

Package ‘enrichplot’

March 30, 2021

Title Visualization of Functional Enrichment Result

Version 1.10.2

Description The 'enrichplot' package implements several visualization methods for interpreting functional enrichment results obtained from ORA or GSEA analysis.

All the visualization methods are developed based on 'ggplot2' graphics.

Depends R (>= 3.5.0)

Imports cowplot, DOSE, ggplot2, ggraph, graphics, grid, igraph, methods, plyr, purrr, RColorBrewer, reshape2, stats, utils, scatterpie, shadowtext, GOSemSim, magrittr

Suggests clusterProfiler, dplyr, europepmc, ggupset, knitr, org.Hs.eg.db, prettydoc, tibble, tidyr, ggforce, AnnotationDbi, ggplotify, ggridges, grDevices, gridExtra, ggnewscale, ggrepel

VignetteBuilder knitr

License Artistic-2.0

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

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

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

Encoding UTF-8

LazyData true

RoxygenNote 7.1.1

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

git_branch RELEASE_3_12

git_last_commit 77ee04f

git_last_commit_date 2021-01-28

Date/Publication 2021-03-29

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

Maintainer Guangchuang Yu <guangchuangyu@gmail.com>

R topics documented:

barplot.enrichResult	2
cnetplot	3
color_palette	5
dotplot	5
dotplot.compareClusterResult-method	7
emapplot	7
emapplot_cluster	9
fortify.compareClusterResult	12
get_igraph	14
get_w	14
ggtable	15
goplot	15
gseadist	16
gseaplot	17
gseaplot2	18
gsearank	19
gsInfo	20
has_pairsim	20
heatplot	21
list2graph	22
pairwise_termsim	22
plotting.clusterProfile	23
pmcplot	24
ridgeplot	25
upsetplot	26
wordcloud_i	27
Index	28

barplot.enrichResult *barplot*

Description

barplot of enrichResult

Usage

```
## S3 method for class 'enrichResult'
barplot(
  height,
  x = "Count",
  color = "p.adjust",
  showCategory = 8,
  font.size = 12,
  title = "",
  label_format = 30,
  ...
)
```

Arguments

height	enrichResult object
x	one of 'Count' and 'GeneRatio'
color	one of 'pvalue', 'p.adjust', 'qvalue'
showCategory	number of categories to show
font.size	font size
title	plot title
label_format	a numeric value sets wrap length, alternatively a custom function to format axis labels. by default wraps names longer than 30 characters
...	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",
cex_category = 1,
cex_gene = 1,
node_label_size = NULL,
cex_label_category = 1,
cex_label_gene = 1,
...
)

```

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".
cex_category	number indicating the amount by which plotting category nodes should be scaled relative to the default.
cex_gene	number indicating the amount by which plotting gene nodes should be scaled relative to the default.
node_label_size	size of node label, this parameter has been changed to cex_label_category and cex_label_gene
cex_label_category	scale of category node label size
cex_label_gene	scale of gene node label size

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	<i>color_palette</i>
---------------	----------------------

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

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 = "",  
  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 = "",
  label_format = 30,
  ...
)

```

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
label_format	a numeric value sets wrap length, alternatively a custom function to format axis labels. by default wraps names longer than 30 characters

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 = 30, color = "p.adjust", layout = "nicely", ...)

emapplot.enrichResult(
  x,
  showCategory = 30,
  color = "p.adjust",
  layout = "nicely",
  node_scale = NULL,
  line_scale = NULL,
  min_edge = 0.2,
  node_label_size = NULL,
  cex_label_category = 1,
  cex_category = NULL,
  cex_line = NULL
)

