Package ‘gg4way’

January 12, 2024

Title 4way Plots of Differential Expression

Version 1.0.1

Description 4way plots enable a comparison of the logFC values from two contrasts of differential gene expression. The gg4way package creates 4way plots using the ggplot2 framework and supports popular Bioconductor objects. The package also provides information about the correlation between contrasts and significant genes of interest.

License MIT + file LICENSE

URL https://github.com/ben-laufer/gg4way

BugReports https://github.com/ben-laufer/gg4way/issues

biocViews Software, Visualization, DifferentialExpression,
  GeneExpression, Transcription, RNASeq, SingleCell, Sequencing

Encoding UTF-8

Roxygen list(markdown = TRUE)

RoxygenNote 7.2.3

Depends R (>= 4.3.0), ggplot2

Imports DESeq2, dplyr, edgeR, ggrepel, glue, janitor, limma, magrittr,
  methods, purrr, rlang, scales, stats, stringr, tibble, tidyr

Suggests airway, BiocStyle, knitr, org.Hs.eg.db, rmarkdown, testthat

VignetteBuilder knitr

Config/testthat/edition 3

LazyData false

git_url https://git.bioconductor.org/packages/gg4way

git_branch RELEASE_3_18

git_last_commit 9616af8

git_last_commit_date 2023-12-08

Repository Bioconductor 3.18

Date/Publication 2024-01-12

Author Benjamin I Laufer [aut, cre],
  Brad A Friedman [aut]

Maintainer Benjamin I Laufer <blaufer@gmail.com>
R topics documented:

.plot4way
.prepareAnnotations
.prepareData
.testCor
.tidyLabel
.totalCounts
.airwayFit
.extractors
.gg4way

Description

Creates a 4way plot

Usage

.plot4way(
  DGEtibble = DGEtibble,
  x = x,
  y = y,
  sep = sep,
  logFCcutoff = logFCcutoff,
  lineColor = lineColor,
  colorKey = colorKey,
  corRes = corRes,
  textKey = textKey,
  hjust = hjust,
  vjust = vjust,
  textSize = textSize,
  label = label
)

Arguments

x Character specifying name of DGE results within object for the x-axis
y Character specifying name of DGE results within object for the y-axis
sep Character specifying the separator between conditions for the contrast
logFCcutoff Numeric for the absolute Log2FC cut-off for DEGs, default is 1
lineColor Color of lines
textSize Numeric specifying size of text with gene overlap category totals
label Character vector specifying genes to label (FALSE for none, TRUE for all blue)
.prepareAnnotations  Prepare annotations

Description
Prepare text annotations of sums for plotting

Usage
```r
.prepareAnnotations(
  totalTibble = totalTibble,
  colorKey = colorKey,
  textNudge = textNudge
)
```

Arguments
- `totalTibble` A tibble of summarized counts
- `textNudge` Numeric specifying nudge of text with gene overlap category totals

Value
A tibble

.prepareData  Prepare data

Description
Prepare data for a 4way plot

Usage
```r
.prepareData(
  DGEdata = DGEdata,
  x = x,
  y = y,
  ID = ID,
  symbol = symbol,
  logFC = logFC,
  FDR = FDR,
  logFCcutoff = logFCcutoff,
  FDRcutoff = FDRcutoff
)
```
.testCor

**Arguments**

DGEdata  The object to plot from:
- limma: A MArrayLM object from eBayes or treat
- edgeR: A list of DGELRT objects from glmQLFTest, glmTreat, or glmLRT
- DESeq2: a DESeqDataSet from DESeq or a list of DESeqResults from results
- Other packages: A list of data.frames, see details section for more information

x  Character specifying name of DGE results within object for the x-axis

y  Character specifying name of DGE results within object for the y-axis

ID  Column name for gene ID

symbol  Column name for gene symbol description

logFC  Column name for logFC values

FDR  Column name for FDR values

logFCcutoff  Numeric for the absolute Log2FC cut-off for DEGs, default is 1

FDRcutoff  Numeric for the FDR cut-off for DEGs, default is 0.05

**Value**

A tibble

**Description**

Test the correlation between DGE contrasts

**Usage**

.testCor(DGEtibble = DGEtibble)

**Arguments**

DGEtibble  A tibble of DGE results

**Value**

A numeric of the Pearson correlation
### .tidyLabel

**Tidy axis labels**

**Description**
Process axis labels from contrast names

**Usage**
```
.tidyLabel(label = NULL, sep = " vs ", labelType = c("x", "y"))
```

**Arguments**
- `label` Character vector specifying genes to label (FALSE for none, TRUE for all blue)
- `sep` Character specifying the separator between conditions for the contrast

**Value**
A call

### .totalCount

**Summarize counts**

**Description**
Create a summary table counts for DGE contrast overlaps for shared (quadrants) and non-shared (lines) DEGs

**Usage**
```
.totalCounts(DGEtibble = DGEtibble, x = x, y = y, logFCcutoff = logFCcutoff)
```

**Arguments**
- `DGEtibble` A tibble of DGE results
- `x` Character specifying name of DGE results within object for the x-axis
- `y` Character specifying name of DGE results within object for the y-axis
- `logFCcutoff` Numeric for the absolute Log2FC cut-off for DEGs, default is 1

**Value**
A tibble
Description

Generate example data from the airway data package using eBayes

Usage

data(airwayFit)

Format

An object of class MArrayLM with 14516 rows and 2 columns.

