

# Package ‘gg4way’

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**Title** 4way Plots of Differential Expression

**Version** 1.11.0

**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>

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## Contents

.checkFeatures	2
.checkNames	3
.plot4way	4
.prepareAnnotations	5
.prepareData	5
.testCor	6
.tidyLabel	7
.totalCounts	7
airwayFit	8
extractors	8
gg4way	9
<b>Index</b>	<b>12</b>

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.checkFeatures	<i>Missing features warning</i>
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### Description

Warn about features not shared between x and y

### Usage

```
.checkFeatures(DGEdata = DGEdata, x = x, y = y, ID = ID)
```

### 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 the name of DGE results within the object for the x-axis
y	Character specifying the name of DGE results within the object for the y-axis
ID	Column name for gene IDs

### Value

A character

---

.checkNames                      *Missing names check*

---

### Description

Check for missing names in the DGEdata object

### Usage

```
.checkNames(  
  DGEdata = DGEdata,  
  x = x,  
  y = y,  
  ID = ID,  
  symbol = symbol,  
  logFC = logFC,  
  FDR = FDR  
)
```

### Arguments

DGEdata	The object to plot from: <ul style="list-style-type: none"><li>• <code>limma</code>: A <code>MArrayLM</code> object from <code>eBayes</code> or <code>treat</code></li><li>• <code>edgeR</code>: A list of <code>DGELRT</code> objects from <code>glmQLFTest</code>, <code>glmTreat</code>, or <code>glmLRT</code></li><li>• <code>DESeq2</code>: a <code>DESeqDataSet</code> from <code>DESeq</code> or a list of <code>DESeqResults</code> from <code>results</code></li><li>• <code>Other packages</code>: A list of <code>data.frames</code>, see details section for more information</li></ul>
x	Character specifying the name of DGE results within the object for the x-axis
y	Character specifying the name of DGE results within the object for the y-axis
ID	Column name for gene IDs
symbol	Column name for gene symbols, which can be the same as the value for the ID column if not present in the object
logFC	Column name for logFC values
FDR	Column name for FDR values

### Value

A character

---

`.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,  
  labelSize = labelSize  
)
```

### Arguments

<code>x</code>	Character specifying the name of DGE results within the object for the x-axis
<code>y</code>	Character specifying the name of DGE results within the object for the y-axis
<code>sep</code>	Character specifying the separator between conditions for the contrast name provided to the x and y arguments
<code>logFCcutoff</code>	Numeric for the absolute logFC cut-off for DEGs (default is 1)
<code>lineColor</code>	Color of lines
<code>textSize</code>	Numeric specifying size of text with gene overlap category totals, where 0 will remove the text
<code>label</code>	Character vector specifying the symbols of genes to label (FALSE for none, TRUE for all blue)
<code>labelSize</code>	Numeric specifying size of text with gene labels

### 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>• <code>limma</code>: A <code>MArrayLM</code> object from <code>eBayes</code> or <code>treat</code></li> <li>• <code>edgeR</code>: A list of <code>DGELRT</code> objects from <code>glmQLFTest</code>, <code>glmTreat</code>, or <code>glmLRT</code></li> <li>• <code>DESeq2</code>: a <code>DESeqDataSet</code> from <code>DESeq</code> or a list of <code>DESeqResults</code> from <code>results</code></li> <li>• Other packages: A list of <code>data.frames</code>, see details section for more information</li> </ul>
x	Character specifying the name of DGE results within the object for the x-axis
y	Character specifying the name of DGE results within the object for the y-axis
ID	Column name for gene IDs
symbol	Column name for gene symbols, which can be the same as the value for the ID column if not present in the object
logFC	Column name for logFC values
FDR	Column name for FDR values
logFCcutoff	Numeric for the absolute logFC cut-off for DEGs (default is 1)
FDRcutoff	Numeric for the FDR cut-off for DEGs (default is 0.05)

**Value**

A [tibble](#)

---

.testCor	<i>Correlation test</i>
----------	-------------------------

---

**Description**

Test the correlation between DGE contrasts

**Usage**