emapplot.compareClusterResult(
  x,
  showCategory = 30,
  color = "p.adjust",
  layout = "nicely",
  split = NULL,
  pie = "equal",
  legend_n = 5,
  cex_category = NULL,
  pie_scale = NULL,
  cex_line = 1,
  min_edge = 0.2,
  cex_label_category = 1,
  node_label_size = NULL
)
```

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
node_scale	scale of node, this parameter has been changed to cex_category
line_scale	scale of line width, this parameter has been changed to cex_line

min_edge	minimum percentage of overlap genes to display the edge, should between 0 and 1, default value is 0.2
node_label_size	size of node label, this parameter has been changed to cex_label_category
cex_label_category	scale of category node label size
cex_category	number indicating the amount by which plotting category nodes should be scaled relative to the default.
cex_line	scale of line width
split	separate result by 'category' variable
pie	proportion of clusters in the pie chart, one of 'equal' (default) or 'Count'
legend_n	number of circle in legend
pie_scale	scale of pie chart or point, this parameter has been changed to "node_scale"

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)
x2 <- pairwise_termsim(x)
emapplot(x2)
```

emapplot_cluster *emapplot_cluster*

Description

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

Usage

```
emapplot_cluster(  
  x,  
  showCategory = nrow(x),  
  color = "p.adjust",  
  label_format = 30,  
  ...  
)  
  
## S4 method for signature 'enrichResult'  
emapplot_cluster(  
  x,  
  showCategory = 30,  
  color = "p.adjust",  
  label_format = 30,  
  ...  
)  
  
## S4 method for signature 'gseaResult'  
emapplot_cluster(  
  x,  
  showCategory = 30,  
  color = "p.adjust",  
  label_format = 30,  
  ...  
)  
  
## S4 method for signature 'compareClusterResult'  
emapplot_cluster(  
  x,  
  showCategory = nrow(x),  
  color = "p.adjust",  
  label_format = 30,  
  ...  
)  
  
emapplot_cluster.enrichResult(  
  x,  
  showCategory = 30,  
  color = "p.adjust",  
  cex_line = 1,  
  with_edge = TRUE,  
  nWords = 4,  
  nCluster = NULL,  
  split = NULL,  
  min_edge = 0.2,  
  cex_label_group = 1,  
  label_style = "shadowtext",  
  group_legend = FALSE,  
  cex_category = 1,  
  label_format = 30,  
  repel = FALSE,
```

```

    ...
)

emapplot_cluster.compareClusterResult(
  x,
  showCategory = 30,
  color = "p.adjust",
  cex_line = 1,
  with_edge = TRUE,
  nWords = 4,
  nCluster = NULL,
  split = NULL,
  min_edge = 0.2,
  cex_label_group = 1,
  pie = "equal",
  legend_n = 5,
  cex_category = 1,
  label_style = "shadowtext",
  group_legend = FALSE,
  label_format = 30,
  repel = FALSE,
  ...
)

```

Arguments

x	enrichment result.
showCategory	number of enriched terms to display
color	variable that used to color enriched terms, e.g. pvalue, p.adjust or qvalue
label_format	a numeric value sets wrap length, alternatively a custom function to format axis labels.
...	Additional parameters used to set the position of the group label. When the parameter repel is set to TRUE, additional parameters will take effect. additional parameters can refer the following parameters. <ul style="list-style-type: none"> • force Force of repulsion between overlapping text labels. Defaults to 1. • nudge_x, nudge_y Horizontal and vertical adjustments to nudge the starting position of each text label. • direction "both", "x", or "y" – direction in which to adjust position of labels.
cex_line	scale of line width
with_edge	if TRUE, draw the edges of the network diagram
nWords	the number of words in the cluster tags
nCluster	the number of clusters
split	separate result by 'category' variable
min_edge	minimum percentage of overlap genes to display the edge, should between 0 and 1, default value is 0.2
cex_label_group	scale of group labels size
label_style	one of "shadowtext" and "ggforce"

group_legend	If TRUE, the grouping legend will be displayed. The default is FALSE
cex_category	number indicating the amount by which plotting category nodes should be scaled relative to the default.
repel	whether to correct the position of the label. Defaults to FALSE.
pie	proportion of clusters in the pie chart, one of 'equal' (default) or 'Count'
legend_n	number of circle in legend

Details

This function visualizes gene sets as a grouped network (i.e. enrichment map). Gene sets with high similarity tend to cluster together, making it easier for interpretation.

