

Package ‘enrichplot’

October 17, 2020

Title Visualization of Functional Enrichment Result

Version 1.8.1

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 (>= 3.4.0)

Imports AnnotationDbi, cowplot, DOSE (>= 3.13.1), europepmc, ggplot2, ggplotify, ggraph, ggridges, GOSemSim, graphics, grDevices, grid, gridExtra, igraph, methods, plyr, purrr, RColorBrewer, reshape2, stats, utils, scatterpie

Suggests clusterProfiler, dplyr, ggupset, knitr, org.Hs.eg.db, prettydoc, tibble, tidyr

VignetteBuilder knitr

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URL <https://github.com/GuangchuangYu/enrichplot>

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

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

Encoding UTF-8

LazyData true

RoxygenNote 7.1.0

git_url <https://git.bioconductor.org/packages/enrichplot>

git_branch RELEASE_3_11

git_last_commit e55d9f1

git_last_commit_date 2020-04-29

Date/Publication 2020-10-16

Author Guangchuang Yu [aut, cre] (<<https://orcid.org/0000-0002-6485-8781>>), Erqiang Hu [ctb]

Maintainer Guangchuang Yu <guangchuangyu@gmail.com>

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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 = "",
  ...
)
```

Arguments

height	enrichResult object
x	one of 'Count' and 'GeneRatio'
color	one of 'pvalue', 'p.adjust', 'qvalue'
showCategory	number of categories to show

font.size	font size
title	plot title
...	other parameter, ignored

Value

ggplot object

Examples

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

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",
  ...
)
```

Arguments

x	enrichment result
showCategory	number of enriched terms to display
foldChange	fold Change
layout	layout of the network
...	additional parameters
colorEdge	whether coloring edge by enriched terms
circular	whether using circular layout
node_label	select which labels to be displayed. 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

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

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

Arguments

object	input object
...	additional parameters
x	variable for x-axis, one of 'GeneRatio' or 'Count'
color	variable that used to color enriched terms, e.g. pvalue, p.adjust or qvalue

<code>showCategory</code>	number of enriched terms to display
<code>size</code>	variable that used to scale the sizes of categories
<code>split</code>	separate result by 'category' variable
<code>font.size</code>	font size
<code>title</code>	plot title

Value

plot

Author(s)

guangchuang yu

Examples

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

`dotplot,compareClusterResult-method`
dotplot

Description

dot plot method

Usage

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

Arguments

object	compareClusterResult object
x	x variable
color	one of pvalue or p.adjust
showCategory	category numbers
split	ONTOLOGY or NULL
font.size	font size
title	figure title
by	one of geneRatio, Percentage or count
includeAll	logical

emapplot

*emapplot***Description**

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

Usage

```
emapplot(x, showCategory = 30, color = "p.adjust", layout = "kk", ...)

## S4 method for signature 'enrichResult'
emapplot(x, showCategory = 30, color = "p.adjust", layout = "nicely", ...)

## S4 method for signature 'gseaResult'
emapplot(x, showCategory = 30, color = "p.adjust", layout = "nicely", ...)

## S4 method for signature 'compareClusterResult'
emapplot(x, showCategory = 5, color = "p.adjust", layout = "nicely", ...)

emapplot.enrichResult(
  x,
  showCategory = 30,
  color = "p.adjust",
  layout = "nicely",
  pie_scale = 1,
  line_scale = 1,
  ...
)
```

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
...	additional parameters
pie_scale	scale of pie plot
line_scale	scale of line width

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.

Value

ggplot object

Author(s)

Guangchuang Yu

Examples

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

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

<code>x</code>	enrichment result.
<code>showCategory</code>	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

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**

<code>x</code>	gseaResult object
<code>geneSetID</code>	gene set ID
<code>title</code>	plot title

Value

ggplot object

Author(s)

Guangchuang Yu

`gsInfo`*gsInfo*

Description

extract gsea result of selected geneSet

Usage`gsInfo(object, geneSetID)`**Arguments**

<code>object</code>	gseaResult object
<code>geneSetID</code>	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)
```

Arguments

x	enrichment result.
showCategory	number of enriched terms to display
foldChange	fold Change

Value

ggplot object

Author(s)

guangchuang yu
Guangchuang Yu

Examples

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

list2graph *convert gene IDs to igraph object*

Description

convert a list of gene IDs to igraph object.

Usage

```
list2graph(inputList)
```

Arguments

inputList a list of gene IDs

Value

a igraph object.

Author(s)

Guangchuang Yu

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

<code>clProf.reshape.df</code>	data frame of compareCluster result
<code>x</code>	x variable
<code>type</code>	one of dot and bar
<code>colorBy</code>	one of pvalue or p.adjust
<code>by</code>	one of percentage and count
<code>title</code>	graph title
<code>font.size</code>	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

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

Value

ggplot object

Author(s)

guangchuang yu

ridgeplot	<i>ridgeplot</i>
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Description

ridgeline plot for GSEA result

Usage

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

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

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

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

Value

ggplot object

Author(s)

Guangchuang Yu

Examples

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

`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

<code>x</code>	object
<code>...</code>	additional parameters
<code>n</code>	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)
```

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