Package ‘ReactomePA’

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Type Package

Title Reactome Pathway Analysis

Version 1.48.0

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. 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


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

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

RoxygenNote 7.3.0

Encoding UTF-8

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**ReactomePA-package**  
**ReactomePA: Reactome Pathway Analysis**

**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.

**Author(s)**

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**See Also**

Useful links:

- [https://yulab-smu.top/biomedical-knowledge-mining-book/](https://yulab-smu.top/biomedical-knowledge-mining-book/)
- Report bugs at [https://github.com/GuangchuangYu/ReactomePA/issues](https://github.com/GuangchuangYu/ReactomePA/issues)

**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


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

---

getALLEG

**Description**
get all entrezgene ID of a specific organism

**Usage**
getALLEG(organism)

**Arguments**
- organism species

**Value**
etrez 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
gsePathway

Value

annotationDb name

Author(s)

Yu Guangchuang

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
```

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)
```

```
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
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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