Package ‘DExMADATA’

February 29, 2024

**Type** Package

**Title** Data package for DExMA package

**Version** 1.10.0

**Description** Data objects needed to `allSameID()` function of DExMA package. There are also some objects that are necessary to be able to apply the examples of the DExMA package, which illustrate package functionality.

**Depends** R (>= 4.1)

**Imports** Biobase

**Suggests** BiocStyle

**biocViews** ExperimentData, OrganismData, MicroarrayData

**License** GPL-2

**Encoding** UTF-8

**LazyData** true

**LazyDataCompression** xz

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**Author** Juan Antonio Villatoro-García [aut, cre], Pedro Carmona-Sáez [aut]

**Maintainer** Juan Antonio Villatoro-García <juananthoniovillatorogarcia@gmail.com>

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DExMAdata-package  

Data for DExMA package

Description

Data objects needed to allSameID() function of DExMA package. There are also some objects that are necessary to be able to apply the examples of the DExMA package, which illustrate package functionality

Author(s)

Juan Antonio Villatoro-García and Pedro Carmona-Sáez

Maintainer: Juan Antonio Villatoro García<juanantoniovillatorogarcia@gmail.com>

Examples

data(avaliableIDs)
data(SynonymsDExMA)

avaliableIDs  

Identifiers available in allSameID() function

Description

avaliableIDs contains the different IDs that can be used in allSameID() function. It could be used before allSameID() function to know what ID can be used and how to write them.

Usage

data(avaliableIDs)

Format

character vector
availableOrganism

Organism available in allSameID() function

Description
availableOrganism contains the differents organism that can be used in allSameID() function. It could be used before allSameID() function to know what organism can be used and how to write them.

Usage
data(availableOrganism)

Format
character vector

DExMAExampleData

DExMA synthetic data

Description
- listMatrixEX is a list of expression matrices with genes in different annotation (entrez and Official Gene symbol annotations)
- listPhenodatas is a list of dataframes objects where each dataframe is a phenodata of each expression matrix of listMatrixEX object
- listExpressionSets is a list of ExpressionSets object that have the same information as listMatrixEX and listPheno.
- ExpressionSetStudy5 is an ExpressionSetObject similar to the ExpressionSets objects of listExpressionSets object
- maObjectDif is the meta-analyis object created from the listMatrixEX and listPhenoDatas objects.
- maObject is the resulting object after setting all the studies in Official Gene Symbol annotation

Usage
data(DExMAExampleData)

Format
list arrays (listMatrixEX), list data.frame (listPhenodatas), list ExpressionSets (listExpressionSets) and list of nested lists (maObjectDif, maObject).
**Source**

listMatrixEX, listPhenodatas, listExpressionSets, ExpressionSetStudy5 are synthetic. maObjectDif was created after using createObjectMA DExMA function to the listExpressionSets object. maObject was obtained after using allSameID function to maObjectDif function.

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### IDsDExMA

<table>
<thead>
<tr>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>IDsDExMA contains the equivalences between the different types of gene IDs. It also contains a column with the organism to which the annotation refers. It is used by allSameID() function to set all the genes of the datasets in the same gene ID.</td>
</tr>
</tbody>
</table>

### Usage

data(IDsDExMA)

### Format

data.frame

### Source

the information needed to make the object was downloaded from Gene Expression Omnibus (GEO) database and from ftp://ftp.ncbi.nih.gov/gene/DATA/gene_info.gz

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### SynonymsDExMA

<table>
<thead>
<tr>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>SynonymsDExMA contains other possible gene names and the organisms they refer to. It is used by allSameID() function to check all the genes of the datasets annotated in Official Gene Symbol.</td>
</tr>
</tbody>
</table>

### Usage

data(SynonymsDExMA)

### Format

data.frame

### Source

the information needed to make the object was downloaded from ftp://ftp.ncbi.nih.gov/gene/DATA/gene_info.gz
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