Package ‘clusterProfiler’

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Type Package
Title statistical analysis and visualization of functional profiles for genes and gene clusters
Version 3.2.5
Maintainer Guangchuang Yu <guangchuangyu@gmail.com>
Description This package implements methods to analyze and visualize functional profiles (GO and KEGG) of gene and gene clusters.
Depends R (>= 3.3.1), DOSE (>= 3.0.1)
Imports AnnotationDbi, ggplot2, GO.db, GOSemSim (>= 2.0.0), IRanges, magrittr, methods, plyr, qvalue, stats, stats4, tidyr, utils
Suggests AnnotationHub, BiocStyle, GSEABase, KEGG.db, knitr, org.Hs.eg.db, pathview, ReactomePA, testthat, topGO
VignetteBuilder knitr
ByteCompile true
License Artistic-2.0
URL https://guangchuangyu.github.io/clusterProfiler
BugReports https://github.com/GuangchuangYu/clusterProfiler/issues
biocViews Annotation, Clustering, GeneSetEnrichment, GO, KEGG, MultipleComparison, Pathways, Reactome, Visualization
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Author Guangchuang Yu [aut, cre], Li-Gen Wang [ctb], Giovanni Dall’Olio [ctb] (formula interface of compareCluster)

R topics documented:

- clusterProfiler-package
- bitr
- bitr_kegg
- browseKEGG
- buildGOmap
- compareCluster
- compareClusterResult-class
clusterProfiler-package

statistical analysis and visualization of functional profiles for genes and gene clusters. The package implements methods to analyze and visualize functional profiles of gene and gene clusters.

Description

This package is designed to compare gene clusters functional profiles.

Details

Package: clusterProfiler
Type: Package
Version: 1.9
Date: 06-13-2013
biocViews: GO, Clustering, Visualization
Depends: AnnotationDbi, GO.db, org.Hs.eg.db, ggplot2, plyr, methods
**bitr**

Suggests: GOSemSim  
License: Artistic-2.0

**Author(s)**

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

**See Also**

compareClusterResult, groupGOResult enrichResult

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**Description**

Biological Id TRanslator

**Usage**

`bitr(geneID, fromType, toType, OrgDb, drop = TRUE)`

**Arguments**

- `geneID`: input gene id
- `fromType`: input id type
- `toType`: output id type
- `OrgDb`: annotation db
- `drop`: drop NA or not

**Value**

- data.frame

**Author(s)**

Guangchuang Yu
browseKEGG

**bitr_kegg**

**Description**

convert biological ID using KEGG API

**Usage**

```r
bitr_kegg(geneID, fromType, toType, organism, drop = TRUE)
```

**Arguments**

- `geneID`: input gene id
- `fromType`: input id type
- `toType`: output id type
- `organism`: supported organism, can be search using `search_kegg_organism` function
- `drop`: drop NA or not

**Value**

data.frame

**Author(s)**

Guangchuang Yu

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browseKEGG

**Description**

open KEGG pathway with web browser

**Usage**

```r
browseKEGG(x, pathID)
```

**Arguments**

- `x`: an instance of enrichResult or gseaResult
- `pathID`: pathway ID

**Value**

url

**Author(s)**

Guangchuang Yu
buildGOmap

Description
building GO mapping files

Usage
buildGOmap(gomap)

Arguments
gomap data.frame with two columns of GO and gene ID

Details
provided by a data.frame of GO (column 1) and gene (column 2) direct annotation this function
will building gene to GO and GO to gene mapping, with directly and indirectly (ancestor GO term)
annotation.

Value
data.frame, GO annotation with indirect annotation

Author(s)
Yu Guangchuang

compareCluster

Description
Given a list of gene set, this function will compute profiles of each gene cluster.

Usage
compareCluster(geneClusters, fun = "enrichGO", data = "", ...)

Arguments
geneClusters a list of entrez gene id. Alternatively, a formula of type Entrez~group
fun One of "groupGO", "enrichGO", "enrichKEGG", "enrichDO" or "enrichPathway".
data if geneClusters is a formula, the data from which the clusters must be extracted.
... Other arguments.
Value
A clusterProfResult instance.

