

# Package ‘ReactomePA’

April 10, 2015

**Type** Package

**Title** Reactome Pathway Analysis

**Version** 1.10.1

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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.

**Dependes** R (>= 3.0.0)

**Imports** DOSE, AnnotationDbi, reactome.db, org.Hs.eg.db, igraph, graphite

**Suggests** clusterProfiler, GOSemSim, ChIPseeker, knitr

**VignetteBuilder** knitr

**License** GPL-2

**biocViews** Pathways, Visualization, Annotation, MultipleComparison, GeneSetEnrichment

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ReactomePA-package     *Reactome Pathway Analysis*

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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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ALLEXTID.Reactome     *ALLEXTID.Reactome*

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**Description**

ALLEXTID.Reactome

**Usage**

```
## S3 method for class Reactome  
ALLEXTID(organism)
```

**Arguments**

organism            organism

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<code>cnetplot</code>	<i>cnetplot</i>
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**Description**

category-gene-net plot

**Usage**

`cnetplot(x, ...)`

**Arguments**

<code>x</code>	enrichResult object
<code>...</code>	additional parameter

**Details**

category gene association

**Value**

figure

**Author(s)**

ygc

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

Datasets sample contains a sample of gene IDs.

---

enrichMap

*enrichMap*


---

**Description**

enrichment map

**Usage**

```
enrichMap(x, ...)
```

**Arguments**

x	enrichResult or gseaResult
...	additional parameter

**Details**

enrichMap

**Value**

figure

**Author(s)**

ygc

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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.

**Usage**

```
enrichPathway(gene, organism = "human", pvalueCutoff = 0.05,
  pAdjustMethod = "BH", qvalueCutoff = 0.2, universe, minGSSize = 5,
  readable = FALSE)
```

**Arguments**

gene	a vector of entrez gene id.
organism	one of "human", "rat", "mouse", "celegans", "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.
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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EXTID2TERMID.Reactome *EXTID2TERMID.Reactome*

---

**Description**

EXTID2TERMID.Reactome

**Usage**

```
## S3 method for class Reactome
EXTID2TERMID(gene, organism)
```

**Arguments**

gene	gene
organism	organism

getGeneSet.Reactome    *getGeneSet.Reactome*

---

**Description**

getGeneSet.Reactome

**Usage**

```
## S3 method for class Reactome
getGeneSet(setType = "Reactome", organism)
```

**Arguments**

setType	gene set type
organism	organism

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gseaplot                    *gseaplot*

---

**Description**

visualize analyzing result of GSEA

**Usage**

```
gseaplot(x, ...)
```

**Arguments**

x	gseaResult object
...	additional parameters

**Details**

plotting function for gseaResult

**Value**

figure

**Author(s)**

ygc

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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, pvalueCutoff = 0.05, pAdjustMethod = "BH",  
           verbose = TRUE)
```

**Arguments**

<code>geneList</code>	order ranked <code>geneList</code>
<code>organism</code>	organism
<code>exponent</code>	weight of each step
<code>nPerm</code>	permutation numbers
<code>minGSSize</code>	minimal size of each <code>geneSet</code> for analyzing
<code>pvalueCutoff</code>	pvalue Cutoff
<code>pAdjustMethod</code>	pvalue adjustment method
<code>verbose</code>	print message or not

**Value**

`gseaResult` object

**Author(s)**

Yu Guangchuang

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`TERM2NAME.Reactome`*TERM2NAME.Reactome*

---

**Description**

`TERM2NAME.Reactome`

**Usage**

```
## S3 method for class Reactome  
TERM2NAME(term, organism)
```

**Arguments**

term	reactome pathway term
organism	organism

---

TERMID2EXTID.Reactome *TERMID2EXTID.Reactome*

---

**Description**

TERMID2EXTID.Reactome

**Usage**

```
## S3 method for class Reactome
TERMID2EXTID(term, organism)
```

**Arguments**

term	reactome pathway term
organism	organism

---

viewPathway *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 parameter

**Details**

plotting reactome pathway



*viewPathway*

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**Value**

plot

**Author(s)**

Yu Guangchuang

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