Package: ReactomePA (via r-universe)

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Type Package

Title Reactome Pathway Analysis

Version 1.49.0

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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. This package is not affiliated with the Reactome team.

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 7.3.0

Encoding UTF-8

Repository https://bioc.r-universe.dev

RemoteUrl https://github.com/bioc/ReactomePA

RemoteRef HEAD

RemoteSha 6ac0ae2d614c9c8040022c3c071079ceede376cc

Contents

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

Description

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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

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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

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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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