

# Package ‘enrichplot’

July 17, 2023

**Title** Visualization of Functional Enrichment Result

**Version** 1.20.0

**Description** The ‘enrichplot’ package implements several visualization methods for interpreting functional enrichment results obtained from ORA or GSEA analysis. It is mainly designed to work with the ‘clusterProfiler’ package suite. All the visualization methods are developed based on ‘ggplot2’ graphics.

**Depends** R (>= 3.5.0)

**Imports** aplot (>= 0.1.4), DOSE (>= 3.16.0), ggnewscale, ggplot2, ggraph, graphics, grid, igraph, methods, plyr, purrr, RColorBrewer, reshape2, rlang, stats, utils, scatterpie, shadowtext, GOSemSim, magrittr, ggtree, yulab.utils (>= 0.0.4)

**Suggests** clusterProfiler, dplyr, europepmc, ggupset, knitr, rmarkdown, org.Hs.eg.db, prettydoc, tibble, tidyr, ggforce, AnnotationDbi, ggplotify, ggridges, grDevices, gridExtra, ggrepel (>= 0.9.0), ggstar, treeio, scales, tidytree, ggtreeExtra, tidydr

**Remotes** YuLab-SMU/tidydr

**VignetteBuilder** knitr

**License** Artistic-2.0

**URL** <https://yulab-smu.top/biomedical-knowledge-mining-book/>

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

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

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autofacet	<i>automatically split barplot or dotplot into several facets</i>
-----------	---

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### Description

automatically split barplot or dotplot into several facets

### Usage

```
autofacet(by = "row", scales = "free", levels = NULL)
```

**Arguments**

by	one of 'row' or 'column'
scales	wether 'fixed' or 'free'
levels	set facet levels

**Value**

a ggplot object

---

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 = "",
  label_format = 30,
  ...
)
```

**Arguments**

height	enrichResult object
x	one of 'Count' and 'GeneRatio'
color	one of 'pvalue', 'p.adjust' and 'qvalue'
showCategory	number of categories to show
font.size	font size
title	plot title
label_format	a numeric value sets wrap length, alternatively a custom function to format axis labels. by default wraps names longer than 30 characters
...	other parameter, ignored

**Value**

ggplot object

**Examples**

```

library(DOSE)
data(geneList)
de <- names(geneList)[1:100]
x <- enrichDO(de)
barplot(x)
# use `showCategory` to select the displayed terms. It can be a number of a vector of terms.
barplot(x, showCategory = 10)
categorys <- c("pre-malignant neoplasm", "intestinal disease",
               "breast ductal carcinoma", "non-small cell lung carcinoma")
barplot(x, showCategory = categorys)

```

---

cnetplot

*cnetplot*


---

**Description**

Gene-Concept Network

**Usage**

```

cnetplot(x, ...)

## S4 method for signature 'enrichResult'
cnetplot(x, ...)

## S4 method for signature 'list'
cnetplot(x, ...)

## S4 method for signature 'gseaResult'
cnetplot(x, ...)

## S4 method for signature 'compareClusterResult'
cnetplot(x, ...)

cnetplot.enrichResult(
  x,
  showCategory = 5,
  foldChange = NULL,
  layout = "kk",
  colorEdge = FALSE,
  circular = FALSE,
  node_label = "all",
  cex_category = 1,
  cex_gene = 1,
  cex_label_category = 1,
  cex_label_gene = 1,

```

```

    color_category = "#E5C494",
    color_gene = "#B3B3B3",
    shadowtext = "all",
    color.params = list(foldChange = NULL, edge = FALSE, category = "#E5C494", gene =
      "#B3B3B3"),
    cex.params = list(category_node = 1, gene_node = 1, category_label = 1, gene_label = 1),
    hilight.params = list(category = NULL, alpha_hilight = 1, alpha_no_hilight = 0.3),
    ...
  )

```

### Arguments

x	Enrichment result.
...	Additional parameters
showCategory	A number or a vector of terms. If it is a number, the first n terms will be displayed. If it is a vector of terms, the selected terms will be displayed.
foldChange	Fold Change of nodes, the default value is NULL. If the user provides the Fold Change value of the nodes, it can be used to set the color of the gene node. Will be removed in the next version.
layout	Layout of the map, e.g. 'star', 'circle', 'gem', 'dh', 'graphopt', 'grid', 'mds', 'randomly', 'fr', 'kk', 'drl' or 'lgl'.
colorEdge	Logical, whether coloring edge by enriched terms, the default value is FALSE. Will be removed in the next version.
circular	Logical, whether using circular layout, the default value is FALSE. Will be removed in the next version.
node_label	Select which labels to be displayed. one of 'category', 'gene', 'all'(the default) and 'none'.
cex_category	Number indicating the amount by which plotting category nodes should be scaled relative to the default, the default value is 1. Will be removed in the next version.
cex_gene	Number indicating the amount by which plotting gene nodes should be scaled relative to the default, the default value is 1. Will be removed in the next version.
cex_label_category	Scale of category node label size, the default value is 1. Will be removed in the next version.
cex_label_gene	Scale of gene node label size, the default value is 1. Will be removed in the next version.
color_category	Color of category node. Will be removed in the next version.
color_gene	Color of gene node. Will be removed in the next version.
shadowtext	select which node labels to use shadow font, one of 'category', 'gene', 'all' and 'none', default is 'all'.
color.params	list, the parameters to control the attributes of highlighted nodes and edges. see the color.params in the following. color.params control the attributes of highlight, it can be referred to the following parameters:

- foldChange Fold Change of nodes for enrichResult, or size of nodes for compareClusterResult, the default value is NULL.
  - edge Logical, whether coloring edge by enriched terms, the default value is FALSE.
  - category Color of category node.
  - gene Color of gene node.
- cex.params list, the parameters to control the size of nodes and labels. see the cex.params in the following. cex.params control the attributes of highlight, it can be referred to the following parameters:
- foldChange only used in compareClusterResult object, fold Change of nodes, the default value is NULL. If the user provides the Fold Change value of the nodes, it can be used to set the size of the gene node.
  - category\_node Number indicating the amount by which plotting category nodes should be scaled relative to the default, the default value is 1.
  - gene\_node Number indicating the amount by which plotting gene nodes should be scaled relative to the default, the default value is 1.
  - category\_label Scale of category node label size, the default value is 1.
  - gene\_label Scale of gene node label size, the default value is 1.
- highlight.params list, the parameters to control the attributes of highlighted nodes and edges. see the highlight.params in the following. highlight.params control the attributes of highlight, it can be referred to the following parameters:
- category category nodes to be highlight.
  - alpha\_highlight alpha of highlighted nodes.
  - alpha\_no\_highlight alpha of unhighlighted nodes.

## Details

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

## Value

ggplot object

## Author(s)

Guangchuang Yu

## Examples