Author(s)
Guangchuang Yu https://guangchuangyu.github.io

See Also
compareClusterResult-class, groupGO enrichGO

Examples
## Not run:
data(gcSample)
xx <- compareCluster(gcSample, fun="enrichKEGG",
                      organism="hsa", pvalueCutoff=0.05)
as.data.frame(xx)
# plot(xx, type="dot", caption="KEGG Enrichment Comparison")

## formula interface
g=df <- data.frame(Entrez=c('1', '100', '1000', '100101467',
                           '100127206', '100128071' ),
                    group = c('A', 'A', 'A', 'B', 'B'),
                    othergroup = c('good', 'good', 'bad', 'bad', 'good', 'bad'))
xx.formula <- compareCluster(Entrez~group, data=mydf,
                               fun='groupGO', OrgDb='org.Hs.eg.db')
as.data.frame(xx.formula)

## formula interface with more than one grouping variable
xx.formula.twogroups <- compareCluster(Entrez~group+othergroup, data=mydf,
                                       fun='groupGO', OrgDb='org.Hs.eg.db')
as.data.frame(xx.formula.twogroups)

## End(Not run)

compareClusterResult-class
Class "compareClusterResult" This class represents the comparison result of gene clusters by GO categories at specific level or GO enrichment analysis.

Description
Class "compareClusterResult" This class represents the comparison result of gene clusters by GO categories at specific level or GO enrichment analysis.

Slots
compareClusterResult cluster comparing result
geneClusters a list of genes
fun one of groupGO, enrichGO and enrichKEGG
_call function call
**Description**

Datasets gcSample contains a sample of gene clusters.

Datasets kegg_species contains kegg species information

**dotplot,compareClusterResult-method**

```
dotplot
```

**Description**

dot plot method

**Usage**

```r
## S4 method for signature 'compareClusterResult'
dotplot(object, x = ~Cluster,
        colorBy = "p.adjust", showCategory = 5, by = "geneRatio",
        includeAll = TRUE, font.size = 12, title = "")
```

**Arguments**

- `object` : compareClusterResult object
- `x` : x variable
- `colorBy` : one of pvalue or p.adjust
- `showCategory` : category numbers
- `by` : one of geneRatio, Percentage or count
- `includeAll` : logical
- `font.size` : font size
- `title` : figure title
download_KEGG

download_KEGG

**Description**

download the latest version of KEGG pathway/module

**Usage**

download_KEGG(species, keggType = "KEGG", keyType = "kegg")

**Arguments**

- **species**: species
- **keggType**: one of 'KEGG' or 'MKEGG'
- **keyType**: supported keyType, see bitr_kegg

**Value**

list

**Author(s)**

Guangchuang Yu

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dropGO

dropGO

**Description**

drop GO term of specific level or specific terms (mostly too general).

**Usage**

dropGO(x, level = NULL, term = NULL)

**Arguments**

- **x**: an instance of 'enrichResult' or 'compareClusterResult'
- **level**: GO level
- **term**: GO term

**Value**

modified version of x

**Author(s)**

Guangchuang Yu
Description

enrichment analysis by DAVID

Usage

enrichDAVID(gene, idType = "ENTREZ_GENE_ID", listType = "Gene", 
minGSSize = 10, maxGSSize = 500, annotation = "GOTERM_BP_FAT", 
pvalueCutoff = 0.05, pAdjustMethod = "BH", qvalueCutoff = 0.2, 
species = NA, david.user)

Arguments

gene input gene
idType id type
listType list Type
minGSSize minimal size of genes annotated for testing
maxGSSize maximal size of genes annotated for testing
annotation david annotation
pvalueCutoff pvalueCutoff
pAdjustMethod one of "BH" and "bonferroni"
qvalueCutoff qvalueCutoff
species species
david.user david user

Value

A enrichResult instance

Author(s)

Guangchuang Yu
enricher

Description
A universal enrichment analyzer

Usage
enricher(gene, pvalueCutoff = 0.05, pAdjustMethod = "BH", universe,
minGSSize = 10, maxGSSize = 500, qvalueCutoff = 0.2, TERM2GENE,
TERM2NAME = NA)

