

# Package ‘enrichplot’

April 15, 2020

**Title** Visualization of Functional Enrichment Result

**Version** 1.6.1

**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), europepmc, ggplot2, ggplotify, ggraph, ggridges, GOSemSim, graphics, grDevices, grid, gridExtra, igraph, methods, purrr, RColorBrewer, reshape2, stats, utils

**Suggests** clusterProfiler, dplyr, ggupset, knitr, org.Hs.eg.db, prettydoc, tibble

**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

**RoxygenNote** 7.0.2

**git\_url** <https://git.bioconductor.org/packages/enrichplot>

**git\_branch** RELEASE\_3\_10

**git\_last\_commit** 67291ef

**git\_last\_commit\_date** 2019-12-13

**Date/Publication** 2020-04-14

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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 = "all",
  ...
)
```

**Arguments**

x	enrichment result
showCategory	number of enriched terms to display
foldChange	fold Change
layout	layout of the network
...	additional parameters
colorEdge	whether coloring edge by enriched terms
circular	whether using circular layout
node_label	select which labels to be displayed. one of 'category', 'gene', 'all' and 'none', default is "all".

**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,  
  size = NULL,  
  split = NULL,  
  font.size = 12,  
  title = "",  
  ...  
)
```

```
## S4 method for signature 'gseaResult'
```

```
dotplot(  
  object,  
  x = "GeneRatio",  
  color = "p.adjust",  
  showCategory = 10,  
  size = NULL,  
  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
size	variable that used to scale the sizes of categories
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**

<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. <code>pvalue</code> , <code>p.adjust</code> or <code>qvalue</code>
<code>layout</code>	layout of the map
<code>...</code>	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

---

ggtable*ggtable*

---

**Description**

plot table

**Usage**

ggtable(d, p = NULL)

**Arguments**

d data frame

p ggplot object to extract color to color rownames(d), optional

**Value**

ggplot object

**Author(s)**

guangchuang yu

---

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

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
geom	label geom, one of 'label' or 'text'
...	additional parameter

### Value

ggplot object

### Author(s)

guangchuang yu

---

gseadist

*gseadist*

---

### Description

plot logFC distribution of selected gene sets

**Usage**

```
gseadist(x, IDs, type = "density")
```

**Arguments**

x	GSEA result
IDs	gene set IDs
type	one of 'density' or 'boxplot'

**Value**

distribution plot

**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)
```

---

`gseaplot2`

*gseaplot2*

---

**Description**

GSEA plot that mimic the plot generated by broad institute's GSEA software

**Usage**

```
gseaplot2(
  x,
  geneSetID,
  title = "",
  color = "green",
  base_size = 11,
  rel_heights = c(1.5, 0.5, 1),
  subplots = 1:3,
  pvalue_table = FALSE,
  ES_geom = "line"
)
```

**Arguments**

x	gseaResult object
geneSetID	gene set ID
title	plot title
color	color of running enrichment score line
base_size	base font size
rel_heights	relative heights of subplots
subplots	which subplots to be displayed
pvalue_table	whether add pvalue table
ES_geom	geom for plotting running enrichment score, one of 'line' or 'dot'

**Value**

plot

**Author(s)**

Guangchuang Yu

---

gsearank

*gsearank*

---

**Description**

plot ranked list of genes with running enrichment score as bar height

**Usage**

```
gsearank(x, geneSetID, title = "")
```

**Arguments**

x	gseaResult object
geneSetID	gene set ID
title	plot title

**Value**

ggplot object

**Author(s)**

Guangchuang Yu

---

 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

---

pmcplot                      *pmcplot*

---

**Description**

PubMed Central Trend plot

**Usage**

```
pmcplot(query, period, proportion = TRUE)
```

**Arguments**

query	query terms
period	period of query in the unit of year
proportion	If TRUE, use query_hits/all_hits, otherwise use query_hits

**Value**

ggplot object

**Author(s)**

guangchuang yu

---

ridgeplot                      *ridgeplot*

---

**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

**Usage**

```
upsetplot(x, ...)
```

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

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

**Arguments**

x                    object  
 ...                additional parameters  
 n                   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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