

Package: enrichplot (via r-universe)

October 9, 2026

Title Visualization of Functional Enrichment Result

Version 1.99.8

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.

Depends R (>= 4.2.0)

Imports aplot (>= 0.2.1), DOSE, dplyr, enrichit (>= 0.1.6), ggfun (>= 0.1.7), ggnewscale, ggplot2 (>= 3.5.0), ggrepel (>= 0.9.0), ggtangle (>= 0.0.9), ggtree, GOSemSim (>= 2.37.2), graphics, grid, igraph, methods, purrr, RColorBrewer, reshape2, rlang, scatterpie, stats, tidydr, utils, yulab.utils (>= 0.2.2)

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as.data.frame.compareClusterResult	
<i>Convert compareClusterResult to data frame</i>	

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	<i>Plotting utility functions for enrichplot package</i>
-----------	--

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

<code>height</code>	enrichResult object
<code>x</code>	one of 'Count' and 'GeneRatio'
<code>color</code>	one of 'pvalue', 'p.adjust' and 'qvalue'
<code>showCategory</code>	number of categories to display or a vector of terms.
<code>font.size</code>	font size
<code>title</code>	plot title
<code>label_format</code>	a numeric value sets wrap length, alternatively a custom function to format axis labels. by default wraps names longer than 30 characters
<code>...</code>	additional parameters

Details

Barplot of enrichResult

Value

ggplot object

Examples

```
## Not run:
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)

## End(Not run)
```

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"))
```

consensusmap	<i>consensusmap</i>
--------------	---------------------

Description

Multi-context mechanism consensus map

Usage

```
consensusmap(
  x,
  fill_var = c("NES", "delta_NES"),
  size_var = c("rewiring_score", "leading_edge_overlap"),
  include_rewiring = TRUE,
  label = c("mechanism_class", "rewiring_score", "none"),
  reference = NULL,
  thresholds = list(rewire = 0.5, nes = 0.2),
  ...
)

## S4 method for signature 'mnseaResult'
consensusmap(
  x,
  fill_var = c("NES", "delta_NES"),
  size_var = c("rewiring_score", "leading_edge_overlap"),
  include_rewiring = TRUE,
  label = c("mechanism_class", "rewiring_score", "none"),
  reference = NULL,
  thresholds = list(rewire = 0.5, nes = 0.2),
  ...
)

## S4 method for signature 'nseaResult'
consensusmap(
  x,
  fill_var = c("NES", "delta_NES"),
  size_var = c("rewiring_score", "leading_edge_overlap"),
  include_rewiring = TRUE,
  label = c("mechanism_class", "rewiring_score", "none"),
  reference = NULL,
  thresholds = list(rewire = 0.5, nes = 0.2),
  ...
)

## S4 method for signature 'list'
consensusmap(
  x,
```

```
fill_var = c("NES", "delta_NES"),
size_var = c("rewiring_score", "leading_edge_overlap"),
include_rewiring = TRUE,
label = c("mechanism_class", "rewiring_score", "none"),
reference = NULL,
thresholds = list(rewire = 0.5, nes = 0.2),
...
)
```

Arguments

x	A mnseaResult, nseaResult, or a named list of results.
fill_var	One of "NES" or "delta_NES"; controls tile fill.
size_var	One of "rewiring_score" or "leading_edge_overlap"; controls point size.
include_rewiring	Logical; whether to draw topology-consistency points.
label	One of "mechanism_class", "rewiring_score", or "none".
reference	An optional reference result used to compute delta_NES. For list input, the first element is used as the default reference.
thresholds	Optional named list with rewire and nes numeric thresholds used to classify mechanism states.
...	Additional parameters passed to plot methods.

Details

consensusmap() creates a pathway by context heatmap. Tile fill represents enrichment strength (NES or delta_NES) and point size represents topology consistency (rewiring_score or leading_edge_overlap). Mechanism class is shown as tile text and point color.

Value

A ggplot object.

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

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 'mnseaResult'  
dotplot(  
  object,  
  x = "share",  
  color = "contribution",  
  showCategory = 10,  
  size = NULL,  
  split = NULL,  
  font.size = 12,  
  title = "",  
  orderBy = "x",  
  label_format = 30,  
  layer = NULL,  
  ...  
)
```

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

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

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

```
dotplot.enrichResult(
```

```

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

dotplot.compareClusterResult(
  object,
  x = "Cluster",
  colorBy = "p.adjust",
  showCategory = 5,
  by = "geneRatio",
  size = "geneRatio",
  split = NULL,
  includeAll = TRUE,
  font.size = 12,
  title = "",
  label_format = 30,
  group = FALSE,
  shape = FALSE,
  facet = NULL,
  strip_width = 15
)