Arguments
- gene: a vector of gene id
- pvalueCutoff: pvalue cutoff
- pAdjustMethod: one of "holm", "hochberg", "hommel", "bonferroni", "BH", "BY", "fdr", "none"
- universe: background genes
- minGSSize: minimal size of genes annotated for testing
- maxGSSize: maximal size of genes annotated for testing
- qvalueCutoff: qvalue cutoff
- TERM2GENE: user input annotation of TERM TO GENE mapping, a data.frame of 2 column with term and gene
- TERM2NAME: user input of TERM TO NAME mapping, a data.frame of 2 column with term and name

Value
A enrichResult instance

Author(s)
Guangchuang Yu

enrichGO

GO Enrichment Analysis of a gene set. Given a vector of genes, this function will return the enrichment GO categories after FDR control.

Description
GO Enrichment Analysis of a gene set. Given a vector of genes, this function will return the enrichment GO categories after FDR control.

Usage
enrichGO(gene, OrgDb, keytype = "ENTREZID", ont = "MF",
pvalueCutoff = 0.05, pAdjustMethod = "BH", universe, qvalueCutoff = 0.2,
minGSSize = 10, maxGSSize = 500, readable = FALSE)
enrichKEGG

Arguments

gene  a vector of entrez gene id.
OrgDb  OrgDb
keytype  keytype of input gene
ont  One of "MF", "BP", and "CC" subontologies.
pvalueCutoff  Cutoff value of pvalue.
pAdjustMethod  one of "holm", "hochberg", "hommel", "bonferroni", "BH", "BY", "fdr", "none"
universe  background genes
qvalueCutoff  qvalue cutoff
minGSSize  minimal size of genes annotated by Ontology term for testing.
maxGSSize  maximal size of genes annotated for testing
readable  whether mapping gene ID to gene Name

Value

An enrichResult instance.

Author(s)

Guangchuang Yu http://ygc.name

See Also

enrichResult-class, compareCluster

Examples

## Not run:
data(gcSample)
yy <- enrichGO(gcSample[[1]], 'org.Hs.eg.db', ont="BP", pvalueCutoff=0.01)
head(summary(yy))
plot(yy)
## End(Not run)

enrichKEGG  KEGG Enrichment Analysis of a gene set. Given a vector of genes, this function will return the enrichment KEGG categories with FDR control.

Description

KEGG Enrichment Analysis of a gene set. Given a vector of genes, this function will return the enrichment KEGG categories with FDR control.

Usage

enrichKEGG(gene, organism = "hsa", keyType = "kegg", pvalueCutoff = 0.05,
pAdjustMethod = "BH", universe, minGSSize = 10, maxGSSize = 500,
qvalueCutoff = 0.2, use_internal_data = FALSE)
enrichMKEGG

Arguments

gene a vector of entrez gene id.
organism supported organism listed in 'http://www.genome.jp/kegg/catalog/org_list.html'
keyType one of "kegg", 'ncbi-geneid', 'ncib-proteinid' and 'uniprot'
pvalueCutoff Cutoff value of pvalue.
pAdjustMethod one of "holm", "hochberg", "hommel", "bonferroni", "BH", "BY", "fdr", "none"
universe background genes
minGSSize minimal size of genes annotated by Ontology term for testing.
maxGSSize maximal size of genes annotated for testing
qvalueCutoff qvalue cutoff
use_internal_data logical, use KEGG.db or latest online KEGG data

Value

A enrichResult instance.

Author(s)

Guangchuang Yu http://ygc.name

See Also

enrichResult-class, compareCluster

Examples

data(gcSample)
yy = enrichKEGG(gcSample[[5]], pvalueCutoff=0.01)
head(summary(yy))
#plot(yy)

enrichMKEGG

KEGG Module Enrichment Analysis of a gene set. Given a vector of genes, this function will return the enrichment KEGG Module categories with FDR control.

Description

KEGG Module Enrichment Analysis of a gene set. Given a vector of genes, this function will return the enrichment KEGG Module categories with FDR control.

