# Package 'ReactomePA'

October 14, 2021

**Type** Package

**Title** Reactome Pathway Analysis

**Version** 1.36.0

**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.

**Depends** R (>= 3.4.0)

**Imports** AnnotationDbi, DOSE (>= 3.5.1), enrichplot, ggplot2, ggraph, reactome.db, igraph, graphite

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

**VignetteBuilder** knitr

**ByteCompile** true

**License** GPL-2

**URL** https://yulab-smu.top/biomedical-knowledge-mining-book/

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

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

**RoxygenNote** 7.1.1

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

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## `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, Visulization |
| 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

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`DataSet` *Datasets sample contains a sample of gene IDs.*

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### Description

Datasets sample contains a sample of gene IDs.

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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.*

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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)
```

---

# `getALLEG` *getALLEG*

## 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*

---

### 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*

---

### 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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# `viewPathway` *viewPathway*

## 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 |
| `...` | additional parameters |

## Details

plotting reactome pathway

## Value

plot

## Author(s)

Yu Guangchuang

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