

# Package ‘clusterProfiler’

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**Type** Package

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

**Version** 2.4.3

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**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 (>= 3.1.0)

**Imports** DOSE, GOSemSim, AnnotationDbi, methods, stats4, plyr, ggplot2, GO.db, KEGGREST, magrittr, qvalue, topGO

**Suggests** BiocStyle, KEGG.db, knitr, org.Hs.eg.db, pathview, ReactomePA, RDAVIDWebService

**VignetteBuilder** knitr

**License** Artistic-2.0

**URL** <https://github.com/GuangchuangYu/clusterProfiler>

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

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

**NeedsCompilation** no

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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

This package is designed to compare gene clusters functional profiles.

## Details

Package: clusterProfiler  
 Type: Package  
 Version: 1.9.  
 Date: 06-13-2013  
 biocViews: GO, Clustering, Visualization  
 Depends: AnnotationDbi, GO.db, org.Hs.eg.db, ggplot2, plyr, methods  
 Suggests: GOSemSim  
 License: Artistic-2.0

**Author(s)**

Guangchuang Yu <guangchuangyu@gmail.com>

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**See Also**

[compareClusterResult](#), [groupGOResult](#) [enrichResult](#)

---

*bitr*

*bitr*

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**Description**

Biological Id TRanslator

**Usage**

```
bitr(geneID, fromType, toType, annoDb, drop = TRUE)
```

**Arguments**

geneID	input gene id
fromType	input id type
toType	output id type
annoDb	annotation db
drop	drop NA or not

**Value**

data.frame

**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**

GO annotation

**Author(s)**

Yu Guangchuang

---

 buildKEGGmap

*buildKEGGmap*


---

**Description**

build KEGG annotation files

**Usage**

```
buildKEGGmap(keggmap, id2name = NULL, organism)
```

**Arguments**

keggmap                    pathway to external ID  
 id2name                    pathway id to pathway name  
 organism                    organism

**Author(s)**

Guangchuang Yu

---

*cnetplot*

*cnetplot*

---

**Description**

category-gene-net plot

**Usage**

```
cnetplot(x, showCategory = 5, categorySize = "geneNum", foldChange = NULL,  
         fixed = TRUE, ...)
```

**Arguments**

<code>x</code>	enrichResult object
<code>showCategory</code>	number of category plotted
<code>categorySize</code>	one of geneNum or pvalue
<code>foldChange</code>	fold change of expression value
<code>fixed</code>	logical
<code>...</code>	additional parameter

**Details**

category gene association

**Value**

plot

**Author(s)**

ygc

---

compareCluster	<i>Compare gene clusters functional profile</i>
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---

### 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 <code>Entrez~group</code>
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 <http://ygc.name>

### See Also

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

### Examples

```
data(gcSample)
xx <- compareCluster(gcSample, fun="enrichKEGG",
                    organism="human", pvalueCutoff=0.05)
summary(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')
summary(xx.formula)

## formula interface with more than one grouping variable
```

```
xx.formula.twogroups <- compareCluster(Entrez~group+othergroup, data=mydf, fun='groupGO')  
summary(xx.formula.twogroups)
```

---

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

### Author(s)

Guangchuang Yu <http://ygc.name>

### See Also

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

---

DataSet

*Datasets gcSample contains a sample of gene clusters.*

---

### Description

Datasets gcSample contains a sample of gene clusters.

---

dotplot,compareClusterResult-method  
*dotplot*

---

**Description**

dot plot method

**Usage**

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

**Arguments**

object	compareClusterResult object
colorBy	one of pvalue or p.adjust
showCategory	category numbers
by	one of geneRatio, Percentage or count
includeAll	logical
font.size	font size
title	figure title

