Package ‘ReactomePA’

January 31, 2017

Type Package
Title Reactome Pathway Analysis
Version 1.18.1
Author Guangchuang Yu <guangchuangyu@gmail.com> with contributions from Vladislav Petyuk
Maintainer Guangchuang Yu <guangchuangyu@gmail.com>
Description This package provides functions for pathway analysis based on REACTOME pathway database. It implements enrichment analysis, gene set enrichment analysis and several functions for visualization.
Depends R (>= 3.3.0), DOSE (>= 2.11.12)
Imports AnnotationDbi, reactome.db, igraph, graphite
Suggests BiocStyle, clusterProfiler, knitr, org.Hs.eg.db, testthat
VignetteBuilder knitr
ByteCompile true
License GPL-2
URL https://guangchuangyu.github.io/ReactomePA
BugReports https://github.com/GuangchuangYu/ReactomePA/issues
biocViews Pathways, Visualization, Annotation, MultipleComparison, GeneSetEnrichment, Reactome
RoxygenNote 5.0.1
NeedsCompilation no

R topics documented:

ReactomePA-package ................................................. 2
DataSet ............................................................... 2
enrichPathway ...................................................... 2
getALLEG ............................................................ 4
getDb ................................................................. 4
gsePathway ........................................................ 5
viewPathway ......................................................... 5

Index 7
ReactomePA-package  Reactome Pathway Analysis

Description

This package is designed for reactome pathway analysis.

Details

Package: ReactomePA  
Type: Package  
Version: 1.9.4  
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)

Guangchuang Yu <guangchuangyu@gmail.com>
Maintainer: Guangchuang Yu <guangchuangyu@gmail.com>

See Also

enrichResult

DataSet  

Datasets sample contains a sample of gene IDs.

Description

Datasets sample contains a sample of gene IDs.

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, 
pAdjustMethod = "BH", qvalueCutoff = 0.2, universe, minGSSize = 10, 
maxGSSize = 500, readable = FALSE)

Arguments

gene a vector of entrez gene id.
organism one of "human", "rat", "mouse", "celegans", "yeast", "zebrafish", "fly".
pvalueCutoff Cutoff value of pvalue.
pAdjustMethod one of "holm", "hochberg", "hommel", "bonferroni", "BH", "BY", "fdr", "none"
qvalueCutoff Cutoff value of qvalue
universe background genes
minGSSize minimal size of genes annotated by Ontology term for testing.
maxGSSize maximal size of each geneSet for analyzing
readable whether mapping gene ID to gene Name

Value

A enrichment instance.

Author(s)

Guangchuang Yu http://ygc.name

See Also

enrichResult-class

Examples


yy = enrichPathway(gene, pvalueCutoff=0.05)

head(summary(yy))

#plot(yy)
**getALLEG**

**Description**
get all entrezgene ID of a specific organism

**Usage**
getALLEG(organism)

**Arguments**
organism species

**Value**
entrez gene ID vector

**Author(s)**
Yu Guangchuang

---

**getDb**

**Description**
mapping organism name to annotationDb package name

**Usage**
getDb(organism)

**Arguments**
organism one of supported organism

**Value**
annotationDb name

**Author(s)**
Yu Guangchuang
gsePathway

Description
Gene Set Enrichment Analysis of Reactome Pathway

Usage
```
gsePathway(geneList, organism = "human", exponent = 1, nPerm = 1000, 
minGSSize = 10, maxGSSize = 500, pvalueCutoff = 0.05, 
pAdjustMethod = "BH", verbose = TRUE, seed = FALSE, by = "fgsea")
```

Arguments
- geneList: order ranked geneList
- organism: organism
- exponent: weight of each step
- nPerm: permutation numbers
- minGSSize: minimal size of each geneSet for analyzing
- maxGSSize: maximal size of each geneSet for analyzing
- pvalueCutoff: pvalue Cutoff
- pAdjustMethod: pvalue adjustment method
- verbose: print message or not
- seed: logical
- by: one of 'fgsea' or 'DOSE'

Value
```
gseaResult object
```

Author(s)
Yu Guangchuang

viewPathway

Description
view reactome pathway

Usage
```
viewPathway(pathName, organism = "human", readable = TRUE, 
foldChange = NULL, ...)```
Arguments

pathName       pathway Name
organism       supported organism
readable       logical
foldChange     fold change
...            additional parameters passed to netplot

Details

plotting reactome pathway

Value

plot

Author(s)

Yu Guangchuang
Index

∗Topic **datasets**
  DataSet, 2

∗Topic **manip**
  enrichPathway, 2

∗Topic **package**
  ReactomePA-package, 2

DataSet, 2

enrichPathway, 2
enrichResult, 2

getALLEG, 4
getDb, 4
gsePathway, 5

netplot, 6

ReactomePA (ReactomePA-package), 2
ReactomePA-package, 2

viewPathway, 5