Package ‘clusterProfiler’

April 7, 2022

Type Package

Title A universal enrichment tool for interpreting omics data

Version 4.2.2

Maintainer Guangchuang Yu <guangchuangyu@gmail.com>

Description This package supports functional characteristics of both coding and non-coding genomics data for thousands of species with up-to-date gene annotation. It provides a universal interface for gene functional annotation from a variety of sources and thus can be applied in diverse scenarios. It provides a tidy interface to access, manipulate, and visualize enrichment results to help users achieve efficient data interpretation. Datasets obtained from multiple treatments and time points can be analyzed and compared in a single run, easily revealing functional consensus and differences among distinct conditions.

Depends R (>= 3.5.0)

Imports AnnotationDbi, downloader, DOSE (>= 3.13.1), dplyr, enrichplot (>= 1.9.3), GO.db, GOSemSim, magrittr, methods, plyr, qvalue, rlang, stats, tidyr, utils, yulab.utils

Suggests AnnotationHub, knitr, rmarkdown, org.Hs.eg.db, prettydoc, ReactomePA, testthat

VignetteBuilder knitr

ByteCompile true

License Artistic-2.0


BugReports https://github.com/GuangchuangYu/clusterProfiler/issues

biocViews Annotation, Clustering, GeneSetEnrichment, GO, KEGG, MultipleComparison, Pathways, Reactome, Visualization

RoxygenNote 7.1.2

git_url https://git.bioconductor.org/packages/clusterProfiler
git_branch RELEASE_3_14

git_last_commit 4ebb9de

git_last_commit_date 2022-01-12
R topics documented:

clusterProfiler-package ........................................... 3
bitr ................................................................. 3
bitr_kegg ............................................................ 4
browseKEGG .......................................................... 4
buildGOmap ............................................................ 5
compareCluster ....................................................... 6
DataSet ............................................................... 7
download_KEGG ....................................................... 7
dropGO ................................................................. 8
enrichDAVID .......................................................... 8
enricher ............................................................... 9
enrichGO .............................................................. 10
enrichKEGG ........................................................... 12
enrichMKEGG ........................................................ 13
enrichWP ............................................................... 14
get_wp_organisms .................................................... 15
Gff2GeneTable ......................................................... 15
go2ont ................................................................. 16
go2term ............................................................... 16
gofilter ............................................................... 17
groupGO .............................................................. 17
groupGOResult-class ................................................. 18
GSEA ................................................................. 19
gseGO ................................................................. 20
gseKEGG ............................................................. 21
gseMKEGG ........................................................... 22
gseWP ................................................................. 23
idType ................................................................. 24
ko2name .............................................................. 25
merge_result .......................................................... 25
plotGOgraph .......................................................... 26
read.gmt ............................................................. 27
search_kegg_organism ................................................. 27
simplify .............................................................. 28
uniprot_get .......................................................... 29

Index 30
clusterProfiler-package

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

Description

The package implements methods to analyze and visualize functional profiles of gene and gene clusters.

bitr

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
**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

---

**browseKEGG**

**Description**

open KEGG pathway with web browser

**Usage**

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

**Arguments**

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

**Value**

url

**Author(s)**

Guangchuang Yu

**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

<table>
<thead>
<tr>
<th>Argument</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>geneClusters</td>
<td>a list of entrez gene id. Alternatively, a formula of type Entrez~group</td>
</tr>
<tr>
<td>fun</td>
<td>One of &quot;groupGO&quot;, &quot;enrichGO&quot;, &quot;enrichKEGG&quot;, &quot;enrichDO&quot; or &quot;enrichPathway&quot;.</td>
</tr>
<tr>
<td>data</td>
<td>if geneClusters is a formula, the data from which the clusters must be extracted.</td>
</tr>
<tr>
<td>...</td>
<td>Other arguments.</td>
</tr>
</tbody>
</table>

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', '100101467',
                           '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
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)

---

### DataSet

Datasets gcSample contains a sample of gene clusters.