Usage

enrichMKEGG(gene, organism = "hsa", keyType = "kegg", pvalueCutoff = 0.05,
pAdjustMethod = "BH", universe, minGSSize = 10, maxGSSize = 500,
qvalueCutoff = 0.2)
Arguments

gene a vector of entrez gene id.
organism supported organism listed in 'http://www.genome.jp/kegg/catalog/org_list.html'
keyType one of "kegg", 'ncbi-geneid', 'ncib-proteinid' and 'uniprot'
pvalueCutoff Cutoff value of pvalue.
pAdjustMethod one of "holm", "hochberg", "hommel", "bonferroni", "BH", "BY", "fdr", "none"
universe background genes
minGSSize minimal size of genes annotated by Ontology term for testing.
maxGSSize maximal size of genes annotated for testing
qvalueCutoff qvalue cutoff

Value

A enrichResult instance.

Description

convert compareClusterResult to a data.frame that ready for plot

Usage

```r
## S3 method for class 'compareClusterResult'
fotify(model, data, showCategory = 5,
by = "geneRatio", includeAll = TRUE)
```

Arguments

model compareClusterResult object
data not use here
showCategory category numbers
by one of geneRatio, Percentage or count
includeAll logical

Value

data.frame

Author(s)

Guangchuang Yu
getGOLevel  

get GOIDs at a specific level

Description
query GOIDs at a specific level.

Usage
getGOLevel(ont, level)

Arguments
ont  Ontology
level GO level

Value
a vector of GOIDs

Author(s)
Guangchuang Yu http://guangchuangyu.github.io

Gff2GeneTable

Description
read GFF file and build gene information table

Usage
Gff2GeneTable(gffFile, compress = TRUE)

Arguments
gffFile  GFF file
compress  compress file or not

Details
given a GFF file, this function extracts information from it and save it in working directory

Value
file save.

Author(s)
Yu Guangchuang
**go2ont**

**Description**
convert goid to ontology (BP, CC, MF)

**Usage**
go2ont(goid)

**Arguments**
goid a vector of GO IDs

**Value**
data.frame

**Author(s)**
Guangchuang Yu

---

**go2term**

**Description**
convert goid to descriptive term

**Usage**
go2term(goid)

**Arguments**
goid a vector of GO IDs

**Value**
data.frame

**Author(s)**
Guangchuang Yu
**gofilter**

**Description**
filter GO enriched result at specific level

**Usage**
```r
gofilter(x, level = 4)
```

**Arguments**
- `x` output from `enrichGO` or `compareCluster`
- `level` GO level

**Value**
updated object

**Author(s)**
Guangchuang Yu

---

**groupGO**

Functional Profile of a gene set at specific GO level. Given a vector of genes, this function will return the GO profile at a specific level.

**Usage**
```r
groupGO(gene, OrgDb, keytype = "ENTREZID", ont = "CC", level = 2, readable = FALSE)
```

**Arguments**
- `gene` a vector of entrez gene id.
- `OrgDb` OrgDb
- `keytype` keytype of input gene
- `ont` One of "MF", "BP", and "CC" subontologies.
- `level` Specific GO Level.
- `readable` if readable is TRUE, the gene IDs will mapping to gene symbols.
Value

A `groupGOResult` instance.

Author(s)

Guangchuang Yu http://ygc.name

See Also

groupGOResult-class, compareCluster

Examples

data(gcSample)
yy <- groupGO(gcSample[[1]], 'org.Hs.eg.db', ont="BP", level=2)
head(summary(yy))
#plot(yy)

groupGOResult-class

Class "groupGOResult" This class represents the result of functional Profiles of a set of gene at specific GO level.

Description

Class "groupGOResult" This class represents the result of functional Profiles of a set of gene at specific GO level.

Slots

  result GO classification result
  ontology Ontology
  level GO level
  organism one of "human", "mouse" and "yeast"
  gene Gene IDs
  readable logical flag of gene ID in symbol or not.