```
## Not run:
library(DOSE)
data(geneList)
de <- names(geneList)[1:100]
x <- enrichDO(de)
x2 <- pairwise_termsim(x)
cnetplot(x2)
# use `layout` to change the layout of map
```

```
cnetplot(x2, layout = "star")
# use `showCategory` to select the displayed terms. It can be a number or a vector of terms.
cnetplot(x2, showCategory = 10)
categorys <- c("pre-malignant neoplasm", "intestinal disease",
              "breast ductal carcinoma", "non-small cell lung carcinoma")
cnetplot(x2, showCategory = categorys)
# 'compareClusterResult' object is also supported.
library(clusterProfiler)
library(DOSE)
library(org.Hs.eg.db)
data(gcSample)
xx <- compareCluster(gcSample, fun="enrichGO", OrgDb="org.Hs.eg.db")
xx2 <- pairwise_termsim(xx)
cnetplot(xx2)

## End(Not run)
```

---

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 = "",  
  orderBy = "x",  
  label_format = 30,  
  ...  
)
```

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

```
dotplot(  
  object,  
  x = "GeneRatio",  
  color = "p.adjust",  
  showCategory = 10,  
  size = NULL,  
  split = NULL,  
  font.size = 12,  
  title = "",  
  orderBy = "x",  
  label_format = 30,  
  ...  
)
```

```
## S4 method for signature 'compareClusterResult'
```

```
dotplot(  
  object,  
  x = "Cluster",  
  color = "p.adjust",  
  showCategory = 5,  
  ...  
)
```



```
    split = NULL,  
    font.size = 12,  
    title = "",  
    by = "geneRatio",  
    size = NULL,  
    includeAll = TRUE,  
    label_format = 30,  
    ...  
)  
  
## S4 method for signature 'enrichResultList'  
dotplot(  
  object,  
  x = "GeneRatio",  
  color = "p.adjust",  
  showCategory = 10,  
  size = NULL,  
  split = NULL,  
  font.size = 12,  
  title = "",  
  orderBy = "x",  
  label_format = 30,  
  ...  
)  
  
## S4 method for signature 'gseaResultList'  
dotplot(  
  object,  
  x = "GeneRatio",  
  color = "p.adjust",  
  showCategory = 10,  
  size = NULL,  
  split = NULL,  
  font.size = 12,  
  title = "",  
  orderBy = "x",  
  label_format = 30,  
  ...  
)  
  
dotplot.enrichResult(  
  object,  
  x = "geneRatio",  
  color = "p.adjust",  
  showCategory = 10,  
  size = NULL,  
  split = NULL,  
  font.size = 12,
```

```

    title = "",
    orderBy = "x",
    label_format = 30,
    decreasing = TRUE
)

dotplot.compareClusterResult(
  object,
  x = "Cluster",
  colorBy = "p.adjust",
  showCategory = 5,
  by = "geneRatio",
  size = "geneRatio",
  split = NULL,
  includeAll = TRUE,
  font.size = 12,
  title = "",
  label_format = 30,
  group = FALSE,
  shape = FALSE
)

```

### Arguments

object	compareClusterResult object
...	additional parameters
x	variable for x-axis, one of 'GeneRatio' and 'Count'
color	variable that used to color enriched terms, e.g. 'pvalue', 'p.adjust' or 'qvalue'
showCategory	A number or a list of terms. If it is a number, the first n terms will be displayed. If it is a list of terms, the selected terms will be displayed.
size	variable that used to scale the sizes of categories, one of "geneRatio", "Percentage" and "count"
split	ONTOLOGY or NULL
font.size	font size
title	figure title
orderBy	The order of the Y-axis
label_format	a numeric value sets wrap length, alternatively a custom function to format axis labels. by default wraps names longer than 30 characters
by	one of "geneRatio", "Percentage" and "count"
includeAll	logical
decreasing	logical. Should the orderBy order be increasing or decreasing?
colorBy	variable that used to color enriched terms, e.g. 'pvalue', 'p.adjust' or 'qvalue'
group	a logical value, whether to connect the nodes of the same group with wires.
shape	a logical value, whether to use nodes of different shapes to distinguish the group it belongs to

**Value**

plot

**Author(s)**

guangchuang yu

**Examples**

```
## Not run:
library(DOSE)
data(geneList)
de <- names(geneList)[1:100]
x <- enrichDO(de)
dotplot(x)
# use `showCategory` to select the displayed terms. It can be a number of a vector of terms.
dotplot(x, showCategory = 10)
categorys <- c("pre-malignant neoplasm", "intestinal disease",
              "breast ductal carcinoma", "non-small cell lung carcinoma")
dotplot(x, showCategory = categorys)
# It can also graph compareClusterResult
data(gcSample)
library(clusterProfiler)
library(DOSE)
library(org.Hs.eg.db)
data(gcSample)
xx <- compareCluster(gcSample, fun="enrichGO", OrgDb="org.Hs.eg.db")
xx2 <- pairwise_termsim(xx)
library(ggstar)
dotplot(xx2)
dotplot(xx2, shape = TRUE)
dotplot(xx2, group = TRUE)
dotplot(xx2, x = "GeneRatio", group = TRUE, size = "count")

## End(Not run)
```

---

drag\_network

*Drag the nodes of a network to update the layout of the network*

---

**Description**

Drag the nodes of a network to update the layout of the network

**Usage**

```
drag_network(p, g = NULL)
```

**Arguments**

`p` the network diagram as a `ggplot/gg/ggraph` object.  
`g` an corresponding `igraph` object. Default is to extract from the `'ggraph'` attribute.

