Package ‘meshr’

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Title Tools for conducting enrichment analysis of MeSH

Description A set of annotation maps describing the entire MeSH assembled using data from MeSH

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R topics documented:

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meshr-package  Enrichment analysis for MeSH terms.

Description

meshr package conducts a MeSH enrichment analysis employing gene-MeSH annotation data. A hypergeometric test accounting for a multiple testing correction is used to find significantly enriched MeSH terms.

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Details
category

This function returns the name of MeSH category.

Usage

\[\text{category}(r)\]
\[\text{category}(r) \leftarrow \text{value}\]

Arguments

\[r\] An object containing annotation information.
\[\text{value}\] The annotation information to set on object.

Author(s)

Koki Tsuyuzaki
database

A function to return the name of MeSH database

Description
This function returns the name of MeSH database.

Usage

```
database(r)
database(r) <- value
```

Arguments

- `r`: An object containing annotation information.
- `value`: The annotation information to set on object.

Author(s)
Koki Tsuyuzaki

geneid.cummeRbund

Test data of significant differentially expressed genes used in cummeRbund package.

Description
This RNA-Seq data were taken from three samples, "iPS", "hESC", and "Fibroblasts". We first create two objects of gene sets, i.e., selected and universal genes, by comparing significantly regulated genes between iPS and hESC under the significance level of 0.05 by getSig method in cummeRbund package. 303 genes were finally choosed and 104 of them were differentially expressed.

Usage

```
data(geneid.cummeRbund)
```

Source


See Also

`sig.geneid.cummeRbund`. 
Examples

data(geneid.cummeRbund)
names(geneid.cummeRbund)

## This data is also available by following scripts.
if(interactive()){
  library(cummeRbund)
  library(org.Hs.eg.db)
  cuff <- readCufflinks(dir = system.file("extdata", package = "cummeRbund"))

  gene.symbols <- annotation(genes(cuff))[,4]
  mySigGeneIds <- getSig(cuff,x="hESC",y="iPS",alpha=0.05,level="genes")
  mySigGenes <- getGenes(cuff,mySigGeneIds)

  sig.gene.symbols <- annotation(mySigGenes[,4]
  gene.symbols <- gene.symbols[!is.na(gene.symbols)]
  sig.gene.symbols <- sig.gene.symbols[!is.na(sig.gene.symbols)]

  geneid.cummeRbund <- select(org.Hs.eg.db, keys=gene.symbols, keytype="SYMBOL", columns="ENTREZID")
  sig.geneid.cummeRbund <- select(org.Hs.eg.db, keys=sig.gene.symbols, keytype="SYMBOL", columns="ENTREZID")

  na.index1 <- which(is.na(geneid.cummeRbund[,2]))
  for (i in na.index1){
    s <- unlist(strsplit(as.character(geneid.cummeRbund[i,][1]), ",")[1]
    sym <- get(s, org.Hs.egALIAS2EG)[1]
    geneid.cummeRbund[i,2] <- as.integer(sym)
  }

  na.index2 <- which(is.na(sig.geneid.cummeRbund[,2]))
  for (i in na.index2){
    s <- unlist(strsplit(as.character(sig.geneid.cummeRbund[i,][1]), ",")[1]
    sym <- get(s, org.Hs.egALIAS2EG)[1]
    sig.geneid.cummeRbund[i,2] <- as.integer(sym)
  }

  geneid.cummeRbund <- geneid.cummeRbund[!duplicated(geneid.cummeRbund[,2]),]
  sig.geneid.cummeRbund <- sig.geneid.cummeRbund[!duplicated(sig.geneid.cummeRbund[,2]),]
}

MeSHHyperGParams-class

Class "MeSHHyperGParams"

Description


Objects from the Class

Objects can be created by calls of the form `new("MeSHHyperGParams", ...)`. 

MeSHHyperGParams-class
Slots

geneIds: Object of class "ANY": A vector of gene identifiers. Numeric and character vectors are probably the only things that make sense. These are the gene ids for the selected gene set.

universeGeneIds: Object of class "ANY": A vector of gene ids in the same format as geneIds defining a subset of the gene ids on the chip that will be used as the universe for the hypergeometric calculation.

annotation: A string giving the name of the gene-MeSH annotation package like MeSH.XXX.eg.db.
category: A string giving the name of the MeSH category like A, B, C, D, ... and so on.
database: A string giving the name of the MeSH database like gendoo, gene2pubmed, ... and so on.
pvalueCutoff: A numeric values between zero and one used as a p-value or FDR cutoff for hypergeometric test depending on pAdjust. The default is set to 0.05.
pAdjust: A string which can be one of the Benjamini-Hochberg procedure (a.k.a. q-value) ("BH"), Q-value ("QV"), empirical Bayes method ("lFDR"), and unadjusted p-value ("none") for multiple testing correction.

Methods

geneIds(p), geneIds(p) <- value Accessor methods for the geneIds.
universeGeneIds(p), universeGeneIds(p) <- value Accessor methods for the geneIds.
annotation(p), annotation(p) <- value Accessor methods for the gene-MeSH annotation data.
pAdjust(p) An accessor method for the choice of a method for multiple testing correction.
pvalueCutoff(p) An accessor method for the choice of a threshold when conducting enrichment analysis.

Author(s)

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See Also

meshr-package, MeSHHyperGResult-class, meshHyperGTest, category, database

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Class "MeSHHyperGResult"

Description

This class represents the results of a test for overrepresentation of MeSH terms among genes in a selected gene set based upon the Hypergeometric distribution.

For details on extracting information from this object, please read the documentation in the MeSHHyperGParams-class.

