Package ‘ReactomePA’

September 16, 2019

Type Package

Title Reactome Pathway Analysis

Version 1.28.0

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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.

Depends R (>= 3.4.0)

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

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

VignetteBuilder knitr

ByteCompile true

License GPL-2

URL https://guangchuangyu.github.io/software/ReactomePA

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

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

RoxygenNote 6.1.0

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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

**DataSet**

*Datasets sample contains a sample of gene IDs.*

**Description**

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

```r
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](http://ygc.name)

**See Also**

- `enrichResult-class`

**Examples**

```r

yy = enrichPathway(gene, pvalueCutoff=0.05)

head(summary(yy))

#plot(yy)
```
**getALLEG**

**Description**
get all entrezgene ID of a specific organism

**Usage**
getALLEG(organism)

**Arguments**
organism, species

**Value**
etrez gene ID vector

**Author(s)**
Yu Guangchuang

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**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
**gsePathway**

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**Description**

Gene Set Enrichment Analysis of Reactome Pathway

**Usage**

```
gsePathway(geneList, organism = "human", exponent = 1, nPerm = 1000,  
minGSSize = 10, maxGSSize = 500, pvalueCutoff = 0.05,  
pAdjustMethod = "BH", verbose = TRUE, seed = FALSE, by = "fgsea")
```

**Arguments**

- `geneList`: order ranked geneList
- `organism`: organism
- `exponent`: weight of each step
- `nPerm`: permutation numbers
- `minGSSize`: minimal size of each geneSet for analyzing
- `maxGSSize`: maximal size of each geneSet for analyzing
- `pvalueCutoff`: pvalue Cutoff
- `pAdjustMethod`: pvalue adjustment method
- `verbose`: print message or not
- `seed`: logical
- `by`: one of 'fgsea' or 'DOSE'

**Value**

`gseaResult` object

**Author(s)**

Yu Guangchuang

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**viewPathway**

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**Description**

view reactome pathway

**Usage**

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

---
viewPathway

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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