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.

Version  2.8.0

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Depends  R (>= 4.1.0)
Imports  markdown, rmarkdown, BiocStyle, knitr, methods, stats, utils,
         fdrtool, MeSHDbi, Category, S4Vectors, BiocGenerics, RSQLite

License  Artistic-2.0

biocViews  AnnotationData, FunctionalAnnotation, Bioinformatics,
            Statistics, Annotation, MultipleComparisons, MeSHDb

VignetteBuilder  knitr

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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.

**Details**

Package: meshr  
Version: 1.2.6  
Date: 3-20-2015  
biocViews: AnnotationData, FunctionalAnnotation, Bioinformatics, Statistics, Annotation, MultipleComparisons  
Depends: R (>= 3.0.1), cummeRbund, org.Hs.eg.db, fdrtool, Category, BiocGenerics, methods, MeSH.db, MeSH.AOR.db, MeSH.PCR.db, MeSHDbi, MeSH.Hsa.eg.db, MeSH.Aca.eg.db, MeSH.Atu.K84.eg.db, MeSH.Bsu.168.eg.db, MeSH.Syn.eg.db  
Imports:  
Suggests:  
License: Artistic-2.0

Index:

meshHyperGTest performs a hypergeometric statistical test.

Further information is available in the vignettes.

**Author(s)**

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**See Also**

MeSHHyperGParams-class, MeSHHyperGResult-class, meshHyperGTest

**Examples**

ls("package:meshr")
### category

**Description**

This function returns the name of MeSH category.

**Usage**

```r
category(r)
category(r) <- value
```

**Arguments**

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

**Author(s)**

Koki Tsuyuzaki

**Examples**

```r
showMethods("category")
```

### database

**Description**

This function returns the name of MeSH database.

**Usage**

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

**Arguments**

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

**Author(s)**

Koki Tsuyuzaki
**Description**


**Objects from the Class**

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

**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.
- `meshdb`: A string giving the name of the MeSH database like MeSH.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.
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.

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See Also
meshr-package, MeSHHyperGParams-class, meshHyperGTest

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

showMethods("meshHyperGTest")
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