

clusterProfiler

October 25, 2011

DataSet

Datasets...

Description

Datasets gcSample contains a sample of gene clusters.

GO2Term

Mapping GOIDs to GO Terms

Description

provide a vector of GOIDs, this function will convert them to corresponding GO Terms

Usage

```
GO2Term(GOID)
```

Arguments

GOID GOID

Value

GO Terms

Author(s)

Guangchuang Yu <http://ygc.name>

HyperG *hypergeometric test*

Description

hypergeometric test for enrichment analysis

Usage

```
HyperG(numWdrawn, numW, numB, numDrawn)
```

Arguments

numWdrawn	number of White balls drawn
numW	number of White balls
numB	number of Black balls
numDrawn	number of balls drawn

Value

pvalue

Author(s)

Guangchuang Yu <http://ygc.name>

clusterProfiler-package
statistical analysis and visulization of functional profiles for genes

Description

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.

Details

This package is designed to compare gene clusters functional profiles.

Package:	clusterProfiler
Type:	Package
Version:	1.0.0
Date:	03-15-2011
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Suggests:	GOSemSim
License:	Artistic-2.0

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See Also

[compareClusterResult](#), [groupGOResult](#) [enrichGOResult](#)

compareCluster *Compare gene clusters functional profile...*

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` and `enrichGO`.
`...` 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"...

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](#) [enrichGOResult](#) [compareCluster](#)

enrichGO

GO Enrichment Analysis of a gene set.

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=0.01, 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.
readable	if readable is TRUE, the gene IDs will mapping to gene symbols.

Value

A `enrichGOResult` instance.

Author(s)

Guangchuang Yu <http://ygc.name>

See Also

[enrichGOResult-class](#), [compareCluster](#)

Examples

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

enrichGOResult-class
Class "enrichGOResult"...

Description

Class "enrichGOResult" This class represents the result of GO enrichment analysis with FDR control.

Author(s)

Guangchuang Yu <http://ygc.name>

See Also

[compareClusterResult](#) [compareCluster](#) [enrichGO](#)

enrichKEGG *KEGG Enrichment Analysis of a gene set.*

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, readable=FALSE)
```

Arguments

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

Value

A `enrichKEGGResult` instance.

Author(s)

Guangchuang Yu <http://ygc.name>

See Also

[enrichKEGGResult-class](#), [compareCluster](#)

Examples

```
data(gcSample)
yy = enrichKEGG(gcSample[[5]], pvalueCutoff=0.01)
head(summary(yy))
#plot(yy)
```

```
enrichKEGGResult-class
      Class "enrichKEGGResult"...
```

Description

Class "enrichKEGGResult" This class represents the result of KEGG enrichment analysis.

Author(s)

Guangchuang Yu <http://ygc.name>

See Also

[compareClusterResult](#) [compareCluster](#) [enrichKEGG](#)

```
geneID2geneName    convert gene IDs to gene Names
```

Description

convert a list of gene IDs to gene Names.

Usage

```
geneID2geneName(geneID.list, organism)
```

Arguments

`geneID.list` a list of gene IDs
`organism` one of human, mouse and yeast.

Value

a list of gene names.

Author(s)

Guangchuang Yu <http://ygc.name>

getGO2ExtID	<i>query genes annotated by given GOIDs</i>
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Description

provide a vector of GOIDs, and organism, this function will return the species specific gene list annotated by the given GOIDs.

Usage

```
getGO2ExtID(GOID, organism)
```

Arguments

GOID	the query GO IDs
organism	one of human, mouse and yeast.

Value

a list of gene IDs, the names of the list is the GOIDs

Author(s)

Guangchuang Yu <http://ygc.name>

getGOLevel	<i>get GOIDs at a specific level</i>
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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>

`getRatio`*getRatio*

Description

provide numerator and denominator, return numerator/denominator

Usage

```
getRatio(a, b)
```

Arguments

a	numerator
b	denominator

Value

numerator/denominator

Author(s)

Guangchuang Yu <http://ygc.name>

`groupGO`*Functional Profile of a gene set at specific GO 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"...

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](#)

pModify

changing title and font size

Description

changing ggplot object's title and font size

Usage

```
pModify(p, title="", font.size=12)
```

Arguments

p	ggplot object
title	graph title
font.size	font size

Details

internal use, not for user.

Author(s)

Guangchuang Yu <http://ygc.name>

path2Name	<i>convert KEGG pathway ID to pathway Name</i>
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Description

provide a vector of KEGG pathway IDs, this function will convert them to corresponding KEGG pathway Names

Usage

```
path2Name (pathIDs)
```

Arguments

pathIDs KEGG pathway IDs

Value

KEGG pathway names

Author(s)

Guangchuang Yu <http://ygc.name>

plot	<i>plot method</i>
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Description

plot method for groupGOResult instance

Arguments

x	A groupGOResult instance
order	logical parameter, order the result by *Count*.
title	graph title
font.size	graph font size
drop	logical parameter, drop void category.

Value

ggplot object

Author(s)

Guangchuang Yu <http://ygc.name>

plotting.barplot *internal function of barplot*

Description

generate a bar plot

Usage

```
plotting.barplot(result, title, font.size=12)
```

Arguments

result	a data frame of enrichment result.
title	graph title
font.size	font size

Details

internal use, not for user.

Value

ggplot object

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="")
```

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 `groupGOREsult` instance

Arguments

`object` A `groupGOREsult` instance

Value

message

Author(s)

Guangchuang Yu <http://ygc.name>

`summary` *summary method*

Description

summary method for `groupGOREsult` instance

Arguments

`object` A `groupGOREsult` instance

Value

A data frame

Author(s)

Guangchuang Yu

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