Package 'methylclockData'

February 26, 2026

Title Data for methylclock package

Description Collection of 9 datasets, andrews and bakulski cord blood,
blood gse35069, blood gse35069 chen, blood gse35069 complete, combined cord blood,
cord bloo d gse68456, gervin and lyle cord blood, guintivano dlpfc and
saliva gse48472". Data downloaded from
[meffil](https://github.com/perishky/meffil/). Data used to estimate
cell counts using Extrinsic epigenetic age acceleration (EEAA) method
Collection of 12 datasets to use with MethylClock package to estimate
chronological and gestational DNA methylationwith estimators to use wit
different methylation clocks

Version 1.18.0

BugReports <https://github.com/isglobal-brge/methylclockData/issues>

URL <https://github.com/isglobal-brge/methylclockData>

biocViews SpecimenSource, ExperimentHub, Tissue, OrganismData,
Homo_sapiens_Data

Imports ExperimentHubData, ExperimentHub, utils

Suggests knitr, BiocStyle, rmarkdown

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NeedsCompilation no

Encoding UTF-8

RoxygenNote 7.1.2

VignetteBuilder knitr

git_url https://git.bioconductor.org/packages/methylclockData

git_branch RELEASE_3_22

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Repository Bioconductor 3.22

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get_coefBLUP *coefBLUP*

Description

`get_coefBLUP` returns the Best Linear Unbiased Prediction (BLUP) clock coefficients

Usage

```
get_coefBLUP()
```

Value

coefBLUP dataset

Examples

```
get_coefBLUP()
```

get_coefBohlin *coefBohlin*

Description

get_coefBohlin returns the Bohlin's clock coefficients

Usage

```
get_coefBohlin()
```

Value

coefBohlin dataset

Examples

```
get_coefBohlin()
```

get_coefEN *coefEN*

Description

get_coefEN returns the Elastic Net (EN) clock coefficients

Usage

```
get_coefEN()
```

Value

coefEN dataset

Examples

```
get_coefEN()
```

---

get_coefEPIC   *coefEPIC*

Description

get_coefEPIC returns the EPIC clock coefficients

Usage

```
get_coefEPIC()
```

Value

coefEPIC dataset

Examples

```
get_coefEPIC()
```

---

get_coefHannum   *coefHannum*

Description

get_coefHannum returns the Hannum's clock coefficients

Usage

```
get_coefHannum()
```

Value

coefHannum dataset

Examples

```
get_coefHannum()
```

get_coefHorvath *coefHorvath*

Description

get_coefHorvath returns the Hobarth's clock coefficients

Usage

```
get_coefHorvath()
```

Value

coefHorvath dataset

Examples

```
get_coefHorvath()
```

get_coefKnightGA *coefKnightGA*

Description

get_coefKnightGA returns the Knight's clock coefficients

Usage

```
get_coefKnightGA()
```

Value

coefKnightGA dataset

Examples

```
get_coefKnightGA()
```

get_coefLeeGA   *coefLeeGA*

Description

get_coefLeeGA returns the Lee's Gestational Age clock coefficients

Usage

```
get_coefLeeGA()
```

Value

coefLeeGA dataset

Examples

```
get_coefLeeGA()
```

get_coefLevine   *coefLevine*

Description

get_coefLevine returns the Levine's clock coefficients

Usage

```
get_coefLevine()
```

Value

coefLevine dataset

Examples

```
get_coefLevine()
```

get_coefMayneGA *coefMayneGA*

Description

get_coefMayneGA returns the Mayne's clock coefficients

Usage

```
get_coefMayneGA()
```

Value

coefMayneGA dataset

Examples

```
get_coefMayneGA()
```

get_coefPedBE *coefPedBE*

Description

get_coefPedBE returns the PedBE's clock coefficients

Usage

```
get_coefPedBE()
```

Value

coefPedBE dataset

Examples

```
get_coefPedBE()
```

---

get_coefSkin *coefSkin*

Description

get_coefSkin returns the Horvath's skin+blood clock coefficients

Usage

```
get_coefSkin()
```

Value

coefSkin dataset

Examples

```
get_coefSkin()
```

---

get_coefTL *coefTL*

Description

get_coefTL returns the Telomere Length clock coefficients

Usage

```
get_coefTL()
```

Value

coefTL dataset

Examples

```
get_coefTL()
```

get_coefWu	*Wu*

Description

`get_coefWu` returns the Wu's clock coefficients

Usage

```
get_coefWu()
```

Value

Wu dataset

Examples

```
get_coefWu()
```

get_cpgs_bn	*cpgs_bn*

Description

`get_cpgs_bn` returns data to use Horvath's CpGs to train a Bayesian Neural Network (BNN)

Usage

```
get_cpgs_bn()
```

Value

cpgs_bn dataset

Examples

```
get_cpgs_bn()
```

get_MethylationDataExample
                                MethylationDataExample55

Description

get_MethylationDataExample MethylationDataExample55 for vignette

Usage

```
get_MethylationDataExample()
```

Value

MethylationDataExample55 dataset

Examples

```
get_MethylationDataExample()
```

get_probeAnnotation21kdatMethUsed
                                probeAnnotation21kdatMethUsed

Description

get_probeAnnotation21kdatMethUsed returns probeAnnotation21kdatMethUsed

Usage

```
get_probeAnnotation21kdatMethUsed()
```

Value

probeAnnotation21kdatMethUsed dataset

Examples

```
get_probeAnnotation21kdatMethUsed()
```

get_references *references*

Description

The methylclockData package is a repository of a few public datasets that needs the *methylclock* package to estimate chronological and gestational DNA methylation (DNAm) age as well as biological age using different methylation clocks.

Usage

```
get_references()
```

Format

A list with different data frame.

blood gse35069 complete methylation profiles from Reinius 2012 for purified blood cell types. It includes CD4T, CD8T, Mono,

blood gse35069 methylation profiles from Reinius 2012 for purified blood cell types. It includes CD4T,CD8T, Mono, Bcell, NK and Gran.

blood gse35069 chen methylation profiles from Chen 2017 blood cell types. It includes CD4T, CD8T, Mono, Bcell, NK, Neu and Eos.

andrews and bakulski cord blood Cord blood reference from Bakulski 2016. It includes Bcell, CD4T, CD8T, Gran, Mono, NK and nRBC.

cord blood gse68456 Cord blood methylation profiles from De 2015. It includes CD4T, CD8T, Mono, Bcell, NK, Neu, Eos and RBC.

gervin and lyle cord blood Cord blood reference generated by Kristina Gervin and Robert Lyle, available at 'miffil' package. It includes CD14, Bcell, CD4T, CD8T, NK, Gran.

saliva gse48472 Reference generated from the multi-tissue pannel from Slieker 2013. It includes Buccal, CD4T, CD8T, Mono, Bcell, NK, Gran.

Details

get_references returns the file with references data

Value

references dataset

Examples

```
get_references()
```

get_TestDataset   *TestDataset*

Description

get_TestDataset returns TestDataset

Usage

```
get_TestDataset()
```

Value

TestDataset dataset

Examples

```
get_TestDataset()
```

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