

# Package ‘enrichplot’

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**Title** Visualization of Functional Enrichment Result

**Version** 1.0.2

**Description** The 'enrichplot' package implements several visualization methods for interpreting functional enrichment results obtained from ORA or GSEA analysis.  
All the visualization methods are developed based on 'ggplot2' graphics.

**Depends** R (>= 3.4.0)

**Imports** AnnotationDbi, cowplot, DOSE (>= 3.5.1), ggplot2, ggraph, ggridges, GOSemSim, graphics, grDevices, grid, igraph, methods, reshape2, UpSetR, utils

**Suggests** clusterProfiler, knitr, org.Hs.eg.db, prettydoc

**VignetteBuilder** knitr

**License** Artistic-2.0

**URL** <https://github.com/GuangchuangYu/enrichplot>

**BugReports** <https://github.com/GuangchuangYu/enrichplot/issues>

**biocViews** Annotation, GeneSetEnrichment, GO, KEGG, Pathways, Software, Visualization

**Encoding** UTF-8

**LazyData** true

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barplot.enrichResult *barplot*

---

## Description

barplot of enrichResult

## Usage

```
## S3 method for class 'enrichResult'
barplot(height, x = "Count", color = "p.adjust",
        showCategory = 8, font.size = 12, title = "", ...)
```

## Arguments

height	enrichResult object
x	one of 'Count' and 'GeneRatio'
color	one of 'pvalue', 'p.adjust', 'qvalue'
showCategory	number of categories to show
font.size	font size
title	plot title
...	other parameter, ignored

## Value

ggplot object

## Examples

```
library(DOSE)
data(geneList)
de <- names(geneList)[1:100]
x <- enrichDO(de)
barplot(x)
```

---

`cnetplot`*cnetplot*

---

**Description**

Gene-Concept Network

**Usage**

```
cnetplot(x, showCategory = 5, foldChange = NULL, layout = "kk", ...)  
  
## S4 method for signature 'enrichResult'  
cnetplot(x, showCategory = 5, foldChange = NULL,  
  layout = "kk", ...)  
  
## S4 method for signature 'gseaResult'  
cnetplot(x, showCategory = 5, foldChange = NULL,  
  layout = "kk", ...)  
  
cnetplot.enrichResult(x, showCategory = 5, foldChange = NULL,  
  layout = "kk", colorEdge = FALSE, circular = FALSE, node_label = TRUE,  
  ...)
```

**Arguments**

<code>x</code>	enrichment result
<code>showCategory</code>	number of enriched terms to display
<code>foldChange</code>	fold Change
<code>layout</code>	layout of the network
<code>...</code>	additional parameters
<code>colorEdge</code>	whether coloring edge by enriched terms
<code>circular</code>	whether using circular layout
<code>node_label</code>	whether display node label

**Details**

plot linkages of genes and enriched concepts (e.g. GO categories, KEGG pathways)

**Value**

ggplot object

**Author(s)**

Guangchuang Yu

**Examples**

```
library(DOSE)
data(geneList)
de <- names(geneList)[1:100]
x <- enrichDO(de)
cnetplot(x)
```

---

color\_palette            *color\_palette*

---

**Description**

create color palette for continuous data

**Usage**

```
color_palette(colors)
```

**Arguments**

colors            colors of length  $\geq 2$

**Value**

color vector

**Author(s)**

guangchuang yu

**Examples**

```
color_palette(c("red", "yellow", "green"))
```

---

dotplot            *dotplot*

---

**Description**

dotplot for enrichment result

**Usage**

```
dotplot(object, ...)
```

```
## S4 method for signature 'enrichResult'
dotplot(object, x = "GeneRatio",
  color = "p.adjust", showCategory = 10, split = NULL, font.size = 12,
  title = "", ...)
```

```
## S4 method for signature 'gseaResult'
dotplot(object, x = "GeneRatio", color = "p.adjust",
  showCategory = 10, split = NULL, font.size = 12, title = "", ...)
```

**Arguments**

object	input object
...	additional parameters
x	variable for x-axis, one of 'GeneRatio' or 'Count'
color	variable that used to color enriched terms, e.g. pvalue, p.adjust or qvalue
showCategory	number of enriched terms to display
split	separate result by 'category' variable
font.size	font size
title	plot title

**Value**

plot

**Author(s)**

guangchuang yu

**Examples**

```
library(DOSE)
data(geneList)
de <- names(geneList)[1:100]
x <- enrichDO(de)
dotplot(x)
```

---

emapplot

*emapplot*

---

**Description**

Enrichment Map for enrichment result of over-representation test or gene set enrichment analysis

**Usage**

```
emapplot(x, showCategory = 30, color = "p.adjust", layout = "kk", ...)
```

```
## S4 method for signature 'enrichResult'
emapplot(x, showCategory = 30, color = "p.adjust",
  layout = "kk", ...)
```

```
## S4 method for signature 'gseaResult'
emapplot(x, showCategory = 30, color = "p.adjust",
  layout = "kk", ...)
```

```
emapplot.enrichResult(x, showCategory = 30, color = "p.adjust",
  layout = "kk", ...)
```

**Arguments**

x	enrichment result.
showCategory	number of enriched terms to display
color	variable that used to color enriched terms, e.g. pvalue, p.adjust or qvalue
layout	layout of the map
...	additional parameters

**Details**

This function visualizes gene sets as a network (i.e. enrichment map). Mutually overlapping gene sets tend to cluster together, making it easier for interpretation.

