

# Package ‘ReactomePA’

April 23, 2016

**Type** Package

**Title** Reactome Pathway Analysis

**Version** 1.14.4

**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.

**Dependes** R (>= 3.1.0)

**Imports** DOSE, AnnotationDbi, reactome.db, igraph, graphite

**Suggests** BiocStyle, clusterProfiler, knitr

**VignetteBuilder** knitr

**License** GPL-2

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

**NeedsCompilation** no

## R topics documented:

ReactomePA-package . . . . .	2
cnetplot . . . . .	2
DataSet . . . . .	3
dotplot . . . . .	3
enrichMap . . . . .	4
enrichPathway . . . . .	5
gseaplot . . . . .	6
gsePathway . . . . .	6
viewPathway . . . . .	7
<b>Index</b>	<b>9</b>

---

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](#)

---

cnetplot                      *cnetplot*

---

### Description

category-gene-net plot

### Usage

```
cnetplot(x, showCategory = 5, categorySize = "geneNum", foldChange = NULL,  
         fixed = TRUE, ...)
```

**Arguments**

x	enrichResult object
showCategory	number of category plotted
categorySize	one of geneNum or pvalue
foldChange	fold change of expression value
fixed	logical
...	additional parameter

**Details**

category gene association

**Value**

plot

**Author(s)**

ygc

---

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

---

**Description**

Datasets sample contains a sample of gene IDs.

---

dotplot	<i>dotplot</i>
---------	----------------

---

**Description**

dot plot of enrichResult

**Usage**

```
dotplot(object, ...)
```

**Arguments**

object	an instance of enrichResult
...	additional parameter

**Value**

ggplot object

**Author(s)**

Guangchuang Yu

---

enrichMap

*enrichMap*

---

**Description**

enrichment map

**Usage**

```
enrichMap(x, n = 50, fixed = TRUE, vertex.label.font = 1, ...)
```

**Arguments**

x	gseaResult or enrichResult object
n	maximum number of category to shown
fixed	if set to FALSE, will invoke tkplot
vertex.label.font	font size of vertex label
...	additional parameters passed to <a href="#">netplot</a>

**Details**

enrichMap

**Value**

figure

**Author(s)**

ygc

---

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, 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", "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.
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)
```

gseaplot

*gseaplot*

---

**Description**

visualize analyzing result of GSEA

**Usage**

```
gseaplot(gseaResult, geneSetID, by = "all")
```

**Arguments**

gseaResult	gseaResult object
geneSetID	geneSet ID
by	one of "runningScore" or "position"

**Details**

plotting function for gseaResult

**Value**

figure

**Author(s)**

ygc

---

gsePathway

*gsePathway*

---

**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**

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

**Value**

gseaResult object

**Author(s)**

Yu Guangchuang

---

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 parameters passed to <a href="#">netplot</a>

**Details**

plotting reactome pathway

**Value**

plot

**Author(s)**

Yu Guangchuang



# Index

\*Topic **datasets**

DataSet, [3](#)

\*Topic **manip**

enrichPathway, [5](#)

\*Topic **package**

ReactomePA-package, [2](#)

cnetplot, [2](#)

DataSet, [3](#)

dotplot, [3](#)

enrichMap, [4](#)

enrichPathway, [5](#)

enrichResult, [2](#)

gseaplot, [6](#)

gsePathway, [6](#)

netplot, [4, 7](#)

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

ReactomePA-package, [2](#)

viewPathway, [7](#)