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 2.10.0

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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")
A function to return the name of MeSH category

Description
This function returns the name of MeSH category.

Usage
\[
\text{category}(r) \\
\text{category}(r) <- \text{value}
\]

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

Author(s)
Koki Tsuyuzaki

Examples
\[
\text{showMethods("category")}
\]

A function to return the name of MeSH database

Description
This function returns the name of MeSH database.

Usage
\[
\text{database}(r) \\
\text{database}(r) <- \text{value}
\]

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

Author(s)
Koki Tsuyuzaki
MeSHHyperGParams-class

Class "MeSHHyperGParams"

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 `universeGeneIds`.
- `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.
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See Also
meshr-package, MeSHHyperGResult-class, meshHyperGTest, category, database

MeSHHyperGResult-class

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.
meshHyperGTest

**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

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**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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