

Package ‘ReactomePA’

October 9, 2013

Type Package

Title Reactome Pathway Analysis

Version 1.4.0

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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.

Depends R (>= 2.10), DOSE

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

Suggests clusterProfiler, GOSemSim, org.Hs.eg.db

License GPL-2

biocViews Bioinformatics, Pathways, Visualization

Collate ‘enrichPathway.R’ ‘zzz.R’ ‘ReactomePA-package.R’

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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, Visualization
Depends: AnnotationDbi, org.Hs.eg.db, igraph, plyr, methods, stats, qvalue, reactome.db
Suggests: GOSemSim, DOSE, clusterProfiler
License: GPL-2

Author(s)

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See Also

[enrichResult](#)

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

Description

Datasets sample contains a sample of gene IDs.

enrichPathway	<i>Pathway Enrichment Analysis of a gene set. Given a vector of genes, this function will return the enriched pathways with FDR control.</i>
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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, pvalueCutoff = 0.05,  
              qvalueCutoff = 0.05, readable = FALSE)
```

Arguments

gene	a vector of entrez gene id.
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)

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See Also

[enrichResult-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)
```

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