# Package ‘ReactomePA’

March 29, 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:

| Topic                  |  |
|------------------------|  |
| 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 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

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

```r
sgePathway(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

```r
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