

Data for DExMA package

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1 Package contents

```
> library(DExMAdata)
> data(IDsDExMA)
> data(SynonymsDExMA)
> data(availableIDs)
> data(availableOrganism)
> data(DExMAExampleData)
```

Firstly, **DExMAExampleData** contains the objects required to perform the **DExMA** package examples:

- **listMatrixEX**: a list of four expression matrices. The first two matrices contain 200 genes annotated in entrez and the other two contains 175 genes annotated in Official Gene Symbol.

```
> class(listMatrixEX)
[1] "list"
> head(listMatrixEX$Study1)
      Sample1 Sample2 Sample3 Sample4
100859927 5.439524 6.253319 2.926444 4.4304023
8086      5.769823 5.971453 1.831349 4.0466288
8212      7.558708 5.957130 2.365252 3.4352889
65985     6.070508 7.368602 2.971158 3.7151784
729522    6.129288 5.774229 3.670696 3.9171749
13        7.715065 7.516471 1.349453 0.3390772
```

- **listPhenodatas**: a list of four phenodatas corresponding to the four expression matrices of the `listMatrixEX` object

```
> class(listPhenodatas)
[1] "list"
> head(listPhenodatas$Study1)
      condition gender  organism race
Sample1 Diseased Female Homo Sapiens AA
Sample2 Diseased Female Homo Sapiens AA
Sample3 Healthy Female Homo Sapiens AA
Sample4 Healthy Female Homo Sapiens H
```

- **listExpressionSets**: a list of four ExpressionSets objects. It contains the same information as `listMatrixEX` and `listPhenodatas` objects.

```
> class(listExpressionSets)
[1] "list"
> listExpressionSets$Study1
ExpressionSet (storageMode: lockedEnvironment)
assayData: 200 features, 4 samples
element names: exprs
```

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```
protocolData: none
phenoData
  rowNames: Sample1 Sample2 Sample3 Sample4
  varLabels: condition gender organism race
  varMetadata: labelDescription
featureData: none
experimentData: use 'experimentData(object)'
Annotation:
```

- **ExpressionSetStudy5**: an ExpressionSet object similar to the ExpressionSets objects of *listExpression*

```
> class(ExpressionSetStudy5)
[1] "ExpressionSet"
attr(,"package")
[1] "Biobase"

> ExpressionSetStudy5
ExpressionSet (storageMode: lockedEnvironment)
assayData: 200 features, 6 samples
  element names: exprs
protocolData: none
phenoData
  rowNames: newSample1 newSample2 ... newSample6 (6 total)
  varLabels: condition gender organism race
  varMetadata: labelDescription
featureData: none
experimentData: use 'experimentData(object)'
Annotation:
```

- **maObjectDif**: the meta-analysis object (*ObjectMA*) created from the listMatrixEX and phenodatas objects information. An *ObjectMA* is the object type used in the DExMA package. This type of object is better explained in the DExMA package.

```
> str(maObjectDif)
List of 4
 $ Study1:List of 2
  ..$ mExpres : num [1:200, 1:4] 5.44 5.77 7.56 6.07 6.13 ...
  .. ..- attr(*, "dimnames")=List of 2
  .. .. ..$ : chr [1:200] "100859927" "8086" "8212" "65985" ...
  .. .. ..$ : chr [1:4] "Sample1" "Sample2" "Sample3" "Sample4"
  ..$ condition: num [1:4] 1 1 0 0
 $ Study2:List of 2
  ..$ mExpres : num [1:200, 1:6] 4.37 5.94 5.29 5.69 5.73 ...
  .. ..- attr(*, "dimnames")=List of 2
  .. .. ..$ : chr [1:200] "100859927" "8086" "8212" "65985" ...
  .. .. ..$ : chr [1:6] "Sample5" "Sample6" "Sample7" "Sample8" ...
  ..$ condition: num [1:6] 1 1 1 0 0 0
 $ Study3:List of 2
  ..$ mExpres : num [1:175, 1:4] 4.5 7.24 6.04 4.96 6.15 ...
  .. ..- attr(*, "dimnames")=List of 2
```

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```
.. .. .$ : chr [1:175] "AAA4" "AAAS" "AABT" "AACS" ...
.. .. .$ : chr [1:4] "Sample11" "Sample12" "Sample13" "Sample14"
..$ condition: num [1:4] 1 1 0 0
$ Study4:List of 2
..$ mExpres : num [1:175, 1:6] 5.37 5.04 6.84 6.94 6 ...
.. ..- attr(*, "dimnames")=List of 2
.. .. .$ : chr [1:175] "AAA4" "ADRACALIN" "AABT" "ACSF1" ...
.. .. .$ : chr [1:6] "Sample15" "Sample16" "Sample17" "Sample18" ...
..$ condition: num [1:6] 1 1 1 0 0 0
```