Value

A MArrayLM

Source

airway

extractors

Helper Functions for gg4way

Description

These helper functions provide data used in the plot:

- getCor: Get the correlation of the logFC of all genes
- getShared: Get only the shared genes that pass the thresholds
- getTotals: Get the totals of overlap categories

Usage

getCor(p1)

getShared(p1)

getTotals(p1)
Arguments

\( p1 \)  The plot from \texttt{gg4way} \\

Value

Each function returns a different result:

\begin{itemize}
\item \texttt{getCor} A numeric
\item \texttt{getShared} A \texttt{tibble}
\item \texttt{getTotals} A \texttt{tabyl}
\end{itemize}

Examples

\begin{verbatim}
data("airwayFit")
p1 <- airwayFit |>
    gg4way(x = "N61311 vs N052611",
          y = "N061011 vs N052611")

## Correlation
getCor(p1)

## Shared
getShared(p1)

## Totals
getTotals(p1)
\end{verbatim}

Description

Create a 4way plot to compare the logFC values from two contrasts of differential gene expression.

Usage

\begin{verbatim}
## Default S3 method:
gg4way(
    DGEdata,
    x = NULL,
    y = NULL,
    ID = "ID",
    symbol = "symbol",
    logFC = "logFC",
\end{verbatim}
FDR = "adj.P.Val",
sep = " vs ",
FDRcutoff = 0.05,
logFCcutoff = 1,
label = FALSE,
colorVector = c("grey80", "firebrick", "forestgreen", "mediumblue"),
lineColor = "grey60",
textSize = 4,
textNudge = 0.25,
...  
]

Arguments

DGEdata The object to plot from:

• limma: A MArrayLM object from eBayes or treat
• edgeR: A list of DGELRT objects from glmQLFTest, glmTreat, or glmLRT
• DESeq2: a DESeqDataSet from DESeq or a list of DESeqResults from results
• Other packages: A list of data.frames, see details section for more information

x Character specifying name of DGE results within object for the x-axis

y Character specifying name of DGE results within object for the y-axis

ID Column name for gene ID

symbol Column name for gene symbol description

logFC Column name for logFC values

FDR Column name for FDR values

sep Character specifying the separator between conditions for the contrast

FDRcutoff Numeric for the FDR cut-off for DEGs, default is 0.05

logFCcutoff Numeric for the absolute Log2FC cut-off for DEGs, default is 1

label Character vector specifying genes to label (FALSE for none, TRUE for all blue)

colorVector Character vector of colors in the following order: "not significant", "significant in x", "significant in y", "significant in both"

lineColor Color of lines

textSize Numeric specifying size of text with gene overlap category totals

textNudge Numeric specifying nudge of text with gene overlap category totals

Details

When a list of data.frames is provided to the DGEdata argument, they should have the following column names and data:
ID  Character vector with the feature ID (i.e. EnsemblID)
symbol  Optional character vector with gene symbol for labels
LogFC  Numeric with the logFC
FDR  Numeric with the FDR

The correlation coefficient is useful for comparing across multiple plots. It’s important to consider whether there are any common factors when comparing values, since that can result in a larger value.

**Value**

A ggplot

**Examples**

```r
data("airwayFit")
airwayFit |> 
  gg4way(x = "N61311 vs N052611",
         y = "N061011 vs N052611")
```
Index

* datasets
  airwayFit, 6
* internal
  .plot4way, 2
  .prepareAnnotations, 3
  .prepareData, 3
  .testCor, 4
  .tidyLabel, 5
  .totalCounts, 5
  .plot4way, 2
  .prepareAnnotations, 3
  .prepareData, 3
  .testCor, 4
  .tidyLabel, 5
  .totalCounts, 5

airway, 6
airwayFit, 6

call, 5

DESeq, 4, 8
DESeqDataSet, 4, 8
DESeqResults, 4, 8
DGELRT, 4, 8
eBayes, 4, 6, 8
extractors, 6
getCor (extractors), 6
getShared (extractors), 6
getTotals (extractors), 6
gg4way, 7, 7
ggplot, 3, 9
glmLRT, 4, 8
glmQLFTest, 4, 8
glmTreat, 4, 8
MArrayLM, 4, 6, 8

results, 4, 8

tabyl, 7
tibble, 3–5, 7
treat, 4, 8