Package ‘ReactomePA’

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Type Package

Title Reactome Pathway Analysis

Version 1.18.1

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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)

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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  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 enrichResult instance.

Author(s)

Guangchuang Yu http://ygc.name

See Also

enrichResult-class

Examples

gene <- c("11171", "8243", "112464", "2194", "9318", "79026", "1654", "65003",
        "6240", "3476", "6238", "1654", "4176", "1017", "249")
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

**Value**
entrez gene ID vector

**Author(s)**
Yu Guangchuang

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**getDb**

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

**Usage**
getDb(organism)

**Arguments**
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