**Value**

an updated `ggplot/gg/ggraph` object

**Examples**

```
## Not run:
library(igraph)
library(ggraph)

flow_info <- data.frame(from = c(1,2,3,3,4,5,6),
                        to = c(5,5,5,6,7,6,7))
g = graph_from_data_frame(flow_info)
p <- ggraph(g, layout='nicely') + geom_node_point() + geom_edge_link()
pp <- drag_network(p)

## End(Not run)
```

---

 emapplot

*emapplot*


---

**Description**

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

**Usage**

```
emapplot(x, ...)
```

## S4 method for signature 'enrichResult'

```
emapplot(x, showCategory = 30, ...)
```

## S4 method for signature 'gseaResult'

```
emapplot(x, showCategory = 30, ...)
```

## S4 method for signature 'compareClusterResult'

```
emapplot(x, showCategory = 30, ...)
```

```
emapplot.enrichResult(
  x,
  showCategory = 30,
  layout = NULL,
  coords = NULL,
```

```
    color = "p.adjust",
    min_edge = 0.2,
    cex_label_category = 1,
    cex_category = 1,
    cex_line = 1,
    shadowtext = TRUE,
    label_style = "shadowtext",
    repel = FALSE,
    node_label = "category",
    with_edge = TRUE,
    group_category = FALSE,
    group_legend = FALSE,
    cex_label_group = 1,
    nWords = 4,
    label_format = 30,
    clusterFunction = stats::kmeans,
    nCluster = NULL,
    layout.params = list(layout = NULL, coords = NULL),
    edge.params = list(show = TRUE, min = 0.2),
    cex.params = list(category_node = 1, category_label = 1, line = 1),
    hilight.params = list(category = NULL, alpha_hilight = 1, alpha_no_hilight = 0.3),
    cluster.params = list(cluster = FALSE, method = stats::kmeans, n = NULL, legend =
      FALSE, label_style = "shadowtext", label_words_n = 4, label_format = 30),
    ...
  )

emapplot.compareClusterResult(
  x,
  showCategory = 30,
  layout = NULL,
  coords = NULL,
  split = NULL,
  pie = "equal",
  legend_n = 5,
  cex_category = 1,
  cex_line = 1,
  min_edge = 0.2,
  cex_label_category = 1,
  shadowtext = TRUE,
  with_edge = TRUE,
  group_category = FALSE,
  label_format = 30,
  group_legend = FALSE,
  node_label = "category",
  label_style = "shadowtext",
  repel = FALSE,
  cex_label_group = 1,
  nWords = 4,
```

```

clusterFunction = stats::kmeans,
nCluster = NULL,
cex_pie2axis = 1,
pie.params = list(pie = "equal", legend_n = 5),
layout.params = list(layout = NULL, coords = NULL),
edge.params = list(show = TRUE, min = 0.2),
cluster.params = list(cluster = FALSE, method = stats::kmeans, n = NULL, legend =
  FALSE, label_style = "shadowtext", label_words_n = 4, label_format = 30),
cex.params = list(category_node = 1, category_label = 1, line = 1, pie2axis = 1,
  label_group = 1),
hilight.params = list(category = NULL, alpha_hilight = 1, alpha_no_hilight = 0.3),
...
)

```

### Arguments

x	Enrichment result.
...	additional parameters
	additional parameters can refer the following parameters.
	<ul style="list-style-type: none"> <li>• force Force of repulsion between overlapping text labels. Defaults to 1.</li> <li>• nudge_x, nudge_y Horizontal and vertical adjustments to nudge the starting position of each text label.</li> <li>• direction "both", "x", or "y" – direction in which to adjust position of labels.</li> <li>• ellipse_style style of ellipse, one of "ggforce" an "polygon".</li> <li>• ellipse_pro numeric indicating confidence value for the ellipses, it can be used only when ellipse_style = "polygon".</li> <li>• alpha the transparency of ellipse fill.</li> <li>• type The type of ellipse. The default "t" assumes a multivariate t-distribution, and "norm" assumes a multivariate normal distribution. "euclid" draws a circle with the radius equal to level, representing the euclidean distance from the center.</li> </ul>
showCategory	A number or a vector of terms. If it is a number, the first n terms will be displayed. If it is a vector of terms, the selected terms will be displayed.
layout	Layout of the map, e.g. 'star', 'circle', 'gem', 'dh', 'graphopt', 'grid', 'mds', 'randomly', 'fr', 'kk', 'drl' or 'lgl'. Will be removed in the next version. Will be removed in the next version.
coords	a data.frame with two columns: 'x' for X-axis coordinate and 'y' for Y-axis coordinate. Will be removed in the next version.
color	Variable that used to color enriched terms, e.g. 'pvalue', 'p.adjust' or 'qvalue'.
min_edge	The minimum similarity threshold for whether two nodes are connected, should be between 0 and 1, default value is 0.2. Will be removed in the next version.
cex_label_category	Scale of category node label size. Will be removed in the next version.
cex_category	Number indicating the amount by which plotting category nodes should be scaled relative to the default. Will be removed in the next version.

