Package ‘DExMAdata’

April 9, 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
git_url https://git.bioconductor.org/packages/DExMAdata
git_branch RELEASE_3_18
git_last_commit 3d2144d
git_last_commit_date 2023-10-24
Repository Bioconductor 3.18
Date/Publication 2024-04-09
Author Juan Antonio Villatoro-García [aut, cre], Pedro Carmona-Sáez [aut]
Maintainer Juan Antonio Villatoro-García <juanantioniovillatorogarcia@gmail.com>

R topics documented:

DExMAdata-package .......................................................... 2
availableIDs .............................................................. 2
availableOrganism ......................................................... 3
**avaliableIDs**

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**

```r
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**

```r
data(avaliableIDs)
```

**Format**

character vector
availableOrganism

<table>
<thead>
<tr>
<th>availableOrganism</th>
<th>Organism available in allSameID() function</th>
</tr>
</thead>
</table>

**Description**

availableOrganism contains the different organisms 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

<table>
<thead>
<tr>
<th>DExMAExampleData</th>
<th>DExMA synthetic data</th>
</tr>
</thead>
</table>

**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-analysis 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.

<table>
<thead>
<tr>
<th>IDsDExMA</th>
<th>Gene ID information</th>
</tr>
</thead>
</table>

Description

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.

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

<table>
<thead>
<tr>
<th>SynonymsDExMA</th>
<th>Other names for identifiers information</th>
</tr>
</thead>
</table>

Description

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.

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
Index

* **Identifiers**
  - availableIDs, 2
  - IDsDExMA, 4
  - SynonymsDExMA, 4

* **Organisms**
  - availableOrganism, 3

* **datasets**
  - DExMAdataset-package, 2

* **objectMA**
  - DExMAExampleData, 3
    - availableIDs, 2
    - availableOrganism, 3
    - DExMAdataset(DExMAdataset-package), 2
    - DExMAdataset-package, 2
    - DExMAExampleData, 3
    - ExpressionSetStudy5(DExMAExampleData), 3
    - IDsDExMA, 4
    - listExpressionSets(DExMAExampleData), 3
    - listMatrixEX(DExMAExampleData), 3
    - listPhenodatas(DExMAExampleData), 3
    - maObject(DExMAExampleData), 3
    - maObjectDif(DExMAExampleData), 3
    - SynonymsDExMA, 4