Package ‘ReactomePA’

January 8, 2024

Type Package
Title Reactome Pathway Analysis
Version 1.46.0
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 (>= 3.3.5), ggraph, reactome.db, igraph, graphite, gson
Suggests BiocStyle, clusterProfiler, knitr, rmarkdown, org.Hs.eg.db, prettydoc, testthat

VignetteBuilder knitr
ByteCompile true
License GPL-2

BugReports https://github.com/GuangchuangYu/ReactomePA/issues
biocViews Pathways, Visualization, Annotation, MultipleComparison, GeneSetEnrichment, Reactome

RoxygenNote 7.2.1
Encoding UTF-8

git_url https://git.bioconductor.org/packages/ReactomePA
git_branch RELEASE_3_18
git_last_commit 4fc270b
git_last_commit_date 2023-10-24

Repository Bioconductor 3.18
Date/Publication 2024-01-07

Author Guangchuang Yu [aut, cre], Vladislav Petyuk [ctb]
**R topics documented:**

- ReactomePA-package ................................................................. 2
- DataSet ................................................................................. 3
- enrichPathway ................................................................. 3
- getALLEG .......................................................................... 4
- getDb .................................................................................. 5
- gsePathway ......................................................................... 5
- gson_Reactome ..................................................................... 6
- reexports ............................................................................ 7
- viewPathway ....................................................................... 7

**Index**

---

**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
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
getALLEG

Value
A enrichResult instance.

Author(s)
Guangchuang Yu http://ygc.name

See Also
enrichResult-class

Examples

```r
yy = enrichPathway(gene, pvalueCutoff=0.05)
head(summary(yy))
#plot(yy)
```

Description
get all entrezgene ID of a specific organism

Usage
getALLEG(organism)

Arguments

organism species

Value
entrez gene ID vector

Author(s)
Yu Guangchuang
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

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

---

gson_Reactome

gson_Reactome

Description

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

Usage

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

Arguments

- `organism` (one of "human", "rat", "mouse", "celegans", "yeast", "zebrafish", "fly").

Value

- a ‘GSON’ object
Examples

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

---

**reexports**

Objects exported from other packages

**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`

---

**viewPathway**

**viewPathway**

**Description**

view reactome pathway

**Usage**

```r
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
Index

* datasets
  * DataSet, 3

* internal
  * reexports, 7

* manip
  * enrichPathway, 3

* package
  * ReactomePA-package, 2

  cnetplot, 7
  cnetplot (reexports), 7

  DataSet, 3
dotplot, 7
dotplot (reexports), 7
emapplot, 7
emapplot (reexports), 7
enrichPathway, 3
enrichResult, 2
geneID, 7
geneID (reexports), 7
geneInCategory, 7
geneInCategory (reexports), 7
getALLEG, 4
getDb, 5
gseaplot, 7
gseaplot (reexports), 7
gsePathway, 5
gson_Reactome, 6

  heatplot, 7
  heatplot (reexports), 7

  ReactomePA (ReactomePA-package), 2
  ReactomePA-package, 2
  reexports, 7
  ridgeplot, 7
  ridgeplot (reexports), 7

viewPathway, 7