Package 'gg4way'

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Title 4way Plots of Differential Expression

Version 1.2.0

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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`.plot4way` *gg4way plot*

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)

Value

A ggplot

.prepareAnnotations *Prepare annotations*

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 *Prepare data*

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 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 infromation
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

.testCor *Correlation test*

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 *airwayFit data*

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:

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)
```

---

gg4way *Create a 4way plot*

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",
```

```
  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 infromation
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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