Package 'clusterProfiler'

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Type Package

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

Version 1.6.0

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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

biocViews Clustering, GO, Pathways, Visualization,MultipleComparisons, GeneSetEnrichment

Collate 'AllGenerics.R' 'clusterProfiler-
package.R' 'compareCluster.R''enrichGO.R' 'enrichKEGG.R' 'GFFparser.R' 'groupGO.R''utilities.R' 'zzz.R'

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R topics documented:

clusterProfiler-package	*statistical analysis and visulization 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, Visulization
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

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buildGOmap	*buildGOmap*

Description

building GO mapping files

Usage

buildGOmap(gomap)

Arguments

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

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 "enrichPathway" .
...	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")

---

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.

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.

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

Description

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.

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)
```

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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   *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

Value

file save.

Author(s)

Yu Guangchuang

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groupGO	*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.*

Description

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

```
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

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.

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 *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 *show method*

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)

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

summary	*summary method*

Description

summary method for compareClusterResult instance

Arguments

object   A compareClusterResult instance.

Value

A data frame

Author(s)

Guangchuang Yu http://ygc.name

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