Package ‘ReactomePA’

March 30, 2021

Type Package

Title Reactome Pathway Analysis

Version 1.34.0

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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://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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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)
```

`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

`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

`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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