```

Arguments

<code>object</code>	compareClusterResult object
<code>...</code>	additional parameters.
<code>x</code>	variable for x-axis, one of 'GeneRatio' and 'Count'
<code>color</code>	variable used to color enriched terms, e.g. 'pvalue', 'p.adjust' or 'qvalue'
<code>showCategory</code>	number of categories to display or a vector of terms.
<code>size</code>	variable used to scale the sizes of categories, one of "geneRatio", "Percentage" and "count". When x is "GeneRatio", the size defaults to "count" (number of genes); pass size = "GeneRatio" to scale point size by the enrichment gene ratio instead.
<code>split</code>	apply showCategory to each category specified by the 'split', e.g., "ONTOL-OGY", "category" and "intersect". Default is NULL and do nothing
<code>font.size</code>	font size
<code>title</code>	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
layer	optional layer or layers to retain for mnseaResult.
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	<i>dotplot2</i>
----------	-----------------

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	<i>emapplot</i>
----------	-----------------

Description

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

Usage

```
emapplot(  
  x,  
  layout = igraph::layout_with_kk,  
  coords = NULL,  
  showCategory = 30,  
  color = "p.adjust",  
  size_category = 1,  
  min_edge = 0.2,  
  color_edge = "grey",  
  size_edge = 0.5,  
  group = NULL,  
  group_legend = TRUE,  
  node_label = "category",  
  node_label_size = 5,  
  pie = "equal",  
  layer = NULL,  
  label_format = 30,  
  clusterFunction = stats::kmeans,  
  nWords = 4,  
  nCluster = NULL,  
  show_category_size_legend = TRUE,  
  edge_filter = "threshold",  
  top_k = 5,  
  target_density = 0.1,  
  edge_diagnostic = FALSE,  
  ...  
)  
  
## S4 method for signature 'enrichResult'  
emapplot(  
  x,  
  layout = igraph::layout_with_kk,  
  coords = NULL,  
  showCategory = 30,  
  color = "p.adjust",  
  size_category = 1,  
  min_edge = 0.2,  
  color_edge = "grey",  
  size_edge = 0.5,  
  group = NULL,  
  group_legend = TRUE,  
  node_label = "category",  
  node_label_size = 5,  
  pie = "equal",  
  layer = NULL,  
  label_format = 30,  
  clusterFunction = stats::kmeans,
```

```

    nWords = 4,
    nCluster = NULL,
    show_category_size_legend = TRUE,
    edge_filter = "threshold",
    top_k = 5,
    target_density = 0.1,
    edge_diagnostic = FALSE,
    ...
)

## S4 method for signature 'gseaResult'
emapplot(
  x,
  layout = igraph::layout_with_kk,
  coords = NULL,
  showCategory = 30,
  color = "p.adjust",
  size_category = 1,
  min_edge = 0.2,
  color_edge = "grey",
  size_edge = 0.5,
  group = NULL,
  group_legend = TRUE,
  node_label = "category",
  node_label_size = 5,
  pie = "equal",
  layer = NULL,
  label_format = 30,
  clusterFunction = stats::kmeans,
  nWords = 4,
  nCluster = NULL,
  show_category_size_legend = TRUE,
  edge_filter = "threshold",
  top_k = 5,
  target_density = 0.1,
  edge_diagnostic = FALSE,
  ...
)

## S4 method for signature 'compareClusterResult'
emapplot(
  x,
  layout = igraph::layout_with_kk,
  coords = NULL,
  showCategory = 30,
  color = "p.adjust",
  size_category = 1,
  min_edge = 0.2,

```

```

    color_edge = "grey",
    size_edge = 0.5,
    group = NULL,
    group_legend = TRUE,
    node_label = "category",
    node_label_size = 5,
    pie = "equal",
    layer = NULL,
    label_format = 30,
    clusterFunction = stats::kmeans,
    nWords = 4,
    nCluster = NULL,
    show_category_size_legend = TRUE,
    edge_filter = "threshold",
    top_k = 5,
    target_density = 0.1,
    edge_diagnostic = FALSE,
    ...
)

## S4 method for signature 'mnseaResult'
emapplot(
  x,
  layout = igraph::layout_with_kk,
  coords = NULL,
  showCategory = 30,
  color = "p.adjust",
  size_category = 1,
  min_edge = 0.2,
  color_edge = "grey",
  size_edge = 0.5,
  group = NULL,
  group_legend = TRUE,
  node_label = "category",
  node_label_size = 5,
  pie = "equal",
  layer = NULL,
  label_format = 30,
  clusterFunction = stats::kmeans,
  nWords = 4,
  nCluster = NULL,
  show_category_size_legend = TRUE,
  edge_filter = "threshold",
  top_k = 5,
  target_density = 0.1,
  edge_diagnostic = FALSE,
  ...
)

```

```

prepare_emapplot_data(
  x,
  showCategory,
  color,
  min_edge,
  size_edge,
  edge_filter = "threshold",
  top_k = 5,
  target_density = 0.1
)