```
.testCor(DGEtibble = DGEtibble)
```

**Arguments**

DGEtibble	A <a href="#">tibble</a> of DGE results
-----------	---

**Value**

A numeric of the Pearson correlation

---

<code>.tidyLabel</code>	<i>Tidy axis labels</i>
-------------------------	-------------------------

---

**Description**

Process axis labels from contrast names

**Usage**

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

**Arguments**

<code>label</code>	Character vector specifying the symbols of genes to label (FALSE for none, TRUE for all blue)
<code>sep</code>	Character specifying the separator between conditions for the contrast name provided to the x and y arguments

**Value**

A [call](#)

---

<code>.totalCounts</code>	<i>Summarize counts</i>
---------------------------	-------------------------

---

**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**

<code>DGEtibble</code>	A <a href="#">tibble</a> of DGE results
<code>x</code>	Character specifying the name of DGE results within the object for the x-axis
<code>y</code>	Character specifying the name of DGE results within the object for the y-axis
<code>logFCcutoff</code>	Numeric for the absolute logFC 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="#">tibble</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,
  textSize = 11,
  textNudge = 0.25,
  labelSize = textSize,
```

```

colorVector = c("grey80", "firebrick", "forestgreen", "mediumblue"),
lineColor = "grey60",
...
)

```

## Arguments

DGEdata	The object to plot from: <ul style="list-style-type: none"> <li>• <code>limma</code>: A <code>MArrayLM</code> object from <code>eBayes</code> or <code>treat</code></li> <li>• <code>edgeR</code>: A list of <code>DGELRT</code> objects from <code>glmQLFTest</code>, <code>glmTreat</code>, or <code>glmLRT</code></li> <li>• <code>DESeq2</code>: a <code>DESeqDataSet</code> from <code>DESeq</code> or a list of <code>DESeqResults</code> from <code>results</code></li> <li>• Other packages: A list of <code>data.frames</code>, see details section for more information</li> </ul>
x	Character specifying the name of DGE results within the object for the x-axis
y	Character specifying the name of DGE results within the object for the y-axis
ID	Column name for gene IDs
symbol	Column name for gene symbols, which can be the same as the value for the ID column if not present in the object
logFC	Column name for logFC values
FDR	Column name for FDR values
sep	Character specifying the separator between conditions for the contrast name provided to the x and y arguments
FDRcutoff	Numeric for the FDR cut-off for DEGs (default is 0.05)
logFCcutoff	Numeric for the absolute logFC cut-off for DEGs (default is 1)
label	Character vector specifying the symbols of genes to label (FALSE for none, TRUE for all blue)
textSize	Numeric specifying size of text with gene overlap category totals, where 0 will remove the text
textNudge	Numeric specifying nudge of text with gene overlap category totals
labelSize	Numeric specifying size of text with gene labels
colorVector	Character vector of colors in the following order: "not significant", "significant in x", "significant in y", "significant in both"
lineColor	Color of lines
...	Support for additional arguments used internally by <code>gg4way.MArrayLM</code> , <code>gg4way.list</code> , and <code>gg4way.DESeqDataSet</code>

## Details

When a named list of `data.frames` is provided to the `DGEdata` argument, each `data.frame` can follow the defaults and have the following columns or specify alternate names for the following to the `ID`, `symbol`, `logFC`, and `FDR` arguments:

ID	Character vector with the feature ID (i.e. EnsemblID)
symbol	Optional character vector with gene symbol for labels

logFC	Numeric with the logFC
adj.P.Val	Numeric with the FDR

The correlation coefficient is useful for comparing across multiple plots. However, it is important to consider whether there are any common factors when comparing values, since that can result in a larger value. Some examples are contrasts with covariates that are shared between groups or contrasts with the same control group.

### Value

A [ggplot](#)

### Examples

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

# Index

- \* **datasets**
  - airwayFit, 8
- \* **internal**
  - .checkFeatures, 2
  - .checkNames, 3
  - .plot4way, 4
  - .prepareAnnotations, 5
  - .prepareData, 5
  - .testCor, 6
  - .tidyLabel, 7
  - .totalCounts, 7
- .checkFeatures, 2
- .checkNames, 3
- .plot4way, 4
- .prepareAnnotations, 5
- .prepareData, 5
- .testCor, 6
- .tidyLabel, 7
- .totalCounts, 7
  
- airway, 8
- airwayFit, 8
  
- call, 7
  
- DESeq, 2, 3, 6, 10
- DESeqDataSet, 2, 3, 6, 10
- DESeqResults, 2, 3, 6, 10
- DGELRT, 2, 3, 6, 10
  
- eBayes, 2, 3, 6, 8, 10
- extractors, 8
  
- getCor (extractors), 8
- getShared (extractors), 8
- getTotals (extractors), 8
- gg4way, 8, 9
- ggplot, 4, 11
- glmLRT, 2, 3, 6, 10
- glmQLFTest, 2, 3, 6, 10
- glmTreat, 2, 3, 6, 10
  
- MArrayLM, 2, 3, 6, 8, 10
  
- results, 2, 3, 6, 10
  
- tabyl, 9
- tibble, 5–7, 9
- treat, 2, 3, 6, 10