Datasets kegg_species contains kegg species information

Datasets DE_GSE8057 contains differential expressed genes obtained from GSE8057 dataset

---

### download_KEGG

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
### 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

### enrichDAVID

**Description**

enrichment analysis by DAVID

**Usage**

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

Arguments

- **gene**: input gene
- **idType**: id type
- **universe**: background genes. If missing, the all genes listed in the database (eg TERM2GENE table) will be used as background.
- **minGSSize**: minimal size of genes annotated for testing
- **maxGSSize**: maximal size of genes annotated for testing
- **annotation**: david annotation
- **pvalueCutoff**: adjusted pvalue cutoff on enrichment tests to report
- **pAdjustMethod**: one of "holm", "hochberg", "hommel", "bonferroni", "BH", "BY", "fdr", "none"
- **qvalueCutoff**: qvalue cutoff on enrichment tests to report as significant. Tests must pass i) pvalueCutoff on unadjusted pvalues, ii) pvalueCutoff on adjusted pvalues and iii) qvalueCutoff on qvalues to be reported.
- **species**: species
- **david.user**: david user

Value

A enrichResult instance

Author(s)

Guangchuang Yu

Description

A universal enrichment analyzer

Usage

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

<table>
<thead>
<tr>
<th>Argument</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>gene</td>
<td>a vector of gene id</td>
</tr>
<tr>
<td>pvalueCutoff</td>
<td>adjusted pvalue cutoff on enrichment tests to report</td>
</tr>
<tr>
<td>pAdjustMethod</td>
<td>one of &quot;holm&quot;, &quot;hochberg&quot;, &quot;hommel&quot;, &quot;bonferroni&quot;, &quot;BH&quot;, &quot;BY&quot;, &quot;fdr&quot;, &quot;none&quot;</td>
</tr>
<tr>
<td>universe</td>
<td>background genes. If missing, the all genes listed in the database (eg TERM2GENE table) will be used as background.</td>
</tr>
<tr>
<td>minGSSize</td>
<td>minimal size of genes annotated for testing</td>
</tr>
<tr>
<td>maxGSSize</td>
<td>maximal size of genes annotated for testing</td>
</tr>
<tr>
<td>qvalueCutoff</td>
<td>qvalue cutoff on enrichment tests to report as significant. Tests must pass i) pvalueCutoff on unadjusted pvalues, ii) pvalueCutoff on adjusted pvalues and iii) qvalueCutoff on qvalues to be reported.</td>
</tr>
<tr>
<td>TERM2GENE</td>
<td>user input annotation of TERM TO GENE mapping, a data.frame of 2 column with term and gene</td>
</tr>
<tr>
<td>TERM2NAME</td>
<td>user input of TERM TO NAME mapping, a data.frame of 2 column with term and name</td>
</tr>
</tbody>
</table>

**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**

```r
enrichGO(
  gene,
  OrgDb,
  keyType = "ENTREZID",
  ont = "MF",
  pvalueCutoff = 0.05,
  pAdjustMethod = "BH",
  universe,
  qvalueCutoff = 0.2,
)```
enrichGO

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 "BP", "MF", and "CC" subontologies, or "ALL" for all three.
pvalueCutoff adjusted pvalue cutoff on enrichment tests to report
pAdjustMethod one of "holm", "hochberg", "hommel", "bonferroni", "BH", "BY", "fdr", "none"
universe   background genes. If missing, the all genes listed in the database (eg TERM2GENE
table) will be used as background.
qvalueCutoff qvalue cutoff on enrichment tests to report as significant. Tests must pass i) 
pvalueCutoff on unadjusted pvalues, ii) pvalueCutoff on adjusted pvalues and iii) qvalueCutoff on qvalues to be reported.
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

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

## End(Not run)
enrichKEGG

**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.
- `keyType`: one of "kegg", 'ncbi-geneid', 'ncib-proteinid' and 'uniprot'
- `pvalueCutoff`: adjusted pvalue cutoff on enrichment tests to report
- `pAdjustMethod`: one of "holm", "hochberg", "hommel", "bonferroni", "BH", "BY", "fdr", "none"
- `universe`: background genes. If missing, the all genes listed in the database (e.g., TERM2GENE table) will be used as background.
- `minGSSize`: minimal size of genes annotated by Ontology term for testing.
- `maxGSSize`: maximal size of genes annotated for testing
- `qvalueCutoff`: qvalue cutoff on enrichment tests to report as significant. Tests must pass i) `pvalueCutoff` on unadjusted pvalues, ii) `pvalueCutoff` on adjusted pvalues and iii) `qvalueCutoff` on qvalues to be reported.
- `use_internal_data`: logical, use KEGG.db or latest online KEGG data

**Value**

A `enrichResult` instance.
### 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