```

Arguments

x	Enrichment result.
layout	igraph layout
coords	optional user-supplied coordinate data.frame with x, y and row names matching node labels.
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'.
size_category	relative size of the categories
min_edge	The minimum similarity threshold for whether two nodes are connected, should be between 0 and 1, default value is 0.2.
color_edge	color of the network edge
size_edge	relative size of edge width
group	Deprecated. group = TRUE is node_label = "category_grouped"; group = FALSE is node_label = "none". Use node_label instead.
group_legend	logical, if TRUE, draw a legend for the groups.
node_label	Select which labels to display and whether the groups are outlined. One of:

node_label	group outline	group labels	category labels
"none"	no	no	no
"category"	no	no	yes
"category_grouped"	yes	no	yes
"group"	yes	yes	no
"all"	yes	yes	yes

node_label_size	size of node label, default is 5.
pie	one of 'equal' or 'Count' to set the slice ratio of the pies
layer	optional layer or layers to retain for mnseaResult plots.
label_format	a numeric value sets wrap length, alternatively a custom function to format axis labels.

clusterFunction	clustering method function, such as <code>stats::kmeans</code> (default), <code>cluster::clara</code> , <code>cluster::fanny</code> , or <code>cluster::pam</code> .
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.
show_category_size_legend	Logical, whether to draw the category-size annotation legend for compareCluster pie charts.
edge_filter	Edge filtering strategy. <code>min_edge</code> applies to all three; <code>top_k</code> only applies to "top_k" and <code>target_density</code> only to "adaptive". Supplying a non-default value for the inactive one warns rather than being ignored silently.
top_k	Number of strongest neighbors per term. Only used when <code>edge_filter = "top_k"</code> .
target_density	Target proportion of unique term pairs. Only used when <code>edge_filter = "adaptive"</code> .
edge_diagnostic	Logical; if TRUE, attach a one-row <code>enrichplot_edge_diagnostic</code> data frame to the returned plot. The diagnostic reports retained pairs, rendered edge rows and graph density.
...	Additional parameters

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 or 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,
  dense_threshold = 0.2
)

```

Arguments

<code>pair_sim</code>	A square numeric similarity matrix.
<code>min_edge</code>	minimum similarity threshold for "threshold" mode.
<code>edge_filter</code>	edge filtering strategy.
<code>top_k</code>	number of neighbors per term for "top_k" mode.
<code>target_density</code>	target proportion of unique pairs for "adaptive".
<code>dense_threshold</code>	density above which a higher threshold is suggested.

Value

A one-row data.frame with retained pair/edge counts, density, filter settings, and a suggestion when the graph is dense.

`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,
  ...
)
```

```

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

## S3 method for class 'mnseaResult'
fortify(
  model,
  data,
  showCategory = 5,
  by = c("p.adjust", "NES", "contribution", "share"),
  order = FALSE,
  drop = FALSE,
  split = NULL,
  level = c("result", "pathway"),
  layer = 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
level	One of "result" or "pathway" for mnseaResult.
layer	Optional layer or layers to retain for pathway-level output.

Value

data.frame
data.frame

Author(s)

Guangchuang Yu

fortify_mnsea_contribution*Plot-facing helpers for mnseaResult*

Description

These helpers convert explanation-ready outputs from enrichit into stable data structures that are easier to consume in enrichplot.

Usage

```
fortify_mnsea_contribution(  
  x,  
  level = c("pathway", "feature"),  
  pathway_id = NULL,  
  layer = NULL,  
  ...  
)  
  
fortify_mnsea_subnetwork(  
  x,  
  pathway_id = NULL,  
  layer = NULL,  
  include_couplings = TRUE,  
  include_isolated = FALSE,  
  ...  
)
```

Arguments

x	A mnseaResult object.
level	One of "pathway" or "feature".
pathway_id	Optional pathway ID.
layer	Optional layer or layers to retain.
...	Additional parameters reserved for future extensions.
include_couplings	Logical, whether to keep inter-layer coupling edges.
include_isolated	Logical, whether to keep nodes without retained edges.

Value

fortify_mnsea_contribution() returns a data.frame. fortify_mnsea_subnetwork() returns a list containing standardized nodes and edges tables together with the selected pathway metadata.

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

get_enrichplot_color	<i>Color utility functions for enrichplot package</i>
----------------------	---

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

<i>ggtable</i>	<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

<i>goplot</i>	<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

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)
```

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

Description

plot logFC distribution of selected gene sets

Usage

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

Arguments

x	GSEA result
IDs	gene set IDs
type	one of 'density' or 'boxplot'

Value

distribution plot

Author(s)

Guangchuang Yu

`gseaplot`*gseaplot*

Description

Visualize 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",  
  ...  
)
```