- **maObjetc**: an *ObjectMA* after setting all the studies of *maObjectDif* in Official Gene Symbol annotation.

```
> str(maObject)
List of 4
$ Study1:List of 2
..$ mExpres : num [1:144, 1:4] 5.44 5.77 7.56 6.07 6.13 ...
.. ..- attr(*, "dimnames")=List of 2
.. .. .$ : chr [1:144] "AAA4" "AAAS" "AABT" "AACS" ...
.. .. .$ : chr [1:4] "Sample1" "Sample2" "Sample3" "Sample4"
..$ condition: num [1:4] 1 1 0 0
$ Study2:List of 2
..$ mExpres : num [1:144, 1:6] 4.37 5.94 5.29 5.69 5.73 ...
.. ..- attr(*, "dimnames")=List of 2
.. .. .$ : chr [1:144] "AAA4" "AAAS" "AABT" "AACS" ...
.. .. .$ : chr [1:6] "Sample5" "Sample6" "Sample7" "Sample8" ...
..$ condition: num [1:6] 1 1 1 0 0 0
$ Study3:List of 2
..$ mExpres : num [1:175, 1:4] 6.37 6.28 4.59 4.6 4.59 ...
.. ..- attr(*, "dimnames")=List of 2
.. .. .$ : chr [1:175] "AARS1" "AATF" "ABCC2" "ABCD1P4" ...
.. .. .$ : chr [1:4] "Sample11" "Sample12" "Sample13" "Sample14"
..$ condition: num [1:4] 1 1 0 0
$ Study4:List of 2
..$ mExpres : num [1:175, 1:6] 5.79 5.59 4.61 4.6 4.63 ...
.. ..- attr(*, "dimnames")=List of 2
.. .. .$ : chr [1:175] "AARS1" "AATF" "ABCC2" "ABCD1P4" ...
.. .. .$ : chr [1:6] "Sample15" "Sample16" "Sample17" "Sample18" ...
..$ condition: num [1:6] 1 1 1 0 0 0
```

On the other hand, **IDsDExMA** and **SynonymsDExMA** are the necessary objects to be able to apply the *allSameID()* function of the package *DExMA*.

IDsDExMA is a dataframe that contains the equivalences between the different types of IDs. It also contains a column with the organism to which the annotation refers.

```
> class(IDsDExMA)
[1] "data.frame"
> length(IDsDExMA)
[1] 4
```

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```
> names(IDsDExMA)
[1] "GeneSymbol" "Entrez"      "Ensembl"    "Organism"
> head(IDsDExMA$Entrez)
[1] "53288" "27777" "27778" "71661" "76253" "78297"
> head(IDsDExMA$Genesymbol)
NULL
> class(SynonymsDExMA)
[1] "data.frame"
> head(SynonymsDExMA)
  Name GeneSymbol Organism
1   Alm      Pzp Mus musculus
2 AI893533      Pzp Mus musculus
4   MAM      Pzp Mus musculus
5   Pzp      Pzp Mus musculus
9  Nat-2     Aanat Mus musculus
10 AA-NAT     Aanat Mus musculus
```

SynonymsDExMA is a data.frame of 3 columns that contains other possible names that a gene can have in a organism and its equivalent annotation in Official Gene Symbol.