<code>cex_line</code>	Scale of line width. Will be removed in the next version.
<code>shadowtext</code>	a logical value, whether to use shadow font.
<code>label_style</code>	style of group label, one of "shadowtext" and "ggforce". Will be removed in the next version.
<code>repel</code>	whether to correct the position of the label. Defaults to FALSE.
<code>node_label</code>	Select which labels to be displayed, one of 'category', 'group', 'all' and 'none'.
<code>with_edge</code>	Logical, if TRUE, draw the edges of the network diagram. Will be removed in the next version.
<code>group_category</code>	a logical, if TRUE, group the category. Will be removed in the next version.
<code>group_legend</code>	Logical, if TRUE, the grouping legend will be displayed. The default is FALSE. Will be removed in the next version.
<code>cex_label_group</code>	Numeric, scale of group labels size, the default value is 1. Will be removed in the next version.
<code>nWords</code>	Numeric, the number of words in the cluster tags, the default value is 4. Will be removed in the next version.
<code>label_format</code>	a numeric value sets wrap length, alternatively a custom function to format axis labels. Will be removed in the next version.
<code>clusterFunction</code>	function of Clustering method, such as <code>stats::kmeans</code> (the default), <code>cluster::clara</code> , <code>cluster::fanny</code> or <code>cluster::pam</code> . Will be removed in the next version.
<code>nCluster</code>	Numeric, the number of clusters, the default value is square root of the number of nodes. Will be removed in the next version.
<code>layout.params</code>	list, the parameters to control the layout. see the <code>layout.params</code> in the following. <code>layout.params</code> control the attributes of layout, it can be referred to the following parameters: <ul style="list-style-type: none"> <li>• <code>layout</code> Layout of the map, e.g. 'star', 'circle', 'gem', 'dh', 'graphopt', 'grid', 'mds', 'randomly', 'fr', 'kk', 'drl' or 'lgl'..</li> <li>• <code>coords</code> a data.frame with two columns: 'x' for X-axis coordinate and 'y' for Y-axis coordinate.</li> </ul>
<code>edge.params</code>	list, the parameters to control the edge. see the <code>edge.params</code> in the following. <code>edge.params</code> control the attributes of edge, it can be referred to the following parameters: <ul style="list-style-type: none"> <li>• <code>show</code> Logical, if TRUE (the default), draw the edges of the network diagram.</li> <li>• <code>min</code> The minimum similarity threshold for whether two nodes are connected, should between 0 and 1, default value is 0.2.</li> </ul>
<code>cex.params</code>	list, the parameters to control the edge. see the <code>cex.params</code> in the following. <code>cex.params</code> control the attributes of edge, it can be referred to the following parameters: <ul style="list-style-type: none"> <li>• <code>category_node</code> Number indicating the amount by which plotting category nodes should be scaled relative to the default.</li> <li>• <code>category_label</code> Scale of category node label size.</li> </ul>

	<ul style="list-style-type: none"> <li>• <code>line</code> Scale of line width.</li> <li>• <code>pie2axis</code> It is used to adjust the relative size of the pie chart on the coordinate axis, the default value is 1.</li> <li>• <code>label_group</code> Numeric, scale of group labels size, the default value is 1.</li> </ul>
<code>highlight.params</code>	list, the parameters to control the attributes of highlighted nodes and edges. see the <code>highlight.params</code> in the following. <code>highlight.params</code> control the attributes of highlight, it can be referred to the following parameters: <ul style="list-style-type: none"> <li>• <code>category</code> category nodes to be highlight.</li> <li>• <code>alpha_highlight</code> alpha of highlighted nodes.</li> <li>• <code>alpha_no_highlight</code> alpha of unhighlighted nodes.</li> </ul>
<code>cluster.params</code>	list, the parameters to control the attributes of highlighted nodes and edges. see the <code>cluster.params</code> in the following. <code>cluster.params</code> control the attributes of highlight, it can be referred to the following parameters: <ul style="list-style-type: none"> <li>• <code>cluster</code> a logical, if TRUE, group the category.</li> <li>• <code>method</code> function of Clustering method, such as <code>stats::kmeans</code>(the default), <code>cluster::clara</code>, <code>cluster::fanny</code> or <code>cluster::pam</code>.</li> <li>• <code>n</code> Numeric, the number of clusters, the default value is square root of the number of nodes.</li> <li>• <code>legend</code> Logical, if TRUE, the grouping legend will be displayed. The default is FALSE.</li> <li>• <code>label_style</code> style of group label, one of "shadowtext" and "ggforce".</li> <li>• <code>label_words_n</code> Numeric, the number of words in the cluster tags, the default value is 4.</li> <li>• <code>label_format</code> a numeric value sets wrap length, alternatively a custom function to format axis labels.</li> </ul>
<code>split</code>	separate result by 'category' variable
<code>pie</code>	proportion of clusters in the pie chart, one of 'equal' (default) and 'Count' Will be removed in the next version.
<code>legend_n</code>	number of circle in legend Will be removed in the next version.
<code>cex_pie2axis</code>	It is used to adjust the relative size of the pie chart on the coordinate axis, the default value is 1. Will be removed in the next version.
<code>pie.params</code>	list, the parameters to control the attributes of pie nodes. see the <code>pie.params</code> in the following. <code>pie.params</code> control the attributes of pie nodes, it can be referred to the following parameters: <ul style="list-style-type: none"> <li>• <code>pie</code> proportion of clusters in the pie chart, one of 'equal' (default) and 'Count'.</li> <li>• <code>legend_n</code> number of circle in legend.</li> </ul>

## 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. When the similarity between terms meets a certain threshold (default is 0.2, adjusted by parameter 'min\_edge'), there will be edges between terms. The stronger the similarity, the shorter and thicker the edges. The similarity between terms is obtained by function 'pairwise\_termsim', the details of similarity calculation can be found in its documentation: [pairwise\\_termsim](#).



