Package 'DExMAdata'

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Type Package

Title Data package for DExMA package

Version 1.20.0

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.

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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

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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

avaliableOrganism *Organism available in allSameID() function*

Description

avaliableOrganism 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(avaliableOrganism)
```

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.

`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

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`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

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