

# Package ‘clusterProfiler’

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**Type** Package

**Title** A universal enrichment tool for interpreting omics data

**Version** 4.13.0

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**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.

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<https://doi.org/10.1016/j.xinn.2021.100141> (paper)

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

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clusterProfiler-package

*clusterProfiler: A universal enrichment tool for interpreting omics data*

---

## 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.

## Author(s)

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**See Also**

Useful links:

- [https://yulab-smu.top/biomedical-knowledge-mining-book/\(docs\)](https://yulab-smu.top/biomedical-knowledge-mining-book/(docs))
- [doi:10.1016/j.xinn.2021.100141](https://doi.org/10.1016/j.xinn.2021.100141) (paper)
- Report bugs at <https://github.com/GuangchuangYu/clusterProfiler/issues>

---

append\_kegg\_category    *append\_kegg\_category*

---

**Description**

add KEGG pathway category information

**Usage**

```
append_kegg_category(x)
```

**Arguments**

x                    KEGG enrichment result

**Details**

This function appends the KEGG pathway category information to KEGG enrichment result (either output of 'enrichKEGG' or 'gseKEGG')

**Value**

update KEGG enrichment result with category information

**Author(s)**

Guangchuang Yu

---

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

**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>
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---

**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	<i>browseKEGG</i>
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---

**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

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

**Arguments**

geneClusters	a list of entrez gene id. Alternatively, a formula of type <code>Entrez~group</code> or a formula of type <code>Entrez   logFC ~ group</code> 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	<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

Datasets kegg\_category contains kegg pathway category information

Datasets DE\_GSE8057 contains differential expressed genes obtained from GSE8057 dataset

---

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

### 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 <code>bitr_kegg</code>

### Value

list

### Author(s)

Guangchuang Yu



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

**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>
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---

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

---

### 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 ' <a href="https://www.genome.jp/kegg/catalog/org_list.html">https://www.genome.jp/kegg/catalog/org_list.html</a> '
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 categories with FDR control.*

---

**Description**

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

**Usage**

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

**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.

---

enrichPC	<i>enrichPC</i>
----------	-----------------

---

**Description**

ORA analysis for Pathway Commons

**Usage**

```
enrichPC(gene, source, keyType = "hgnc", ...)
```

**Arguments**

gene	a vector of genes (either hgnc symbols or uniprot IDs)
source	Data source of Pathway Commons, e.g., 'reactome', 'kegg', 'pathbank', 'net-path', 'panther', etc.
keyType	specify the type of input 'gene' (one of 'hgnc' or 'uniprot')
...	additional parameters, see also the parameters supported by the <code>enricher()</code> function

**Details**

This function performs over-representation analysis using Pathway Commons

**Value**

A `enrichResult` instance

---

enrichWP	<i>enrichWP</i>
----------	-----------------

---

**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 <code>get_wp_organisms()</code> function
...	additional parameters, see also the parameters supported by the <code>enricher()</code> function

**Details**

This function performs over-representation analysis using WikiPathways

**Value**

A `enrichResult` instance

**Author(s)**

Guangchuang Yu

---

getPPI	<i>getPPI</i>
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---

**Description**

getPPI



**Usage**

```

getPPI(
  x,
  ID = 1,
  taxID = "auto",
  required_score = NULL,
  network_type = "functional",
  add_nodes = 0,
  show_query_node_labels = 0,
  output = "igraph"
)

```

**Arguments**

x	an ‘enrichResult‘ object or a vector of proteins, e.g. ‘c("PTCH1", "TP53", "BRCA1", "BRCA2")‘
ID	ID or index to extract genes in the enriched term(s) if ‘x‘ is an ‘enrichResult‘ object
taxID	NCBI taxon identifiers (e.g. Human is 9606, see: [STRING organisms](https://string-db.org/cgi/input.pl?input_page_active_form=organisms)).
required_score	threshold of significance to include a interaction, a number between 0 and 1000 (default depends on the network)
network_type	network type: functional (default), physical
add_nodes	adds a number of proteins with to the network based on their confidence score (default:1)
show_query_node_labels	when available use submitted names in the preferredName column when (0 or 1) (default:0)
output	one of ‘data.frame‘ or ‘igraph‘

**Details**

[Getting the STRING network interactions](https://string-db.org/cgi/help.pl?sessionId=btsvnCeNrBk7).

**Value**

a ‘data.frame‘ or an ‘igraph‘ object

**Author(s)**

Yonghe Xia and modified by Guangchuang Yu

---

<code>getTaxID</code>	<i>getTaxID</i>
-----------------------	-----------------

---

**Description**

Convert species scientific name to taxonomic ID

**Usage**

```
getTaxID(species)
```

**Arguments**

<code>species</code>	scientific name of a species
----------------------	------------------------------

**Value**

taxonomic ID

**Author(s)**

Guangchuang Yu

---

<code>getTaxInfo</code>	<i>getTaxInfo</i>
-------------------------	-------------------

---

**Description**

Query taxonomy information from 'stringdb' or 'ensembl' web services

**Usage**

```
getTaxInfo(species, source = "stringdb")
```

**Arguments**

<code>species</code>	scientific name of a species
<code>source</code>	one of 'stringdb' or 'ensembl'

**Value**

a 'data.frame' of query information

**Author(s)**

Guangchuang Yu

---

get_wp_organisms	<i>get_wp_organism</i>
------------------	------------------------

---

**Description**

list supported organism of WikiPathways

**Usage**

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

---

**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](#) [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 ' <a href="https://www.genome.jp/kegg/catalog/org_list.html">https://www.genome.jp/kegg/catalog/org_list.html</a> '
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 ' <a href="https://www.genome.jp/kegg/catalog/org_list.html">https://www.genome.jp/kegg/catalog/org_list.html</a> '
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

---

gsePC

*gsePC*


---

**Description**

GSEA analysis for Pathway Commons

**Usage**

```
gsePC(geneList, source, keyType, ...)
```

**Arguments**

geneList	a ranked gene list
source	Data source of Pathway Commons, e.g., 'reactome', 'kegg', 'pathbank', 'net-path', 'panther', etc.
keyType	specify the type of input 'gene' (one of 'hgnc' or 'uniprot')
...	additional parameters, see also the parameters supported by the GSEA() function

**Details**

This function performs GSEA using Pathway Commons

**Value**

A gseaResult instance

---

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	<i>Build KEGG annotation for novel species using KEGG Mapper</i>
------------------	--

---

**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()` function.

---

idType	<i>idType</i>
--------	---------------

---

**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	<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.pc

*read.gmt.pc*

---

**Description**

Parse gmt file from Pathway Common

**Usage**

```
read.gmt.pc(gmtfile, output = "data.frame")
```

**Arguments**

gmtfile	A gmt file
output	one of 'data.frame' or 'GSON'

**Details**

This function parse gmt file downloaded from Pathway common

**Value**

A data.frame or A GSON object depends on the value of 'output'

---

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** [buildGOMap](#), [read.blast2go](#), [read.gaf](#)

**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](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**

<code>x</code>	output of enrichGO
<code>cutoff</code>	similarity cutoff
<code>by</code>	feature to select representative term, selected by 'select_fun' function
<code>select_fun</code>	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**

retrieves 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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