```
## S4 method for signature 'mnseaResult'
```

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

```
gseaplot.gseaResult(  
  x,
```

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

Arguments

<code>x</code>	<code>gseaResult</code> object
<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 indicating the maximum/minimal running enrichment score
<code>layer</code>	Optional mnsea layer. When NULL, use collapsed scores.

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("NES", "p.adjust"),
  pvalue_table_rownames = "Description",
  ES_geom = "line",
  layer = NULL
)
```

Arguments

<code>x</code>	<code>gseaResult</code> object
<code>geneSetID</code>	gene set ID
<code>title</code>	plot title
<code>color</code>	color of running enrichment score line
<code>base_size</code>	base font size
<code>rel_heights</code>	relative heights of subplots
<code>subplots</code>	which subplots to be displayed
<code>pvalue_table</code>	whether add pvalue table
<code>pvalue_table_columns</code>	selected columns to be plotted in the <code>pvalue_table</code> . Defaults to <code>c("NES", "p.adjust")</code> , but can be set to any columns of the enrichment result (e.g. <code>"pvalue"</code> , <code>"qvalue"</code>).
<code>pvalue_table_rownames</code>	selected column as the rownames of the <code>pvalue_table</code> . If set to <code>NULL</code> , no rownames will be displayed.
<code>ES_geom</code>	geom for plotting running enrichment score, one of <code>'line'</code> or <code>'dot'</code>
<code>layer</code>	Optional <code>mnsea</code> layer. When <code>NULL</code> , use collapsed scores.

Value

plot

Author(s)

Guangchuang Yu

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

Description

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

Usage

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

Arguments

- | | |
|-----------|--|
| x | gseaResult object |
| geneSetID | gene set ID |
| title | plot title |
| output | one of 'plot' or 'table' (for exporting data) |
| layer | Optional mnsea layer. When NULL, use collapsed scores. |

Value

ggplot object

Author(s)

Guangchuang Yu

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

Description

extract gsea result of selected geneSet

Usage

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

Arguments

- | | |
|-----------|---|
| object | gseaResult object |
| geneSetID | gene set ID |
| ... | additional arguments passed to methods (e.g. layer for mnseaResult) |

Value

data.frame

Author(s)

Guangchuang Yu

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

Description

Heatmap-like plot for functional classification

Usage

```
heatplot(  
  x,  
  showCategory = 30,  
  showTop = NULL,  
  symbol = "rect",  
  foldChange = NULL,  
  pvalue = NULL,  
  label_format = 30,  
  pathway_id = NULL,  
  layer = NULL,  
  value = c("score", "abs_score", "share", "contribution"),  
  ...  
)  
  
## S4 method for signature 'enrichResult'  
heatplot(  
  x,  
  showCategory = 30,  
  showTop = NULL,  
  symbol = "rect",  
  foldChange = NULL,  
  pvalue = NULL,  
  label_format = 30,  
  pathway_id = NULL,  
  layer = NULL,  
  value = c("score", "abs_score", "share", "contribution"),  
  ...  
)  
  
## S4 method for signature 'gseaResult'  
heatplot(  
  x,  
  showCategory = 30,  
  showTop = NULL,  
  symbol = "rect",  
  foldChange = NULL,  
  pvalue = NULL,  
  label_format = 30,  
  pathway_id = NULL,  
  layer = NULL,  
  value = c("score", "abs_score", "share", "contribution"),  
  ...  
)
```

```

    x,
    showCategory = 30,
    showTop = NULL,
    symbol = "rect",
    foldChange = NULL,
    pvalue = NULL,
    label_format = 30,
    pathway_id = NULL,
    layer = NULL,
    value = c("score", "abs_score", "share", "contribution"),
    ...
)

## S4 method for signature 'mnseaResult'
heatplot(
  x,
  showCategory = 30,
  showTop = NULL,
  symbol = "rect",
  foldChange = NULL,
  pvalue = NULL,
  label_format = 30,
  pathway_id = NULL,
  layer = NULL,
  value = c("score", "abs_score", "share", "contribution"),
  ...
)

prepare_heatplot_data(x, showCategory, showTop, foldChange, pvalue)

```

Arguments

x	enrichment result.
showCategory	number of enriched terms to display
showTop	number of top genes ranked by <code>abs(foldChange) * frequency</code> to be shown in the heatmap, default <code>NULL</code> 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
pathway_id	optional pathway ID for pathway-specific <code>mnseaResult</code> heatmaps.
layer	optional layer or layers to retain for <code>mnseaResult</code> plots.
value	fill value for <code>mnseaResult</code> ; use "share" or "contribution" for term-layer heatmaps and "score" or "abs_score" for pathway-specific feature heatmaps.
...	Additional parameters

Value

ggplot object

Author(s)

Guangchuang Yu

Examples

```
## Not run:
library(DOSE)
data(geneList)
de <- names(geneList)[1:100]
x <- enrichDO(de)
heatplot(x)

## End(Not run)
```

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

Description

Horizontal plot for GSEA result

Usage

```
hplot(x, geneSetID, layer = NULL)
```

Arguments

- x gseaResult object
- geneSetID gene set ID
- layer Optional mnsea layer. When NULL, use collapsed scores.

