

Package ‘enrichplot’

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Title Visualization of Functional Enrichment Result

Version 1.31.0

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.

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Contents

enrichplot-package	2
autofacet	3
barplot.enrichResult	4
cnetplot.enrichResult	5
color_palette	7
dotplot	7
dotplot2	11
emapplot	12
fortify.compareClusterResult	14
geom_gsea_gene	15
ggtable	16
goplot	17
gseadist	18
gseaplot	19
gseaplot2	20
gsearank	21
gsInfo	22
heatplot	22
hplot	24
pairwise_termsim	24
plotting.clusterProfile	26
pmcplot	27
reexports	27
ridgeplot	28
set_enrichplot_color	29
ssplot	30
treeplot	32
upsetplot	37
volplot	38
Index	40

enrichplot-package	<i>enrichplot: Visualization of Functional Enrichment Result</i>
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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.

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See Also

Useful links:

- <https://yulab-smu.top/contribution-knowledge-mining/>
- Report bugs at <https://github.com/GuangchuangYu/enrichplot/issues>

autofacet

automatically split barplot or dotplot into several facets

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 or a vector of terms.
barplot(x, showCategory = 10)
```

```
categorys <- c("urinary bladder cancer", "bronchiolitis obliterans",  
              "aortic aneurysm", "esophageal cancer")  
barplot(x, showCategory = categorys)
```

cnetplot.enrichResult *cnetplot*

Description

category-gene-network plot

Usage

```
## S3 method for class 'enrichResult'  
cnetplot(  
  x,  
  layout = igraph::layout_with_kk,  
  showCategory = 5,  
  color_category = "#E5C494",  
  size_category = 1,  
  color_item = "#B3B3B3",  
  size_item = 1,  
  color_edge = "grey",  
  size_edge = 0.5,  
  node_label = "all",  
  foldChange = NULL,  
  highlight = "none",  
  highlight_alpha = 0.3,  
  ...  
)
```

```
## S3 method for class 'gseaResult'  
cnetplot(  
  x,  
  layout = igraph::layout_with_kk,  
  showCategory = 5,  
  color_category = "#E5C494",  
  size_category = 1,  
  color_item = "#B3B3B3",  
  size_item = 1,  
  color_edge = "grey",  
  size_edge = 0.5,  
  node_label = "all",  
  foldChange = NULL,  
  highlight = "none",  
  highlight_alpha = 0.3,  
  ...  
)
```

```

)

## S3 method for class 'compareClusterResult'
cnetplot(
  x,
  layout = igraph::layout_with_kk,
  showCategory = 5,
  color_category = "#E5C494",
  size_category = 1,
  color_item = "#B3B3B3",
  size_item = 1,
  color_edge = "grey",
  size_edge = 0.5,
  node_label = "all",
  foldChange = NULL,
  highlight = "none",
  highlight_alpha = 0.3,
  pie = "equal",
  ...
)

```

Arguments

<code>x</code>	input object
<code>layout</code>	network layout
<code>showCategory</code>	selected category to be displayed
<code>color_category</code>	color of category node
<code>size_category</code>	relative size of the category
<code>color_item</code>	color of item node
<code>size_item</code>	relative size of the item (e.g., genes)
<code>color_edge</code>	color of edge
<code>size_edge</code>	relative size of edge
<code>node_label</code>	one of 'all', 'none', 'category', 'item', 'exclusive' or 'share'
<code>foldChange</code>	numeric values to color the item (e.g, foldChange of gene expression values)
<code>highlight</code>	selected category to be highlighted
<code>highlight_alpha</code>	transparent value for not selected to be highlight
<code>...</code>	additional parameters
<code>pie</code>	one of 'equal' or 'Count' to set the slice ratio of the pies

See Also

[cnetplot][ggtangle::cnetplot]

color_palette	<i>color_palette</i>
---------------	----------------------

Description

create color palette for continuous data

Usage

```
color_palette(colors)
```

Arguments

colors colors of length ≥ 2

Value

color vector

Author(s)

guangchuang yu

Examples

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

dotplot	<i>dotplot</i>
---------	----------------

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,
```

```

    facet = NULL,
    strip_width = 15
)

