Package ‘clusterProfiler’

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Type Package
Title statistical analysis and visualization of functional profiles
for genes and gene clusters
Version 3.2.14
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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NeedsCompilation no
Author Guangchuang Yu [aut, cre],
Li-Gen Wang [ctb],
Giovanni Dall’Olio [ctb] (formula interface of compareCluster)

R topics documented:

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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.

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**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
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 | bitr_kegg |

**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

**Author(s)**
Guangchuang Yu

---

browseKEGG

| browseKEGG | 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

**Author(s)**
Yu Guangchuang

**compareCluster**

**Compare gene clusters functional profile**

**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

```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', '10001467',
                            '10012706', '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
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**

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

See Also
  groupGOResult enrichResult compareCluster

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

dotplot, compareClusterResult-method

Description
dot plot method

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

---

**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
enrichGO

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(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
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

See Also
enrichResult-class, compareCluster

Examples

data(geneList)
  de <- names(geneList)[1:100]
  yy <- enrichKEGG(de, 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)
fortify.compareClusterResult

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

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

Value
data.frame

Author(s)
Guangchauang Yu
getGOLevel  

**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](http://guangchuangyu.github.io)

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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
```r
go2ont(goid)
```

### Arguments
- `goid` a vector of GO IDs

### Value
data.frame

### Author(s)
Guangchuang Yu

---

**go2term**

### Description
convert goid to descriptive term

### Usage
```r
go2term(goid)
```

### Arguments
- `goid` a vector of GO IDs

### Value
data.frame

### Author(s)
Guangchuang Yu
gofilter

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

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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

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

arguments

gene a vector of entrez gene id.
0rgDb 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
GSEA

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**

```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
Description

Gene Set Enrichment Analysis of KEGG Module

Usage

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>
<th>list ID types supported by annoDb</th>
</tr>
</thead>
<tbody>
<tr>
<td><strong>Usage</strong></td>
<td>idType(OrgDb = &quot;org.Hs.eg.db&quot;)</td>
</tr>
<tr>
<td><strong>Arguments</strong></td>
<td>OrgDb: annotation db</td>
</tr>
<tr>
<td><strong>Value</strong></td>
<td>character vector</td>
</tr>
</tbody>
</table>

**Author(s)**

Guangchuang Yu

---

**merge_result**

<table>
<thead>
<tr>
<th>Description</th>
<th>merge a list of enrichResult objects to compareClusterResult</th>
</tr>
</thead>
<tbody>
<tr>
<td><strong>Usage</strong></td>
<td>merge_result(enrichResultList)</td>
</tr>
<tr>
<td><strong>Arguments</strong></td>
<td>enrichResultList: a list of enrichResult objects</td>
</tr>
<tr>
<td><strong>Value</strong></td>
<td>a compareClusterResult instance</td>
</tr>
</tbody>
</table>

**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",
     category = 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
category ONTOLOGY or NULL
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 plotGOgraph

Description

plot GO graph

Usage

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

Arguments

<table>
<thead>
<tr>
<th>Argument</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>x</td>
<td>output of enrichGO or gseGO</td>
</tr>
<tr>
<td>firstSigNodes</td>
<td>number of significant nodes (rectangle nodes in the graph)</td>
</tr>
<tr>
<td>useInfo</td>
<td>additional info</td>
</tr>
<tr>
<td>sigForAll</td>
<td>if TRUE the score/p-value of all nodes in the DAG is shown, otherwise only score will be shown</td>
</tr>
<tr>
<td>useFullNames</td>
<td>logical</td>
</tr>
<tr>
<td>...</td>
<td>additional parameter of showSigOfNodes, please refer to topGO</td>
</tr>
</tbody>
</table>

Value

GO DAG graph

Author(s)

Guangchuang Yu

See Also

showSigOfNodes

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

<table>
<thead>
<tr>
<th>Argument</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>clProf.reshape.df</td>
<td>data frame of compareCluster result</td>
</tr>
<tr>
<td>x</td>
<td>x variable</td>
</tr>
<tr>
<td>type</td>
<td>one of dot and bar</td>
</tr>
<tr>
<td>colorBy</td>
<td>one of pvalue or p.adjust</td>
</tr>
<tr>
<td>by</td>
<td>one of percentage and count</td>
</tr>
<tr>
<td>title</td>
<td>graph title</td>
</tr>
<tr>
<td>font.size</td>
<td>graph font size</td>
</tr>
</tbody>
</table>

Value

ggplot object
**read.gmt**

**Author(s)**

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

---

**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](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)

## 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)**

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**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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