Objects from the Class

Objects can be created by calls of the form new("MeSHHyperGResult", ...).
Slots

meshCategory: Object of class "character" representing the category of MeSH terms tested.

meshAnnotation: Object of class "character". The name of the annotation data used in the analysis.

meshDatabase: Object of class "character". The name of the database used in the analysis.

ORA: Object of class "data.frame". MeSH IDs, MeSH Terms, P-value, and other statistics is returned.

Methods

meshCategory signature(r = "MeSHHyperGResult"): Returns the MeSH category used in the analysis.

meshAnnotation signature(r = "MeSHHyperGResult"): Returns the name of the annotation data used in the analysis.

meshDatabase signature(r = "MeSHHyperGResult"): Returns the name of the database used in the analysis.

meshIds signature(r = "MeSHHyperGResult"): Returns the character vector of the MeSH IDs identified as significant in the analysis.

meshTerms signature(r = "MeSHHyperGResult"): Returns the character vector of the MeSH terms identified as significant in the analysis.

pvalues signature(r = "MeSHHyperGResult"): Returns the associated p-values of significantly enriched MeSH terms.

summary signature(r = "MeSHHyperGResult"): Returns a data.frame summarizing the test result. Optional arguments pvalue and categorySize allow specification of maximum p-value and minimum categorySize, respectively. Optional argument htmlLinks is a logical value indicating whether to add HTML links (useful in conjunction with xtables print method with type set to "html").

show signature(object = "MeSHHyperGResult"): Return a short description of the result.

save.pdf signature(object = "MeSHHyperGResult"): Return PDF files corresponding PMCID. This function is available only when using gene2pubmed as database

Author(s)

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See Also

meshr-package, MeSHHyperGParams-class, meshHyperGTest
meshHyperGTest  

Hypergeometric Tests for MeSH term association

Description

Given a `MeSHHyperGParams` object containing a set of selected and background gene IDs, and gene-MeSH annotation data of interest, `meshHyperGTest` performs Hypergeometric test for over-representation of each MeSH term accounting for the multiple testing correction.

Arguments

- `p`  
  A `MeSHHyperGParams` object

Details

For details on creating `MeSHHyperGParams` object, please read the documentation in the `MeSHHyperGParams-class`.

Value

A `MeSHHyperGResult` object.

Author(s)

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See Also

- `meshr-package`
- `MeSHHyperGParams-class`
- `MeSHHyperGResult-class`

Examples

```r
data(geneid.cummeRbund)
data(sig.geneid.cummeRbund)

meshParams <- new("MeSHHyperGParams", geneIds=sig.geneid.cummeRbund[,2], universeGeneIds=geneid.cummeRbund[,2], annotation="MeSH.Hsa.eg.db", category="Z", database="gene2pubmed", pvalueCutoff=0.05, pAdjust="none")

meshR <- meshHyperGTest(meshParams)
```

PMCID  

PUBMEDID - PMCID correspondence

Description

PUBMEDID - PMCID correspondence. This data is used by `save.pdf` function

Usage

data(PMCID)
**Examples**

```r
data(PMCID)
names(PMCID)
```

---

**Description**

This RNA-Seq data were taken from three samples, "iPS", "hESC", and "Fibroblasts". We first create two objects of gene sets, i.e., selected and universal genes, by comparing significantly regulated genes between iPS and hESC under the significance level of 0.05 by getSig method in `cummeRbund` package. 303 genes were finally choosed and 104 of them were differentially expressed.

**Usage**

```r
data(sig.geneid.cummeRbund)
```

**Source**


**See Also**

`geneid.cummeRbund`.

**Examples**

```r
## This data is also available by following scripts.
if(interactive()){
  library(cummeRbund)
  library(org.Hs.eg.db)
  cuff <- readCufflinks(dir = system.file("extdata", package = "cummeRbund"))
  gene.symbols <- annotation(genes(cuff))[,4]
  mySigGeneIds <- getSig(cuff,x='hESC',y='iPS',alpha=0.05,level='genes')
  mySigGenes <- getGenes(cuff,mySigGeneIds)
  sig.gene.symbols <- annotation(mySigGenes[,4])
  gene.symbols <- gene.symbols[!is.na(gene.symbols)]
  sig.gene.symbols <- sig.gene.symbols[!is.na(sig.gene.symbols)]
  geneid.cummeRbund <- select(org.Hs.eg.db, keys=gene.symbols, keytype="SYMBOL", columns="ENTREZID")
  sig.geneid.cummeRbund <- select(org.Hs.eg.db, keys=sig.gene.symbols, keytype="SYMBOL", columns="ENTREZID")
}
```

```r
ga <- geneid.cummeRbund
na.index1 <- which(is.na(geneid.cummeRbund[,2]))
for (i in na.index1){
  s <- unlist(strsplit(as.character(geneid.cummeRbund[i,][1]), ","))[1]
  geneid.cummeRbund[i,][2] <- s
}
```
sym <- get(s, org.Hs.egALIAS2EG)[1]
geneid.cummeRbund[i,2] <- as.integer(sym)
}

na.index2 <- which(is.na(sig.geneid.cummeRbund[,2]))
for (i in na.index2){
  s <- unlist(strsplit(as.character(sig.geneid.cummeRbund[i,][1]), ",\"))[1]
  sym <- get(s, org.Hs.egALIAS2EG)[1]
  sig.geneid.cummeRbund[i,2] <- as.integer(sym)
}

geneid.cummeRbund <- geneid.cummeRbund[!duplicated(geneid.cummeRbund[,2]), ]
sig.geneid.cummeRbund <- sig.geneid.cummeRbund[!duplicated(sig.geneid.cummeRbund[,2]), ]
}
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