

# 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.

**License** MIT + file LICENSE

**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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 dotplotGsea

*dotplotGsea*


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### Description

dotplotGsea

### Arguments

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

### Value

a ggplot object.

### Author(s)

Jun Zhang

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 gseaNb

*gseaNb*


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

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

**Value**

a ggplot object.

**Author(s)**

Jun Zhang

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