Package ‘gg4way’

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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.

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

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

biocViews Software, Visualization, DifferentialExpression,
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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
)
```
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

.totalCounts
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
### airwayFit

**Description**
Generate example data from the airway data package using eBayes

**Usage**
```r
data(airwayFit)
```

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

**Value**
A `MArrayLM`

**Source**
`airway`

### extractors

**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**
```r
getCor(p1)
getShared(p1)
geTotals(p1)
```
Arguments

p1 The plot from gg4way

Value

Each function returns a different result:

- `getCor` A numeric
- `getShared` A tibble
- `getTotals` A tabyl

Examples

data("airwayFit")
p1 <- airwayFit |> gg4way(x = "N61311 vs N052611", y = "N061011 vs N052611")

## Correlation
getCor(p1)

## Shared
getShared(p1)

## Totals
getTotals(p1)

Description

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

Usage

## Default S3 method:
gg4way(
  DGEdata,
  x = NULL,
  y = NULL,
  ID = "ID",
  symbol = "symbol",
  logFC = "logFC",
)
\begin{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,
...
\end{verbatim}

**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

- **...**  
  Support for additional arguments used internally by gg4way.MArrayLM, gg4way.list, and gg4way.DESeqDataSet

**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

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