Package ‘ReactomePA’

March 21, 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

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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)

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See Also

enrichResult
\begin{verbatim}
\textbf{Description} 

Datasets sample contains a sample of gene IDs.

\textbf{enrichPathway} 

Pathway Enrichment Analysis of a gene set. Given a vector of genes, this function will return the enriched pathways with FDR control.

\textbf{Usage} 

\begin{verbatim}
enrichPathway(
    gene,
    organism = "human",
    pvalueCutoff = 0.05,
    pAdjustMethod = "BH",
    qvalueCutoff = 0.2,
    universe,
    minGSSize = 10,
    maxGSSize = 500,
    readable = FALSE
)
\end{verbatim}

\textbf{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
\end{verbatim}
\end{verbatim}
getALLEG

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

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**

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**getDb**

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**Description**

mapping organism name to annotationDb package name

**Usage**

ggetDb(organism)

**Arguments**

organism one of supported organism

**Value**

annotationDb name

**Author(s)**

Yu Guangchuang

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**gsePathway**

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**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)
```

---

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

---

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
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