Package 'enrichplot'

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Title Visualization of Functional Enrichment Result

Version 1.32.1

Description The 'enrichplot' package provides visualization methods for interpreting functional enrichment results from ORA or GSEA analyses.
It is designed to work with the 'clusterProfiler' ecosystem and builds on 'ggplot2' for flexible and extensible graphics.

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enrichplot-package *enrichplot: Visualization of Functional Enrichment Result*

Description

The 'enrichplot' package provides visualization methods for interpreting functional enrichment results from ORA or GSEA analyses. It is designed to work with the 'clusterProfiler' ecosystem and builds on 'ggplot2' for flexible and extensible 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

---

as.data.frame.compareClusterResult *Convert compareClusterResult to data frame*

Description

Convert compareClusterResult to data frame

Usage

```
## S3 method for class 'compareClusterResult'
as.data.frame(x, ...)
```

Arguments

x	compareClusterResult object
...	additional parameters

Value

data frame

`autofacet` *Plotting utility functions for enrichplot package*

Description

This file contains plotting and visualization helper functions for enrichplot Automatically split barplot or dotplot into several facets

Usage

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

Arguments

`by`	one of 'row' or 'column'
`scales`	whether '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 display or a vector of terms.
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
...	additional parameters

Details

Barplot of enrichResult

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

---

cnetplot.enrichResult *Category-Gene-Network Plot*

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,
  categorySizeBy = ~itemNum,
  node_label = "all",
  node_label_size = NULL,
  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,
  categorySizeBy = ~itemNum,
  node_label = "all",
  node_label_size = NULL,
  foldChange = NULL,
  fc_threshold = NULL,
  hilight = "none",
  hilight_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,
  categorySizeBy = ~itemNum,
  node_label = "all",
  node_label_size = NULL,
  foldChange = NULL,
  fc_threshold = NULL,
  hilight = "none",
  hilight_alpha = 0.3,
  ...
)
```

Arguments

x	input object
layout	network layout
showCategory	number of categories to display or a vector of terms.
color_category	color of category nodes
size_category	relative size of the category nodes
color_item	color of item nodes
size_item	relative size of the item nodes (e.g., genes)
color_edge	color of edge
size_edge	relative size of edge
categorySizeBy	An expression (e.g., `itemNum`, `p.adjust`) or a formula (e.g., `~ -log10(p.adjust)`) to set the category node size. For `compareClusterResult`, this controls the category pie size.
node_label	one of 'all', 'none', 'category', 'item', 'exclusive' or 'share'. 'exclusive' labels genes that uniquely belong to categories; 'share' labels genes that are shared between categories.
node_label_size	size of category/item labels, or `NULL` for the ggtangle default.
foldChange	numeric values to color the item (e.g., fold change 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).
hilight	selected categories to be highlighted
hilight_alpha	transparency value for non-highlighted items
...	additional parameters. For `compareClusterResult`, `pie`, `split`, and `includeAll` may be supplied through these additional parameters.

See Also

cnetplot

color_palette *Create color palette for continuous data*

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 *dotplot*

Description

Dot plot 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 used to color enriched terms, e.g. 'pvalue', 'p.adjust' or 'qvalue'
showCategory	number of categories to display or a vector of terms.
size	variable 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 value
decreasing	logical. Should the orderBy order be increasing or decreasing?
colorBy	variable 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 (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)
    categories <- c("pre-malignant neoplasm", "intestinal disease",
                    "breast ductal carcinoma", "non-small cell lung carcinoma")
    dotplot(x, showCategory = categories)
    # 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,
  coords = NULL,
  showCategory = 30,
  color = "p.adjust",
  size_category = 1,
  min_edge = 0.2,
  edge_filter = "threshold",
  top_k = 5,
  target_density = 0.1,
  edge_diagnostic = FALSE,
  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

x	Enrichment result.
...	Additional parameters
showCategory	number of categories to display or a vector of terms.
layout	igraph layout
coords	Optional coordinate data.frame with x, y columns and row names matching node labels.
color	Variable 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, between 0 and 1 (default 0.2).
edge_filter	Edge filtering strategy: "threshold" (default), "top_k", or "adaptive".
top_k	Number of strongest neighbors per term in top-k mode.
target_density	Target proportion of unique term pairs in adaptive mode.
edge_diagnostic	Logical; attach a density data.frame to the returned plot when TRUE.
color_edge	color of the network edge
size_edge	relative size of edge width
node_label	Select which labels to display, 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
label_format	a numeric value sets wrap length, alternatively a custom function to format axis labels.
clusterFunction	clustering method function, such as stats::kmeans (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 the function pairwise_termsim. Details of the 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)
    categories <- c("pre-malignant neoplasm", "intestinal disease",
                    "breast ductal carcinoma")
    emapplot(x2, showCategory = categories)

    # 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_edge_density *Diagnose enrichment-map edge density*

Description

Diagnose enrichment-map edge density

Usage