Value

ggplot object

Examples

```
## Not run:
library(clusterProfiler)
library(org.Hs.eg.db)
library(enrichplot)
library(GOsemSim)
library(DOSE)
data(geneList)
gene <- names(geneList)[abs(geneList) > 2]
ego <- enrichGO(gene = gene,
  universe      = names(geneList),
  OrgDb         = org.Hs.eg.db,
  ont           = "CC",
  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_cluster(ego2, showCategory = 80)

## End(Not run)
```

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

get_igraph	<i>Get an iGraph object</i>
------------	-----------------------------

Description

Get an iGraph object

Usage

```
get_igraph(x, y, n, color, cex_line, min_edge)
```

Arguments

x	enrichment result.
y	as.data.frame(x).
n	number of enriched terms to display.
color	variable that used to color enriched terms, e.g. pvalue, p.adjust or qvalue.
cex_line	scale of line width.
min_edge	minimum percentage of overlap genes to display the edge, should between 0 and 1, default value is 0.2.

Value

an iGraph object

get_w	<i>A function for get sel_w and net_w</i>
-------	---

Description

A function for get sel_w and net_w

Usage

```
get_w(wordd)
```

Arguments

wordd	clusters
-------	----------

`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

gseadist

gseadist

Description

plot logFC distribution of selected gene sets

Usage

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


Arguments

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

Value

distribution plot

Author(s)

Guangchuang Yu

gseaplot

gseaplot

Description

visualize analyzing result of GSEA

Usage

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

```
## S4 method for signature 'gseaResult'
```

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

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

Arguments

x	object of gsea result
geneSetID	geneSet ID
by	one of "runningScore" or "position"
title	plot title
...	additional parameters
color	color of line segments
color.line	color of running enrichment score line
color.vline	color of vertical line which indicating the maximum/minimal running enrichment score

Details

plotting function for gseaResult

Value

ggplot2 object
ggplot2 object

Author(s)

Guangchuang Yu

Examples

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

`gseaplot2`

gseaplot2

Description

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

Usage

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

Arguments

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

Value

plot

Author(s)

Guangchuang Yu

gsearank

gsearank

Description

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

Usage

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

Arguments

x	gseaResult object
geneSetID	gene set ID
title	plot title

Value

ggplot object

Author(s)

Guangchuang Yu

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

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

has_pairsim	<i>Check whether the similarity matrix exists</i>
-------------	---

Description

Check whether the similarity matrix exists

Usage

```
has_pairsim(x)
```

Arguments

x	result of enrichment analysis
---	-------------------------------

`heatplot`*heatplot*

Description

heatmap like plot for functional classification

Usage

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

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

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

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

Arguments

<code>x</code>	enrichment result.
<code>showCategory</code>	number of enriched terms to display
<code>foldChange</code>	fold Change
<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

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	<i>convert gene IDs to igraph object</i>
------------	--

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

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

Description

Get the similarity matrix

Usage

```
pairwise_termsim(x, method = "JC", semData = NULL, showCategory = 30)

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

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

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

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

```

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

```

Arguments

x	enrichment result.
method	method of calculating the similarity between nodes, one of "Resnik", "Lin", "Rel", "Jiang", "Wang" and "JC"(Jaccard similarity coefficient) methods.
semData	GOSemSimDATA object
showCategory	number of enriched terms to display

Details

This function add similarity matrix to the termsim slot of enrichment result.

Examples