**Value**

ggplot object

**Author(s)**

Guangchuang Yu

**Examples**

```
## Not run:
library(DOSE)
data(geneList)
de <- names(geneList)[1:100]
x <- enrichDO(de)
x2 <- pairwise_termsim(x)
emapplot(x2)
# use `layout` to change the layout of map
emapplot(x2, layout = "star")
# use `showCategory` to select the displayed terms. It can be a number of a vector of terms.
emapplot(x2, showCategory = 10)
categorys <- c("pre-malignant neoplasm", "intestinal disease",
              "breast ductal carcinoma")
emapplot(x2, showCategory = categorys)

# It can also graph compareClusterResult
library(clusterProfiler)
library(DOSE)
library(org.Hs.eg.db)
data(gcSample)
xx <- compareCluster(gcSample, fun="enrichGO", OrgDb="org.Hs.eg.db")
xx2 <- pairwise_termsim(xx)
emapplot(xx2)

## End(Not run)
```

---

emapplot_cluster	<i>Functional grouping network diagram for enrichment result of over-representation test or gene set enrichment analysis</i>
------------------	--

---

**Description**

This function has been replaced by ‘emapplot’.

**Usage**

```
emapplot_cluster(x, ...)
```

**Arguments**

x enrichment result  
... additional parameters. Please refer to: [emapplot](#).

**Value**

ggplot2 object

---

fortify.compareClusterResult  
*fortify*

---

**Description**

convert compareClusterResult to a data.frame that ready for plot  
convert enrichResult object for ggplot2

**Usage**

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

**Arguments**

model 'enrichResult' or 'compareClusterResult' object  
data not use here  
showCategory Category numbers to show

by	one of Count and GeneRatio
split	separate result by 'split' variable
includeAll	logical
order	logical
drop	logical
...	additional parameter

**Value**

data.frame  
data.frame

**Author(s)**

Guangchuang Yu

---

geom_gsea_gene	<i>geom_gsea_gene</i>
----------------	-----------------------

---

**Description**

label genes in running score plot

**Usage**

```
geom_gsea_gene(
  genes,
  mapping = NULL,
  geom = ggplot2::geom_text,
  ...,
  geneSet = NULL
)
```

**Arguments**

genes	selected genes to be labeled
mapping	aesthetic mapping, default is NULL
geom	geometric layer to plot the gene labels, default is geom_text
...	additional parameters passed to the 'geom'
geneSet	choose which gene set(s) to be label if the plot contains multiple gene sets

**Value**

ggplot object

**Author(s)**

Guangchuang Yu

---

ggtable	<i>ggtable</i>
---------	----------------

---

**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	<i>goplot</i>
--------	---------------

---

**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

**Examples**

```
## Not run:
library(clusterProfiler)
data(geneList, package = "DOSE")
de <- names(geneList)[1:100]
yy <- enrichGO(de, 'org.Hs.eg.db', ont="BP", pvalueCutoff=0.01)
goplot(yy)
goplot(yy, showCategory = 5)

## End(Not run)
```

---

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 <- gseD0(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	<i>gsearank</i>
----------	-----------------

---

**Description**

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

**Usage**

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

**Arguments**

x	gseaResult object
geneSetID	gene set ID
title	plot title
output	one of 'plot' or 'table' (for exporting data)

**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, ...)
```

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

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

```
heatplot.enrichResult(
  x,
  showCategory = 30,
  symbol = "rect",
```

```
    foldChange = NULL,  
    pvalue = NULL,  
    label_format = 30  
  )
```

### Arguments

x	enrichment result.
showCategory	number of enriched terms to display
...	Additional parameters
symbol	symbol of the nodes, one of "rect"(the default) and "dot" by default wraps names longer than 30 characters
foldChange	fold Change.
pvalue	pvalue of genes
label_format	a numeric value sets wrap length, alternatively a custom function to format axis labels.

### Value

ggplot object

### Author(s)

guangchuang yu  
Guangchuang Yu

### Examples

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

---

pairwise\_termsim      *pairwise\_termsim*

---

### Description

Get the similarity matrix

**Usage**

```

pairwise_termsim(x, method = "JC", semData = NULL, showCategory = 200)

## S4 method for signature 'enrichResult'
pairwise_termsim(x, method = "JC", semData = NULL, showCategory = 200)

## S4 method for signature 'gseaResult'
pairwise_termsim(x, method = "JC", semData = NULL, showCategory = 200)

## S4 method for signature 'compareClusterResult'
pairwise_termsim(x, method = "JC", semData = NULL, showCategory = 200)

pairwise_termsim.enrichResult(
  x,
  method = "JC",
  semData = NULL,
  showCategory = 200
)

pairwise_termsim.compareClusterResult(
  x,
  method = "JC",
  semData = NULL,
  showCategory = 200
)

```

**Arguments**

x	enrichment result.
method	method of calculating the similarity between nodes, one of "Resnik", "Lin", "Rel", "Jiang", "Wang" and "JC"(Jaccard similarity coefficient) methods.
semData	GOSemSimDATA object, can be obtained through <a href="#">godata</a> function in GOSemSim package.
showCategory	number of enriched terms to display, default value is 200.

**Details**

This function add similarity matrix to the termsim slot of enrichment result. Users can use the 'method' parameter to select the method of calculating similarity. The Jaccard correlation coefficient(JC) is used by default, and it applies to all situations. When users want to calculate the correlation between GO terms or DO terms, they can also choose "Resnik", "Lin", "Rel" or "Jiang" (they are semantic similarity calculation methods from GOSemSim packages), and at this time, the user needs to provide 'semData' parameter, which can be obtained through [godata](#) function in GOSemSim package.

**Examples**

