Package 'enrichplot'

October 14, 2021

Title Visualization of Functional Enrichment Result

Version 1.12.3

Description The 'enrichplot' package implements several visualization methods for interpreting functional enrichment results obtained from ORA or GSEA analysis.
All the visualization methods are developed based on 'ggplot2' graphics.

Depends R (>= 3.5.0)

Imports cowplot, DOSE (>= 3.16.0), ggplot2, ggraph, graphics, grid,
igraph, methods, plyr, purrr, RColorBrewer, reshape2, stats,
utils, scatterpie, shadowtext, GOSemSim, magrittr, ggtree

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

VignetteBuilder knitr

License Artistic-2.0

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

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

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

Encoding UTF-8

LazyData true

RoxygenNote 7.1.1

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R **topics documented:**

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barplot.enrichResult   *barplot*

Description

barplot of enrichResult

Usage

```
## S3 method for class 'enrichResult'
barplot(
  height,
  x = "Count",
  color = "p.adjust",
  showCategory = 8,
  font.size = 12,
  title = "",
  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 that 30 characters
`...`	other parameter, ignored

Value

ggplot object

Examples

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

---

cnetplot *cnetplot*

Description

Gene-Concept Network

Usage

```
cnetplot(x, showCategory = 5, foldChange = NULL, layout = "kk", ...)

## S4 method for signature 'enrichResult'
cnetplot(x, showCategory = 5, foldChange = NULL, layout = "kk", ...)

## S4 method for signature 'gseaResult'
cnetplot(x, showCategory = 5, foldChange = NULL, layout = "kk", ...)
```

```
## S4 method for signature 'compareClusterResult'
cnetplot(x, showCategory = 5, foldChange = NULL, layout = "kk", ...)

cnetplot.enrichResult(
  x,
  showCategory = 5,
  foldChange = NULL,
  layout = "kk",
  colorEdge = FALSE,
  circular = FALSE,
  node_label = "all",
  cex_category = 1,
  cex_gene = 1,
  cex_label_category = 1,
  cex_label_gene = 1,
  color_category = "#E5C494",
  color_gene = "#B3B3B3",
  shadowtext = "all",
  ...
)
```

Arguments

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

Details

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

Value

ggplot object

Author(s)

Guangchuang Yu

Examples

```
## Not run:
    library(DOSE)
    data(geneList)
    de <- names(geneList)[1:100]
    x <- enrichDO(de)
    x2 <- pairwise_termsim(x)
    cnetplot(x2)
    # use `layout` to change the layout of map
    cnetplot(x2, layout = "star")
  # use `showCategory` to select the displayed terms. It can be a number of a vector of terms.
    cnetplot(x2, showCategory = 10)
    categorys <- c("pre-malignant neoplasm", "intestinal disease",
                   "breast ductal carcinoma", "non-small cell lung carcinoma")
    cnetplot(x2, showCategory = categorys)
    # 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)
    cnetplot(xx2)

## End(Not run)
```

---

color_palette	*color_palette*

Description

create color palette for continuous data

Usage

```
color_palette(colors)
```

Arguments

colors   colors of length >=2

Value

color vector

Author(s)

guangchuang yu

Examples

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

---

dotplot	*dotplot*

Description

dotplot for enrichment result

Usage

```
dotplot(object, ...)

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

## S4 method for signature 'gseaResult'
dotplot(
  object,
  x = "GeneRatio",
  color = "p.adjust",
  showCategory = 10,
```

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

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

  dotplot.enrichResult(
    object,
    x = "geneRatio",
    color = "p.adjust",
    showCategory = 10,
    size = NULL,
    split = NULL,
    font.size = 12,
    title = "",
    orderBy = "x",
    label_format = 30,
    decreasing = TRUE
  )

  dotplot.compareClusterResult(
    object,
    x = "Cluster",
    colorBy = "p.adjust",
    showCategory = 5,
    by = "geneRatio",
    size = "geneRatio",
    split = NULL,
    includeAll = TRUE,
```

```
    font.size = 12,
    title = "",
    label_format = 30,
    group = FALSE,
    shape = FALSE
)
```

