Package ‘clusterProfiler’

September 24, 2012

Type  Package
Title  statistical analysis and visualization of functional profiles for genes and gene clusters
Version  1.4.0
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Description  The package implements methods to analyze and visualize functional profiles (GO and KEGG) of gene and gene clusters.
Depends  R (>= 2.10), ggplot2
Imports  methods, stats4, DBI, plyr, AnnotationDbi, GO.db, KEGG.db, org.Hs.eg.db, DOSE
Suggests  GOSemSim, ReactomePA
License  Artistic-2.0
URL  http://www.jclinbioinformatics.com/content/1/1/15
biocViews  Bioinformatics, Clustering, GO, Pathways, Visualization,MultipleComparisons

R topics documented:
clusterProfiler-package .................................................. 2
buildGOmap .................................................. 2
compareCluster ............................................. 3
compareClusterResult-class ........................................ 4
DataSet .................................................... 4
enrichGO ................................................... 4
enrichKEGG .................................................. 5
getGOLevel .................................................. 6
Gff2GeneTable ................................................ 6
groupGO .................................................... 7
groupGOResult-class ......................................... 8
plot ....................................................... 8
plotting.clusterProfile ....................................... 9
show ....................................................... 9
summary .................................................... 10
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: 1.0.0
Date: 03-15-2011
biocViews: GO, Clustering, Visualization
Depends: AnnotationDbi, GO.db, org.Hs.eg.db, ggplot2, plyr, methods
Suggests: GOSemSim
License: Artistic-2.0

Author(s)

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See Also

compareClusterResult, groupGOResult, enrichResult

buildGOmap

Description

building GO mapping files

Usage

buildGOmap(gomap)

Arguments

gomap data.frame with two columns names "entrezgene", and "go_accession"
compareCluster

Details

provided by a data.frame of gene and GO directly annotation file this function will building gene to
GO and GO to gene mapping, with directly and undirectly annotation.

Value

files save in the the working directory

Author(s)

Yu Guangchuang

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compareCluster   Compare gene clusters functional profile Given a list of gene set, this
function will compute profiles of each gene cluster.

Description

Compare gene clusters functional profile Given a list of gene set, this function will compute profiles
of each gene cluster.

Usage

compareCluster(geneClusters, fun = "enrichGO", ...)

Arguments

geneClusters    a list of entrez gene id.
fun             One of "groupGO", "enrichGO", "enrichKEGG", "enrichDO" or "enrichPath-
                way".
...             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")
Class "compareClusterResult" This class represents the comparison result of gene clusters by GO categories at specific level or GO enrichment analysis.

Author(s)

Guangchuang Yu http://ygc.name

See Also

groupGOResult enrichResult compareCluster

Description

Datasets gcSample contains a sample of gene clusters.

enrichGO

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

Usage

enrichGO(gene, organism = "human", ont = "MF", pvalueCutoff = 0.05, qvalueCutoff = 0.05, readable = FALSE)

Arguments

gene a vector of entrez gene id.
organism Currently, only "human", "mouse" and "yeast" supported.
ont One of "MF", "BP", and "CC" subontologies.
pvalueCutoff Cutoff value of pvalue.
qvalueCutoff Cutoff value of qvalue.
readable if readable is TRUE, the gene IDs will mapping to gene symbols.
enrichKEGG

Value
A enrichResult instance.

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

See Also
enrichResult-class, compareCluster

Examples
#data(gcSample)
#yy <- enrichGO(gcSample[[1]], organism="human", ont="BP", pvalueCutoff=0.01)
#head(summary(yy))
#plot(yy)

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 = "human", pvalueCutoff = 0.05, qvalueCutoff = 0.05, readable = FALSE)

Arguments
gene a vector of entrez gene id.
organism Currently, only "human" and "mouse" supported.
pvalueCutoff Cutoff value of pvalue.
qvalueCutoff Cutoff value of qvalue.
readable if readable is TRUE, the gene IDs will mapping to gene symbols.

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)

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

Description
read GFF file and build gene information table

Usage
Gff2GeneTable(gffFile)

Arguments
gffFile GFF file

Details
given the GFF file, this function will extract information and save it in working directory
Functional Profile of a gene set at specific GO level. Given a vector of genes, this function will return the GO profile at specific level.

Usage

```r
groupGO(gene, organism = "human", ont = "CC", level = 2, readable = FALSE)
```

Arguments

- `gene`: a vector of entrez gene id.
- `organism`: Currently, only "human" and "mouse" supported.
- `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](http://ygc.name)

See Also

`groupGOResult-class`, `compareCluster`

Examples

```r
data(gcSample)
yy <- groupGO(gcSample[[1]], organism="human", ont="BP", level=2)
head(summary(yy))
#plot(yy)
```
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.

Author(s)

Guangchuang Yu http://ygc.name

See Also

compareClusterResult compareCluster groupGO

plot

plot method

Description

plot method generics

Arguments

... Additional argument list

Value

plot

Author(s)

Guangchuang Yu http://ygc.name
plotting.clusterProfile

Description
Internal plot function for plotting compareClusterResult

Usage
plotting.clusterProfile(clProf.reshape.df, type = "dot", by = "percentage", title = "", font.size = 12)

Arguments
- clProf.reshape.df: data frame of compareCluster result
- type: one of dot and bar
- by: one of percentage and count
- title: graph title
- font.size: graph font size

Value
ggplot object

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

show

Description
show method for compareClusterResult instance
show method for groupGOResult instance

Arguments
- object: A compareClusterResult instance.
- object: A groupGOResult instance

Value
message
message
Author(s)

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**summary**

**summary method**

Description

summary method for `compareClusterResult` instance

Arguments

object A `compareClusterResult` instance.

Value

A data frame

Author(s)

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Index

*Topic **classes**
  compareClusterResult-class, 4
  groupGOResult-class, 8

*Topic **datasets**
  DataSet, 4

*Topic **manip**
  compareCluster, 3
  enrichGO, 4
  enrichKEGG, 5
  groupGO, 7

*Topic **package**
  clusterProfiler-package, 2

buildGOmap, 2

clusterProfiler
  (clusterProfiler-package), 2
  clusterProfiler-package, 2
  compareCluster, 3, 4, 5, 7, 8
  compareClusterResult, 2, 8
  compareClusterResult-class, 4

DataSet, 4

enrichGO, 3, 4
enrichKEGG, 5
enrichResult, 2, 4

gcSample (DataSet), 4
getGOlevel, 6
Gff2GeneTable, 6

groupGO, 3, 7, 8