```
emapplot_edge_density(
  pair_sim,
  min_edge = 0.2,
  edge_filter = "threshold",
  top_k = 5,
```

```
  target_density = 0.1
)
```

Arguments

pair_sim	square numeric similarity matrix.
min_edge	minimum similarity threshold.
edge_filter	edge filtering strategy.
top_k	number of neighbors per term.
target_density	target adaptive density.

Value

A one-row data.frame with retained-pair counts and density.

---

enrichplot-common-params

Shared parameters for enrichment plots

Description

Shared parameters for enrichment plots

Arguments

color	variable used to color enriched terms, e.g. 'pvalue', 'p.adjust', or 'qvalue'.
showCategory	number of categories to display, or a vector of terms.
size	variable used to scale category size, one of "geneRatio", "Percentage", or "count".
split	apply showCategory to each category specified by split, e.g., "ONTOLOGY", "category", or "intersect". Default is NULL.
font.size	font size.
title	figure title.
label_format	a numeric wrap width, or a custom function to format axis labels.
includeAll	logical value.

enrichplot-term-params
Shared term-plot parameters

Description

Shared term-plot parameters

Arguments

showCategory	number of categories to display, or a vector of terms.
color	variable used to color enriched terms, e.g. 'pvalue', 'p.adjust', or 'qvalue'.
label_format	a numeric wrap width, or a custom function to format axis labels.

enrichplot_point_shape
Predefined color palettes

Description

Predefined color palettes

Usage

```
enrichplot_point_shape
```

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 *geom_gsea_gene*

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

get_enrichplot_color *Color utility functions for enrichplot package*

Description

This file contains all color-related helper functions Get default enrichplot colors

Usage

```
get_enrichplot_color(n = 2)
```

Arguments

n	number of colors (2 or 3)

Value

color vector

---

ggtable *ggtable*

Description

plot table

Usage

```
ggtable(d, p = NULL)
```

Arguments

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

Value

ggplot object

Author(s)

guangchuang yu

---

goplot *goplot*

Description

Plot induced GO DAG of significant terms

Usage

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

## S4 method for signature 'enrichResult'
goplot(
  x,
  showCategory = 10,
  color = "p.adjust",
  layout = 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 categories to display, or a vector of terms.
color	variable 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 parameters.

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 GSEA analysis results

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	gseaResult object
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 indicating the maximum/minimal running enrichment score

Details

Plotting function for gseaResult

Value

ggplot2 object

ggplot2 object

Author(s)

Guangchuang Yu

Examples

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

---

gseaplot2 *gseaplot2*

Description

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

Usage

```
gseaplot2(
  x,
  geneSetID,
  title = "",
  color = "green",
  base_size = 11,
  rel_heights = c(1.5, 0.5, 1),
  subplots = 1:3,
  pvalue_table = FALSE,
  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` *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,
  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) or "dot"
foldChange	fold change.
pvalue	pvalue of genes
label_format	a numeric value sets wrap length, alternatively a custom function to format axis labels. by default wraps names longer than 30 characters

Value

ggplot object

Author(s)

Guangchuang Yu

Examples

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

hplot *hplot*

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

manhattanplot *manhattanplot*

Description

Manhattan plot for enrichment result

Usage

```
manhattanplot(x, ...)

## S4 method for signature 'enrichResult'
manhattanplot(
  x,
  color = "p.adjust",
  showCategory = 5,
  size = "Count",
  split = NULL,
  font.size = 12,
  title = "",
  label_format = 30,
```

```
  ...
)

## S4 method for signature 'gseaResult'
manhattanplot(
  x,
  color = "p.adjust",
  showCategory = 5,
  size = "Count",
  split = NULL,
  font.size = 12,
  title = "",
  label_format = 30,
  ...
)

## S4 method for signature 'compareClusterResult'
manhattanplot(
  x,
  color = "p.adjust",
  showCategory = 5,
  split = NULL,
  font.size = 12,
  title = "",
  size = "Count",
  includeAll = TRUE,
  label_format = 30,
  ...
)

## S4 method for signature 'enrichResultList'
manhattanplot(
  x,
  color = "p.adjust",
  showCategory = 5,
  size = "Count",
  split = NULL,
  font.size = 12,
  title = "",
  label_format = 30,
  ...
)

## S4 method for signature 'gseaResultList'
manhattanplot(
  x,
  color = "p.adjust",
  showCategory = 5,
```

```
  size = "Count",
  split = NULL,
  font.size = 12,
  title = "",
  label_format = 30,
  ...
)

## S4 method for signature 'list'
manhattanplot(
  x,
  color = "p.adjust",
  showCategory = 5,
  size = "Count",
  split = NULL,
  font.size = 12,
  title = "",
  label_format = 30,
  ...
)
```

