

Package ‘ReactomePA’

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Type Package

Title Reactome Pathway Analysis

Version 1.12.3

Author Guangchuang Yu <guangchuangyu@gmail.com>

Maintainer Guangchuang Yu <guangchuangyu@gmail.com>

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.

Depends R (>= 3.1.0)

Imports DOSE, AnnotationDbi, reactome.db, igraph, graphite

Suggests clusterProfiler, knitr, BiocStyle

VignetteBuilder knitr

License GPL-2

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

NeedsCompilation no

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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)

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

See Also

[enrichResult](#)

cnetplot *cnetplot*

Description

category-gene-net plot

Usage

```
cnetplot(x, ...)
```

Arguments

x enrichResult object
... additional parameter

Details

category gene association

Value

figure

Author(s)

ygc

DataSet

Datasets sample contains a sample of gene IDs.

Description

Datasets sample contains a sample of gene IDs.

enrichMap

enrichMap

Description

enrichment map

Usage

enrichMap(x, ...)

Arguments

x	enrichResult or gseaResult
...	additional parameter

Details

enrichMap

Value

figure

Author(s)

ygc

enrichPathway	<i>Pathway Enrichment Analysis of a gene set. Given a vector of genes, this function will return the enriched pathways with FDR control.</i>
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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)

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)
```

gseaplot	<i>gseaplot</i>
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Description

visualize analyzing result of GSEA

Usage

```
gseaplot(gseaResult, geneSetID, by = "all")
```

Arguments

gseaResult	gseaResult object
geneSetID	geneSet ID
by	one of "runningScore" or "position"

Details

plotting function for gseaResult

Value

figure

Author(s)

ygc

gsePathway	<i>gsePathway</i>
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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

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

Value

gseaResult object

Author(s)

Yu Guangchuang

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

Value

plot

viewPathway

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Author(s)

Yu Guangchuang

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