Package 'ReactomePA'

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Type Package

Title Reactome Pathway Analysis

Version 1.56.0

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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, enrichplot, enrichit, ggplot2 (>= 3.3.5), ggraph, reactome.db, igraph, graphite, gson, yulab.utils (>= 0.1.5)

Suggests clusterProfiler, knitr, rmarkdown, org.Hs.eg.db, prettydoc, testthat

VignetteBuilder knitr

ByteCompile true

License GPL-2

URL https://yulab-smu.top/contribution-knowledge-mining/

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

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

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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:

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See Also

Useful links:

- https://yulab-smu.top/contribution-knowledge-mining/
- Report bugs at 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.

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,
  pvalueCutoff = 0.05,
  pAdjustMethod = "BH",
  universe = NULL,
  minGSSize = 10,
  maxGSSize = 500,
  qvalueCutoff = 0.2,
  organism = "human",
  readable = FALSE
)
```

Arguments

gene	a vector of entrez gene id.
pvalueCutoff	Cutoff value of pvalue.
pAdjustMethod	one of "holm", "hochberg", "hommel", "bonferroni", "BH", "BY", "fdr", "none"
universe	background genes
minGSSize	minimal size of genes annotated by Ontology term for testing.
maxGSSize	maximal size of each geneSet for analyzing
qvalueCutoff	Cutoff value of qvalue
organism	one of "human", "rat", "mouse", "celegans", "yeast", "zebrafish", "fly".
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

---

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,
  pvalueCutoff = 0.05,
  pAdjustMethod = "BH",
  verbose = TRUE,
  nPerm = 1000,
  method = "multilevel",
  adaptive = FALSE,
  minPerm = 101,
  maxPerm = 1e+05,
  pvalThreshold = 0.1
)
```

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
`pvalueCutoff`	pvalue Cutoff
`pAdjustMethod`	pvalue adjustment method
`verbose`	print message or not
`nPerm`	The number of permutations for the "permute" method

method	one of "sample", "permute", "multilevel"
adaptive	logical
minPerm	minimal number of permutations for the "multilevel" method
maxPerm	maximal number of permutations for the "multilevel" method
pvalThreshold	The p-value threshold for the "multilevel" method

Value

gseaResult object

Author(s)

Yu Guangchuang

`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)
```

reexports *Objects exported from other packages*

Description

These objects are imported from other packages. Follow the links below to see their documentation.

enrichit geneID, geneInCategory

enrichplot cnetplot, dotplot, emapplot, gseaplot, heatplot, ridgeplot

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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