Package 'EpiMix.data'

November 10, 2026

Title Data for the EpiMix package

Version 1.14.0

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

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`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

Examples

```
## Not run:
data("EPIC_lncRNA_probes")

## End(Not run)
```

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

Description

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

Usage

```
EPIC_miRNA_probes
```

Format

A dataframe with 23,907 rows and 4 columns

Examples

```
## 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

```
EpigenomeMap
```

Format

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

Examples

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

## End(Not run)
```

`HM450_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

```
HM450_lncRNA_probes
```

Format

A character vector with 108202 elements

Examples

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

## End(Not run)
```

`HM450_miRNA_probes` *A dataframe that maps CpG probes genes to microRNA genes.*

Description

A dataframe that maps CpG probes genes to microRNA genes.

Usage

```
HM450_miRNA_probes
```

Format

A dataframe with 17,495 rows and 4 columns

Examples

```
## Not run:
data("HM450_miRNA_probes")

## End(Not run)
```

`lncRNA.data` *Toy lncRNA expression dataset for demonstration purpose.*

Description

This is a subset of lncRNA 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 micoRNA 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

```
## 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

```
## 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

```
## Not run:
data("Sample_EpiMixResults_Regular")

## 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

```
## Not run:
data("TCGA_BatchData")

## End(Not run)
```

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