```

Arguments

<code>object</code>	compareClusterResult object
<code>...</code>	additional parameters
<code>x</code>	variable for x-axis, one of 'GeneRatio' and 'Count'
<code>color</code>	variable that used to color enriched terms, e.g. 'pvalue', 'p.adjust' or 'qvalue'
<code>showCategory</code>	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.
<code>size</code>	variable that used to scale the sizes of categories, one of "geneRatio", "Percentage" and "count"
<code>split</code>	apply 'showCategory' to each category specified by the 'split', e.g., "ONTOLOGY", "category" and "intersect". Default is NULL and do nothing
<code>font.size</code>	font size
<code>title</code>	figure title
<code>orderBy</code>	The order of the Y-axis
<code>label_format</code>	a numeric value sets wrap length, alternatively a custom function to format axis labels. by default wraps names longer than 30 characters
<code>by</code>	one of "geneRatio", "Percentage" and "count"
<code>includeAll</code>	logical
<code>decreasing</code>	logical. Should the orderBy order be increasing or decreasing?
<code>colorBy</code>	variable that used to color enriched terms, e.g. 'pvalue', 'p.adjust' or 'qvalue'
<code>group</code>	a logical value, whether to connect the nodes of the same group with wires.
<code>shape</code>	a logical value, whether to use nodes of different shapes to distinguish the group it belongs to
<code>facet</code>	apply 'facet_grid' to the plot by specified variable, e.g., "ONTOLOGY", "category" and "intersect".
<code>strip_width</code>	width of strip text, a.k.a facet label.

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)
```

dotplot2

*dotplot2***Description**

compare two clusters in the compareClusterResult object

Usage

```
dotplot2(object, x = "FoldEnrichment", vars = NULL, label = "auto", ...)
```

Arguments

object	a compareClusterResult object
x	selected variable to visualize in x-axis
vars	selected Clusters to be compared, only length of two is supported
label	to label the Clusters in the plot, should be a named vector
...	additional parameters passed to dotplot

Value

a ggplot object

Author(s)

Guangchuang Yu

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_internal(  
  x,  
  layout = igraph::layout_with_kk,  
  showCategory = 30,  
  color = "p.adjust",  
  size_category = 1,  
  min_edge = 0.2,  
  color_edge = "grey",  
  size_edge = 0.5,  
  node_label = "category",  
  pie = "equal",  
  group = FALSE,  
  group_style = "ggforce",  
  label_group_style = "shaddowtext",  
  label_format = 30,  
  clusterFunction = stats::kmeans,  
  nWords = 4,  
  nCluster = NULL  
)
```

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.
layout	igraph layout
color	Variable that used to color enriched terms, e.g. 'pvalue', 'p.adjust' or 'qvalue'.
size_category	relative size of the categories
min_edge	The minimum similarity threshold for whether two nodes are connected, should be between 0 and 1, default value is 0.2.
color_edge	color of the network edge
size_edge	relative size of edge width
node_label	Select which labels to be displayed, one of 'category', 'group', 'all' and 'none'.
pie	one of 'equal' or 'Count' to set the slice ratio of the pies
group	logical, if TRUE, group the category.
group_style	style of ellipse, one of "ggforce" and "polygon".
label_group_style	style of group label, one of "shadowtext" and "ggforce".
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.
nWords	Numeric, the number of words in the cluster tags, the default value is 4.
nCluster	Numeric, the number of clusters, the default value is square root of the number of nodes.