Value

horizontal plot

Author(s)

Guangchuang Yu

import_enrichr	<i>import_enrichr</i>
----------------	-----------------------

Description

Import enrichr results

Usage

```
import_enrichr(  
  x,  
  db = 1,  
  gene = NULL,  
  universe = NULL,  
  ontology = "UNKNOWN",  
  organism = "UNKNOWN",  
  keytype = "UNKNOWN",  
  pAdjustMethod = "BH",  
  ...  
)
```

Arguments

x	result table (data.frame) or the list of tables returned by <code>enrichR::enrichr()</code>
db	if x is a list, the name or index of the database table to import
gene	query gene vector used in the analysis
universe	background gene vector used in the analysis
ontology, organism, keytype	metadata stored in the object slots
pAdjustMethod	method used to compute p.adjust when the table has no adjusted p-value column
...	additional parameters passed to as_enrichResult

Details

Converts the output of `enrichR::enrichr()` (a list of result tables, one per database, or a single result table) into an `enrichResult` object compatible with 'enrichplot' visualizations. The gene vector used in the analysis should be supplied for exact GeneRatio values; universe enables BgRatio/RichFactor calculation.

Value

An `enrichResult` object

import_fgsea	<i>import_fgsea</i>
--------------	---------------------

Description

Import fgsea results

Usage

```
import_fgsea(
  x,
  stats,
  geneSets = NULL,
  setType = "UNKNOWN",
  organism = "UNKNOWN",
  keytype = "UNKNOWN",
  exponent = 1,
  scoreType = "std",
  pAdjustMethod = "BH",
  ...
)
```

Arguments

x	result table returned by <code>fgsea::fgsea()</code>
stats	named numeric vector of ranked statistics, sorted in descending order (sorted automatically with a warning if not)
geneSets	the pathways list used as <code>fgsea()</code> input
setType, organism, keytype	metadata stored in the object slots
exponent, scoreType	parameters used to recompute missing rank/leading_edge/core_enrichment columns
pAdjustMethod	method used to compute <code>p.adjust</code> when the table has no adjusted p-value column
...	additional parameters passed to as_gseaResult

Details

Converts the result table returned by `fgsea::fgsea()` into a `gseaResult` object. The ranked statistics vector (`stats`) used as `fgsea()` input is required, as most GSEA visualizations consume the ranked list. Passing the pathways list used in the analysis enables exact running-score plots; without it, gene sets are rebuilt from the leading edge and plots are approximate.

Value

A `gseaResult` object

import_gprofiler2	<i>import_gprofiler2</i>
-------------------	--------------------------

Description

Import g:Profiler (gprofiler2) results

Usage

```
import_gprofiler2(  
  x,  
  gene = NULL,  
  ontology = "UNKNOWN",  
  organism = "UNKNOWN",  
  keytype = "UNKNOWN",  
  pAdjustMethod = "BH",  
  ...  
)
```

Arguments

x	the object returned by <code>gprofiler2::gost()</code> , or its <code>result</code> component
gene	query gene vector; used only when the table has no <code>query_size</code> column
ontology, organism, keytype	metadata stored in the object slots
pAdjustMethod	method used to compute <code>p.adjust</code> when the table has no adjusted p-value column
...	additional parameters passed to as_enrichResult

Details

Converts the result of `gprofiler2::gost()` (the list it returns, or its `result` data.frame) into an `enrichResult` object. Only the over-representation mode is mapped in this version.

Value

An `enrichResult` object

import_webgestalt	<i>import_webgestalt</i>
-------------------	--------------------------

Description

Import WebGestaltR results

Usage

```
import_webgestalt(  
  x,  
  gene = NULL,  
  universe = NULL,  
  ontology = "UNKNOWN",  
  organism = "UNKNOWN",  
  keytype = "UNKNOWN",  
  pAdjustMethod = "BH",  
  ...  
)
```

Arguments

x	result table (data.frame) returned by WebGestaltR()
gene	query gene vector used in the analysis
universe	background gene vector used in the analysis
ontology, organism, keytype	metadata stored in the object slots
pAdjustMethod	method used to compute p.adjust when the table has no adjusted p-value column
...	additional parameters passed to as_enrichResult

Details

Converts the result table returned by WebGestaltR() into an enrichResult object. The gene vector used in the analysis should be supplied for exact GeneRatio values.

