

Package ‘enrichplot’

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Title Visualization of Functional Enrichment Result

Version 1.31.2

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

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Author Guangchuang Yu [aut, cre] (ORCID:
<https://orcid.org/0000-0002-6485-8781>),
 Chun-Hui Gao [ctb] (ORCID: <https://orcid.org/0000-0002-1445-7939>)

Maintainer Guangchuang Yu <guangchuangyu@gmail.com>

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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.

Author(s)

Maintainer: Guangchuang Yu <guangchuangyu@gmail.com> ([ORCID](#))

Other contributors:

- Chun-Hui Gao <gaospecial@gmail.com> ([ORCID](#)) [contributor]

See Also

Useful links:

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

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

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,  
  fc_threshold = NULL,  
  hilight = "none",  
  hilight_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,  
  fc_threshold = NULL,  
  hilight = "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,
  fc_threshold = NULL,
  highlight = "none",
  highlight_alpha = 0.3,
  pie = "equal",
  ...
)

```

Arguments

x	input object
layout	network layout
showCategory	selected category to be displayed
color_category	color of category node
size_category	relative size of the category
color_item	color of item node
size_item	relative size of the item (e.g., genes)
color_edge	color of edge
size_edge	relative size of edge
node_label	one of 'all', 'none', 'category', 'item', 'exclusive' or 'share'
foldChange	numeric values to color the item (e.g, foldChange of gene expression values)
fc_threshold	threshold for filtering genes by absolute fold change (e.g., fc_threshold = 1 keeps only genes with foldChange > 1)
highlight	selected category to be highlighted
highlight_alpha	transparent value for not selected to be highlight
...	additional parameters
pie	one of 'equal' or 'Count' to set the slice ratio of the pies

See Also

[cnetplot][ggangle::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

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	apply 'showCategory' to each category specified by the 'split', e.g., "ONTOLOGY", "category" and "intersect". Default is NULL and do nothing
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
facet	apply 'facet_grid' to the plot by specified variable, e.g., "ONTOLOGY", "category" and "intersect".
strip_width	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 or 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

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

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",
  node_label_size = 5,
```

```

    pie = "equal",
    label_format = 30,
    clusterFunction = stats::kmeans,
    nWords = 4,
    nCluster = NULL
  )

```

Arguments

<code>x</code>	Enrichment result.
<code>...</code>	Additional parameters
<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>layout</code>	igraph layout
<code>color</code>	Variable that used to color enriched terms, e.g. 'pvalue', 'p.adjust' or 'qvalue'.
<code>size_category</code>	relative size of the categories
<code>min_edge</code>	The minimum similarity threshold for whether two nodes are connected, should be between 0 and 1, default value is 0.2.
<code>color_edge</code>	color of the network edge
<code>size_edge</code>	relative size of edge width
<code>node_label</code>	Select which labels to be displayed, one of 'category', 'group', 'all' and 'none'.
<code>node_label_size</code>	size of node label, default is 5.
<code>pie</code>	one of 'equal' or 'Count' to set the slice ratio of the pies
<code>label_format</code>	a numeric value sets wrap length, alternatively a custom function to format axis labels.
<code>clusterFunction</code>	function of Clustering method, such as stats::kmeans(the default), cluster::clara, cluster::fanny or cluster::pam.
<code>nWords</code>	Numeric, the number of words in the cluster tags, the default value is 4.
<code>nCluster</code>	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	<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 = 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

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

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)
```

<code>gseaplot2</code>	<i>gseaplot2</i>
------------------------	------------------

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

<code>gsearank</code>	<i>gsearank</i>
-----------------------	-----------------

Description

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

Usage

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

Arguments

- | | |
|------------------------|---|
| <code>x</code> | <code>gseaResult</code> object |
| <code>geneSetID</code> | gene set ID |
| <code>title</code> | plot title |
| <code>output</code> | one of 'plot' or 'table' (for exporting data) |

Value

`ggplot` object

Author(s)

Guangchuang Yu

<code>gsInfo</code>	<i>gsInfo</i>
---------------------	---------------

Description

extract gsea result of selected geneSet

Usage

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

Arguments

- | | |
|------------------------|--------------------------------|
| <code>object</code> | <code>gseaResult</code> object |
| <code>geneSetID</code> | 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,
  showTop = NULL,
  symbol = "rect",
  foldChange = NULL,
  pvalue = NULL,
  label_format = 30
)
```

Arguments

x	enrichment result.
showCategory	number of enriched terms to display
...	Additional parameters
showTop	number of top genes ranked by abs(foldChange) * frequency to be shown in the heatmap, default NULL means all genes are shown
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

pmcplot

Description

PubMed Central Trend plot

Usage

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

Arguments

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

Value

ggplot object

Author(s)

guangchuang yu

reexports

Objects exported from other packages

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

x	gseaResult object
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.
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)

```

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 = "identity",  
  ...  
)
```

Arguments

colors	user provided color vector
type	one of 'color', 'colour' or 'fill'
name	name of the color legend
.fun	force to use user provided color scale function
reverse	whether reverse the color scheme, default is TRUE as it is more significant for lower pvalue
transform	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
...	additional parameter that passed to the color scale function

Value

a color scale

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

Description

Similarity Space Plot for enrichment analysis

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(),
  node_label = "group",
  ...
)
```

```
ssplot.compareClusterResult(
  x,
  showCategory = 30,
  pie = "equal",
  drfun = NULL,
  dr.params = list(),
  node_label = "group",
  ...
)
```

Arguments

- | | |
|-----|-----------------------|
| x | Enrichment result. |
| ... | additional parameters |
- additional parameters can refer the following parameters.
- layout igraph layout function for node positioning
 - 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 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'.
 - node_label_size size of node label, default is 5.
 - pie one of 'equal' or 'Count' to set the slice ratio of the pies (for 'compareClusterResult' only).
 - 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.

	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'.
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

Details

Creates 2D visualization of enrichment results using dimension reduction techniques to show relationships between terms based on similarity.

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

Description

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

Creates hierarchical tree visualization of enriched terms based on similarity

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_internal(
  x,
  showCategory = 30,
  color = "p.adjust",
  size_var = c("Count", "setSize"),
  nCluster = 5,
  cluster_method = "ward.D",
  label_format = 30,
  fontsize_tiplab = 4,
  fontsize_cladelab = 4,
  group_color = NULL,
  extend = 0.3,
  highlight = TRUE,
  align = "both",
  hexpand = 0.1,
  tiplab_offset = 0.2,
  cladelab_offset = 1
)
```

Arguments

x	enrichment result.
...	additional parameters
showCategory	number of enriched terms to display

color	variable to color nodes, e.g. 'p.adjust', 'pvalue', or 'qvalue'
size_var	variable for node size, e.g. 'Count' (for enrichResult) or 'setSize' (for gseaResult)
nCluster	number of clusters for tree cutting
cluster_method	hierarchical clustering method
label_format	wrap length for labels or custom formatting function
fontsize_tiplab	font size for tip labels
fontsize_cladelab	font size for clade labels
group_color	vector of colors for groups
extend	extend length for clade labels
hilight	whether to highlight clades
align	alignment for highlight rectangles
hexpand	expand x limits by amount of xrange * hexpand
tiplab_offset	offset for tip labels
cladelab_offset	offset for clade labels

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
ggplot2 object representing the tree plot

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)

```

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)
```

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