Package ‘clusterProfiler’

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Type Package
Title statistical analysis and visualization of functional profiles for genes and gene clusters
Version 3.2.11
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 (>= 3.3.1), DOSE (>= 3.0.1)
Imports AnnotationDbi, ggplot2, GO.db, GOSemSim (>= 2.0.0), IRanges,
    magrittr, methods, plyr, qvalue, stats, stats4, tidyr, utils
Suggests AnnotationHub, BiocStyle, GSEABase, KEGG.db, knitr,
    org.Hs.eg.db, pathview, ReactomePA, testthat, topGO
VignetteBuilder knitr
ByteCompile true
License Artistic-2.0
URL https://guangchuangyu.github.io/clusterProfiler
BugReports https://github.com/GuangchuangYu/clusterProfiler/issues
biocViews Annotation, Clustering, GeneSetEnrichment, GO, KEGG,
    MultipleComparison, Pathways, Reactome, Visualization
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NeedsCompilation no
Author Guangchuang Yu [aut, cre],
    Li-Gen Wang [ctb],
    Giovanni Dall’Olio [ctb] (formula interface of compareCluster)

R topics documented:

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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.

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
Description

Biological Id TRanslator

Usage

\texttt{bitr(geneID, fromType, toType, OrgDb, drop = TRUE)}

Arguments

\begin{itemize}
  \item \texttt{geneID} \hspace{1cm} input gene id
  \item \texttt{fromType} \hspace{1cm} input id type
  \item \texttt{toType} \hspace{1cm} output id type
  \item \texttt{OrgDb} \hspace{1cm} annotation db
  \item \texttt{drop} \hspace{1cm} drop NA or not
\end{itemize}

Value

\texttt{data.frame}

Author(s)

Guangchuang Yu
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

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**

**Description**
building GO mapping files

**Usage**
buildGOmap(gomap)

**Arguments**
gomap data.frame with two columns of GO and gene ID

**Details**
provided by a data.frame of GO (column 1) and gene (column 2) direct annotation this function will building gene to GO and GO to gene mapping, with directly and indirectly (ancestor GO term) annotation.

**Value**
data.frame, GO annotation with indirect annotation

**Author(s)**
Yu Guangchuang

**compareCluster**

*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.
compareClusterResult-class

Value

A clusterProfResult instance.

Author(s)

Guangchuang Yu [https://guangchuangyu.github.io](https://guangchuangyu.github.io)

See Also

compareClusterResult-class, groupGO enrichGO

Examples

```r
## 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)
```

---

```r
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
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,
  colorBy = "p.adjust", showCategory = 5, by = "geneRatio",
  category = NULL, includeAll = TRUE, font.size = 12, title = "")

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

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
Description

enrichment analysis by DAVID

Usage

enrichDAVID(gene, idType = "ENTREZ_GENE_ID", listType = "Gene", 
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
listType list Type
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 qvalueCutoff
species species
david.user david user

Value

A enrichResult instance

Author(s)

Guangchuang Yu
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

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)
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

Value

An enrichResult instance.

Author(s)

Guangchuang Yu [http://ygc.name](http://ygc.name)

See Also

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

Examples

```r
## Not run:
data(geneList)
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)
```
enrichMKEGG

Arguments

gene a vector of entrez gene id.
organism supported organism listed in 'http://www.genome.jp/kegg/catalog/org_list.html'
keyType one of "kegg", 'ncbi-geneid', 'ncib-proteinid' and 'uniprot'
pvalueCutoff 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)
  de <- names(geneList)[1:100]
  yy <- enrichMKEGG(de, pvalueCutoff=0.01)
  head(summary(yy))
  #plot(yy)

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

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

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

Description

convert compareClusterResult to a data.frame that ready for plot

Usage

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

Arguments

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

Value

data.frame

Author(s)

Guangchuang Yu
getGOLevel  

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

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**

Description
convert goid to ontology (BP, CC, MF)

Usage
```r
go2ont(goid)
```

Arguments
- `goid`: a vector of GO IDs

Value
data.frame

Author(s)
Guangchuang Yu

**go2term**

Description
convert goid to descriptive term

Usage
```r
go2term(goid)
```

Arguments
- `goid`: a vector of GO IDs

Value
data.frame

Author(s)
Guangchuang Yu
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 keytype 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

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 http://ygc.name

See Also

compareClusterResult compareCluster groupGO
GSEA

Description

a universal gene set enrichment analysis tool

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
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
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 'http://www.genome.jp/kegg/catalog/org_list.html'
keyType one of "kegg", 'nebi-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
**Description**

Gene Set Enrichment Analysis of KEGG Module

**Usage**

```r
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 'http://www.genome.jp/kegg/catalog/org_list.html'
- `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
merge_result

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

merge_result

Description
merge a list of enrichResult objects to compareClusterResult

Usage
merge_result(enrichResultList)

Arguments
enrichResultList

Value
a compareClusterResult instance

Author(s)
Guangchuang Yu
Description

plot method generics

Usage

```r
## S4 method for signature 'compareClusterResult,ANY'
plot(x, type = "dot",
     colorBy = "p.adjust", showCategory = 5, by = "geneRatio",
     category = NULL, 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
- `category`: ONTOLOGY or NULL
- `includeAll`: logical
- `font.size`: font size
- `title`: figure title
- `...`: Additional argument list

Value

plot

Author(s)

Guangchuang Yu [http://ygc.name](http://ygc.name)

Description

plot GO graph

Usage

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

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

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

- **clProf.reshape.df**: data frame of compareCluster result
- **x**: x variable
- **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
read.gmt

Author(s)
Guangchuang Yu http://ygc.name

Description
parse gmt file to a data.frame

Usage
read.gmt(gmtfile)

Arguments
gmtfile gmt file

Value
data.frame

Author(s)
Guangchuang Yu

search_kegg_organism

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

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

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

Value
data.frame

Author(s)
Guangchuang Yu
simplify

simplify method

Description

simplify output from enrichGO by removing redundancy of enriched GO terms
simplify output from compareCluster by removing redundancy of enriched GO terms

Usage

```r
## S4 method for signature 'enrichResult'
simplify(x, cutoff = 0.7, by = "p.adjust",
        select_fun = min, measure = "Wang", semData = NULL)
```

```r
## 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
- Guangchuang Yu

References

issue #28 [https://github.com/GuangchuangYu/clusterProfiler/issues/28](https://github.com/GuangchuangYu/clusterProfiler/issues/28)
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

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