Package ‘enrichplot’

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Title Visualization of Functional Enrichment Result

Version 1.4.0

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 (>= 3.5.1), europepmc, ggplot2, ggplotify, ggraph, ggridges, GOSemSim, graphics, grDevices, grid, gridExtra, igraph, methods, purrr, RColorBrewer, reshape2, stats, UpSetR, utils

Suggests clusterProfiler, dplyr, knitr, org.Hs.eg.db, prettydoc

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

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

Maintainer Guangchuang Yu <`guangchuangyu@gmail.com`>

R topics documented:

`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", ...)

cnetplot.enrichResult(x, showCategory = 5, foldChange = NULL,
  layout = "kk", colorEdge = FALSE, circular = FALSE,
  node_label = TRUE, ...)
```

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`	whether display node label

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

Value

plot

Author(s)

guangchuang yu

Examples

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

`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 = "kk", ...)

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

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

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

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.enrichResult` *fortify*

Description

convert enrichResult object for ggplot2

Usage

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

Arguments

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

Value

data.frame

`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

`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)
```

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

`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)

## 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, ...)
```

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)
```

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