

# Package ‘ReactomePA’

November 8, 2025

**Type** Package

**Title** Reactome Pathway Analysis

**Version** 1.55.0

**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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**Author** Guangchuang Yu [aut, cre],  
Vladislav Petyuk [ctb]

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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 | <i>getALLEG</i> |
|----------|-----------------|

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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 | <i>getDb</i> |
|-------|--------------|

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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

gsePathway

*gsePathway***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**

|               |                                                               |
|---------------|---------------------------------------------------------------|
| geneList      | order ranked geneList                                         |
| organism      | organism                                                      |
| exponent      | weight of each step                                           |
| minGSSize     | minimal size of each geneSet for analyzing                    |
| maxGSSize     | maximal size of each geneSet for analyzing                    |
| eps           | This parameter sets the boundary for calculating the p value. |
| pvalueCutoff  | pvalue Cutoff                                                 |
| pAdjustMethod | pvalue adjustment method                                      |
| verbose       | print message or not                                          |
| seed          | logical                                                       |
| by            | one of 'fgsea' or 'DOSE'                                      |
| ...           | 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](#), [emapplot](#), [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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