Package ‘clusterProfiler’

January 14, 2017

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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     Li-Gen Wang [ctb],
     Giovanni Dall’Olio [ctb] (formula interface of compareCluster)

R topics documented:

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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.

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
Author(s)

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

See Also

compareClusterResult, groupGOResult enrichResult

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`  
`biir_kegg`

**Description**
convert biological ID using KEGG API

**Usage**

```
bitr_kegg(geneID, fromType, toType, organism, drop = TRUE)
```

**Arguments**
- **geneID** input gene id
- **fromType** input id type
- **toType** output id type
- **organism** supported organism, can be search using `search_kegg_organism` function
- **drop** drop NA or not

**Value**
data.frame

**Author(s)**
Guangchuang Yu

---

`browseKEGG`  
`browseKEGG`

**Description**
open KEGG pathway with web browser

**Usage**

```
browseKEGG(x, pathID)
```

**Arguments**
- **x** an instance of enrichResult or gseaResult
- **pathID** pathway ID

**Value**
url

**Author(s)**
Guangchuang Yu
buildGOmap

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.
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'),
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)
Author(s)
Guangchuang Yu https://guangchuangyu.github.io

See Also
    groupGOResult enrichResult compareCluster

---

**DataSet**

Datasets gcSample contains a sample of gene clusters.

Datasets kegg_species contains kegg species information

---

**Description**

dot plot method

**Usage**

```r
## 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
Description

download the latest version of KEGG pathway/module

Usage

download_KEGG(species, keggType = "KEGG", keyType = "kegg")

Arguments

species 
keggType 
keyType 

Value

list

Author(s)

Guangchuang Yu

Description

drop GO term of specific level or specific terms (mostly too general).

Usage

dropGO(x, level = NULL, term = NULL)

Arguments

x 
level 
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
enrichGO

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)
enrichKEGG

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
minGSize minimal size of genes annotated by Ontology term for testing.
maxGSize 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

See Also
enrichResult-class, compareCluster

Examples

## 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, minGSize = 10, maxGSize = 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)

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 'http://www.genome.jp/kegg/catalog/org_list.html'
keyType one of "kegg", 'ncbi-geneid', 'ncib-proteinid' and 'uniprot'
pvalueCutoff Cutoff value of pvalue.
adjMethod one of "holm", "hochberg", "hommel", "bonferroni", "BH", "BY", "fdr", "none"
universe background genes
minGSize minimal size of genes annotated by Ontology term for testing.
maxGSize 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

## 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  get GOIDs at a specific level

**Description**

query GOIDs at a specific level.

**Usage**

getGOLevel(ont, level)

**Arguments**

<table>
<thead>
<tr>
<th>ont</th>
<th>Ontology</th>
</tr>
</thead>
<tbody>
<tr>
<td>level</td>
<td>GO level</td>
</tr>
</tbody>
</table>

**Value**

a vector of GOIDs

**Author(s)**

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

---

Gff2GeneTable  Gff2GeneTable

**Description**

read GFF file and build gene information table

**Usage**

Gff2GeneTable(gffFile, compress = TRUE)

**Arguments**

<table>
<thead>
<tr>
<th>gffFile</th>
<th>GFF file</th>
</tr>
</thead>
<tbody>
<tr>
<td>compress</td>
<td>compress file or not</td>
</tr>
</tbody>
</table>

**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**

go2ont(goid)

**Arguments**

| goid | a vector of GO IDs |

**Value**

data.frame

**Author(s)**

Guangchuang Yu

---

**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

**Description**

filter GO enriched result at specific level

**Usage**

```r
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**

```r
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)
```
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
gseGO

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", '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

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 '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
### idType

**Description**

list ID types supported by annoDb

**Usage**

```r
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**

```r
merge_result(enrichResultList)
```

**Arguments**

- `enrichResultList` : a list of enrichResult objects

**Value**

a compareClusterResult instance

**Author(s)**

Guangchuang Yu
plot method

Description
plot method generics

Usage
## 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

plotGOgraph

Description
plot GO graph

Usage
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
- **useFullName**: 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(c1Prof.reshape.df, x = ~Cluster, type = "dot", colorBy = "p.adjust", by = "geneRatio", title = "", font.size = 12)

Arguments

- **c1Prof.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

Description
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 '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
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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