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)
```

```
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
...	additional parameter
order	logical
drop	logical

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

<i>gseadist</i>	<i>gseadist</i>
-----------------	-----------------

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

x	object of gsea result
geneSetID	geneSet ID
by	one of "runningScore" or "position"
title	plot title
...	additional parameters
color	color of line segments
color.line	color of running enrichment score line
color.vline	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,
  pvalue_table_columns = c("pvalue", "p.adjust"),
  pvalue_table_rownames = "Description",
  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
pvalue_table_columns	selected columns to be plotted in the 'pvalue_table'
pvalue_table_rownames	selected column as the rownames of the 'pvalue_table'. If set to NULL, no rownames will be displayed.
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 = "", 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	<i>gsInfo</i>
--------	---------------

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	<i>heatplot</i>
----------	-----------------

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

Examples

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

hplot	<i>hplot</i>
-------	--------------

Description

Horizontal plot for GSEA result

Usage

```
hplot(x, geneSetID)
```

Arguments

x	gseaResult object
geneSetID	gene set ID

Value

horizontal plot

Author(s)

Guangchuang Yu

pairwise_termsim	<i>pairwise_termsim</i>
------------------	-------------------------

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 godata .
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](#).

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://yulab-smu.top>

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](#)
ggtangle [cnetplot](#), [geom_cnet_label](#)

ridgeplot

ridgeplot

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

<code>x</code>	<code>gseaResult</code> object
<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>fill</code>	one of "pvalue", "p.adjust", "qvalue"
<code>core_enrichment</code>	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)
```

set_enrichplot_color *set_enrichplot_color*

Description

helper function to set color for enrichplot

Usage

```
set_enrichplot_color(
  colors = get_enrichplot_color(2),
  type = "color",
  name = NULL,
  .fun = NULL,
  reverse = TRUE,
  transform = "log10",
  ...
)
```

Arguments

colors	user provided color vector
type	one of 'color', 'colour' or 'fill'
name	name of the color legend

<code>.fun</code>	force to use user provided color scale function
<code>reverse</code>	whether reverse the color scheme, default is TRUE as it is more significant for lower pvalue
<code>transform</code>	transform the color scale, default is "log10" as p-values operate over a wide range of orders of magnitude, set to 'identity' to disable the transformation
<code>...</code>	additional parameter that passed to the color scale function

Value

a color scale

ssplot	<i>ssplot</i>
--------	---------------

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,
  dr.params = list(),
  group = TRUE,
  node_label = "group",
  ...
)
```

```
ssplot.compareClusterResult(
  x,
  showCategory = 30,
  pie = "equal",
  drfun = NULL,
```

```

dr.params = list(),
group = TRUE,
node_label = "group",
...
)

```

Arguments

x	Enrichment result.
...	additional parameters
	additional parameters can refer the following parameters.
	• color Variable that used to color enriched terms, e.g. 'pvalue', 'p.adjust' or 'qvalue'. the starting position of each text label. • size_edge 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. • size_category Number indicating the amount by which plotting category nodes should be scaled relative to the default. • label_style style of group label, one of "shadowtext" and "ggforce". • group Logical, if TRUE, the grouping legend will be displayed. The default is FALSE. • 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 .
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.
drfun	The function used for dimension reduction, e.g. stats::cmdscale (the default), vegan::metaMDS, or ape::pcoa.
dr.params	list, the parameters of tidydr::dr. one of 'category', 'group', 'all' and 'none'.
group	logical, if TRUE, group the category.
node_label	Select which labels to be displayed, one of 'category', 'group', 'all' and 'none'.
pie	one of 'equal' or 'Count' to set the slice ratio of the pies

Value

ggplot object

Author(s)

