

# Package ‘ReactomePA’

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**Type** Package

**Title** Reactome Pathway Analysis

**Version** 1.18.1

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**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

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ReactomePA-package	<i>Reactome Pathway Analysis</i>
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### 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](#)

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DataSet	<i>Datasets sample contains a sample of gene IDs.</i>
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### Description

Datasets sample contains a sample of gene IDs.

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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, 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)
```

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`getALLEG``getALLEG`

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**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``getDb`

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**Description**

mapping organism name to annotationDb package name

**Usage**

```
getDb(organism)
```

**Arguments**

organism      one of supported organism

**Value**

annotationDb name

**Author(s)**

Yu Guangchuang

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gsePathway

*gsePathway*


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**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

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viewPathway

*viewPathway*


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**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 <a href="#">netplot</a>

**Details**

plotting reactome pathway

**Value**

plot

**Author(s)**

Yu Guangchuang

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