Package 'enrichplot'

October 16, 2019

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

License Artistic-2.0

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 6.1.1

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

git_branch RELEASE_3_9

git_last_commit 6ffe5d9

git_last_commit_date 2019-05-02

Date/Publication 2019-10-15

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)
```

Index