Author(s)

Guangchuang Yu http://ygc.name

See Also

  compareClusterResult compareCluster groupGO
Description

a universal gene set enrichment analysis tool

Usage

GSEA(geneList, exponent = 1, nPerm = 1000, minGSSize = 10,
    maxGSSize = 500, pvalueCutoff = 0.05, pAdjustMethod = "BH", TERM2GENE,
    TERM2NAME = NA, verbose = TRUE, seed = FALSE, by = "fgsea")

Arguments

geneList          order ranked geneList
exponent          weight of each step
nPerm             number of permutations
minGSSize         minimal size of each geneSet for analyzing
maxGSSize         maximal size of genes annotated for testing
pvalueCutoff      pvalue cutoff
pAdjustMethod     p value adjustment method
TERM2GENE         user input annotation of TERM TO GENE mapping, a data.frame of 2 column
                  with term and gene
TERM2NAME         user input of TERM TO NAME mapping, a data.frame of 2 column with term
                  and name
verbose           logical
seed              logical
by                one of `fgsea` or `DOSE`

Value

gseaResult object

Author(s)

Guangchuang Yu
Description

Gene Set Enrichment Analysis of Gene Ontology

Usage

gseGO(geneList, ont = "BP", OrgDb, keytype = "ENTREZID", exponent = 1,
nPerm = 1000, minGSSize = 10, maxGSSize = 500, pvalueCutoff = 0.05,
pAdjustMethod = "BH", verbose = TRUE, seed = FALSE, by = "fgsea")

Arguments

geneList order ranked geneList
ont one of "BP", "MF", "CC" or "GO"
OrgDb OrgDb
keytype keytype of gene
exponent weight of each step
nPerm permutation numbers
minGSSize minimal size of each geneSet for analyzing
maxGSSize maximal size of genes annotated for testing
pvalueCutoff pvalue Cutoff
pAdjustMethod pvalue adjustment method
verbose print message or not
seed logical
by one of `fgsea` or `DOSE`

Value

gseaResult object

Author(s)

Yu Guangchuang
Description

Gene Set Enrichment Analysis of KEGG

Usage

gseKEGG(geneList, organism = "hsa", keyType = "kegg", exponent = 1, nPerm = 1000, minGSSize = 10, maxGSSize = 500, pvalueCutoff = 0.05, pAdjustMethod = "BH", verbose = TRUE, use_internal_data = FALSE, seed = FALSE, by = "fgsea")

Arguments

geneList order ranked geneList
organism supported organism listed in 'http://www.genome.jp/kegg/catalog/org_list.html'
keyType one of "kegg", 'ncbi-geneid', 'ncib-proteinid' and 'uniprot'
exponent weight of each step
nPerm permutation numbers
minGSSize minimal size of each geneSet for analyzing
maxGSSize maximal size of genes annotated for testing
pvalueCutoff pvalue Cutoff
pAdjustMethod pvalue adjustment method
verbose print message or not
use_internal_data logical, use KEGG.db or latest online KEGG data
seed logical
by one of 'fgsea' or 'DOSE'

Value

gseaResult object

Author(s)

Yu Guangchuang
Description
Gene Set Enrichment Analysis of KEGG Module

Usage
```r
gseMKEGG(geneList, organism = "hsa", keyType = "kegg", exponent = 1,
nPerm = 1000, minGSSize = 10, maxGSSize = 500, pvalueCutoff = 0.05,
pAdjustMethod = "BH", verbose = TRUE, seed = FALSE, by = "fgsea")
```

Arguments
- `geneList`: order ranked geneList
- `organism`: supported organism listed in 'http://www.genome.jp/kegg/catalog/org_list.html'
- `keyType`: one of "kegg", 'ncbi-geneid', 'ncib-proteinid' and 'uniprot'
- `exponent`: weight of each step
- `nPerm`: permutation numbers
- `minGSSize`: minimal size of each geneSet for analyzing
- `maxGSSize`: maximal size of genes annotated for testing
- `pvalueCutoff`: pvalue Cutoff
- `pAdjustMethod`: pvalue adjustment method
- `verbose`: print message or not
- `seed`: logical
- `by`: one of 'fgsea' or 'DOSE'

Value
- gseaResult object

Author(s)
- Yu Guangchuang
### idType

**Description**
list ID types supported by annoDb

**Usage**
```
idType(OrgDb = "org.Hs.eg.db")
```

**Arguments**
- `OrgDb` annotation db

**Value**
character vector

**Author(s)**
Guangchuang Yu

---

### merge_result

**Description**
merge a list of enrichResult objects to compareClusterResult

**Usage**
```
merge_result(enrichResultList)
```

**Arguments**
- `enrichResultList` a list of enrichResult objects

**Value**
a compareClusterResult instance

**Author(s)**
Guangchuang Yu
plot method

Description
plot method generics

Usage
## S4 method for signature 'compareClusterResult,ANY'
plot(x, type = "dot",
     colorBy = "p.adjust", showCategory = 5, by = "geneRatio",
     includeAll = TRUE, font.size = 12, title = ""

