Package ‘ReactomePA’

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Type Package
Title Reactome Pathway Analysis
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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)
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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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Other contributors:

• Vladislav Petyuk <petyuk@gmail.com> [contributor]

See Also

Useful links:

• https://yulab-smu.top/biomedical-knowledge-mining-book/
• Report bugs at 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**

```r
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](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))

getdb

getdb

Description

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)
Value

annotationDb name

Author(s)

Yu Guangchuang

Description

Gene Set Enrichment Analysis of Reactome Pathway

Usage

```r
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

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)

---

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

```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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