Guangchuang Yu

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

treeplot

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,
leave_fontsize = 4,
clade_fontsize = 4,
offset = rel(1),
offset_tiplab = rel(1),
hclust_method = "ward.D",
group_color = NULL,
extend = 0.3,
highlight = TRUE,
hexpand = 0.1,
align = "both",
highlight.params = list(highlight = 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,
  leave_fontsize = 4,
  clade_fontsize = 4,
  offset = rel(1),
  pie = "equal",
  legend_n = 3,
  offset_tiplab = rel(1),
  hclust_method = "ward.D",
  group_color = NULL,
  extend = 0.3,
  highlight = 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),
    highlight.params = list(hilighit = TRUE, align = "both"),
    clusterPanel.params = list(clusterPanel = "heatMap", pie = "equal", legend_n = 3,
        colnames_angle = 0),
    offset.params = list(bar_tree = rel(1), tiplab = rel(1), extend = 0.3, hexpand = 0.1),
    ...
)

```

Arguments

<code>x</code>	enrichment result.
<code>...</code>	additional parameters
<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>nWords</code>	The number of words in the cluster tags. Will be removed in the next version.
<code>nCluster</code>	The number of clusters, the default value is 5. Will be removed in the next version.
<code>cex_category</code>	Number indicating the amount by which plotting category. nodes should be scaled relative to the default. 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.
<code>label_format_cladelab</code>	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.
<code>label_format_tiplab</code>	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.
<code>leave_fontsize</code>	The size of tiplabel, default is 4.
<code>clade_fontsize</code>	The size of cladelabel, default is 4.
<code>offset</code>	rel object or numeric value, distance bar and tree, offset of bar and text from the clade, default is <code>rel(1)</code> , meaning $1 * 1.2 * x_range_of_tree$ plus <code>distance_between_tree_and_tiplab</code> ($1 * (1.2 * x_range_of_tree + distance_between_tree_and_tiplab)$). Will be removed in the next version.
<code>offset_tiplab</code>	tiplab offset, rel object or numeric value, the bigger the number, the farther the distance between the node and the branch. The default is <code>rel(1)</code> , when <code>geneClusterPanel = "pie"</code> , meaning $1 * max_radius_of_the_pies$; when <code>geneClusterPanel = "heatMap"</code> , meaning $1 * 0.16 * column_number_of_heatMap * x_range_of_tree$; when <code>geneClusterPanel = "dotplot"</code> , meaning $1 * 0.09 * column_number_of_dotplot * x_range_of_tree$. Will be removed in the next version.
<code>hclust_method</code>	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.
<code>group_color</code>	A vector of group colors, the length of the vector should be the same as <code>nCluster</code> . 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: • hilight Logical value, if TRUE(default), add ggtree::geom_hilight() layer. • align control the align direction of the edge of high light rectangular. Options is 'none', 'left', 'right', 'both (default)'.
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: • bar_tree 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 ($1 * (1.2 * x_range_of_tree + distance_between_tree_and_tiplab)$). • 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 $1 * max_radius_of_the_pies$; when clusterPanel = "heatMap", meaning $1 * 0.16 * column_number_of_heatMap * x_range_of_tree$; when clusterPanel = "dotplot", meaning $1 * 0.09 * column_number_of_dotplot * x_range_of_tree$. • 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.
 - `colnames_angle` set the angle of colnames.

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` 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, hilight = 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)

```

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)
```

volplot*volplot*

Description

volcano plot for enrichment result

Usage

```
volplot(
  x,
  color = "zScore",
  xintercept = 1,
  yintercept = 2,
  showCategory = 5,
  label_format = 30,
  ...
)

## S4 method for signature 'enrichResult'
volplot(
  x,
  color = "zScore",
  xintercept = 1,
  yintercept = 2,
  showCategory = 5,
  label_format = 30,
  ...
)

volplot.enrichResult(
  x,
  color = "zScore",
  xintercept = 1,
  yintercept = 2,
  showCategory = 5,
```

