Package 'clusterProfiler'

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Type Package

Title A universal enrichment tool for interpreting omics data

Version 4.8.3

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 univeral 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 (>= 3.23.2), dplyr, enrichplot (>= 1.9.3), GO.db, GOSemSim (>= 2.26.1), gson (>= 0.0.7), magrittr, methods, plyr, qvalue, rlang, stats, tidyr, utils, yulab.utils (>= 0.0.7)

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

VignetteBuilder knitr

ByteCompile true

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URL https://yulab-smu.top/biomedical-knowledge-mining-book/ (docs), https://doi.org/10.1016/j.xinn.2021.100141 (paper)

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

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

Encoding UTF-8

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Author Guangchuang Yu [aut, cre, cph]
    (<https://orcid.org/0000-0002-6485-8781>),
    Li-Gen Wang [ctb],
    Erqiang Hu [ctb],
    Xiao Luo [ctb],
    Meijun Chen [ctb],
    Giovanni Dall'Olio [ctb],
    Wanqian Wei [ctb],
    Chun-Hui Gao [ctb] (<https://orcid.org/0000-0002-1445-7939>)

R **topics documented:**

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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   *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   *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*

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 undirectly (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 = "",
  source_from = NULL,
  ...
)
```

Arguments

geneClusters	a list of entrez gene id. Alternatively, a formula of type `Entrez~group` or a formula of type `Entrez	logFC ~ group` for "gseGO", "gseKEGG" and "GSEA".
fun	One of "groupGO", "enrichGO", "enrichKEGG", "enrichDO" or "enrichPathway" . Users can also supply their own function.
data	if geneClusters is a formula, the data from which the clusters must be extracted.
source_from	If using a custom function in "fun", provide the source package as a string here. Otherwise, the function will be obtained from the global environment.
...	Other arguments.

Value

A `clusterProfResult` instance.

Author(s)

Guangchuang Yu <https://yulab-smu.top>

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")
dotplot(xx)

## formula interface
mydf <- data.frame(Entrez=c('1', '100', '1000', '100101467',
                            '100127206', '100128071'),
                   logFC = c(1.1, -0.5, 5, 2.5, -3, 3),
                   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.*

Description

Datasets gcSample contains a sample of gene clusters.

Datasets kegg_species contains kegg species information

Datasets DE_GSE8057 contains differential epxressed genes obtained from GSE8057 dataset

---

download_KEGG   *download_KEGG*

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 *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 *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 (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

---

enricher *enricher*

Description

A universal enrichment analyzer

Usage

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

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.
gson	a GSON object, if not NULL, use it as annotation data.
TERM2GENE	user input annotation of TERM TO GENE mapping, a data.frame of 2 column with term and gene. Only used when gson is NULL.
TERM2NAME	user input of TERM TO NAME mapping, a data.frame of 2 column with term and name. Only used when gson is NULL.

Value

A enrichResult instance

Author(s)

Guangchuang Yu <https://yulab-smu.top>

---

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

Description

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

Usage

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

Arguments

gene	a vector of entrez gene id.
OrgDb	OrgDb
keyType	keytype of input gene
ont	One of "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://yulab-smu.top

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 'https://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 <https://yulab-smu.top>

See Also

[enrichResult-class](), [compareCluster]()

Examples

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

## End(Not run)
```

---

enrichMKEGG   *KEGG Module Enrichment Analysis of a gene set. Given a vector of*
                               genes, this function will return the enrichment KEGG Module cate-
                               gories with FDR control.

Description

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

Usage

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

Arguments

gene	a vector of entrez gene id.
organism	supported organism listed in 'https://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.

Value

A enrichResult instance.

---

enrichWP   *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_organism*

Description

list supported organism of WikiPathways

Usage

```
get_wp_organisms()
```

Details

This function extracts information from 'https://wikipathways-data.wmcloud.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

```
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   *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

```
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 https://yulab-smu.top

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://yulab-smu.top>

See Also

[compareClusterResult](compareCluster) [compareCluster](groupGO) 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",
  gson = NULL,
  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	one of "holm", "hochberg", "hommel", "bonferroni", "BH", "BY", "fdr", "none"
gson	a GSON object, if not NULL, use it as annotation data.
TERM2GENE	user input annotation of TERM TO GENE mapping, a data.frame of 2 column with term and gene. Only used when gson is NULL.

