Package ‘ReactomePA’

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Type Package
Title Reactome Pathway Analysis
Version 1.20.0
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 (>= 3.3.1), DOSE (>= 3.0.0)
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
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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.

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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.
enrichPathway

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", "3836", "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
- species

**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
  - 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