Package 'ReactomePA'

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Type Package

Title Reactome Pathway Analysis

Version 1.0.1

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Description This package provides functions for pathway analysis based on REACTOME pathway database. It will implement enrichment analysis, gene set enrichment analysis and functional modules detection.

Dependes R (>= 2.10)

Imports methods, AnnotationDbi, reactome.db, stats4, plyr, igraph0,qvalue, graphics, org.Hs.eg.db

Suggests clusterProfiler, DOSE, GOSemSim

License GPL-2

biocViews Bioinformatics, Pathways, Visualization

Collate 'enrichPathway.R' 'zzz.R' 'cnetplot.R' 'geneID2Name.R' 'pathID2Name.R' 'ReactomePA-package.R'

R topics documented:

ReactomePA-package   *Reactome Pathway Analysis*

Description

This package is designed for reactome pathway analysis.

Details

Package:	ReactomePA
Type:	Package
Version:	0.2.1
Date:	02-09-2012
biocViews:	Bioinformatics, Pathway, Visulization
Depends:	AnnotationDbi, org.Hs.eg.db, igraph0, plyr, methods, stats, qvalue, reactome.db
Suggests:	GOSemSim, DOSE, clusterProfiler
License:	GPL-2

Author(s)

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See Also

enrichPathwayResult

DataSet   *Datasets sample contains a sample of gene IDs.*

Description

Datasets sample contains a sample of gene IDs.

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enrichPathway   *Pathway Enrichment Analysis of a gene set. Given a vector of genes,*
                            this function will return the enriched pathways with FDR control.

Description

Pathway Enrichment Analysis of a gene set. Given a vector of genes, this function will return the enriched pathways with FDR control.

Usage

```
enrichPathway(gene, organism = "human",
  pvalueCutoff = 0.05, qvalueCutoff = 0.05,
  readable = FALSE)
```

Arguments

gene	a vector of entrez gene id.
organism	Currently, only "human" 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 enrichPathwayResult instance.

Author(s)

Guangchuang Yu <http://ygc.name>

See Also

[enrichPathwayResult-class](#)

Examples

```
gene <- c("11171", "8243", "112464", "2194",
"9318", "79026", "1654", "65003",
"6240", "3476", "6238", "3836",
"4176", "1017", "249")
yy = enrichPathway(gene, pvalueCutoff=0.05)
head(summary(yy))
#plot(yy)
```

---

enrichPathwayResult-class

Class "enrichPathwayResult"

Description

This class represents the result of Pathway enrichment analysis.

Methods

In the code snippets below, x is a enrichPathwayResult object.

show show(x) show analysis summary.

summary summary(x) return enrichment result in a data frame.

plot plot(x) visualize enrichment result.

See ?show, ?summary, and ?plot for details of operations on enrichPathwayResult objects.

Author(s)

Guangchuang Yu http://ygc.name

See Also

enrichPathway

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geneID2Name   *convert gene IDs to gene Names*

Description

convert gene IDs to gene Names.

Usage

```
geneID2Name(geneID, annoDb = "org.Hs.eg.db")
```

Arguments

geneID	a vector of gene IDs
annoDb	annotation package name.

Value

a vector of gene names.

Author(s)

Guangchuang Yu http://ygc.name

Examples

```
gene <- as.character(1:10)
geneID2Name(gene, annoDb="org.Hs.eg.db")
```

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pathID2Name   *pathID2Name*

Description

Mapping Pathway ID to Pathway Name

Usage

```
pathID2Name(pathID)
```

Arguments

pathID	query Path ID

Value

Pathway Name

Author(s)

Guangchuang Yu <http://ygc.name>

Examples

```
pathID2Name("1221632")
```

---

plot	*plot method*

Description

plot method for `enrichPathwayResult` instance

Arguments

x	A `enrichPathwayResult` instance.
...	Additional argument list

Value

plot

Author(s)

Guangchuang Yu <http://ygc.name>

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show	*show method*

Description

show method for `enrichPathwayResult` instance

Arguments

object	A `enrichPathwayResult` instance.

Value

message

Author(s)

Guangchuang Yu <http://ygc.name>

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summary   *summary method*

Description

summary method for `enrichPathwayResult` instance

Arguments

object   A `enrichPathwayResult` instance.

Value

A data frame

Author(s)

Guangchuang Yu <http://ygc.name>

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