```

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

## End(Not run)

```

plotting.clusterProfile

plotting-clusterProfile

Description

Internal plot function for plotting compareClusterResult

Usage

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

Arguments

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

Value

ggplot object

Author(s)

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

pmcplot

pmcplot

Description

PubMed Central Trend plot

Usage

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

Arguments

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

Value

ggplot object

Author(s)

guangchuang yu

`ridgeplot`*ridgeplot*

Description

ridgeline plot for GSEA result

Usage

```

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

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

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

```

Arguments

<code>x</code>	<code>gseaResult</code> object
<code>showCategory</code>	number of categories for plotting
<code>fill</code>	one of "pvalue", "p.adjust", "qvalue"
<code>core_enrichment</code>	whether only using <code>core_enriched</code> genes
<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

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)
```

wordcloud_i	<i>Get cluster labels</i>
-------------	---------------------------

Description

Get cluster labels

Usage

```
wordcloud_i(cluster, pdata2, nWords)
```

Arguments

cluster	a cluster name
pdata2	the data section of the ggraph object
nWords	the number of words in the cluster tags

Index

barplot.enrichResult, 2

cnetplot, 3

cnetplot,compareClusterResult-method (cnetplot), 3

cnetplot,enrichResult-method (cnetplot), 3

cnetplot,gseaResult-method (cnetplot), 3

cnetplot.enrichResult (cnetplot), 3

color_palette, 5

dotplot, 5

dotplot,compareClusterResult,ANY-method (dotplot,compareClusterResult-method), 7

dotplot,compareClusterResult-method, 7

dotplot,enrichResult-method (dotplot), 5

dotplot,gseaResult-method (dotplot), 5

emapplot, 7

emapplot,compareClusterResult-method (emapplot), 7

emapplot,enrichResult-method (emapplot), 7

emapplot,gseaResult-method (emapplot), 7

emapplot.compareClusterResult (emapplot), 7

emapplot.enrichResult (emapplot), 7

emapplot_cluster, 9

emapplot_cluster,compareClusterResult-method (emapplot_cluster), 9

emapplot_cluster,enrichResult-method (emapplot_cluster), 9

emapplot_cluster,gseaResult-method (emapplot_cluster), 9

emapplot_cluster.compareClusterResult (emapplot_cluster), 9

emapplot_cluster.enrichResult (emapplot_cluster), 9

fortify.compareClusterResult, 12

fortify.enrichResult (fortify.compareClusterResult), 12

get_igraph, 14

get_w, 14

ggtable, 15

goplot, 15

goplot,enrichResult-method (goplot), 15

goplot,gseaResult-method (goplot), 15

goplot.enrichResult (goplot), 15

gseadist, 16

gseaplot, 17

gseaplot,gseaResult-method (gseaplot), 17

gseaplot.gseaResult (gseaplot), 17

gseaplot2, 18

gsearank, 19

gsInfo, 20

has_pairsim, 20

heatplot, 21

heatplot,enrichResult-method (heatplot), 21

heatplot,gseaResult-method (heatplot), 21

heatplot.enrichResult (heatplot), 21

list2graph, 22

pairwise_termsim, 22

pairwise_termsim,compareClusterResult-method (pairwise_termsim), 22

pairwise_termsim,enrichResult-method (pairwise_termsim), 22

pairwise_termsim,gseaResult-method (pairwise_termsim), 22

pairwise_termsim.compareClusterResult (pairwise_termsim), 22

pairwise_termsim.enrichResult (pairwise_termsim), 22

plotting.clusterProfile, 23

pmcplot, 24

ridgeplot, 25

ridgeplot,gseaResult-method (ridgeplot), 25

ridgeplot.gseaResult (ridgeplot), 25

upsetplot, [26](#)
upsetplot, enrichResult, ANY-method
 (upsetplot), [26](#)
upsetplot, enrichResult-method
 (upsetplot), [26](#)
upsetplot, gseaResult (upsetplot), [26](#)
upsetplot, gseaResult-method
 (upsetplot), [26](#)

wordcloud_i, [27](#)