Package ‘clusterProfiler’

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Type Package

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

Version 3.18.0

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Description This package implements methods to analyze and visualize functional profiles (GO and KEGG) of gene and gene clusters.

Depends R (>= 3.4.0)

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

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

VignetteBuilder knitr

ByteCompile true

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

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

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Li-Gen Wang [ctb],
Giovanni Dall’Olio [ctb] (formula interface of compareCluster)
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
```
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
**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", "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

```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)

<table>
<thead>
<tr>
<th>Dataset</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>gcSample</td>
<td>Datasets gcSample contains a sample of gene clusters.</td>
</tr>
<tr>
<td>kegg_species</td>
<td>Datasets kegg_species contains kegg species information</td>
</tr>
</tbody>
</table>

### download_KEGG

**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

**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

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**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
)
Arguments

gene  input gene
idType  id type
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 for testing
maxGSSize  maximal size of genes annotated for testing
annotation  david annotation
pvalueCutoff  adjusted p-value cutoff on enrichment tests to report
pAdjustMethod  one of "holm", "hochberg", "hommel", "bonferroni", "BH", "BY", "fdr", "none"
qvalueCutoff  q-value cutoff on enrichment tests to report as significant. Tests must pass i) pvalueCutoff on unadjusted p-values, ii) pvalueCutoff on adjusted p-values and iii) qvalueCutoff on q-values to be reported.
species  species
david.user  david user

Value

A enrichResult instance

Author(s)

Guangchuang Yu

Description

A universal enrichment analyzer

Usage

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

**Arguments**

- `gene` (a vector of gene id)
- `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.
- `minGSSize` (minimal size of genes annotated 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.
- `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

---

```r
enrichGO(gene, OrgDb, keyType = "ENTREZID", ont = "MF", pvalueCutoff = 0.05, pAdjustMethod = "BH", universe, qvalueCutoff = 0.2, minGSSize = 10, maxGSSize = 500, readable = FALSE, pool = FALSE)
```

**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**

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

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

See Also

enrichResult-class, compareCluster

Examples

```r
## 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

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.
enrichKEGG

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', 'ncbi-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 (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.
use_internal_data logical, use KEGG.db or latest online KEGG data

Value

A enrichResult instance.

Author(s)

Guangchuang Yu http://guangchuangyu.github.io

See Also

enrichResult-class, compareCluster

Examples

data(geneList, package='DOSE')
de <- names(geneList)[1:100]
yy <- enrichKEGG(de, pvalueCutoff=0.01)
head(yy)
enrichMKEGG  

**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
- `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

Description

list supported organism of WikiPathways

Usage

get_wp_organisms()

Details

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

Value

supported organism list
**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
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`: 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](http://guangchuangyu.github.io)

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

See Also

- compareClusterResult
- compareCluster
- groupGO
- GSEA

**GSEA**

Description

a universal gene set enrichment analysis tools

Usage

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

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

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 gene list
- organism: supported organism listed in 'http://www.genome.jp/kegg/catalog/org_list.html'
- keyType: one of 'kegg', 'ncbi-geneid', 'ncbi-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, ...)

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

---

<table>
<thead>
<tr>
<th>idType</th>
<th>idType</th>
</tr>
</thead>
</table>

**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

---

**KEGG_path2extid**

**Description**

query all genes in a KEGG pathway or module

**Usage**

`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

---

**ko2name**

**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

plotGOgraph

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 (retangle 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
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

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 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(
ex,  
cutoff = 0.7,  
by = "p.adjust",  
select_fun = min,  
measure = "Wang",  
semData = NULL
)

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

## S4 method for signature 'compareClusterResult'
simplify(
ex,  
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](https://github.com/GuangchuangYu/clusterProfiler/issues/28)
- issue #162 [https://github.com/GuangchuangYu/clusterProfiler/issues/162](https://github.com/GuangchuangYu/clusterProfiler/issues/162)

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**uniprot_get**

**Description**
- retrieve annotation data from uniprot

**Usage**

```r
uniprot_get(taxID)
```

**Arguments**
- `taxID` taxonomy ID

**Value**
- gene table data frame

**Author(s)**
- guangchuang yu
viewKEGG

**Description**

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

**Usage**

```r
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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