Package 'GseaVis'

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Title Implement for 'GSEA' Enrichment Visualization

Version 0.0.5

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Description Mark your interesting genes on plot and support more parameters to handle your own gene set enrichment analysis plot.

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Encoding UTF-8

RoxygenNote 7.2.1

Imports aplot, DOSE, dplyr, ggplot2, ggpp, ggrepel, ggsci, grDevices, magrittr, purrr, RColorBrewer, reshape2, stringr, tibble, utils

URL https://github.com/junjunlab/GseaVis

BugReports https://github.com/junjunlab/GseaVis/issues

NeedsCompilation no

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Depends R (>= 3.5.0)

Repository CRAN

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R topics documented:

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dotplotGsea   *dotplotGsea*

Description

dotplotGsea

Arguments

data	GSEA enrich object from clusterProfiler, defalut is NULL.
pval	pvalue cutoff to select significant terms, defalut is NULL.
pajust	adjusted pvalue cutoff to select significant terms, defalut is 0.05.
order.by	the X axis, defalut is "GeneRatio".
str.width	the width of term name, defalut is 50.
base_size	theme base size, defalut is 12.
topn	show the top terms, defalut is NULL.
scales	facet scales, defalut is "free_x".
add.seg	whether add segment line to point, defalut is "FALSE".
line.col	segment line color, defalut is "grey80".
line.size	segment line size, defalut is 1.5.
line.type	segment line type, defalut is "solid".

Value

a ggplot object.

Author(s)

Jun Zhang

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gseaNb   *gseaNb*

Description

gseaNb

Arguments

`object`	GSEA enrich results.
`subPlot`	which plot to show, 1/2/3, default is 3.
`lineSize`	curve line size. default is 0.8.
`geneSetID`	which pathway name to plot.
`rmSegment`	whether to remove segment on the curve plot, default is FALSE.
`termWidth`	the width or the term name, defalut is 40.
`segCol`	segment color on the curves, defalut is "red".
`addGene`	whether add gene name on the curve, defalut is FALSE.
`geneCol`	gene name label color, defalut is NULL.
`arrowAngle`	arrow angle, defalut is 20.
`arrowLength`	arrow line length, defalut is 0.2.
`arrowEnd`	arrow end, defalut is "last".
`arrowType`	arrow type, defalut is "closed".
`curveCol`	curve color, defalut is c("#76BA99", "#EB4747", "#996699").
`htCol`	heatmap color, defalut is c("#08519C", "#A50F15").
`rankCol`	gene rank fill color, defalut is c("#08519C", "white", "#A50F15").
`rankSeq`	gene rank plot X axis breaks, defalt is 5000.
`htHeight`	the relative height when "subplot = 2" to the vertical line plot, defalut is 0.3.
`force`	the gene label force, refer to geom_text_repel function, defalut is 20.
`max.overlaps`	refer to geom_text_repel function, defalut is 50.
`geneSize`	gene label text size, defalut is 4.
`newGsea`	whether show new style of plot, defalut is FALSE.
`addPoint`	new style plot with point layer, defalut is TRUE.
`newCurveCol`	new style plot curve color, defalut is c("#336699", "white", "#993399").
`newHtCol`	new style plot heatmap color, defalut is c("#336699", "white", "#993399").
`rmHt`	whether remove new style plot heatmap, defalut is FALSE.
`addPval`	whether add pvalue and NES, defalut is FALSE.
`pvalX`	set pvalue label x position, defalut is 0.9.
`pvalY`	set pvalue label y position, defalut is 0.9.
`pvalSize`	set pvalue label text size, defalut is 4.
`pCol`	pvalue label color, defalut is "grey30".
`pHjust`	pvalue label hjust, defalut is 1.
`rmPrefix`	whether remove GO term prefix like "GOBP/KEGG/CC/MF_*", defalut is TRUE.
`nesDigit`	the NES score digits retained, defalut is 2.
`pDigit`	the pvalue and pajust value digits retained, defalut is 2.
`markTopgene`	whether add top n genes on plot, defalut is FALSE.

topGeneN	the number of genes to be marked on plot, defalut is 5.
kegg	whether input is gseKEGG object, defalut is FALSE.
legend.position	
	the legend position, defalut is "right".
whether	add target gene expression heatmap, defalut is FALSE.
exp	the expression matrix,tpm/fpkm/rpkm format, defalut is NULL.
scale.exp	whether scale the expression matrix, defalut is TRUE.
sample.order	the expression matrix sample orders, defalut is NULL.
exp.col	the expression colors, defalut is c('blue','white','red').
ht.legend	whether show the heatmap legend, defalut is TRUE.
ght.relHight	the relative height to the main plot, defalut is 0.4.
ght.geneText.size	
	the gene lable text size, defalut is 6.
ght.facet	whether facet expression heatmap, defalut is FALSE.
ght.facet.scale	
	the facet plot scale argumrnt, defalut is "free".
termID.order	the facet term ID orders, defalut is NULL.
rank.gene	add your gene label on rank plot, defalut is NULL.
rank.gene.nudgey	
	the gene label nudge y on rank plot, defalut is 2.

Value

ggplot2 object

Author(s)

Jun Zhang

Examples

```
# load data
test_data <- system.file("extdata", "gseaRes.RDS", package = "GseaVis")
gseaRes <- readRDS(test_data)

# all plot
gseaNb(object = gseaRes,
      geneSetID = 'GOBP_NUCLEOSIDE_DIPHOSPHATE_METABOLIC_PROCESS',
      subPlot = 2)
```

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gsInfo   *gsInfo*

Description

gsInfo

Usage

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

Arguments

object	gseaResult object
geneSetID	gene set ID

Value

data.frame

Author(s)

Guangchuang Yu

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volcanoGsea   *volcanoGsea*

Description

volcanoGsea

Usage

```
volcanoGsea(
  data = NULL,
  NES.cutoff = 1,
  pvalue.cutoff = NULL,
  p.adjust.CUTOFF = 0.05,
  nudge.y = c(0, 0),
  topN = 5,
  point.size = 3,
  point.color = c("#CC3333", "#CCCCCC", "#0099CC"),
  ...
)
```

Arguments

`data`	GSEA enrich object from clusterProfiler, defalut is NULL.
`NES.cutoff`	NES cutoff to select significant terms, defalut is 1.
`pvalue.cutoff`	pvalue cutoff to select significant terms, defalut is NULL.
`p.adjust.CUTOFF`	
	adjusted pvalue cutoff to select significant terms, defalut is 0.05.
`nudge.y`	y shift to ajust label, defalut is c(0,0).
`topN`	top term to show, defalut is 5.
`point.size`	point size, defalut is 3.
`point.color`	point color, defalut is c('#CC3333','#CCCCCC','#0099CC').
`...`	other arguments passed by geom_text_repel.

Value

a ggplot object.

Author(s)

Jun Zhang

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