

Package ‘DExMAdata’

January 22, 2026

Type Package

Title Data package for DExMA package

Version 1.19.0

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 devel

git_last_commit aa10ee3

git_last_commit_date 2025-10-29

Repository Bioconductor 3.23

Date/Publication 2026-01-22

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

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

Contents

DExMAdata-package	2
avaliableIDs	2
avaliableOrganism	3

DEXMAExampleData	3
IDsDEXMA	4
SynonymsDEXMA	4
Index	5

DEXMAdata-package	<i>Data for DEXMA package</i>
-------------------	-------------------------------

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	<i>Identifiers available in allSameID() function</i>
--------------	--

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	<i>Organism available in allSameID() function</i>
-------------------	---

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	<i>DExMA synthetic data</i>
------------------	-----------------------------

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.

 IDsDExMA

Gene ID information

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

 SynonymsDExMA

Other names for identifiers information

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**

- avaliableIDs, [2](#)
 - IDsDExMA, [4](#)
 - SynonymsDExMA, [4](#)

- * **Organisms**

- avaliableOrganism, [3](#)

- * **datasets**

- DExMadata-package, [2](#)

- * **objectMA**

- DExMAExampleData, [3](#)

avaliableIDs, [2](#)

avaliableOrganism, [3](#)

DExMadata (DExMadata-package), [2](#)

DExMadata-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](#)