

Package ‘clusterProfiler’

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Type Package

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

Version 3.16.1

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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
(>= 1.7.1), 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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URL <https://guangchuangyu.github.io/software/clusterProfiler>

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

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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*

Description

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

bitr	<i>bitr</i>
------	-------------

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	<i>bitr_kegg</i>
-----------	------------------

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*

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`*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	<i>Compare gene clusters functional profile</i>
----------------	---

Description

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

Usage

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

Arguments

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

Value

A clusterProfResult instance.

Author(s)

Guangchuang Yu <https://guangchuangyu.github.io>

See Also

[compareClusterResult-class](#), [groupGO](#) [enrichGO](#)

Examples

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

## formula interface
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	<i>Datasets gcSample contains a sample of gene clusters.</i>
---------	--

Description

Datasets gcSample contains a sample of gene clusters.

Datasets kegg_species contains kegg species information

download_KEGG	<i>download_KEGG</i>
---------------	----------------------

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

dropGO	<i>dropGO</i>
--------	---------------

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	<i>enrichDAVID</i>
-------------	--------------------

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 (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	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

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 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

enrichGO	<i>GO Enrichment Analysis of a gene set. Given a vector of genes, this function will return the enrichment GO categories after FDR control.</i>
----------	---

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 "BP", "MF", and "CC" subontologies, or "ALL" for all three.
pvalueCutoff	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

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	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	<i>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.</i>
-------------	--

Description

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

Usage

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

Arguments

gene	a vector of entrez gene id.
organism	supported organism listed in ' http://www.genome.jp/kegg/catalog/org_list.html '
keyType	one of "kegg", 'ncbi-geneid', 'ncib-proteinid' and 'uniprot'
pvalueCutoff	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.

Gff2GeneTable	<i>Gff2GeneTable</i>
---------------	----------------------

Description

read GFF file and build gene information table

Usage

```
Gff2GeneTable(gffFile, compress = TRUE)
```

Arguments

<code>gffFile</code>	GFF file
<code>compress</code>	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	<i>go2ont</i>
--------	---------------

Description

convert goid to ontology (BP, CC, MF)

Usage

```
go2ont(goid)
```

Arguments

<code>goid</code>	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

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	<i>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.</i>
---------	--

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)
```

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 <https://guangchuangyu.github.io>

See Also

[compareClusterResult](#) [compareCluster](#) [groupGO](#)

GSEA

GSEA

Description

a universal gene set enrichment analysis tools

Usage

```
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	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

gseGO

gseGO

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

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

gseMKEGG

gseMKEGG

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

idType

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

KEGG_path2extid	<i>KEGG_path2extid</i>
-----------------	------------------------

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	<i>ko2name</i>
---------	----------------

Description

convert ko ID to descriptive name

Usage

```
ko2name(ko)
```

Arguments

ko	ko ID
----	-------

Value

data.frame

Author(s)

guangchuang yu

merge_result	<i>merge_result</i>
--------------	---------------------

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	<i>plotGOgraph</i>
-------------	--------------------

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

read.gmt

Description

parse gmt file to a data.frame

Usage

```
read.gmt(gmtfile)
```

Arguments

gmtfile	gmt file
---------	----------

Value

data.frame

Author(s)

Guangchuang Yu

search_kegg_organism *search_kegg_organism*

Description

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

Usage

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

Arguments

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

Value

data.frame

Author(s)

Guangchuang Yu

simplify *simplify method*

Description

simplify output from enrichGO and gseGO 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 'gseaResult'
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

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References

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

uniprot_get	<i>uniprot_get</i>
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Description

retrieve annotation data from uniprot

Usage

```
uniprot_get(taxID)
```

Arguments

taxID	taxonomy ID
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Value

gene table data frame

Author(s)

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viewKEGG	<i>viewKEGG function is for visualize KEGG pathways works with enrichResult object to visualize enriched KEGG pathway</i>
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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

References

Luo et al. (2013) Pathview: an R/Bioconductor package for pathway-based data integration and visualization. *Bioinformatics* (Oxford, England), 29:14 1830–1831, 2013. ISSN 1367-4803 <http://bioinformatics.oxfordjournals.org/content/abstract/29/14/1830.abstract> PMID: 23740750

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