

Package ‘ReactomePA’

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Type Package

Title Reactome Pathway Analysis

Version 1.10.1

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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.

Dependes R (>= 3.0.0)

Imports DOSE, AnnotationDbi, reactome.db, org.Hs.eg.db, igraph, graphite

Suggests clusterProfiler, GOSemSim, ChIPseeker, knitr

VignetteBuilder knitr

License GPL-2

biocViews Pathways, Visualization, Annotation, MultipleComparison, GeneSetEnrichment

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ReactomePA-package *Reactome Pathway Analysis*

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](#)

ALLEXTID.Reactome *ALLEXTID.Reactome*

Description

ALLEXTID.Reactome

Usage

```
## S3 method for class Reactome  
ALLEXTID(organism)
```

Arguments

organism organism

<code>cnetplot</code>	<i>cnetplot</i>
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Description

category-gene-net plot

Usage

`cnetplot(x, ...)`

Arguments

<code>x</code>	enrichResult object
<code>...</code>	additional parameter

Details

category gene association

Value

figure

Author(s)

ygc

<code>DataSet</code>	<i>Datasets sample contains a sample of gene IDs.</i>
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Description

Datasets sample contains a sample of gene IDs.

`enrichMap`*enrichMap*

Description

enrichment map

Usage`enrichMap(x, ...)`**Arguments**

<code>x</code>	enrichResult or gseaResult
<code>...</code>	additional parameter

Details`enrichMap`**Value**

figure

Author(s)

ygc

`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, organism = "human", pvalueCutoff = 0.05,  
  pAdjustMethod = "BH", qvalueCutoff = 0.2, universe, minGSSize = 5,  
  readable = FALSE)
```

Arguments

gene	a vector of entrez gene id.
organism	one of "human", "rat", "mouse", "celegans", "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.
readable	whether mapping gene ID to gene Name

Value

A enrichResult instance.

Author(s)

Guangchuan 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)
```

EXTID2TERMID.Reactome *EXTID2TERMID.Reactome*

Description

EXTID2TERMID.Reactome

Usage

```
## S3 method for class Reactome
EXTID2TERMID(gene, organism)
```

Arguments

gene	gene
organism	organism

getGeneSet.Reactome *getGeneSet.Reactome*

Description

getGeneSet.Reactome

Usage

```
## S3 method for class Reactome
getGeneSet(setType = "Reactome", organism)
```

Arguments

setType	gene set type
organism	organism

gseaplot *gseaplot*

Description

visualize analyzing result of GSEA

Usage

```
gseaplot(x, ...)
```

Arguments

x	gseaResult object
...	additional parameters

Details

plotting function for gseaResult

Value

figure

Author(s)

ygc

`gsePathway`*gsePathway*

Description

Gene Set Enrichment Analysis of Reactome Pathway

Usage

```
gsePathway(geneList, organism = "human", exponent = 1, nPerm = 1000,  
           minGSSize = 10, pvalueCutoff = 0.05, pAdjustMethod = "BH",  
           verbose = TRUE)
```

Arguments

<code>geneList</code>	order ranked geneList
<code>organism</code>	organism
<code>exponent</code>	weight of each step
<code>nPerm</code>	permutation numbers
<code>minGSSize</code>	minimal size of each geneSet for analyzing
<code>pvalueCutoff</code>	pvalue Cutoff
<code>pAdjustMethod</code>	pvalue adjustment method
<code>verbose</code>	print message or not

Value

`gseaResult` object

Author(s)

Yu Guangchuang

`TERM2NAME.Reactome`*TERM2NAME.Reactome*

Description

`TERM2NAME.Reactome`

Usage

```
## S3 method for class Reactome  
TERM2NAME(term, organism)
```

Arguments

term	reactome pathway term
organism	organism

TERMID2EXTID.Reactome *TERMID2EXTID.Reactome*

Description

TERMID2EXTID.Reactome

Usage

```
## S3 method for class Reactome
TERMID2EXTID(term, organism)
```

Arguments

term	reactome pathway term
organism	organism

viewPathway *viewPathway*

Description

view reactome pathway

Usage

```
viewPathway(pathName, organism = "human", readable = TRUE,
  foldChange = NULL, ...)
```

Arguments

pathName	pathway Name
organism	supported organism
readable	logical
foldChange	fold change
...	additional parameter

Details

plotting reactome pathway

viewPathway

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Value

plot

Author(s)

Yu Guangchuang

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