Package ‘ReactomePA’

March 7, 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, markdown, 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 2024-03-06
Author Guangchuang Yu [aut, cre],
Vladislav Petyuk [ctb]
ReactomePA-package

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
**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
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
**getDb**

---

**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

---

**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

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

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

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