```r
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**: adjusted pvalue cutoff on enrichment tests to report

#### Examples

```r
## Not run:
data(geneList, package='DOSE')
de <- names(geneList)[1:100]
yy <- enrichKEGG(de, pvalueCutoff=0.01)
head(yy)
## End(Not run)
```
**enrichWP**

- **pAdjustMethod**: one of "holm", "hochberg", "hommel", "bonferroni", "BH", "BY", "fdr", "none"
- **universe**: background genes. If missing, the all genes listed in the database (eg TERM2GENE table) will be used as background.
- **minGSSize**: minimal size of genes annotated by Ontology term for testing.
- **maxGSSize**: maximal size of genes annotated for testing.
- **qvalueCutoff**: qvalue cutoff on enrichment tests to report as significant. Tests must pass i) `pvalueCutoff` on unadjusted pvalues, ii) `pvalueCutoff` on adjusted pvalues and iii) `qvalueCutoff` on qvalues to be reported.

**Value**

A enrichResult instance.

---

### enrichWP

**Description**

ORA analysis for WikiPathways

**Usage**

`enrichWP(gene, organism, ...)`

**Arguments**

- **gene**: a vector of entrez gene id
- **organism**: supported organisms, which can be accessed via the get_wp_organisms() function
- **...**: additional parameters, see also the parameters supported by the enricher() function

**Details**

This function performs over-representation analysis using WikiPathways

**Value**

A enrichResult instance

**Author(s)**

Guangchuang Yu
**get_wp_organisms**

---

**get_wp_organisms**  
**get_wp_organism**

---

**Description**
list supported organism of WikiPathways

**Usage**

```r
get_wp_organisms()
```

**Details**
This function extracts information from 'https://data.wikipathways.org/current/gmt/' and lists all supported organisms

**Value**
supported organism list

**Author(s)**
Guangchuang Yu

---

**Gff2GeneTable**  
**Gff2GeneTable**

---

**Description**
read GFF file and build gene information table

**Usage**

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

Arguments

x output from enrichGO or compareCluster
level GO level

Value
updated object

Author(s)
Guangchuang Yu

groupGO

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.
OrgDb OrgDb
keyType key type 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://guangchuangyu.github.io

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)

---

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.
A universal gene set enrichment analysis tool

Usage

```r
GSEA(
  geneList,
  exponent = 1,
  minGSSize = 10,
  maxGSSize = 500,
  eps = 1e-10,
  pvalueCutoff = 0.05,
  pAdjustMethod = "BH",
  TERM2GENE,
  TERM2NAME = NA,
  verbose = TRUE,
  seed = FALSE,
  by = "fgsea",
  ...)
```

Arguments

- `geneList` order ranked geneList
- `exponent` weight of each step
- `minGSSize` minimal size of each geneSet for analyzing
- `maxGSSize` maximal size of genes annotated for testing
- `eps` This parameter sets the boundary for calculating the p value.
- `pvalueCutoff` adjusted 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'
... other parameter

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,
minGSSize = 10, maxGSSize = 500,
eps = 1e-10,
pvalueCutoff = 0.05,
pAdjustMethod = "BH",
verbose = TRUE, seed = FALSE, by = "fgsea",
... )

Arguments
geneList order ranked geneList
ont one of "BP", "MF", and "CC" subontologies, or "ALL" for all three.
OrgDb OrgDb
keyType keytype of gene
exponent weight of each step
minGSSize minimal size of each geneSet for analyzing
maxGSSize maximal size of genes annotated for testing
eps This parameter sets the boundary for calculating the p value.
pvalueCutoff pvalue Cutoff
pAdjustMethod pvalue adjustment method
verbose print message or not
seed logical
by one of 'fgsea' or 'DOSE'
... other parameter

Value
gseaResult object

Author(s)
Yu Guangchuang

gseKEGG

Description
Gene Set Enrichment Analysis of KEGG

Usage
gseKEGG(
geneList,
organism = "hsa",
keyType = "kegg",
exponent = 1,
minGSSize = 10,
maxGSSize = 500,
eps = 1e-10,
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
- `minGSSize` minimal size of each geneSet for analyzing
- `maxGSSize` maximal size of genes annotated for testing
- `eps` This parameter sets the boundary for calculating the p value.
- `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'
- `...` other parameter