Arguments

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

Value

plot

Author(s)

guangchuang yu

Examples

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

## End(Not run)
```

---

emapplot   *emapplot*

Description

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

Usage

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

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

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

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

emapplot.enrichResult(
```

```
  x,
  showCategory = 30,
  layout = NULL,
  coords = NULL,
  color = "p.adjust",
  min_edge = 0.2,
  cex_label_category = 1,
  cex_category = 1,
  cex_line = 1,
  shadowtext = TRUE,
  label_style = "shadowtext",
  repel = FALSE,
  node_label = "category",
  with_edge = TRUE,
  group_category = FALSE,
  group_legend = FALSE,
  cex_label_group = 1,
  nWords = 4,
  label_format = 30,
  clusterFunction = stats::kmeans,
  nCluster = NULL,
  ...
)

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

```
    cex_pie2axis = 1,
    ...
)
```

Arguments

x	Enrichment result.
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.
...	additional parameters
	additional parameters can refer the following parameters.

- force Force of repulsion between overlapping text labels. Defaults to 1.
- nudge_x,nudge_y Horizontal and vertical adjustments to nudge the starting position of each text label.
- direction "both", "x", or "y" – direction in which to adjust position of labels.
- ellipse_style style of ellipse, one of "ggforce" an "polygon".
- ellipse_pro numeric indicating confidence value for the ellipses, it can be used only when ellipse_style = "polygon".
- alpha the transparency of ellipse fill.
- type The type of ellipse. The default "t" assumes a multivariate t-distribution, and "norm" assumes a multivariate normal distribution. "euclid" draws a circle with the radius equal to level, representing the euclidean distance from the center.

layout	Layout of the map, e.g. 'star', 'circle', 'gem', 'dh', 'graphopt', 'grid', 'mds', 'randomly', 'fr', 'kk', 'drl' or 'lgl'.
coords	a data.frame with two columns: 'x' for X-axis coordinate and 'y' for Y-axis coordinate.
color	Variable that used to color enriched terms, e.g. 'pvalue', 'p.adjust' or 'qvalue'.
min_edge	The minimum similarity threshold for whether two nodes are connected, should between 0 and 1, default value is 0.2.
cex_label_category	Scale of category node label size.
cex_category	Number indicating the amount by which plotting category nodes should be scaled relative to the default.
cex_line	Scale of line width
shadowtext	a logical value, whether to use shadow font.
label_style	style of group label, one of "shadowtext" and "ggforce".
repel	whether to correct the position of the label. Defaults to FALSE.
node_label	Select which labels to be displayed, one of 'category', 'group', 'all' and 'none'.
with_edge	Logical, if TRUE (the default), draw the edges of the network diagram.
group_category	a logical, if TRUE(the default), group the category.
group_legend	Logical, if TRUE, the grouping legend will be displayed. The default is FALSE.

cex_label_group

          Numeric, scale of group labels size, the default value is 1.

nWords   Numeric, the number of words in the cluster tags, the default value is 4.

label_format   a numeric value sets wrap length, alternatively a custom function to format axis labels.

clusterFunction

          function of Clustering method, such as stats::kmeans(the default), cluster::clara, cluster::fanny or cluster::pam.

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

split   separate result by 'category' variable

pie   proportion of clusters in the pie chart, one of 'equal' (default) and 'Count'

legend_n   number of circle in legend

cex_pie2axis   It is used to adjust the relative size of the pie chart on the coordinate axis, the default value is 1.

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", "non-small cell lung carcinoma")
```

```
        emapplot(x2, 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)
        emapplot(xx2)

    ## End(Not run)
```

---

emapplot_cluster   *Functional grouping network diagram for enrichment result of over-representation test or gene set enrichment analysis*

Description

This function has been replaced by 'emapplot'.

Usage

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

Arguments

x	enrichment result
...	additional parameters. Please refer to: emapplot.

