

# Package ‘gg4way’

May 21, 2024

**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 | <i>gg4way plot</i> |
|-----------|--------------------|

---

### 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: <ul style="list-style-type: none"> <li>• limma: A <a href="#">MArrayLM</a> object from <a href="#">eBayes</a> or <a href="#">treat</a></li> <li>• edgeR: A list of <a href="#">DGELRT</a> objects from <a href="#">glmQLFTest</a>, <a href="#">glmTreat</a>, or <a href="#">glmLRT</a></li> <li>• DESeq2: a <a href="#">DESeqDataSet</a> from <a href="#">DESeq</a> or a list of <a href="#">DESeqResults</a> from <a href="#">results</a></li> <li>• Other packages: A list of data.frames, see details section for more information</li> </ul> |
| 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:

|                        |  |
|------------------------|--|
| <code>getCor</code>    | Get the correlation of the logFC of all genes      |
| <code>getShared</code> | Get only the shared genes that pass the thresholds |
| <code>getTotals</code> | 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 <a href="#">tibble</a> |
| getTotals | A <a href="#">tabyl</a>  |

**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: <ul style="list-style-type: none"> <li>limma: A <a href="#">MArrayLM</a> object from <a href="#">eBayes</a> or <a href="#">treat</a></li> <li>edgeR: A list of <a href="#">DGELRT</a> objects from <a href="#">glmQLFTest</a>, <a href="#">glmTreat</a>, or <a href="#">glmLRT</a></li> <li>DESeq2: a <a href="#">DESeqDataSet</a> from <a href="#">DESeq</a> or a list of <a href="#">DESeqResults</a> from <a href="#">results</a></li> <li>Other packages: A list of data.frames, see details section for more information</li> </ul> |
| 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 <code>gg4way.MArrayLM</code> , <code>gg4way.list</code> , and <code>gg4way.DESeqDataSet</code>  |

## 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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