```
    label_format = 30,  
    font.size = 12,  
    size = 5  
  )
```

Arguments

x	enrichment result.
color	selected variable to color the dots
xintercept	value to set x intercept
yintercept	value to set y intercept
showCategory	number of most significant enriched terms or selected terms to display determined by the variable selected to color the dots
label_format	a numeric value sets wrap length, alternatively a custom function to format axis labels.
...	Additional parameters
font.size	font size for 'theme_dose()'
size	font size to label selected categories specified by showCategory

Value

ggplot object

Author(s)

Guangchuang Yu

Examples

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

Index

- * **internal**
 - enrichplot-package, [2](#)
 - reexports, [27](#)
- autofacet, [3](#)
- barplot.enrichResult, [4](#)
- cnetplot, [27](#)
- cnetplot(reexports), [27](#)
- cnetplot.compareClusterResult(cnetplot.enrichResult), [5](#)
- cnetplot.enrichResult, [5](#)
- cnetplot.gseaResult(cnetplot.enrichResult), [5](#)
- color_palette, [7](#)
- dotplot, [7](#)
- dotplot,compareClusterResult,ANY-method(dotplot), [7](#)
- dotplot,compareClusterResult-method(dotplot), [7](#)
- dotplot,enrichResult-method(dotplot), [7](#)
- dotplot,enrichResultList,ANY-method(dotplot), [7](#)
- dotplot,enrichResultList-method(dotplot), [7](#)
- dotplot,gseaResult-method(dotplot), [7](#)
- dotplot,gseaResultList,ANY-method(dotplot), [7](#)
- dotplot,gseaResultList-method(dotplot), [7](#)
- dotplot.compareClusterResult(dotplot), [7](#)
- dotplot.enrichResult(dotplot), [7](#)
- dotplot2, [11](#)
- emapplot, [12](#), [31](#)
- emapplot,compareClusterResult-method(emapplot), [12](#)
- emapplot,enrichResult-method(emapplot), [12](#)
- emapplot,gseaResult-method(emapplot), [12](#)
- emapplot_internal(emapplot), [12](#)
- enrichplot(enrichplot-package), [2](#)
- enrichplot-package, [2](#)
- facet_grid, [27](#)
- facet_grid(reexports), [27](#)
- fortify.compareClusterResult, [14](#)
- fortify.enrichResult(fortify.compareClusterResult), [14](#)
- geom_cnet_label, [27](#)
- geom_cnet_label(reexports), [27](#)
- geom_gsea_gene, [15](#)
- ggtable, [16](#)
- ggtitle, [27](#)
- ggtitle(reexports), [27](#)
- godata, [25](#)
- goplot, [17](#)
- goplot,enrichResult-method(goplot), [17](#)
- goplot,gseaResult-method(goplot), [17](#)
- gseadist, [18](#)
- gseaplot, [19](#)
- gseaplot,gseaResult-method(gseaplot), [19](#)
- gseaplot.gseaResult(gseaplot), [19](#)
- gseaplot2, [20](#)
- gsearank, [21](#)
- gsInfo, [22](#)
- heatplot, [22](#)
- heatplot,enrichResult-method(heatplot), [22](#)
- heatplot,gseaResult-method(heatplot), [22](#)
- heatplot.enrichResult(heatplot), [22](#)

hplot, 24

pairwise_termsim, 13, 24

pairwise_termsim,compareClusterResult-method
 (pairwise_termsim), 24

pairwise_termsim,enrichResult-method
 (pairwise_termsim), 24

pairwise_termsim,gseaResult-method
 (pairwise_termsim), 24

pairwise_termsim.compareClusterResult
 (pairwise_termsim), 24

pairwise_termsim.enrichResult
 (pairwise_termsim), 24

plot_list, 27

plot_list (reexports), 27

plotting.clusterProfile, 26

pmcplot, 27

reexports, 27

ridgeplot, 28

ridgeplot,gseaResult-method
 (ridgeplot), 28

ridgeplot.gseaResult (ridgeplot), 28

set_enrichplot_color, 29

ssplot, 30

ssplot,compareClusterResult-method
 (ssplot), 30

ssplot,enrichResult-method (ssplot), 30

ssplot,gseaResult-method (ssplot), 30

ssplot.compareClusterResult (ssplot), 30

ssplot.enrichResult (ssplot), 30

treeplot, 32

treeplot,compareClusterResult-method
 (treeplot), 32

treeplot,enrichResult-method
 (treeplot), 32

treeplot,gseaResult-method (treeplot),
 32

treeplot.compareClusterResult
 (treeplot), 32

treeplot.enrichResult (treeplot), 32

upsetplot, 37

upsetplot,enrichResult,ANY-method
 (upsetplot), 37

upsetplot,enrichResult-method
 (upsetplot), 37

upsetplot,gseaResult (upsetplot), 37

upsetplot,gseaResult-method
 (upsetplot), 37

volplot, 38

volplot,enrichResult-method (volplot),
 38

volplot.enrichResult (volplot), 38