```
## Not run:
```

```
library(clusterProfiler)
library(org.Hs.eg.db)
library(enrichplot)
library(GOsemSim)
library(DOSE)
data(geneList)
gene <- names(geneList)[abs(geneList) > 2]
ego <- enrichGO(gene = gene,
  universe      = names(geneList),
  OrgDb         = org.Hs.eg.db,
  ont           = "BP",
  pAdjustMethod = "BH",
  pvalueCutoff  = 0.01,
  qvalueCutoff  = 0.05,
  readable      = TRUE)
d <- godata('org.Hs.eg.db', ont="BP")
ego2 <- pairwise_termsim(ego, method="Wang", semData = d)
emapplot(ego2)
emapplot_cluster(ego2)

## End(Not run)
```

---

plotting.clusterProfile

*plotting-clusterProfile*

---

## Description

Internal plot function for plotting compareClusterResult

## Usage

```
plotting.clusterProfile(
  clProf.reshape.df,
  x = ~Cluster,
  type = "dot",
  colorBy = "p.adjust",
  by = "geneRatio",
  title = "",
  font.size = 12
)
```

## Arguments

clProf.reshape.df	data frame of compareCluster result
x	x variable
type	one of dot and bar

colorBy	one of pvalue or p.adjust
by	one of percentage and count
title	graph title
font.size	graph font size

**Value**

ggplot object

**Author(s)**

Guangchuang Yu <https://guangchuangyu.github.io>

---

pmcplot	<i>pmcplot</i>
---------	----------------

---

**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

---

reexports	<i>Objects exported from other packages</i>
-----------	---

---

**Description**

These objects are imported from other packages. Follow the links below to see their documentation.

**aplot** [plot\\_list](#)

**ggplot2** [facet\\_grid](#), [ggtitle](#)

---

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

---

**Description**

ridgeline plot for GSEA result

**Usage**

```
ridgeplot(  
  x,  
  showCategory = 30,  
  fill = "p.adjust",  
  core_enrichment = TRUE,  
  label_format = 30,  
  ...  
)  
  
## S4 method for signature 'gseaResult'  
ridgeplot(  
  x,  
  showCategory = 30,  
  fill = "p.adjust",  
  core_enrichment = TRUE,  
  label_format = 30,  
  ...  
)  
  
ridgeplot.gseaResult(  
  x,  
  showCategory = 30,  
  fill = "p.adjust",  
  core_enrichment = TRUE,  
  label_format = 30,  
  orderBy = "NES",  
  decreasing = FALSE  
)
```

**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

label_format	a numeric value sets wrap length, alternatively a custom function to format axis labels.
...	additional parameters by default wraps names longer than 30 characters
orderBy	The order of the Y-axis
decreasing	logical. Should the orderBy order be increasing or decreasing?

**Value**

ggplot object

**Author(s)**

Guangchuang Yu

**Examples**

```
library(DOSE)
data(geneList)
x <- gseD0(geneList)
ridgeplot(x)
```

---

ssplot

*ssplot*


---

**Description**

Similarity space plot of enrichment analysis results.

**Usage**

```
ssplot(x, ...)

## S4 method for signature 'enrichResult'
ssplot(x, showCategory = 30, ...)

## S4 method for signature 'gseaResult'
ssplot(x, showCategory = 30, ...)

## S4 method for signature 'compareClusterResult'
ssplot(x, showCategory = 30, ...)

ssplot.enrichResult(
  x,
  showCategory = 30,
  drfun = NULL,
  with_edge = FALSE,
  dr.params = list(),
```



```

    group_category = TRUE,
    node_label = "group",
    ...
)

ssplot.compareClusterResult(
  x,
  showCategory = 30,
  split = NULL,
  pie = "equal",
  drfun = NULL,
  with_edge = FALSE,
  cex_pie2axis = 0.0125,
  dr.params = list(),
  group_category = TRUE,
  node_label = "group",
  ...
)

```

### Arguments

**x** Enrichment result.

**...** additional parameters

additional parameters can refer the following parameters.

- **coords** a data.frame with two columns: 'x' for X-axis coordinate and 'y' for Y-axis coordinate.
- **color** Variable that used to color enriched terms, e.g. 'pvalue', 'p.adjust' or 'qvalue'. the starting position of each text label.
- **cex\_line** Scale of line width.
- **min\_edge** The minimum similarity threshold for whether two nodes are connected, should between 0 and 1, default value is 0.2.
- **cex\_label\_category** Scale of category node label size.
- **cex\_category** Number indicating the amount by which plotting category nodes should be scaled relative to the default.
- **shadowtext** a logical value, whether to use shadow font.
- **label\_style** style of group label, one of "shadowtext" and "ggforce".
- **repel** whether to correct the position of the label. Defaults to FALSE.
- **group\_legend** Logical, if TRUE, the grouping legend will be displayed. The default is FALSE.
- **cex\_label\_group** Numeric, scale of group labels size, the default value is 1.
- **nWords** Numeric, the number of words in the cluster tags, the default value is 4.
- **label\_format** a numeric value sets wrap length, alternatively a custom function to format axis labels.
- **clusterFunction** function of Clustering method, such as stats::kmeans(the default), cluster::clara, cluster::fanny or cluster::pam.

- `nCluster` Numeric, the number of clusters, the default value is square root of the number of nodes.

additional parameters can refer the `emapplot` function: [emapplot](#).

<code>showCategory</code>	A number or a vector of terms. If it is a number, the first n terms will be displayed. If it is a vector of terms, the selected terms will be displayed.
<code>drfun</code>	The function used for dimension reduction, e.g. <code>stats::cmdscale</code> (the default), <code>vegan::metaMDS</code> , or <code>ape::pcoa</code> .
<code>with_edge</code>	Logical, if TRUE, draw the edges of the network diagram. Will be removed in the next version.
<code>dr.params</code>	list, the parameters of <code>tidydr::dr</code> . one of 'category', 'group', 'all' and 'none'.
<code>group_category</code>	a logical, if TRUE, group the category. Will be removed in the next version.
<code>node_label</code>	Select which labels to be displayed, one of 'category', 'group', 'all' and 'none'.
<code>split</code>	separate result by 'category' variable
<code>pie</code>	proportion of clusters in the pie chart, one of 'equal' (default) and 'Count' Will be removed in the next version.
<code>cex_pie2axis</code>	It is used to adjust the relative size of the pie chart on the coordinate axis, the default value is 0.0125.

## Value

ggplot object

## Examples

