Package ‘EpiMix.data’

February 22, 2024

Title  Data for the EpiMix package
Version  1.4.0
Description  Supporting data for the EpiMix R package.
It include:
- HM450_lncRNA_probes.rda
- HM450_miRNA_probes.rda
- EPIC_lncRNA_probes.rda
- EPIC_miRNA_probes.rda
- EpigenomeMap.rda
- LUAD.sample.annotation
- TCGA_BatchData
- MET.data
- mRNA.data
- microRNA.data
- lncRNA.data
- Sample_EpiMixResults_lncRNA
- Sample_EpiMixResults_miRNA
- Sample_EpiMixResults_Regular
- Sample_EpiMixResults_Enhancer
- lncRNA expression data of tumors from TCGA that are stored in the ExperimentHub.
License  GPL-3
Encoding  UTF-8
Depends  R (>= 4.2.0), ExperimentHub (>= 0.99.6)
Suggests  rmarkdown, knitr
biocViews  ExperimentData, ExperimentHub, Genome, RNASEqData,
           ExpressionData
NeedsCompilation  no
RoxygenNote  7.2.3
VignetteBuilder  knitr
BugReports  https://github.com/gevaertlab/EpiMix/issues
git_url  https://git.bioconductor.org/packages/EpiMix.data
git_branch  RELEASE_3_18
EPIC_lncRNA_probes

A character vector that maps CpG probes to lncRNA genes. The vectors names are genes and the values are CpG probes.

Description

A character vector that maps CpG probes to lncRNA genes. The vectors names are genes and the values are CpG probes.

Usage

EPIC_lncRNA_probes

Format

A character vector with 205645 elements.
EPIC_miRNA_probes

Examples

```r
## Not run:
data("EPIC_miRNA_probes")
## End(Not run)
```

Description

A dataframe that maps CpG probes genes to microRNA genes. The vectors names are genes and the values are CpG probes.

Usage

```r
EPIC_miRNA_probes
```

Format

A dataframe with 23,907 rows and 4 columns.

Examples

```r
## Not run:
data("EPIC_miRNA_probes")
## End(Not run)
```

EpigenomeMap

A list that map epigenome groups to epigenome IDs

Description

The data were generated from the RoadmapEpigenomic project (Nature, PMID: 25693563, figure 2).

Usage

```r
EpigenomeMap
```

Format

A list with 17 elements. The names are epigenome/tissue groups and the values are epigenome IDs for specific cells.
Example

```r
# Not run:
data("EpigenomeMap")

# End(Not run)
```

**Description**

A character vector that maps CpG probes to lncRNA genes. The vectors names are genes and the values are CpG probes.

**Usage**

```r
HM450_lncRNA_probes
```

**Format**

A character vector with 108202 elements.

**Examples**

```r
# Not run:
data("HM450_lncRNA_probes")

# End(Not run)
```

**Description**

A dataframe that maps CpG probes genes to microRNA genes.

**Usage**

```r
HM450_miRNA_probes
```

**Format**

A dataframe with 17,495 rows and 4 columns.
IncRNA.data

Examples

## Not run:
data("HM450_miRNA_probes")

## End(Not run)

---

lncRNA.data  Toy IncRNA expression dataset for demonstration purpose.

Description

This is a subset of IncRNA expression data from TCGA-LUAD, used for testing the program.

Usage

lncRNA.data

Format

a matrix

Examples

## Not run:
data("lncRNA.data")

## End(Not run)

---

LUAD.sample.annotation  toy dataset for sample annotation

Description

a dataframe with two columns: the first column is the patient identifier, and the second column is the sample annotation

Usage

LUAD.sample.annotation

Format

a dataframe
Examples
   ## Not run:
   data("LUAD.sample.annotation")
   ## End(Not run)

MET.data
Toy DNA methylation dataset for demonstration purpose.

Description
This is a subset of DNA methylation data from TCGA-LUAD, used for testing the program.

Usage
MET.data

Format
a matrix

Examples
   ## Not run:
   data("MET.data")
   ## End(Not run)

microRNA.data
Toy microRNA expression dataset for demonstration purpose.

Description
This is a subset of microRNA expression data from TCGA-LUAD, used for testing the program.

Usage
microRNA.data

Format
a matrix

Examples
   ## Not run:
   data("microRNA.data")
   ## End(Not run)
**mRNA.data**

*Toy gene expression dataset for demonstration purpose.*

**Description**

This is a subset of gene expression data from TCGA-LUAD, used for testing the program.

**Usage**

`mRNA.data`

**Format**

a matrix

**Examples**

```r
## Not run:
data("mRNA.data")
## End(Not run)
```

---

**Sample_EpiMixResults_Enhancer**

*toy dataset for EpiMix output with Enhancer mode*

**Description**

a list object returned from EpiMix

**Usage**

`Sample_EpiMixResults_Enhancer`

**Format**

a list

**Examples**

```r
## Not run:
data("Sample_EpiMixResults_Enhancer")
## End(Not run)
```
Sample_EpiMixResults_LncRNA

toy dataset for EpiMix output with LncRNA mode

Description
a list object returned from EpiMix

Usage
Sample_EpiMixResults_LncRNA

Format
a list

Examples
## Not run:
data("Sample_EpiMixResults_LncRNA")
## End(Not run)

Sample_EpiMixResults_miRNA

toy dataset for EpiMix output with miRNA mode

Description
a list object returned from EpiMix

Usage
Sample_EpiMixResults_miRNA

Format
a list

Examples
## Not run:
data("Sample_EpiMixResults_miRNA")
## End(Not run)
Sample_EpiMixResults-Regular

**toy dataset for EpiMix output with Regular mode**

**Description**
a list object returned from EpiMix

**Usage**
Sample_EpiMixResults-Regular

**Format**
a list

**Examples**

```r
## Not run:
data("Sample_EpiMixResultsRegular")
## End(Not run)
```

TCGA_BatchData

* A dataframe with the batch information of TCGA patient.

**Description**
a dataframe with two columns: the first column is the patient identifier, and the second column is the technical batch

**Usage**
TCGA_BatchData

**Format**
a dataframe

**Examples**

```r
## Not run:
data("TCGA_BatchData")
## End(Not run)
```
Index

* internal
  EPIC_lncRNA_probes, 2
  EPIC_miRNA_probes, 3
  EpigenomeMap, 3
  HM450_lncRNA_probes, 4
  HM450_miRNA_probes, 4
  lncRNA.data, 5
  LUAD.sample.annotation, 5
  MET.data, 6
  microRNA.data, 6
  mRNA.data, 7
  Sample_EpiMixResults_Enhancer, 7
  Sample_EpiMixResults_lncRNA, 8
  Sample_EpiMixResults_miRNA, 8
  Sample_EpiMixResults_Regular, 9
  TCGA_BatchData, 9

EPIC_lncRNA_probes, 2
EPIC_miRNA_probes, 3
EpigenomeMap, 3

HM450_lncRNA_probes, 4
HM450_miRNA_probes, 4

lncRNA.data, 5
LUAD.sample.annotation, 5

MET.data, 6
microRNA.data, 6
mRNA.data, 7

Sample_EpiMixResults_Enhancer, 7
Sample_EpiMixResults_lncRNA, 8
Sample_EpiMixResults_miRNA, 8
Sample_EpiMixResults_Regular, 9

TCGA_BatchData, 9