Arguments
x
  compareClusterResult object
type
  one of bar or dot
colorBy
  one of pvalue or p.adjust
showCategory
  category numbers
by
  one of geneRatio, Percentage or count
includeAll
  logical
font.size
  font size
title
  figure title
...
  Additional argument list

Value
plot

Author(s)
Guangchuang Yu [http://ygc.name](http://ygc.name)

plotGOgraph method

Description
plot GO graph

Usage
plotGOgraph(x, firstSigNodes = 10, useInfo = "all", sigForAll = TRUE, 
useFullNames = TRUE, ...)

plotGOgraph
Arguments

- **x**: output of enrichGO or gseGO
- **firstSigNodes**: number of significant nodes (rectangle nodes in the graph)
- **useInfo**: additional info
- **sigForAll**: if TRUE the score/p-value of all nodes in the DAG is shown, otherwise only score will be shown
- **useFullNames**: logical
- **...**: additional parameter of showSigOfNodes, please refer to topGO

Value

GO DAG graph

Author(s)

Guangchuang Yu

See Also

- showSigOfNodes

Description

Internal plot function for plotting compareClusterResult

Usage

```r
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 p-value or p.adjust
- **by**: one of percentage and count
- **title**: graph title
- **font.size**: graph font size

Value

ggplot object
read.gmt

Author(s)
Guangchuang Yu http://ygc.name

---

read.gmt

Description
parse gmt file to a data.frame

Usage
read.gmt(gmtfile)

Arguments
gmtfile gmt file

Value
data.frame

Author(s)
Guangchuang Yu

---

search_kegg_organism

Description
search kegg organism, listed in http://www.genome.jp/kegg/catalog/org_list.html

Usage
search_kegg_organism(str, by = "scientific_name", ignore.case = FALSE)

Arguments
str string
by one of 'kegg.code', 'scientific_name' and 'common_name'
ignore.case TRUE or FALSE

Value
data.frame

Author(s)
Guangchuang Yu
**simplify**

```
simplify method
```

**Description**

simplify output from enrichGO by removing redundancy of enriched GO terms
simplify output from compareCluster by removing redundancy of enriched GO terms

**Usage**

```r
## S4 method for signature 'enrichResult'
simplify(x, cutoff = 0.7, by = "p.adjust",
         select_fun = min, measure = "Wang", semData = NULL)
```

```r
## S4 method for signature 'compareClusterResult'
simplify(x, cutoff = 0.7, by = "p.adjust",
         select_fun = min, measure = "Wang", semData = NULL)
```

**Arguments**

- `x`  
  output of enrichGO
- `cutoff`  
  similarity cutoff
- `by`  
  feature to select representative term, selected by `select_fun` function
- `select_fun`  
  function to select feature passed by `by` parameter
- `measure`  
  method to measure similarity
- `semData`  
  GOSemSimDATA object

**Value**

updated enrichResult object
updated compareClusterResult object

**Author(s)**

Guangchuang Yu
Guangchuang Yu

**References**

issue #28 [https://github.com/GuangchuangYu/clusterProfiler/issues/28](https://github.com/GuangchuangYu/clusterProfiler/issues/28)
viewKEGG function is for visualize KEGG pathways works with enrichResult object to visualize enriched KEGG pathway

Description

viewKEGG function is for visualize KEGG pathways works with enrichResult object to visualize enriched KEGG pathway

Usage

viewKEGG(obj, pathwayID, foldChange, color.low = "green", color.high = "red", kegg.native = TRUE, out.suffix = "clusterProfiler")

Arguments

obj
pathwayID
foldChange
color.low
color.high
kegg.native
out.suffix

enrichResult object
pathway ID or index
fold change values
color of low foldChange genes
color of high foldChange genes
logical
suffix of output file

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