

# Package ‘clusterProfiler’

November 4, 2018

**Type** Package

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

**Version** 3.10.0

**Maintainer** Guangchuang Yu <guangchuangyu@gmail.com>

**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, DOSE (>= 3.5.1), enrichplot (>= 0.99.7),  
ggplot2, GO.db, GOSemSim, magrittr, methods, plyr, qvalue,  
rvcheck, stats, tidyr, utils

**Suggests** AnnotationHub, GSEABase, KEGG.db, knitr, org.Hs.eg.db,  
prettydoc, pathview, ReactomePA, testthat

**VignetteBuilder** knitr

**ByteCompile** true

**License** Artistic-2.0

**URL** <https://guangchuangyu.github.io/software/clusterProfiler>

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

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

**RoxygenNote** 6.1.0

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Li-Gen Wang [ctb],  
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* The package implements methods to analyze and visualize functional profiles of gene and gene clusters.

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**Description**

statistical analysis and visualization of functional profiles for genes and gene clusters The package implements methods to analyze and visualize functional profiles of gene and gene clusters.

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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>
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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

*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 = "", ...)
```

**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)
```

---

compareClusterResult-class

*Class "compareClusterResult" This class represents the comparison result of gene clusters by GO categories at specific level or GO enrichment analysis.*

---

### Description

Class "compareClusterResult" This class represents the comparison result of gene clusters by GO categories at specific level or GO enrichment analysis.

### Slots

compareClusterResult cluster comparing result  
 geneClusters a list of genes  
 fun one of groupGO, enrichGO and enrichKEGG  
 .call function call

### Author(s)

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

### See Also

[groupGOResult](#) [enrichResult](#) [compareCluster](#)

---

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

---

dotplot,compareClusterResult-method  
*dotplot*

---

## Description

dot plot method

## Usage

```
## S4 method for signature 'compareClusterResult'
dotplot(object, x = ~Cluster,
  color = "p.adjust", showCategory = 5, split = NULL,
  font.size = 12, title = "", by = "geneRatio", includeAll = TRUE)
```

## Arguments

object	compareClusterResult object
x	x variable
color	one of pvalue or p.adjust
showCategory	category numbers
split	ONTOLOGY or NULL
font.size	font size
title	figure title
by	one of geneRatio, Percentage or count
includeAll	logical

---

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 <code>bitr_kegg</code>

## 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
minGSSize	minimal size of genes annotated for testing
maxGSSize	maximal size of genes annotated for testing
annotation	david annotation
pvalueCutoff	pvalueCutoff
pAdjustMethod	one of "BH" and "bonferroni"
qvalueCutoff	qvalutCutoff
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
pAdjustMethod	one of "holm", "hochberg", "hommel", "bonferroni", "BH", "BY", "fdr", "none"
universe	background genes
minGSSize	minimal size of genes annotated for testing
maxGSSize	maximal size of genes annotated for testing
qvalueCutoff	qvalue cutoff
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 "MF", "BP", and "CC" subontologies.
pvalueCutoff	Cutoff value of pvalue.
pAdjustMethod	one of "holm", "hochberg", "hommel", "bonferroni", "BH", "BY", "fdr", "none"
universe	background genes
qvalueCutoff	qvalue cutoff
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	<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>
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---

**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="http://www.genome.jp/kegg/catalog/org_list.html">http://www.genome.jp/kegg/catalog/org_list.html</a> '
keyType	one of "kegg", 'ncbi-geneid', 'ncib-proteinid' and 'uniprot'
pvalueCutoff	Cutoff value of pvalue.
pAdjustMethod	one of "holm", "hochberg", "hommel", "bonferroni", "BH", "BY", "fdr", "none"
universe	background genes
minGSSize	minimal size of genes annotated by Ontology term for testing.
maxGSSize	maximal size of genes annotated for testing
qvalueCutoff	qvalue cutoff
use_internal_data	logical, use KEGG.db or latest online KEGG data

**Value**

A enrichResult instance.