Value

ggplot2 object

---

fortify.compareClusterResult
                    fortify

Description

convert compareClusterResult to a data.frame that ready for plot

convert enrichResult object for ggplot2

Usage

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

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

Arguments

model	'enrichResult' or 'compareClusterResult' object
data	not use here
showCategory	Category numbers to show
by	one of Count and GeneRatio
split	separate result by 'split' variable
includeAll	logical
order	logical
drop	logical
...	additional parameter

Value

data.frame

data.frame

Author(s)

Guangchuang Yu

---

ggtable *ggtable*

Description

plot table

Usage

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

Arguments

d   data frame

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

Value

ggplot object

Author(s)

guangchuang yu

---

goplot *goplot*

Description

plot induced GO DAG of significant terms

Usage

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

## S4 method for signature 'enrichResult'
goplot(
  x,
```

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

## S4 method for signature 'gseaResult'
goplot(
    x,
    showCategory = 10,
    color = "p.adjust",
    layout = "sugiyama",
    geom = "text",
    ...
)

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

Arguments

x	enrichment result.
showCategory	number of enriched terms to display
color	variable that used to color enriched terms, e.g. pvalue, p.adjust or qvalue
layout	layout of the map
geom	label geom, one of 'label' or 'text'
...	additional parameter

Value

ggplot object

Author(s)

Guangchuang Yu

Examples

```
## Not run:
library(clusterProfiler)
    data(geneList, package = "DOSE")
```

```
de <- names(geneList)[1:100]
yy <- enrichGO(de, 'org.Hs.eg.db', ont="BP", pvalueCutoff=0.01)
    goplot(yy)
    goplot(yy, showCategory = 5)

## End(Not run)
```

---

gseadist   *gseadist*

Description

plot logFC distribution of selected gene sets

Usage

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

Arguments

x   GSEA result

IDs   gene set IDs

type   one of 'density' or 'boxplot'

Value

distribution plot

Author(s)

Guangchuang Yu

---

gseaplot   *gseaplot*

Description

visualize analyzing result of GSEA

Usage

```
gseaplot(x, geneSetID, by = "all", title = "", ...)

## S4 method for signature 'gseaResult'
gseaplot(
  x,
  geneSetID,
  by = "all",
  title = "",
  color = "black",
  color.line = "green",
  color.vline = "#FA5860",
  ...
)

gseaplot.gseaResult(
  x,
  geneSetID,
  by = "all",
  title = "",
  color = "black",
  color.line = "green",
  color.vline = "#FA5860",
  ...
)
```

Arguments

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

---

gseaplot2 *gseaplot2*

Description

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

Usage

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

Arguments

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

Value

plot

Author(s)

Guangchuang Yu

---

gsearank *gsearank*

Description

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

Usage

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

Arguments

x	gseaResult object
geneSetID	gene set ID
title	plot title

Value

ggplot object

Author(s)

Guangchuang Yu

---

gsInfo *gsInfo*

Description

extract gsea result of selected geneSet

Usage

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

Arguments

object	gseaResult object
geneSetID	gene set ID

Value

data.frame

Author(s)

Guangchuang Yu

| heatplot | *heatplot* |

Description

heatmap like plot for functional classification

Usage

```
heatplot(x, showCategory = 30, foldChange = NULL)

## S4 method for signature 'enrichResult'
heatplot(x, showCategory = 30, foldChange = NULL)

## S4 method for signature 'gseaResult'
heatplot(x, showCategory = 30, foldChange = NULL)

heatplot.enrichResult(
  x,
  showCategory = 30,
  foldChange = NULL,
  label_format = 30
)
```

Arguments

x	enrichment result.
showCategory	number of enriched terms to display
foldChange	fold Change
label_format	a numeric value sets wrap length, alternatively a custom function to format axis labels. by default wraps names longer that 30 characters

Value

ggplot object

Author(s)

guangchuang yu

Guangchuang Yu

Examples

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

---

pairwise_termsim   *pairwise_termsim*

Description

Get the similarity matrix

Usage

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

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

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

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

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

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

Arguments

x	enrichment result.
method	method of calculating the similarity between nodes, one of "Resnik", "Lin", "Rel", "Jiang" , "Wang" and "JC"(Jaccard similarity coefficient) methods.

semData   GOSemSimDATA object, can be obtained through godata function in GOSem-
                 Sim package.

showCategory   number of enriched terms to display, default value is 200.

Details

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

Examples

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

## End(Not run)
```

---

plotting.clusterProfile

                         plotting-clusterProfile

Description

Internal plot function for plotting compareClusterResult

Usage

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

Arguments

clProf.reshape.df

                data frame of compareCluster result

x	x variable
type	one of dot and bar
colorBy	one of pvalue or p.adjust
by	one of percentage and count
title	graph title
font.size	graph font size