TERM2NAME	user input of TERM TO NAME mapping, a data.frame of 2 column with term and name. Only used when gson is NULL.
verbose	logical
seed	logical
by	one of 'fgsea' or 'DOSE'
...	other parameter

Value

gseaResult object

Author(s)

Guangchuang Yu <https://yulab-smu.top>

---

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 'https://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 'https://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

---

gseWP   *gseWP*

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 GSEA() function

Details

This function performs GSEA using WikiPathways

Value

A gseaResult instance

Author(s)

Guangchuang Yu

---

gson_GO   *gson_KEGG*

Description

download the latest version of KEGG pathway and stored in a 'GSON' object

Usage

```
gson_GO(OrgDb, keytype = "ENTREZID", ont = "BP")
```

Arguments

`OrgDb`	OrgDb
`keytype`	keytype of genes.
`ont`	one of "BP", "MF", "CC", and "ALL"

Value

a 'GSON' object

`gson_KEGG`	*gson_KEGG*

Description

download the latest version of KEGG pathway and stored in a 'GSON' object

Usage

```
gson_KEGG(species, KEGG_Type = "KEGG", keyType = "kegg")
```

Arguments

`species`	species
`KEGG_Type`	one of "KEGG" and "MKEGG"
`keyType`	one of "kegg", 'ncbi-geneid', 'ncib-proteinid' and 'uniprot'.

Value

a 'GSON' object

Author(s)

Guangchuang Yu

---

gson_KEGG_mapper   *Build KEGG annotation for novel species using KEGG Mapper*

Description

KEGG Mapper service can annotate protein sequences for novel species with KO database, and KO annotation need to be converted into Pathway or Module annotation, which can then be used in 'clusterProfiler'

Usage

```
gson_KEGG_mapper(
  file,
  format = c("BLAST", "Ghost", "Kofam"),
  type = c("pathway", "module"),
  species = NULL,
  ...
)
```

Arguments

`file`	the name of the file which comes from the KEGG Mapper service, see Details for file format
`format`	string indicate format of KEGG Mapper result
`type`	string indicate annotation database
`species`	your species, NULL if ignored
`...`	pass to gson::gson()

Details

File is a two-column dataset with K numbers in the second column, optionally preceded by the user's identifiers in the first column. This is consistent with the output files of automatic annotation servers, BlastKOALA, GhostKOALA, and KofamKOALA. KOALA (KEGG Orthology And Links Annotation) is KEGG's internal annotation tool for K number assignment of KEGG GENES using SSEARCH computation. BlastKOALA and GhostKOALA assign K numbers to the user's sequence data by BLAST and GHOSTX searches, respectively, against a nonredundant set of KEGG GENES. KofamKOALA is a new member of the KOALA family available at GenomeNet using the HMM profile search, rather than the sequence similarity search, for K number assignment. see https://www.kegg.jp/blastkoala/, https://www.kegg.jp/ghostkoala/ and https://www.genome.jp/tools/kofamkoala/ for more information.

Value

a gson instance

Examples

```
## Not run:
 file = system.file('extdata', "kegg_mapper_blast.txt", package='clusterProfiler')
 gson_KEGG_mapper(file, format = "BLAST", type = "pathway")

## End(Not run)
```

---

gson_WP   *gson_WP*

Description

Download the latest version of WikiPathways data and stored in a 'GSON' object

Usage

```
gson_WP(organism)
```

Arguments

organism   supported organism, which can be accessed via the get_wp_organisms() func-
              tion.

---

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

---

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 *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

parse_gff   *parse_gff*

Description

parse GAF files

Usage

```
parse_gff(GafFile, nrows = -1)
```

Arguments

GafFile   GAF file

nrows   a parameter

Details

given a GAF file, this function extracts the information from it

Value

a list with two dataframes

plotGOgraph   *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

Value

GO DAG graph

Author(s)

Guangchuang Yu

---

reexports	*Objects exported from other packages*

Description

These objects are imported from other packages. Follow the links below to see their documentation.

DOSE geneID, geneInCategory, gsfilter, setReadable

dplyr arrange, filter, group_by, mutate, n, rename, select, slice, summarise

enrichplot cnetplot, dotplot, emapplot, goplot, gseaplot, heatplot, ridgeplot

GOSemSim read.blast2go

gson read.gmt, read.gmt.wp

magrittr %<>%, %>%

---

search_kegg_organism   *search_kegg_organism*

Description

search kegg organism, listed in https://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

---

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

Author(s)

Guangchuang Yu

Gwang-Jin Kim and 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

retreve annotation data from uniprot

Usage

```
uniprot_get(taxID)
```

Arguments

taxID   taxonomy ID

Value

gene table data frame

Author(s)

guangchuang yu

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