Package ‘clusterProfiler’

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Type Package

Title statistical analysis and visulization 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

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biocViews Bioinformatics, Clustering, GO, Pathways, Visualization,MultipleComparisons

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

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

`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

`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.

`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)
```

`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

`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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