```
## Not run:
library(clusterProfiler)
library(org.Hs.eg.db)
library(enrichplot)
library(GOsemSim)
library(DOSE)
data(geneList)
gene <- names(geneList)[abs(geneList) > 2]
ego <- enrichGO(gene = gene,
  universe = names(geneList),
  OrgDb = org.Hs.eg.db,
  ont = "BP",
  pAdjustMethod = "BH",
  pvalueCutoff = 0.01,
  qvalueCutoff = 0.05,
  readable = TRUE)
d <- godata('org.Hs.eg.db', ont="BP")
ego2 <- pairwise_termsim(ego, method = "Wang", semData = d)
ssplot(ego2)

## End(Not run)
```

---

treeplot	<i>treeplot</i>
----------	-----------------

---

### Description

Functional grouping tree diagram for enrichment result of over-representation test or gene set enrichment analysis.

### Usage

```
treeplot(x, ...)

## S4 method for signature 'enrichResult'
treeplot(x, ...)

## S4 method for signature 'gseaResult'
treeplot(x, ...)

## S4 method for signature 'compareClusterResult'
treeplot(x, ...)

treeplot.enrichResult(
  x,
  showCategory = 30,
  color = "p.adjust",
  nWords = 4,
  nCluster = 5,
  cex_category = 1,
  label_format = NULL,
  label_format_cladelab = 30,
  label_format_tiplab = NULL,
  fontsize = 4,
  offset = rel(1),
  offset_tiplab = rel(1),
  hclust_method = "ward.D",
  group_color = NULL,
  extend = 0.3,
  hilight = TRUE,
  hexpand = 0.1,
  align = "both",
  hilight.params = list(hilight = TRUE, align = "both"),
  offset.params = list(bar_tree = rel(1), tiplab = rel(1), extend = 0.3, hexpand = 0.1),
  cluster.params = list(method = "ward.D", n = 5, color = NULL, label_words_n = 4,
    label_format = 30),
  ...
)
```