Value

An enrichResult object

manhattanplot	<i>manhattanplot</i>
---------------	----------------------

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

mechanismflow

mechanismflow

Description

Pathway state transition flow

Usage

```
mechanismflow(
  x,
  reference = NULL,
  flow_var = c("NES", "delta_NES", "leading_edge_size"),
  thresholds = list(rewire = 0.5, nes = 0.2),
  ...
)

## S4 method for signature 'mnseaResult'
mechanismflow(
  x,
  reference = NULL,
  flow_var = c("NES", "delta_NES", "leading_edge_size"),
  thresholds = list(rewire = 0.5, nes = 0.2),
  ...
)

## S4 method for signature 'nseaResult'
```

```
mechanismflow(  
  x,  
  reference = NULL,  
  flow_var = c("NES", "delta_NES", "leading_edge_size"),  
  thresholds = list(rewire = 0.5, nes = 0.2),  
  ...  
)  
  
## S4 method for signature 'list'  
mechanismflow(  
  x,  
  reference = NULL,  
  flow_var = c("NES", "delta_NES", "leading_edge_size"),  
  thresholds = list(rewire = 0.5, nes = 0.2),  
  ...  
)
```

Arguments

x	A mnseaResult, nseaResult, or a named list of results.
reference	An optional reference result used to compute delta_NES. For list input, the first element is used as the default reference.
flow_var	One of "NES", "delta_NES", or "leading_edge_size"; controls flow magnitude (line width and point size).
thresholds	Optional named list with rewire and nes numeric thresholds used to classify mechanism states.
...	Additional parameters passed to plot methods.

Details

mechanismflow() draws pathway state transitions across contexts (conditions or layers). Line width and point size encode flow magnitude, while point shape encodes the mechanism state.

Value

A ggplot object.

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

Description

Get the similarity matrix

Usage

```
pairwise_termsim(  
  x,  
  method = "JC",  
  semData = NULL,  
  showCategory = NULL,  
  layer = NULL  
)  
  
## S4 method for signature 'enrichResult'  
pairwise_termsim(  
  x,  
  method = "JC",  
  semData = NULL,  
  showCategory = NULL,  
  layer = NULL  
)  
  
## S4 method for signature 'gseaResult'  
pairwise_termsim(  
  x,  
  method = "JC",  
  semData = NULL,  
  showCategory = NULL,  
  layer = NULL  
)  
  
## S4 method for signature 'mnseaResult'  
pairwise_termsim(  
  x,  
  method = "JC",  
  semData = NULL,  
  showCategory = NULL,  
  layer = NULL  
)  
  
## S4 method for signature 'compareClusterResult'  
pairwise_termsim(  
  x,  
  method = "JC",  
  semData = NULL,  
  showCategory = NULL,  
  layer = NULL  
)  
  
prepare_pairwise_termsim_data(x, showCategory)  
  
pairwise_termsim.enrichResult(  
  x,  
  method = "JC",  
  semData = NULL,  
  showCategory = NULL,  
  layer = NULL  
)
```

```

    x,
    method = "JC",
    semData = NULL,
    showCategory = NULL
  )

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

```

Arguments

<code>x</code>	enrichment result.
<code>method</code>	method of calculating the similarity between nodes, one of "Resnik", "Lin", "Rel", "Jiang", "Wang", and "JC" (Jaccard similarity coefficient) methods.
<code>semData</code>	GOSemSimDATA object, can be obtained through <code>GOSemSim::godata</code> .
<code>showCategory</code>	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.
<code>layer</code>	optional layer or layers to retain when computing feature overlap for <code>mnseaResult</code> ; when NULL, features from all layers are used.

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)

```

phaseplot

phaseplot

Description

Phase plot for enrichment-shift versus rewiring

Usage

```

phaseplot(
  x,
  reference = NULL,
  selected_layer = NULL,
  reference_layer = NULL,
  x_axis = NULL,
  size_var = c("leading_edge_size", "leading_edge_overlap"),
  showCategory = 30,
  thresholds = list(rewire = 0.5, nes = 0.2),
  ...
)

## S4 method for signature 'nseaResult'
phaseplot(
  x,
  reference = NULL,
  selected_layer = NULL,
  reference_layer = NULL,
  x_axis = NULL,
  size_var = c("leading_edge_size", "leading_edge_overlap"),
  showCategory = 30,
  thresholds = list(rewire = 0.5, nes = 0.2),
  ...
)