```
> class(SynonymsDExMA)
[1] "data.frame"
> head(SynonymsDExMA)
  Name GeneSymbol Organism
1   Alm      Pzp Mus musculus
2 AI893533      Pzp Mus musculus
4   MAM      Pzp Mus musculus
5   Pzp      Pzp Mus musculus
9  Nat-2     Aanat Mus musculus
10 AA-NAT     Aanat Mus musculus
```

avaliabileIDs is a character vector that contains the different IDs that are available to use in *allSameID* function. It is recommended to look this object before making use of *allSameID* function.

```
> avaliabileIDs
[1] "Entrez"      "Ensembl"    "GeneSymbol"
```

avaliabileOrganism is a character vector that contains the different organism that are available to use in *allSameID* function. Like **avaliabileIDs** object, it is recommended to look this object before making use of *allSameID* function.

```
> avaliabileOrganism
[1] "Bos taurus"          "Caenorhabditis elegans"
[3] "Canis familiaris"   "Danio rerio"
```

```
[5] "Drosophila melanogaster" "Gallus gallus"  
[7] "Homo sapiens"          "Mus musculus"  
[9] "Rattus norvegicus"     "Arabidopsis thaliana"  
[11] "Saccharomyces cerevisiae" "Escherichia coli"
```

2 Sources

listMatrixEX, **lisPhenodatas**, **listExpressionSets** and **ExpressionSetStudy5** example objects are synthetic.

The **maObjectDif** example object have been created after applying *createObjectMA()* function from **DExMA** package to *listMatrixEX* and *listPhenodatas* objects.

The **maObject** example object have been obtained after applying *allSameID()* function from **DExMA** package to *maObjectDif*

IDsDExMA and **SynonymsDExMA** objects have been constructed using the information available in NCBI GEO [1] and in the NCBI's gene database [2]

3 Session info

```
R version 4.4.0 beta (2024-04-15 r86425)  
Platform: x86_64-pc-linux-gnu  
Running under: Ubuntu 22.04.4 LTS  
  
Matrix products: default  
BLAS: /home/biocbuild/bbs-3.19-bioc/R/lib/libRblas.so  
LAPACK: /usr/lib/x86_64-linux-gnu/lapack/liblapack.so.3.10.0  
  
locale:  
 [1] LC_CTYPE=en_US.UTF-8      LC_NUMERIC=C  
 [3] LC_TIME=en_GB            LC_COLLATE=C  
 [5] LC_MONETARY=en_US.UTF-8  LC_MESSAGES=en_US.UTF-8  
 [7] LC_PAPER=en_US.UTF-8    LC_NAME=C  
 [9] LC_ADDRESS=C            LC_TELEPHONE=C  
[11] LC_MEASUREMENT=en_US.UTF-8 LC_IDENTIFICATION=C  
  
time zone: America/New_York  
tzcode source: system (glibc)  
  
attached base packages:  
[1] stats      graphics  grDevices  utils      datasets  methods   base  
  
other attached packages:  
[1] DExMAdata_1.12.0  
  
loaded via a namespace (and not attached):  
 [1] BiocManager_1.30.22 compiler_4.4.0      fastmap_1.1.1  
 [4] BiocStyle_2.32.0   cli_3.6.2          htmltools_0.5.8.1
```

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```
[7] tools_4.4.0      yaml_2.3.8      Biobase_2.64.0
[10] rmarkdown_2.26   knitr_1.46      BiocGenerics_0.50.0
[13] digest_0.6.35    xfun_0.43       rlang_1.1.3
[16] evaluate_0.23
```

References

- [1] Barret T., Wilhite S., Ledoux P. and et al. *NCBI GEO: archive for functional genomics data sets—update Nucleic Acids Research*, 991-995, 2013 <https://doi.org/10.1093/nar/gks1193>
- [2] *Database resources of the National Center for Biotechnology information Nucleic Acids Research*, volume 47, Pages D23–D28, 2019 <https://doi.org/10.1093/nar/gky1069>