**Value**

ggplot object

**Author(s)**

Guangchuang Yu

**Examples**

```
library(DOSE)
data(geneList)
de <- names(geneList)[1:100]
x <- enrichDO(de)
emapplot(x)
```

---

fortify.enrichResult *fortify*

---

**Description**

convert enrichResult object for ggplot2

**Usage**

```
## S3 method for class 'enrichResult'
fortify(model, data, showCategory = 5, by = "Count",
        order = FALSE, drop = FALSE, split = NULL, ...)
```

**Arguments**

model	enrichResult object
data	not use here
showCategory	Category numbers to show
by	one of Count and GeneRatio
order	logical
drop	logical
split	separate result by 'split' variable
...	additional parameter

**Value**

data.frame

---

`goplot`

*goplot*

---

**Description**

plot induced GO DAG of significant terms

**Usage**

```
goplot(x, showCategory = 10, color = "p.adjust", layout = "sugiyama",  
      geom = "text", ...)
```

```
## S4 method for signature 'enrichResult'  
goplot(x, showCategory = 10, color = "p.adjust",  
      layout = "sugiyama", geom = "text", ...)
```

```
## S4 method for signature 'gseaResult'  
goplot(x, showCategory = 10, color = "p.adjust",  
      layout = "sugiyama", geom = "text", ...)
```

```
goplot.enrichResult(x, showCategory = 10, color = "p.adjust",  
                   layout = "sugiyama", geom = "text", ...)
```

**Arguments**

<code>x</code>	enrichment result.
<code>showCategory</code>	number of enriched terms to display
<code>color</code>	variable that used to color enriched terms, e.g. pvalue, p.adjust or qvalue
<code>layout</code>	layout of the map
<code>geom</code>	label geom, one of 'label' or 'text'
<code>...</code>	additional parameter

**Value**

ggplot object

**Author(s)**

guangchuang yu

---

`gseaplot`*gseaplot*

---

**Description**

visualize analyzing result of GSEA

**Usage**

```
gseaplot(x, geneSetID, by = "all", title = "", ...)  
  
## S4 method for signature 'gseaResult'  
gseaplot(x, geneSetID, by = "all", title = "",  
         color = "black", color.line = "green", color.vline = "#FA5860", ...)  
  
gseaplot.gseaResult(x, geneSetID, by = "all", title = "", color = "black",  
                   color.line = "green", color.vline = "#FA5860", ...)
```

**Arguments**

<code>x</code>	object of gsea result
<code>geneSetID</code>	geneSet ID
<code>by</code>	one of "runningScore" or "position"
<code>title</code>	plot title
<code>...</code>	additional parameters
<code>color</code>	color of line segments
<code>color.line</code>	color of running enrichment score line
<code>color.vline</code>	color of vertical line which indicating the maximum/minimal running enrichment score

**Details**

plotting function for gseaResult

**Value**

ggplot2 object  
ggplot2 object

**Author(s)**

Guangchuang Yu

**Examples**

```
library(DOSE)  
data(geneList)  
x <- gseDO(geneList)  
gseaplot(x, geneSetID=1)
```



---

 gsInfo

*gsInfo*


---

**Description**

extract gsea result of selected geneSet

**Usage**

```
gsInfo(object, geneSetID)
```

**Arguments**

object	gseaResult object
geneSetID	gene set ID

**Value**

data.frame

**Author(s)**

Guangchuang Yu

---

heatplot

*heatplot*


---

**Description**

heatmap like plot for functional classification

**Usage**

```
heatplot(x, showCategory = 30, foldChange = NULL)
```

```
## S4 method for signature 'enrichResult'
heatplot(x, showCategory = 30, foldChange = NULL)
```

```
## S4 method for signature 'gseaResult'
heatplot(x, showCategory = 30, foldChange = NULL)
```

```
heatplot.enrichResult(x, showCategory = 30, foldChange = NULL)
```

**Arguments**

x	enrichment result.
showCategory	number of enriched terms to display
foldChange	fold Change

**Value**

ggplot object

**Author(s)**

guangchuang yu

Guangchuang Yu

**Examples**

```
library(DOSE)
data(geneList)
de <- names(geneList)[1:100]
x <- enrichDO(de)
heatplot(x)
```

---

list2graph

*convert gene IDs to igraph object*

---

**Description**

convert a list of gene IDs to igraph object.

**Usage**

```
list2graph(inputList)
```

**Arguments**

inputList      a list of gene IDs

**Value**

a igraph object.

**Author(s)**

Guangchuang Yu

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ridgeplot	<i>ridgeplot</i>
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---

## Description

ridgeline plot for GSEA result

## Usage

```
ridgeplot(x, showCategory = 30, fill = "p.adjust", core_enrichment = TRUE)

## S4 method for signature 'gseaResult'
ridgeplot(x, showCategory = 30, fill = "p.adjust",
  core_enrichment = TRUE)

ridgeplot.gseaResult(x, showCategory = 30, fill = "p.adjust",
  core_enrichment = TRUE)
```

## Arguments

x	gseaResult object
showCategory	number of categories for plotting
fill	one of "pvalue", "p.adjust", "qvalue"
core_enrichment	whether only using core_enriched genes

## Value

ggplot object

## Author(s)

Guangchuang Yu

## Examples

```
library(DOSE)
data(geneList)
x <- gseDO(geneList)
ridgeplot(x)
```

---

`upsetplot`*upsetplot method*

---

**Description**

upsetplot method generics  
upsetplot

**Usage**

```
upsetplot(x, ...)  
  
## S4 method for signature 'enrichResult'  
upsetplot(x, n = 10, ...)
```

**Arguments**

<code>x</code>	object
<code>...</code>	additional parameters
<code>n</code>	number of categories to be plotted

**Value**

plot

**Author(s)**

Guangchuang Yu

**Examples**

```
require(DOSE)  
data(geneList)  
de=names(geneList)[1:100]  
x <- enrichDO(de)  
upsetplot(x, 8)
```

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