**Author(s)**

Guangchuang Yu <http://ygc.name>

**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 ' <a href="http://www.genome.jp/kegg/catalog/org_list.html">http://www.genome.jp/kegg/catalog/org_list.html</a> '
keyType	one of "kegg", 'ncbi-geneid', 'ncib-proteinid' and 'uniprot'
pvalueCutoff	Cutoff value of pvalue.
pAdjustMethod	one of "holm", "hochberg", "hommel", "bonferroni", "BH", "BY", "fdr", "none"
universe	background genes
minGSSize	minimal size of genes annotated by Ontology term for testing.
maxGSSize	maximal size of genes annotated for testing
qvalueCutoff	qvalue cutoff

**Value**

A `enrichResult` instance.

---

```
fortify.compareClusterResult  
  fortify
```

---

**Description**

convert compareClusterResult to a data.frame that ready for plot

**Usage**

```
## S3 method for class 'compareClusterResult'  
fortify(model, data, showCategory = 5,  
  by = "geneRatio", split = NULL, includeAll = TRUE)
```

**Arguments**

model	compareClusterResult object
data	not use here
showCategory	category numbers
by	one of geneRatio, Percentage or count
split	ONTOLOGY or NULL
includeAll	logical

**Value**

data.frame

**Author(s)**

Guangchuang Yu

---

```
getGOLevel          get GOIDs at a specific level
```

---

**Description**

query GOIDs at a specific level.

**Usage**

```
getGOLevel(ont, level)
```

**Arguments**

ont	Ontology
level	GO level

**Value**

a vector of GOIDs

**Author(s)**

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

---

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

**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	<i>go2ont</i>
--------	---------------

---

**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	<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://ygc.name>

## 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	<i>Class "groupGOResult" This class represents the result of functional Profiles of a set of gene at specific GO level.</i>
---------------------	---

---

**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, nPerm = 1000, minGSSize = 10,
     maxGSSize = 500, pvalueCutoff = 0.05, pAdjustMethod = "BH",
     TERM2GENE, TERM2NAME = NA, verbose = TRUE, seed = FALSE,
     by = "fgsea")
```

**Arguments**

geneList	order ranked geneList
exponent	weight of each step
nPerm	number of permutations
minGSSize	minimal size of each geneSet for analyzing
maxGSSize	maximal size of genes annotated for testing
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'

**Value**

gseaResult object

**Author(s)**

Guangchuang Yu

---

gseGO	<i>gseGO</i>
-------	--------------

---

**Description**

Gene Set Enrichment Analysis of Gene Ontology

**Usage**

```
gseGO(geneList, ont = "BP", OrgDb, keyType = "ENTREZID",
      exponent = 1, nPerm = 1000, minGSSize = 10, maxGSSize = 500,
      pvalueCutoff = 0.05, pAdjustMethod = "BH", verbose = TRUE,
      seed = FALSE, by = "fgsea")
```

**Arguments**

geneList	order ranked geneList
ont	one of "BP", "MF", "CC" or "GO"
OrgDb	OrgDb
keyType	keytype of gene
exponent	weight of each step
nPerm	permutation numbers

minGSSize	minimal size of each geneSet for analyzing
maxGSSize	maximal size of genes annotated for testing
pvalueCutoff	pvalue Cutoff
pAdjustMethod	pvalue adjustment method
verbose	print message or not
seed	logical
by	one of 'fgsea' or 'DOSE'

**Value**

gseaResult object

**Author(s)**

Yu Guangchuang

---

gseKEGG	<i>gseKEGG</i>
---------	----------------

---

**Description**

Gene Set Enrichment Analysis of KEGG

**Usage**

```
gseKEGG(geneList, organism = "hsa", keyType = "kegg", exponent = 1,
        nPerm = 1000, minGSSize = 10, maxGSSize = 500,
        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="http://www.genome.jp/kegg/catalog/org_list.html">http://www.genome.jp/kegg/catalog/org_list.html</a> '
keyType	one of "kegg", 'ncbi-geneid', 'ncib-proteinid' and 'uniprot'
exponent	weight of each step
nPerm	permutation numbers
minGSSize	minimal size of each geneSet for analyzing
maxGSSize	maximal size of genes annotated for testing
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'

