

# clusterProfiler

October 25, 2011

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DataSet

*Datasets...*

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## Description

Datasets gcSample contains a sample of gene clusters.

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GO2Term

*Mapping GOIDs to GO Terms*

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## 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>

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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>

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

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**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
biocViews:	GO, Clustering, Visulization
Depends:	AnnotationDbi, GO.db, org.Hs.eg.db, ggplot2, plyr, methods
Suggests:	GOSemSim
License:	Artistic-2.0

**Author(s)**

Guangchuang Yu <guangchuangyu@gmail.com>

Maintainer: Guangchuang Yu <guangchuangyu@gmail.com>

**See Also**

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

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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](#)

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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>

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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>

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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.
```

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### 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](#)

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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>

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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>

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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>

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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>

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`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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