

# Package ‘ReactomePA’

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**Type** Package

**Title** Reactome Pathway Analysis

**Version** 1.51.0

**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. This package is not affiliated with the Reactome team.

**Depends** R (>= 3.4.0)

**Imports** AnnotationDbi, DOSE (>= 3.5.1), enrichplot, ggplot2 (>= 3.3.5), ggraph, reactome.db, igraph, graphite, gson, yulab.utils (>= 0.1.5)

**Suggests** BiocStyle, clusterProfiler, knitr, rmarkdown, org.Hs.eg.db, prettydoc, testthat

**VignetteBuilder** knitr

**ByteCompile** true

**License** GPL-2

**URL** <https://yulab-smu.top/contribution-knowledge-mining/>

**BugReports** <https://github.com/GuangchuangYu/ReactomePA/issues>

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

**RoxygenNote** 7.3.2

**Encoding** UTF-8

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ReactomePA-package	<i>ReactomePA: Reactome Pathway Analysis</i>
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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. This package is not affiliated with the Reactome team.

### Author(s)

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

Other contributors:

- Vladislav Petyuk <petyuk@gmail.com> [contributor]

### See Also

Useful links:

- <https://yulab-smu.top/biomedical-knowledge-mining-book/>
- Report bugs at <https://github.com/GuangchuangYu/ReactomePA/issues>

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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,  
  minGSSize = 10,  
  maxGSSize = 500,  
  eps = 1e-10,  
  pvalueCutoff = 0.05,  
  pAdjustMethod = "BH",  
  verbose = TRUE,  
  seed = FALSE,  
  by = "fgsea",  
  ...  
)
```

**Arguments**

<code>geneList</code>	order ranked geneList
<code>organism</code>	organism
<code>exponent</code>	weight of each step
<code>minGSSize</code>	minimal size of each geneSet for analyzing
<code>maxGSSize</code>	maximal size of each geneSet for analyzing
<code>eps</code>	This parameter sets the boundary for calculating the p value.
<code>pvalueCutoff</code>	pvalue Cutoff
<code>pAdjustMethod</code>	pvalue adjustment method
<code>verbose</code>	print message or not
<code>seed</code>	logical
<code>by</code>	one of 'fgsea' or 'DOSE'
<code>...</code>	other parameter

**Value**

gseaResult object

**Author(s)**

Yu Guangchuang

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gson_Reactome	<i>gson_Reactome</i>
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**Description**

download the latest version of Reactome and stored in a 'GSON' object

**Usage**

```
gson_Reactome(organism = "human")
```

**Arguments**

organism            one of "human", "rat", "mouse", "celegans", "yeast", "zebrafish", "fly".

**Value**

a 'GSON' object

**Examples**

```
## Not run:
rec_gson <- gson_Reactome("human")

## End(Not run)
```

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reexports	<i>Objects exported from other packages</i>
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**Description**

These objects are imported from other packages. Follow the links below to see their documentation.

**DOSE** [geneID](#), [geneInCategory](#)

**enrichplot** [cnetplot](#), [dotplot](#), [emaplot](#), [gseaplot](#), [heatplot](#), [ridgeplot](#)

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viewPathway	<i>viewPathway</i>
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**Description**

view reactome pathway

**Usage**

```
viewPathway(  
  pathName,  
  organism = "human",  
  readable = TRUE,  
  foldChange = NULL,  
  keyType = "ENTREZID",  
  layout = "kk"  
)
```

**Arguments**

pathName	pathway Name
organism	supported organism
readable	logical
foldChange	fold change
keyType	keyType of gene ID (i.e. names of foldChange, if available)
layout	graph layout

**Details**

plotting reactome pathway

**Value**

plot

**Author(s)**

Yu Guangchuang

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