**Value**

gseaResult object

**Author(s)**

Yu Guangchuang

---

gseMKEGG	<i>gseMKEGG</i>
----------	-----------------

---

**Description**

Gene Set Enrichment Analysis of KEGG Module

**Usage**

```
gseMKEGG(geneList, organism = "hsa", keyType = "kegg", exponent = 1,
  nPerm = 1000, minGSSize = 10, maxGSSize = 500,
  pvalueCutoff = 0.05, pAdjustMethod = "BH", verbose = TRUE,
  seed = FALSE, by = "fgsea")
```

**Arguments**

geneList	order ranked geneList
organism	supported organism listed in ' <a href="http://www.genome.jp/kegg/catalog/org_list.html">http://www.genome.jp/kegg/catalog/org_list.html</a> '
keyType	one of "kegg", 'ncbi-geneid', 'ncib-proteinid' and 'uniprot'
exponent	weight of each step
nPerm	permutation numbers
minGSSize	minimal size of each geneSet for analyzing
maxGSSize	maximal size of genes annotated for testing
pvalueCutoff	pvalue Cutoff
pAdjustMethod	pvalue adjustment method
verbose	print message or not
seed	logical
by	one of 'fgsea' or 'DOSE'

**Value**

gseaResult object

**Author(s)**

Yu Guangchuang

---

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

---

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`*plotGOgraph*

---

**Description**

plot GO graph

**Usage**

```
plotGOgraph(x, firstSigNodes = 10, useInfo = "all", sigForAll = TRUE,
  useFullNames = TRUE, ...)
```

**Arguments**

<code>x</code>	output of <code>enrichGO</code> or <code>gseGO</code>
<code>firstSigNodes</code>	number of significant nodes (rectangle nodes in the graph)
<code>useInfo</code>	additional info
<code>sigForAll</code>	if TRUE the score/p-value of all nodes in the DAG is shown, otherwise only score will be shown
<code>useFullNames</code>	logical
<code>...</code>	additional parameter of <code>showSigOfNodes</code> , please refer to <code>topGO</code>

**Value**

GO DAG graph

**Author(s)**

Guangchuang Yu

**See Also**

[showSigOfNodes](#)

---

`plotting.clusterProfile`*plotting-clusterProfile*

---

**Description**

Internal plot function for plotting `compareClusterResult`

**Usage**

```
plotting.clusterProfile(clProf.reshape.df, x = ~Cluster, type = "dot",
  colorBy = "p.adjust", by = "geneRatio", title = "",
  font.size = 12)
```

**Arguments**

<code>clProf.reshape.df</code>	data frame of compareCluster result
<code>x</code>	x variable
<code>type</code>	one of dot and bar
<code>colorBy</code>	one of pvalue or p.adjust
<code>by</code>	one of percentage and count
<code>title</code>	graph title
<code>font.size</code>	graph font size

**Value**

ggplot object

**Author(s)**

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

---

`read.gmt`

*read.gmt*

---

**Description**

parse gmt file to a data.frame

**Usage**

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

**Arguments**

<code>gmtfile</code>	gmt file
----------------------	----------

**Value**

data.frame

**Author(s)**

Guangchuang Yu



---

search_kegg_organism	<i>search_kegg_organism</i>
----------------------	-----------------------------

---

**Description**

search kegg organism, listed in [http://www.genome.jp/kegg/catalog/org\\_list.html](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	<i>simplify method</i>
----------	------------------------

---

**Description**

simplify output from enrichGO by removing redundancy of enriched GO terms

simplify output from enrichGO 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
x	output of gseGO
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 gseaResult object  
 updated compareClusterResult object

**Author(s)**

Guangchuang Yu  
 Gwang-Jin Kim  
 Guangchuang Yu

**References**

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

---

uniprot\_get

*uniprot\_get*


---

**Description**

retrieve annotation data from uniprot

**Usage**

```
uniprot_get(taxID)
```

**Arguments**

taxID	taxonomy ID
-------	-------------

**Value**

gene table data frame

**Author(s)**

guangchuang yu

---

viewKEGG

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

---

**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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