

# Package ‘ReactomePA’

October 9, 2013

**Type** Package

**Title** Reactome Pathway Analysis

**Version** 1.4.0

**Author** Guangchuang Yu <guangchuangyu@gmail.com>

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

**Description** This package provides functions for pathway analysis based on REACTOME pathway database. It will implement enrichment analysis, gene set enrichment analysis and functional modules detection.

**Depends** R (>= 2.10), DOSE

**Imports** methods, AnnotationDbi, reactome.db, org.Hs.eg.db, stats4,plyr, igraph, qvalue, graphics

**Suggests** clusterProfiler, GOSemSim, org.Hs.eg.db

**License** GPL-2

**biocViews** Bioinformatics, Pathways, Visualization

**Collate** ‘enrichPathway.R’ ‘zzz.R’ ‘ReactomePA-package.R’

## R topics documented:

ReactomePA-package . . . . .	2
DataSet . . . . .	2
enrichPathway . . . . .	3

<b>Index</b>	<b>4</b>
--------------	----------

---

ReactomePA-package      *Reactome Pathway Analysis*

---

### Description

This package is designed for reactome pathway analysis.

### Details

Package:      ReactomePA  
Type:          Package  
Version:       0.2.1  
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	<i>Pathway Enrichment Analysis of a gene set. Given a vector of genes, this function will return the enriched pathways with FDR control.</i>
---------------	--

---

### 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, pvalueCutoff = 0.05,  
              qvalueCutoff = 0.05, readable = FALSE)
```

### Arguments

gene	a vector of entrez gene id.
pvalueCutoff	Cutoff value of pvalue.
qvalueCutoff	Cutoff value of qvalue.
readable	if readable is TRUE, the gene IDs will mapping to gene symbols.

### 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)
```

# Index

\*Topic **datasets**

DataSet, [2](#)

\*Topic **manip**

enrichPathway, [3](#)

\*Topic **package**

ReactomePA-package, [2](#)

DataSet, [2](#)

enrichPathway, [3](#)

enrichResult, [2](#)

ReactomePA (ReactomePA-package), [2](#)

ReactomePA-package, [2](#)

sample (DataSet), [2](#)