Package ‘ReactomePA’

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Title Reactome Pathway Analysis
Version 1.48.0
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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)
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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)**

**Maintainer:** Guangchuang Yu <guangchuangyu@gmail.com>

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

**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)

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**DataSet**

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

**Description**

Datasets sample contains a sample of gene IDs.
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

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

entrez gene ID vector

Author(s)

Yu Guangchuang

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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

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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

gson_Reactome

download the latest version of Reactome and stored in a 'GSON' object

Usage

```r
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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