```

treeplot.compareClusterResult(
  x,
  showCategory = 5,
  color = "p.adjust",
  nWords = 4,
  nCluster = 5,
  cex_category = 1,
  split = NULL,
  label_format = NULL,
  label_format_cladelab = 30,
  label_format_tiplab = NULL,
  fontsize = 4,
  offset = rel(1),
  pie = "equal",
  legend_n = 3,
  offset_tiplab = rel(1),
  hclust_method = "ward.D",
  group_color = NULL,
  extend = 0.3,
  hilight = TRUE,
  geneClusterPanel = "heatMap",
  hexpand = 0.1,
  align = "both",
  cluster.params = list(method = "ward.D", n = 5, color = NULL, label_words_n = 4,
    label_format = 30),
  hilight.params = list(hilight = TRUE, align = "both"),
  clusterPanel.params = list(clusterPanel = "heatMap", pie = "equal", legend_n = 3),
  offset.params = list(bar_tree = rel(1), tiplab = rel(1), extend = 0.3, hexpand = 0.1),
  ...
)

```

### Arguments

x	enrichment result.
...	additional parameters
showCategory	number of enriched terms to display
color	variable that used to color enriched terms, e.g. pvalue, p.adjust or qvalue
nWords	The number of words in the cluster tags. Will be removed in the next version.
nCluster	The number of clusters, the default value is 5. Will be removed in the next version.
cex_category	Number indicating the amount by which plotting category. nodes should be scaled relative to the default. Will be removed in the next version.
label_format	a numeric value sets wrap length, alternatively a custom function to format axis labels.
label_format_cladelab	label_format for group labels, a numeric value sets wrap length, alternatively a custom function to format axis labels. Will be removed in the next version.

label_format_tiplab	label_format for tiplabs, a numeric value sets wrap length, alternatively a custom function to format axis labels. Will be removed in the next version.
fontsize	The size of text, default is 4.
offset	rel object or numeric value, distance bar and tree, offset of bar and text from the clade, default is rel(1), meaning $1 * 1.2 * x\_range\_of\_tree$ plus distance_between_tree_and_tiplab ( $1 * (1.2 * x\_range\_of\_tree + distance\_between\_tree\_and\_tiplab)$ ). Will be removed in the next version.
offset_tiplab	tiplab offset, rel object or numeric value, the bigger the number, the farther the distance between the node and the branch. The default is rel(1), when geneClusterPanel = "pie", meaning $1 * max\_radius\_of\_the\_pies$ ; when geneClusterPanel = "heatMap", meaning $1 * 0.16 * column\_number\_of\_heatMap * x\_range\_of\_tree$ ; when geneClusterPanel = "dotplot", meaning $1 * 0.09 * column\_number\_of\_dotplot * x\_range\_of\_tree$ . Will be removed in the next version.
hclust_method	Method of hclust. This should be (an unambiguous abbreviation of) one of "ward.D", "ward.D2", "single", "complete", "average" (= UPGMA), "mcquitty" (= WPGMA), "median" (= WPGMC) or "centroid" (= UPGMC). Will be removed in the next version.
group_color	A vector of group colors, the length of the vector should be the same as nCluster. Will be removed in the next version.
extend	Numeric, extend the length of bar, default is 0.3. Will be removed in the next version.
hilight	Logical value, if TRUE(default), add ggtree::geom_hilight() layer. Will be removed in the next version.
hexpand	expand x limits by amount of xrange * hexpand. Will be removed in the next version.
align	control the align direction of the edge of high light rectangular. Options is 'none', 'left', 'right', 'both (default)'. Will be removed in the next version.
hilight.params	list, the parameters to control the attributes of highlight layer. see the hilight.params in the following. hilight.params control the attributes of highlight layer, it can be referred to the following parameters: <ul style="list-style-type: none"> <li>• hilight Logical value, if TRUE(default), add ggtree::geom_hilight() layer.</li> <li>• align control the align direction of the edge of high light rectangular. Options is 'none', 'left', 'right', 'both (default)'.</li> </ul>
offset.params	list, the parameters to control the offset. see the offset.params in the following. offset.params control the attributes of offset, it can be referred to the following parameters: <ul style="list-style-type: none"> <li>• bar_tree rel object or numeric value, distance bar and tree, offset of bar and text from the clade, default is rel(1), meaning <math>1 * 1.2 * x\_range\_of\_tree</math> plus distance_between_tree_and_tiplab (<math>1 * (1.2 * x\_range\_of\_tree + distance\_between\_tree\_and\_tiplab)</math>).</li> <li>• tiplab tiplab offset, rel object or numeric value, the bigger the number, the farther the distance between the node and the branch. The default is rel(1), when clusterPanel = "pie", meaning <math>1 * max\_radius\_of\_the\_pies</math>; when</li> </ul>

- clusterPanel = "heatMap", meaning  $1 * 0.16 * \text{column\_number\_of\_heatMap} * \text{x\_range\_of\_tree}$ ; when clusterPanel = "dotplot", meaning  $1 * 0.09 * \text{column\_number\_of\_dotplot} * \text{x\_range\_of\_tree}$ .
- extend Numeric, extend the length of bar, default is 0.3.
  - hexpand expand x limits by amount of xrange \* hexpand.
- cluster.params list, the parameters to control the attributes of highlighted nodes and edges. see the cluster.params in the following. cluster.params control the attributes of highlight, it can be referred to the following parameters:
- method function of Clustering method, such as stats::kmeans(the default), cluster::clara, cluster::fanny or cluster::pam.
  - n Numeric, the number of clusters, the default value is square root of the number of nodes.
  - color A vector of group colors, the length of the vector should be the same as nCluster.
  - label\_words\_n Numeric, the number of words in the cluster tags, the default value is 4.
  - label\_format A numeric value sets wrap length, alternatively a custom function to format axis labels.
- split Separate result by 'category' variable.
- pie Used only when geneClusterPanel = "pie", proportion of clusters in the pie chart, one of 'equal' (default) and 'Count'. Will be removed in the next version.
- legend\_n Number of circle in legend, the default value is 3. Will be removed in the next version.
- geneClusterPanel one of "heatMap"(default), "dotplot", "pie". Will be removed in the next version.
- clusterPanel.params list, the parameters to control the attributes of cluster panel. see the clusterPanel.params in the following. clusterPanel.params control the attributes of cluster panel, it can be referred to the following parameters:
- clusterPanel one of "heatMap"(default), "dotplot", "pie".
  - pie pUsed only when ClusterPanel = "pie", proportion of clusters in the pie chart, one of 'equal' (default) and 'Count'.
  - legend\_n number of circle in legend.

## Details

This function visualizes gene sets as a tree. Gene sets with high similarity tend to cluster together, making it easier for interpretation.

## Value

ggplot object

**Examples**

```

## Not run:
library(clusterProfiler)
library(org.Hs.eg.db)
library(enrichplot)
library(GOsemSim)
library(ggplot2)
library(DOSE)
data(geneList)
gene <- names(geneList)[abs(geneList) > 2]
ego <- enrichGO(gene = gene,
  universe      = names(geneList),
  OrgDb         = org.Hs.eg.db,
  ont           = "BP",
  pAdjustMethod = "BH",
  pvalueCutoff  = 0.01,
  qvalueCutoff  = 0.05,
  readable      = TRUE)
d <- godata('org.Hs.eg.db', ont="BP")
ego2 <- pairwise_termsim(ego, method = "Wang", semData = d)
treeplot(ego2, showCategory = 30)
# use `highlight = FALSE` to remove ggtree::geom_highlight() layer.
treeplot(ego2, showCategory = 30, highlight = FALSE)
# use `offset` parameter to adjust the distance of bar and tree.
treeplot(ego2, showCategory = 30, highlight = FALSE, offset = rel(1.5))
# use `offset_tiplab` parameter to adjust the distance of nodes and branches.
treeplot(ego2, showCategory = 30, highlight = FALSE, offset_tiplab = rel(1.5))
keep <- rownames(ego2@termsim)[c(1:10, 16:20)]
keep
treeplot(ego2, showCategory = keep)
treeplot(ego2, showCategory = 20,
  group_color = c("#999999", "#E69F00", "#56B4E9", "#009E73", "#F0E442"))
# It can also graph compareClusterResult
data(gcSample)
xx <- compareCluster(gcSample, fun="enrichKEGG",
  organism="hsa", pvalueCutoff=0.05)
xx <- pairwise_termsim(xx)
treeplot(xx)

# use `geneClusterPanel` to change the gene cluster panel.
treeplot(xx, geneClusterPanel = "dotplot")

treeplot(xx, geneClusterPanel = "pie")

## End(Not run)

```

**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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