Package ‘clusterProfiler’

April 25, 2017

Type Package

Title statistical analysis and visualization of functional profiles
  for genes and gene clusters

Version 3.4.0

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 (>= 3.1.3)

Imports AnnotationDbi, ggplot2, GO.db, GOSemSim (>= 2.0.0), magrittr,
  methods, plyr, qvalue, rvcheck, stats, stats4, tidyR, utils

Suggests AnnotationHub, GSEABase, KEGG.db, knitr, org.Hs.eg.db,
  prettydoc, 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

RoxygenNote 5.0.1

NeedsCompilation no

Author Guangchuang Yu [aut, cre],
  Li-Gen Wang [ctb],
  Giovanni Dall’Olio [ctb] (formula interface of compareCluster)

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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

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**

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

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**Description**

convert biological ID using KEGG API

**Usage**

```
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
browseKEGG

Description
open KEGG pathway with web browser

Usage
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
**compareCluster**

*Author(s)*

Yu Guangchuang

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**compareCluster**

*Compare gene clusters functional profile*

---

**Description**

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

**Usage**

```r
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](https://guangchuangyu.github.io)

**See Also**

- `compareClusterResult-class`, `groupGO`, `enrichGO`

**Examples**

```r
## 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
mydf <- data.frame(Entrez=c("1", "100", "1000", "100010147", 
                           "100127206", "100128071"),
                   group = c("A", "A", "A", "B", "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

```r
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

**Author(s)**

Guangchuang Yu [https://guangchuangyu.github.io](https://guangchuangyu.github.io)

**See Also**

- `groupGOResult`
- `enrichResult`
- `compareCluster`

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**DataSet**

*Datasets gcSample contains a sample of gene clusters.*

**Description**

Datasets gcSample contains a sample of gene clusters.

Datasets kegg_species contains kegg species information
Description
dot plot method

Usage
```r
## S4 method for signature 'compareClusterResult'
dotplot(object, x = ~Cluster,
        colorBy = "p.adjust", showCategory = 5, by = "geneRatio",
        split = NULL, 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
- `split`: ONTOLOGY or NULL
- `includeAll`: logical
- `font.size`: font size
- `title`: figure title

Description
download the latest version of KEGG pathway/module

Usage
```r
download KEgg(species, keggType = "KEGG", keyType = "kegg")
```

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

Value
- list
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

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**enricher**

**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
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, pool = FALSE)

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
pool If ont='ALL', whether pool 3 GO sub-ontologies

Value

An enrichResult instance.

Author(s)

Guangchuang Yu https://guangchuangyu.github.io

See Also

enrichResult-class, compareCluster
Examples

```r
## Not run:
data(geneList)
de <- names(geneList)[1:100]
yy <- enrichGO(de, 'org.Hs.eg.db', ont="BP", pvalueCutoff=0.01)
head(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**

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

**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](http://ygc.name)

**See Also**

- enrichResult-class, compareCluster
enrichMKEGG

Examples

data(geneList)
dec <- names(geneList)[1:10]
yy <- enrichMKEGG(de, pvalueCutoff=0.01)
head(yy)

enrichMKEGG

KEGG Module Enrichment Analysis of a gene set. Given a vector of
genes, this function will return the enrichment KEGG Module cate-
gories 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', 'ncbi-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.
fortify.compareClusterResult

Description
convert compareClusterResult to a data.frame that ready for plot

Usage

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

Arguments

- `model`: compareClusterResult object
- `data`: not use here
- `showCategory`: category numbers
- `by`: one of geneRatio, Percentage or count
- `split`: ONTOLOGY or NULL
- `includeAll`: logical

Value
data.frame

Author(s)
Guangchuang Yu

getGOLevel

get GOIDs at a specific level

Description
query GOIDs at a specific level.

Usage

```r
getGOLevel(ont, level)
```

Arguments

- `ont`: Ontology
- `level`: GO level
go2ont

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

<table>
<thead>
<tr>
<th>Argument</th>
<th>Description</th>
</tr>
</thead>
</table>
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 |
`go2term`

**Value**

data.frame

**Author(s)**

Guangchuang Yu

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`gofilter`

**Description**

filter GO enriched result at specific level

**Usage**

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.*

**Description**

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](http://ygc.name)

**See Also**

`groupGOResult-class`, `compareCluster`

**Examples**

```r
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.

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

GSEA

Description

a universal gene set enrichment analysis tools

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
gseGO

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

gseGO
gseGO

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’
**gseKEGG**

**Value**

gseaResult object

**Author(s)**

Yu Guangchuang

---

**Description**

Gene Set Enrichment Analysis of KEGG

**Usage**

```r
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
**gseMKEGG**

**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**

<table>
<thead>
<tr>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>list ID types supported by annoDb</td>
</tr>
</tbody>
</table>

**Usage**

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

**Arguments**

- `OrgDb` annotation db

**Value**

character vector

**Author(s)**

Guangchuang Yu

---

**KEGG_path2extid**

<table>
<thead>
<tr>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>query all genes in a KEGG pathway or module</td>
</tr>
</tbody>
</table>

**Usage**

```r
KEGG_path2extid(keggID, species = sub("\d+$", "", keggID),
keggType = "Path", keyType = "kegg")
```

**Arguments**

- `keggID` KEGG ID, path or module ID
- `species` species
- `keggType` one of 'Path' or 'Module'
- `keyType` KEGG gene type, one of "ncbi-proteinid", "ncbi-geneid", "uniprot", or "kegg"

**Value**

extid 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
plot method

Description
plot method generics

Usage
## S4 method for signature 'compareClusterResult,ANY'
plot(x, type = "dot", colorBy = "p.adjust", showCategory = 5, by = "geneRatio",
      split = NULL, 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
split ONTOLOGY or NULL
includeAll logical
font.size font size
title figure title
... Additional argument list
plotGOgraph

Value

plot

Author(s)

Guangchuang Yu http://ygc.name

Description

plot GO graph

Usage

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

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
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 http://ygc.name

read.gmt

Description
parse gmt file to a data.frame

Usage
read.gmt(gmtfile)

Arguments
- gmtfile: gmt file
search_kegg_organism

Value
data.frame

Author(s)
Guangchuang Yu

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

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

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

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

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

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  
enrichResult object

pathwayID  
pathway ID or index

foldChange  
fold change values

color.low  
color of low foldChange genes

color.high  
color of high foldChange genes

kegg.native  
logical

out.suffix  
suffix of output file
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