Package ‘gg4way’

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Title 4way Plots of Differential Expression

Version 1.0.2

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, GeneExpression, Transcription, RNASeq, SingleCell, Sequencing

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Depends R (>= 4.3.0), ggplot2

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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

Value

A ggplot

Description

Prepare text annotations of sums for plotting

Usage

.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

Description

Prepare data for a 4way plot

Usage

.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 `MArryLM` object from `eBayes` or `treat`
  • `edgeR`: A list of `DGEList` objects from `glmQLFTest`, `glmTreat`, or `glmLRT`
  • `DESeq2`: A `DESeqData` 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**  
```r
.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**  
```r
.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 gg4way

Value

Each function returns a different result:

<table>
<thead>
<tr>
<th>Function</th>
<th>Type</th>
</tr>
</thead>
<tbody>
<tr>
<td>getCor</td>
<td>A numeric</td>
</tr>
<tr>
<td>getShared</td>
<td>A tibble</td>
</tr>
<tr>
<td>getTotals</td>
<td>A tabyl</td>
</tr>
</tbody>
</table>

Examples

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

  ## Correlation
  getCor(p1)

  ## Shared
  getShared(p1)

  ## Totals
  getTotals(p1)

---

**gg4way**

Create a 4way plot

Description

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

Usage

```r
## Default S3 method:
gg4way(
    DGEdata,
    x = NULL,
    y = NULL,
    ID = "ID",
    symbol = "symbol",
    logFC = "logFC",
```
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:
## gg4way

<table>
<thead>
<tr>
<th>Feature</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>ID</td>
<td>Character vector with the feature ID (i.e. EnsemblID)</td>
</tr>
<tr>
<td>symbol</td>
<td>Optional character vector with gene symbol for labels</td>
</tr>
<tr>
<td>LogFC</td>
<td>Numeric with the logFC</td>
</tr>
<tr>
<td>FDR</td>
<td>Numeric with the FDR</td>
</tr>
</tbody>
</table>

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")
```
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