**Value**

gseaResult object

**Author(s)**

Yu Guangchuang

**Description**

Gene Set Enrichment Analysis of KEGG Module

**Usage**

gseMKEGG(
  geneList,
  organism = "hsa",
  keyType = "kegg",
  exponent = 1,
  minGSSize = 10,
  maxGSSize = 500,
  eps = 1e-10,
  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
minGSSize    minimal size of each geneSet for analyzing
maxGSSize    maximal size of genes annotated for testing
eps          This parameter sets the boundary for calculating the p value.
pvalueCutoff pvalue Cutoff
pAdjustMethod pvalue adjustment method
verbose      print message or not
seed         logical
by           one of 'fgsea' or 'DOSE'
...          other parameter

Value

gseaResult object

Author(s)

Yu Guangchuang

Description

GSEA analysis for WikiPathways

Usage

gseWP(geneList, organism, ...)

idType

Arguments

geneList ranked gene list
organism supported organisms, which can be accessed via the get_wp_organisms() function
...
additional parameters, see also the parameters supported by the enricher() function

Details

This function performs GSEA using WikiPathways

Value

A gseaResult instance

Author(s)

Guangchuang Yu

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
ko2name

Description
convert ko ID to descriptive name

Usage
ko2name(ko)

Arguments
ko ko ID

Value
data.frame

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
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
read.gmt

Description
parse gmt file to a data.frame

Usage
read.gmt(gmtfile)
read.gmt.wp(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,
use_internal_data = TRUE
)

Arguments
str string
by one of 'kegg.code', 'scientific_name' and 'common_name'
ignore.case TRUE or FALSE
use_internal_data logical, use kegg_species.rda or latest online KEGG data
Value
data.frame

Author(s)
Guangchuang Yu

Description
simplify output from enrichGO and gseGO 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 'gseaResult'
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
)
```
uniprot_get

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
Gwang-Jin Kim and Guangchuang Yu
Guangchuang Yu

References

issue #28 https://github.com/GuangchuangYu/clusterProfiler/issues/28
issue #162 https://github.com/GuangchuangYu/clusterProfiler/issues/162

uniprot_get  uniprot_get

Description

retrieve annotation data from uniprot

Usage

uniprot_get(taxID)

Arguments

taxID         taxonomy ID

Value

gene table data frame

Author(s)

guangchuang yu
Index

* **classes**
  - `groupGOResult-class`, 18

* **datasets**
  - `DataSet`, 7

* **manip**
  - `compareCluster`, 6
  - `enrichGO`, 10
  - `enrichKEGG`, 12
  - `groupGO`, 17

`bitr`, 3
`bitr_kegg`, 4
`browseKEGG`, 4
`buildGOmap`, 5

`clusterProfiler`
  - (`clusterProfiler-package`), 3
`clusterProfiler-package`, 3
`compareCluster`, 6, 11, 13, 18, 19
`compareClusterResult`, 19

`DataSet`, 7
`DE_GSE8057 (DataSet)`, 7
`download_KEGG`, 7
`dropGO`, 8

`enrichDAVID`, 8
`enricher`, 9
`enrichGO`, 6, 10
`enrichKEGG`, 12
`enrichMKEGG`, 13
`enrichWP`, 14

`gcSample (DataSet)`, 7
`get_wp_organisms`, 15
`Gff2GeneTable`, 15
`go2ont`, 16
`go2term`, 16
`gofilter`, 17
`groupGO`, 6, 17, 19
`groupGOResult-class`, 18

GSEA, 19
`gseGO`, 20
`gseKEGG`, 21
`gseMKEGG`, 22
`gseWP`, 23
`idType`, 24
`kegg_species (DataSet)`, 7
`ko2name`, 25
`merge_result`, 25
`plotGOgraph`, 26
`read.gmt`, 27

`search_kegg_organism`, 27
`show,groupGOResult-method`
  - (`groupGOResult-class`), 18
`simplify`, 28
`simplify,compareClusterResult-method`
  - (`simplify`), 28
`simplify,enrichResult-method`
  - (`simplify`), 28
`simplify,gseaResult-method (simplify)`, 28

`uniprot_get`, 29