Arguments

x	enrichment result.
...	additional parameters.
color	variable used to color enriched terms, e.g. 'pvalue', 'p.adjust', or 'qvalue'.
showCategory	number of categories to display, or a vector of terms.
size	variable used to scale category size, one of "geneRatio", "Percentage", or "count".
split	apply showCategory to each category specified by split, e.g., "ONTOLOGY", "category", or "intersect". Default is NULL.
font.size	font size.
title	figure title.
label_format	a numeric wrap width, or a custom function to format axis labels.
includeAll	logical value.

Value

ggplot object

Author(s)

Guangchuang Yu

pairwise_termsim *pairwise_termsim*

Description

Get the similarity matrix

Usage

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

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

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

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

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

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

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 GOSemSim::godata.
showCategory	number of enriched terms to be calculated. The default value is the number of enriched terms, or 200 if the number of enriched terms exceeds 200.

Details

This function adds a similarity matrix to the termsim slot of the enrichment result. Users can use the method parameter to select the method of calculating the 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 the 'GOSemSim' package), and at this time, the user needs to provide the semData parameter, which can be obtained through GOSemSim::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

Internal plot function for plotting compareClusterResult

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()`

DOSE `theme_dose()`

enrichit `geneID()`, `geneInCategory()`, `gseaScores()`

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,
  stat = "density_ridges"
)
```

Arguments

x	gseaResult object
showCategory	number of categories to display or a vector of terms.
fill	one of "pvalue", "p.adjust", "qvalue"
core_enrichment	whether to use only core_enriched genes
label_format	a numeric value setting the wrap length, alternatively a custom function to format axis labels.
...	additional parameters.
orderBy	The order of the Y-axis
decreasing	logical. Should the orderBy order be increasing or decreasing?
stat	statistic passed to ggridges::geom_density_ridges().

Value

ggplot object

Author(s)

Guangchuang Yu

Examples

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

`set_enrichplot_color` *Helper function to set color scale for enrichplot*

Description

Helper function to set color scale 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
`transform`	transform the color scale
`...`	additional parameters

Value

a color scale

Author(s)

Guangchuang Yu

ssplot *ssplot*

Description

Similarity Space Plot for enrichment analysis

Usage

```
ssplot(x, showCategory = 30, ..., min_edge = 0.2, size_edge = 0.5)

## S4 method for signature 'enrichResult'
ssplot(x, showCategory = 30, ..., min_edge = 0.2, size_edge = 0.5)

## S4 method for signature 'gseaResult'
ssplot(x, showCategory = 30, ..., min_edge = 0.2, size_edge = 0.5)

## S4 method for signature 'compareClusterResult'
ssplot(x, showCategory = 30, ..., min_edge = 0.2, size_edge = 0.5)

ssplot.enrichResult(
  x,
  showCategory = 30,
  drfun = NULL,
  dr.params = list(),
  node_label = "group",
  min_edge = 0.2,
  size_edge = 0.5,
  ...
)

ssplot.compareClusterResult(
  x,
  showCategory = 30,
  pie = "equal",
  drfun = NULL,
  dr.params = list(),
  node_label = "group",
  min_edge = 0.2,
  size_edge = 0.5,
  ...
)
```

Arguments

x	Enrichment result.
showCategory	number of categories to display or a vector of terms.

...	additional parameters Additional plotting parameters are inherited from emapplot().
min_edge	Minimum similarity threshold for connecting two nodes.
size_edge	Relative size of edge width.
drfun	Function used for dimension reduction. The default, stats::cmdscale, performs classical multidimensional scaling (MDS); this is one available reduction method.
dr.params	Named list of arguments passed separately to drfun via tidydr::dr.
node_label	Select which labels to display, 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.

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.

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,
  hilight = 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 `hilight = FALSE` to remove ggtree::geom_hilight() layer.
treeplot(ego2, showCategory = 30, hilight = FALSE)
# use `offset` parameter to adjust the distance of bar and tree.
treeplot(ego2, showCategory = 30, hilight = 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

Upsetplot

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

```
library(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 setting the 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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