## S4 method for signature 'mnseaResult'
phaseplot(
  x,
  reference = NULL,

```

```

    selected_layer = NULL,
    reference_layer = NULL,
    x_axis = NULL,
    size_var = c("leading_edge_size", "leading_edge_overlap"),
    showCategory = 30,
    thresholds = list(rewire = 0.5, nes = 0.2),
    ...
  )

```

Arguments

<code>x</code>	A <code>nseaResult</code> or <code>mnseaResult</code> object.
<code>reference</code>	An optional reference result (another <code>nseaResult</code> , <code>mnseaResult</code> , or a <code>results</code> <code>data.frame</code>). When supplied, <code>phaseplot()</code> computes <code>delta_NES = NES - reference_NES</code> and uses it as the default x-axis.
<code>selected_layer</code>	Optional layer name for <code>mnseaResult</code> .
<code>reference_layer</code>	Optional reference layer name for <code>mnseaResult</code> .
<code>x_axis</code>	One of "delta_NES" or "NES". By default, delta_NES is used when reference is supplied, otherwise NES.
<code>size_var</code>	One of "leading_edge_size" or "leading_edge_overlap".
<code>showCategory</code>	Number (or vector) of pathways to display.
<code>thresholds</code>	Optional named list with <code>rewire</code> and <code>nes</code> numeric thresholds used to classify mechanism states.
<code>...</code>	Additional parameters passed to plot methods.

Details

`phaseplot()` places each pathway on a two-dimensional plane: enrichment strength (or shift) on the x-axis and rewiring score on the y-axis. Point size and color encode leading-edge information and mechanism class.

Value

A `ggplot` object.

`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,
  width = NULL
)
```

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
width	width of the plot

Value

ggplot object

Author(s)

Guangchuang Yu <https://yulab-smu.top>

pmcplot

pmcplot

Description

PubMed Central Trend plot

Usage

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

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.
data	Optional data.frame with query, year, query_hits, and all_hits columns. When supplied, no Europe PMC request is made.

Value

ggplot object

Author(s)

Guangchuang Yu

prepare_cnetplot_data *Category-Gene-Network Plot*

Description

Category-gene-network plot

Usage

```
prepare_cnetplot_data(x, showCategory, foldChange)
```

```
## 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,
  highlight = "none",
  highlight_alpha = 0.3,
  ...
)
```

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

prepare_mnsea_cnetplot_data(
  x,
  pathway_id,
  layer,
  include_couplings,
  include_isolated = FALSE
)

## S3 method for class 'mnseaResult'
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,
  highlight = "none",
  highlight_alpha = 0.3,
```

```

    pathway_id = NULL,
    layer = NULL,
    include_couplings = TRUE,
    ...
)

## 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,
  highlight = "none",
  highlight_alpha = 0.3,
  ...
)

```

Arguments

x	input object
showCategory	number of categories to display or a vector of terms.
foldChange	numeric values to color the item (e.g., fold change of gene expression values)
layout	network layout
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 the node label text. When NULL (default) the built-in label size is used.
fc_threshold	threshold for filtering genes by absolute fold change (e.g., <code>fc_threshold = 1</code> keeps only genes with <code>lfc > 1</code>).
highlight	selected categories to be highlighted
highlight_alpha	transparency value for non-highlighted items
...	additional parameters. Legacy <code>categorySize</code> , <code>circular</code> , <code>colorEdge</code> , <code>pie</code> , <code>split</code> , and <code>includeAll</code> arguments are also accepted.
pathway_id	optional pathway ID for <code>mnseaResult</code> subnetworks.
layer	optional layer or layers to retain for <code>mnseaResult</code> plots.
include_couplings	logical, whether inter-layer coupling edges should be kept in <code>mnseaResult</code> network plots.
include_isolated	logical, whether isolated feature nodes should be kept in <code>mnseaResult</code> subnetworks.

Details

For `mnseaResult`, `cnetplot()` visualizes a pathway-specific multilayer subnetwork returned by `fortify_mnsea_subnetwork()`. Feature nodes are grouped by layer, a synthetic pathway node is added as the anchor, and optional coupling edges connect features across layers.

See Also

[cnetplot](#)

rewireplot

rewireplot

Description

Pathway-specific rewiring plot

Usage

```
rewireplot(x, ...)

## S4 method for signature 'nseaResult'
rewireplot(x, ...)

## S4 method for signature 'mnseaResult'
rewireplot(x, ...)
```

Arguments

`x` A `mnseaResult` object.
`...` Additional parameters passed to plot methods.

Value

A `ggplot` object.

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

Description

Ridgeline plot for GSEA result

Usage

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

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

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

```

    layer = NULL,
    ...
)

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

Arguments

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

Value

ggplot object

Author(s)

