Package ‘EpiMix.data’

April 4, 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**

**Description**

A list that map epigenome groups to epigenome IDs

**Usage**

```r
EpigenomeMap
```

**Format**

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

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

```r
## 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**

```r
## 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
**IncRNA.data**

**Examples**

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

---

**Description**

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

**Usage**

IncRNA.data

**Format**

a matrix

**Examples**

```r
## Not run:
data("IncRNA.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

```r
## 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

```r
MET.data
```

Format

a matrix

Examples

```r
## 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

```r
microRNA.data
```

Format

a matrix

Examples

```r
## 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

```r
## 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

```r
## 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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