Package 'ReactomePA'

April 10, 2023

Type Package

Title Reactome Pathway Analysis

Version 1.42.0

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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 (>= 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

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

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

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

RoxygenNote 7.2.1

Encoding UTF-8

git_url https://git.bioconductor.org/packages/ReactomePA

git_branch RELEASE_3_16

git_last_commit db48e25

git_last_commit_date 2022-11-01

Date/Publication 2023-04-10

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

R topics documented:

`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)

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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

```
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 *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*

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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gson_Reactome *gson_Reactome*

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)
```

`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

Details

plotting reactome pathway

Value

plot

Author(s)

Yu Guangchuang

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