---

download.KEGG      *download.KEGG*

---

**Description**

download the latest version of KEGG pathway

**Usage**

```
download.KEGG(species)
```

**Arguments**

species	species
---------	---------

**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", listType = "Gene",  
  minGSSize = 5, annotation = "GOTERM_BP_ALL", pvalueCutoff = 0.05,  
  pAdjustMethod = "BH", qvalueCutoff = 0.2, species = NA,  
  david.user = "clusterProfiler@hku.hk")
```

**Arguments**

gene	input gene
idType	id type
listType	list Type
minGSSize	minGSSize
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 = 5, 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
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, organism = "human", ont = "MF", pvalueCutoff = 0.05,
         pAdjustMethod = "BH", universe, qvalueCutoff = 0.2, minGSSize = 5,
         readable = FALSE)
```

**Arguments**

gene	a vector of entrez gene id.
organism	One of "anopheles", "arabidopsis", "bovine", "canine", "celegans", "chicken", "chimp", "coelicolor", "ecolik12", "ecsakai", "fly", "gondii", "human", "malaria", "mouse", "pig", "rat", "rhesus", "xenopus", "yeast" and "zebrafish".
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.
readable	whether mapping gene ID to gene Name

**Value**

A enrichResult instance.

**Author(s)**

Guangchuang Yu <http://ygc.name>

**See Also**

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

**Examples**

```
## Not run:
data(gcSample)
yy <- enrichGO(gcSample[[1]], organism="human", ont="BP", pvalueCutoff=0.01)
head(summary(yy))
plot(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 = "human", pvalueCutoff = 0.05,
  pAdjustMethod = "BH", universe, minGSSize = 5, qvalueCutoff = 0.2,
  readable = FALSE, use_internal_data = FALSE)
```

**Arguments**

gene	a vector of entrez gene id.
organism	One of "anopheles", "arabidopsis", "bovine", "canine", "chicken", "chimp", "ecoli12", "ecsakai", "fly", "human", "malaria", "mouse", "pig", "rat", "rhesus", "worm", "xenopus", "yeast" and "zebrafish".
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.
qvalueCutoff	qvalue cutoff
readable	whether mapping gene ID to gene Name
use_internal_data	logical, if TRUE, use KEGG.db. default is FALSE, will download online KEGG data

**Value**

A enrichResult instance.

**Author(s)**

Guangchuang Yu <http://ygc.name>

**See Also**

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

**Examples**

```
data(gcSample)
yy = enrichKEGG(gcSample[[5]], pvalueCutoff=0.01)
head(summary(yy))
#plot(yy)
```

---

enrichMap

*enrichMap*

---

**Description**

enrichment map

**Usage**

```
enrichMap(x, n = 50, fixed = TRUE, vertex.label.font = 1, ...)
```

**Arguments**

x	gseaResult or enrichResult object
n	maximum number of category to shown
fixed	if set to FALSE, will invoke tkplot
vertex.label.font	font size of vertex label
...	additional parameter

**Details**

enrichMap

**Value**

figure

**Author(s)**

ygc

fortify.compareClusterResult  
*fortify*

---

**Description**

fortify

**Usage**

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

**Arguments**

model	compareClusterResult object
data	not use here
showCategory	category numbers
by	one of geneRatio, Percentage or count
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://ygc.name>

---

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

---

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, organism = "human", ont = "CC", level = 2,  
        readable = FALSE)
```

### Arguments

gene	a vector of entrez gene id.
organism	One of "anopheles", "arabidopsis", "bovine", "canine", "chicken", "chimp", "coelicolor", "ecolik12", "ecsakai", "fly", "gondii", "human", "malaria", "mouse", "pig", "rat", "rhesus", "worm", "xenopus", "yeast" and "zebrafish".
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]], organism="human", 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  
 geneInCategory gene and category association  
 readable logical flag of gene ID in symbol or not.

### Author(s)

Guangchuang Yu <http://ygc.name>

### See Also

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

---

GSEA

*GSEA*

---

### Description

a universal gene set enrichment analysis tools

### Usage