Guangchuang Yu

Examples

```

library(DOSE)
data(geneList)
x <- gseD0(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, ...)  
  
## S4 method for signature 'enrichResult'  
ssplot(  
  x,  
  showCategory = 30,  
  ...,  
  min_edge = 0.2,  
  size_edge = 0.5,  
  edge_filter = "threshold",  
  top_k = 5,  
  target_density = 0.1,  
  edge_diagnostic = FALSE  
)  
  
## S4 method for signature 'gseaResult'  
ssplot(  
  x,  
  showCategory = 30,  
  ...,  
  min_edge = 0.2,  
  size_edge = 0.5,  
  edge_filter = "threshold",  
  top_k = 5,  
  target_density = 0.1,  
  edge_diagnostic = FALSE  
)  
  
## S4 method for signature 'mnseaResult'  
ssplot(  
  x,  
  showCategory = 30,  
  ...,  
  min_edge = 0.2,  
  size_edge = 0.5,  
  edge_filter = "threshold",  
  top_k = 5,  
  target_density = 0.1,
```

```
    edge_diagnostic = FALSE
)

## S4 method for signature 'compareClusterResult'
ssplot(
  x,
  showCategory = 30,
  ...,
  min_edge = 0.2,
  size_edge = 0.5,
  edge_filter = "threshold",
  top_k = 5,
  target_density = 0.1,
  edge_diagnostic = FALSE
)

ssplot.enrichResult(
  x,
  showCategory = 30,
  drfun = NULL,
  dr.params = list(),
  node_label = "group",
  min_edge = 0.2,
  size_edge = 0.5,
  edge_filter = "threshold",
  top_k = 5,
  target_density = 0.1,
  edge_diagnostic = FALSE,
  ...
)

ssplot.compareClusterResult(
  x,
  showCategory = 30,
  pie = "equal",
  drfun = NULL,
  dr.params = list(),
  node_label = "group",
  min_edge = 0.2,
  size_edge = 0.5,
  edge_filter = "threshold",
  top_k = 5,
  target_density = 0.1,
  edge_diagnostic = FALSE,
  ...
)
```

Arguments

x

Enrichment result.

...

additional parameters

Additional plotting parameters are inherited from `emapplot()`.

showCategory

number of categories to display or a vector of terms.

min_edge

The minimum similarity threshold for connecting two nodes; should be between 0 and 1. Passed to `emapplot()`.

size_edge

Relative size of the edge width. Passed to `emapplot()`.

edge_filter

Edge filtering strategy: "threshold" (default), "top_k", or "adaptive". Edge filtering affects display only and does not change the dimension-reduction input.

top_k

Number of strongest neighbors retained per term when `edge_filter = "top_k"`.

target_density

Target proportion of unique term pairs when `edge_filter = "adaptive"`.

edge_diagnostic

Logical; if TRUE, attach a one-row edge-density diagnostic data frame to the returned plot.

drfun

Function used for dimension reduction. The default, `stats::cmdscale`, performs classical multidimensional scaling (MDS); this is one available reduction method. Supply another function here when needed.

dr.params

A named list of arguments passed separately to `drfun` via `tidydr::dr`.

node_label

Select which labels to display and whether the groups are outlined. One of:

node_label	group outline	group labels	category labels
"none"	no	no	no
"category"	no	no	yes
"category_grouped"	yes	no	yes
"group"	yes	yes	no
"all"	yes	yes	yes

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)
# Edge controls are forwarded to emapplot; increase min_edge for a
# less dense display when showing many terms.
ssplot(ego2, showCategory = 50, min_edge = 0.4, size_edge = 0.5)

## 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"),
  split = NULL,
  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)
split	optional result column used to keep split metadata available for faceting
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
highlight	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
Upsetplot

Usage

```

upsetplot(
  x,
  n = 10,
  type = "boxplot",
  layer = NULL,
  value = c("score", "abs_score"),
  core_enrichment = FALSE,
  ...
)

## S4 method for signature 'enrichResult'
upsetplot(
  x,
  n = 10,
  type = "boxplot",
  layer = NULL,
  value = c("score", "abs_score"),
  core_enrichment = FALSE,
  ...
)

## S4 method for signature 'gseaResult'
upsetplot(
  x,
  n = 10,
  type = "boxplot",
  layer = NULL,
  value = c("score", "abs_score"),
  core_enrichment = FALSE,
  ...
)

```

```
## S4 method for signature 'mnseaResult'
upsetplot(
  x,
  n = 10,
  type = "boxplot",
  layer = NULL,
  value = c("score", "abs_score"),
  core_enrichment = FALSE,
  ...
)
```

Arguments

x	object
n	number of categories to be plotted
type	one of 'boxplot' or 'violin' for gseaResult / mnseaResult
layer	Optional mnsea layer. When NULL, use collapsed scores.
value	score summary to display for overlapping features.
core_enrichment	logical. Should only core mnsea features be used?
...	additional parameters

Value

plot

Author(s)

Guangchuang Yu

Examples

```
## Not run:
library(DOSE)
data(geneList)
de <- names(geneList)[1:100]
x <- enrichDO(de)
upsetplot(x, 8)

## End(Not run)
```

volplot	<i>volplot</i>
---------	----------------

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

```
## Not run:
library(DOSE)
data(geneList)
de <- names(geneList)[1:100]
x <- enrichDO(de)
volplot(x)

## End(Not run)
```

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