Package ‘ReactomePA’

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Type Package

Title Reactome Pathway Analysis

Version 1.57.0

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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

RoxygenNote 7.3.3

Encoding UTF-8

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Contents

`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`>

Other contributors:

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

See Also

Useful links:

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

```
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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