Value

ggplot object

Author(s)

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

---

  pmcplot   *pmcplot*

Description

PubMed Central Trend plot

Usage

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

Arguments

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

Value

ggplot object

Author(s)

guangchuang yu

---

ridgeplot   *ridgeplot*

Description

ridgeline plot for GSEA result

Usage

```
ridgeplot(
  x,
  showCategory = 30,
  fill = "p.adjust",
  core_enrichment = TRUE,
  label_format = 30,
  ...
)

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

ridgeplot.gseaResult(
  x,
  showCategory = 30,
  fill = "p.adjust",
  core_enrichment = TRUE,
  label_format = 30,
  orderBy = "NES",
  decreasing = FALSE
)
```

Arguments

x	gseaResult object
showCategory	number of categories for plotting
fill	one of "pvalue", "p.adjust", "qvalue"
core_enrichment	
	whether only using core_enriched genes
label_format	a numeric value sets wrap length, alternatively a custom function to format axis labels.
...	additional parameters by default wraps names longer that 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 <- gseDO(geneList)
ridgeplot(x)
```

---

treeplot	*treeplot*

Description

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

Usage

```
treeplot(x, showCategory = 30, color = "p.adjust", label_format = 30, ...)

## S4 method for signature 'enrichResult'
treeplot(x, showCategory = 30, color = "p.adjust", label_format = 30, ...)

## S4 method for signature 'gseaResult'
treeplot(x, showCategory = 30, color = "p.adjust", label_format = 30, ...)
```

```
## S4 method for signature 'compareClusterResult'
treeplot(x, showCategory = 5, color = "p.adjust", label_format = 30, ...)

treeplot.enrichResult(
  x,
  showCategory = 30,
  color = "p.adjust",
  nWords = 4,
  nCluster = 5,
  cex_category = 1,
  label_format = 30,
  xlim = NULL,
  fontsize = 4,
  offset = NULL,
  offset_tiplab = 0.35,
  hclust_method = "ward.D",
  group_color = NULL,
  extend = 0.3,
  hilight = TRUE,
  ...
)

treeplot.compareClusterResult(
  x,
  showCategory = 5,
  color = "p.adjust",
  nWords = 4,
  nCluster = 5,
  cex_category = 1,
  split = NULL,
  label_format = 30,
  xlim = NULL,
  fontsize = 4,
  offset = NULL,
  pie = "equal",
  legend_n = 3,
  offset_tiplab = 0.5,
  hclust_method = "ward.D",
  group_color = NULL,
  extend = 0.3,
  hilight = TRUE,
  ...
)
```

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
`label_format`	a numeric value sets wrap length, alternatively a custom function to format axis labels.
`...`	additional parameters
`nWords`	The number of words in the cluster tags.
`nCluster`	The number of clusters, the default value is 5.
`cex_category`	Number indicating the amount by which plotting category. nodes should be scaled relative to the default.
`xlim`	Limits for the x axes, e.g. c(0, 40). If the picture is not displayed completely, the user can increase this value.
`fontsize`	The size of text, default is 4.
`offset`	Distance bar and tree, offset of bar and text from the clade.
`offset_tiplab`	Tiplab offset, the bigger the number, the farther the distance between the node and the branch. The default value is 0.35.
`hclust_method`	Method of hclust. This should be (an unambiguous abbreviation of) one of "ward.D", "ward.D2", "single", "complete", "average" (= UPGMA), "mcquitty" (= WPGMA), "median" (= WPGMC) or "centroid" (= UPGMC).
`group_color`	A vector of group colors, the length of the vector should be the same as nCluster.
`extend`	Numeric, extend the length of bar, default is 0.3.
`hilight`	Logical value, if TRUE(default), add ggtree::geom_hilight() layer.
`split`	Separate result by 'category' variable.
`pie`	Proportion of clusters in the pie chart, one of 'equal' (default) and 'Count'.
`legend_n`	Number of circle in legend, the default value is 3.

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(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 = 8)
  # use `offset_tiplab` parameter to adjust the distance of nodes and branches.
  treeplot(ego2, showCategory = 30, hilight = FALSE, offset_tiplab = 0.3)
  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"))

## 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)
```

Index