```
GSEA(geneList, exponent = 1, nPerm = 1000, minGSSize = 10,
     pvalueCutoff = 0.05, pAdjustMethod = "BH", TERM2GENE, TERM2NAME = NA,
     verbose = TRUE)
```

**Arguments**

geneList	order ranked geneList
exponent	weight of each step
nPerm	number of permutations
minGSSize	minimal size of each geneSet for analyzing
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

**Value**

gseaResult object

**Author(s)**

Guangchuang Yu

---

gseaplot

*gseaplot*

---

**Description**

visualize analyzing result of GSEA

**Usage**

```
gseaplot(gseaResult, geneSetID, by = "all")
```

**Arguments**

gseaResult	gseaResult object
geneSetID	geneSet ID
by	one of "runningScore" or "position"

**Details**

plotting function for gseaResult

**Value**

ggplot2 object

**Author(s)**

ygc

gseGO

*gseGO***Description**

Gene Set Enrichment Analysis of Gene Ontology

**Usage**

```
gseGO(geneList, ont = "BP", organism = "human", exponent = 1,
      nPerm = 1000, minGSSize = 10, pvalueCutoff = 0.05,
      pAdjustMethod = "BH", verbose = TRUE)
```

**Arguments**

geneList	order ranked geneList
ont	one of "BP", "MF", "CC" or "GO"
organism	One of "anopheles", "arabidopsis", "bovine", "canine", "chicken", "chimp", "coelicolor", "ecolik12", "ecsakai", "fly", "gondii", "human", "malaria", "mouse", "pig", "rat", "rhesus", "worm", "xenopus", "yeast" and "zebrafish".
exponent	weight of each step
nPerm	permutation numbers
minGSSize	minimal size of each geneSet for analyzing
pvalueCutoff	pvalue Cutoff
pAdjustMethod	pvalue adjustment method
verbose	print message or not

**Value**

gseaResult object

**Author(s)**

Yu Guangchuang

---

gseKEGG

*gseKEGG*

---

### Description

Gene Set Enrichment Analysis of KEGG

### Usage

```
gseKEGG(geneList, organism = "human", exponent = 1, nPerm = 1000,  
        minGSSize = 10, pvalueCutoff = 0.05, pAdjustMethod = "BH",  
        use_internal_data = FALSE, verbose = TRUE)
```

### Arguments

geneList	order ranked geneList
organism	One of "anopheles", "arabidopsis", "bovine", "canine", "chicken", "chimp", "ecoli12", "ecsakai", "fly", "human", "malaria", "mouse", "pig", "rat", "rhesus", "worm", "xenopus", "yeast" and "zebrafish".
exponent	weight of each step
nPerm	permutation numbers
minGSSize	minimal size of each geneSet for analyzing
pvalueCutoff	pvalue Cutoff
pAdjustMethod	pvalue adjustment method
use_internal_data	whether use KEGG.db or not
verbose	print message or not

### Value

gseaResult object

### Author(s)

Yu Guangchuang

---

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

---

**Description**

list ID types supported by annoDb

**Usage**

```
idType(annoDb = "org.Hs.eg.db")
```

**Arguments**

annoDb            annotation db

**Value**

character vector

**Author(s)**

Guangchuang Yu

---

<i>merge_result</i>	<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

---

plot	<i>plot method</i>
------	--------------------

---

## Description

plot method generics

## Usage

```
## S4 method for signature 'compareClusterResult,ANY'  
plot(x, type = "dot",  
     colorBy = "p.adjust", showCategory = 5, by = "geneRatio",  
     includeAll = TRUE, font.size = 12, title = "")
```

## Arguments

x	compareClusterResult object
type	one of bar or dot
colorBy	one of pvalue or p.adjust
showCategory	category numbers
by	one of geneRatio, Percentage or count
includeAll	logical
font.size	font size
title	figure title
...	Additional argument list

## Value

plot

## Author(s)

Guangchuang Yu <http://ygc.name>

---

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

**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

**See Also**

[showSigOfNodes](#)

---

plotting.clusterProfile  
*plotting-clusterProfile*

---

### Description

Internal plot function for plotting compareClusterResult

### Usage

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

### Arguments

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

### Value

ggplot object

### Author(s)

Guangchuang Yu <http://ygc.name>

---

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

---

### 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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