

# Package: methylclockData (via r-universe)

October 10, 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 blood gse68456, gervin and lyle cord blood, quintivano 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 methylation with estimators to use with different methylation clocks

**Version** 1.20.0

**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

**License** MIT + file LICENSE

**NeedsCompilation** no

**Encoding** UTF-8

**RoxygenNote** 7.1.2

**VignetteBuilder** knitr

**Config/pak/sysreqs**  
make libbz2-dev libicu-dev liblzma-dev libpng-dev libxml2-dev libssl-dev xz-utils zlib1g-dev

**Repository** Bioconductor 3.23

**Date/Publication** 2026-04-28 12:34:50 UTC

**RemoteUrl** <https://github.com/bioc/methylclockData>

**RemoteRef** RELEASE\_3\_23

**RemoteSha** c5eeb1b85d32d331a9197fc5a2d655e72b648a2b

Contents

|                                             |           |
|---------------------------------------------|-----------|
| get_coefBLUP . . . . .                      | 2         |
| get_coefBohlin . . . . .                    | 3         |
| get_coefEN . . . . .                        | 3         |
| get_coefEPIC . . . . .                      | 4         |
| get_coefHannum . . . . .                    | 4         |
| get_coefHorvath . . . . .                   | 5         |
| get_coefKnightGA . . . . .                  | 5         |
| get_coefLeeGA . . . . .                     | 6         |
| get_coefLevine . . . . .                    | 6         |
| get_coefMayneGA . . . . .                   | 7         |
| get_coefPedBE . . . . .                     | 7         |
| get_coefSkin . . . . .                      | 8         |
| get_coefTL . . . . .                        | 8         |
| get_coefWu . . . . .                        | 9         |
| get_cpgs_bn . . . . .                       | 9         |
| get_MethylationDataExample . . . . .        | 10        |
| get_probeAnnotation21kdatMethUsed . . . . . | 10        |
| get_references . . . . .                    | 11        |
| get_TestDataset . . . . .                   | 12        |
| <b>Index</b>                                | <b>13</b> |

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|              |                 |
|--------------|-----------------|
| get_coefBLUP | <i>coefBLUP</i> |
|--------------|-----------------|

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Description

get\_coefBLUP returns the Best Linear Unbiased Prediction (BLUP) clock coefficients

Usage

get\_coefBLUP()

Value

coefBLUP dataset

Examples

get\_coefBLUP()

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|                |                   |
|----------------|-------------------|
| get_coefBohlin | <i>coefBohlin</i> |
|----------------|-------------------|

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**Description**

get\_coefBohlin returns the Bohlin's clock coefficients

**Usage**

```
get_coefBohlin()
```

**Value**

coefBohlin dataset

**Examples**

```
get_coefBohlin()
```

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|            |               |
|------------|---------------|
| get_coefEN | <i>coefEN</i> |
|------------|---------------|

---

**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()
```

---

|                              |                    |
|------------------------------|--------------------|
| <code>get_coefHorvath</code> | <i>coefHorvath</i> |
|------------------------------|--------------------|

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### **Description**

`get_coefHorvath` returns the Hobarth's clock coefficients

### **Usage**

```
get_coefHorvath()
```

### **Value**

`coefHorvath` dataset

### **Examples**

```
get_coefHorvath()
```

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|                               |                     |
|-------------------------------|---------------------|
| <code>get_coefKnightGA</code> | <i>coefKnightGA</i> |
|-------------------------------|---------------------|

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### **Description**

`get_coefKnightGA` returns the Knight's clock coefficients

### **Usage**

```
get_coefKnightGA()
```

### **Value**

`coefKnightGA` dataset

### **Examples**

```
get_coefKnightGA()
```

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|               |                  |
|---------------|------------------|
| get_coefLeeGA | <i>coefLeeGA</i> |
|---------------|------------------|

---

**Description**

get\_coefLeeGA returns the Lee's Gestational Age clock coefficients

**Usage**

```
get_coefLeeGA()
```

**Value**

coefLeeGA dataset

**Examples**

```
get_coefLeeGA()
```

---

|                |                   |
|----------------|-------------------|
| get_coefLevine | <i>coefLevine</i> |
|----------------|-------------------|

---

**Description**

get\_coefLevine returns the Levine's clock coefficients

**Usage**

```
get_coefLevine()
```

**Value**

coefLevine dataset

**Examples**

```
get_coefLevine()
```

---

|                              |                          |
|------------------------------|--------------------------|
| <code>get_coefMayneGA</code> | <code>coefMayneGA</code> |
|------------------------------|--------------------------|

---

**Description**

`get_coefMayneGA` returns the Mayne's clock coefficients

**Usage**

```
get_coefMayneGA()
```

**Value**

`coefMayneGA` dataset

**Examples**

```
get_coefMayneGA()
```

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|                            |                        |
|----------------------------|------------------------|
| <code>get_coefPedBE</code> | <code>coefPedBE</code> |
|----------------------------|------------------------|

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**Description**

`get_coefPedBE` returns the PedBE's clock coefficients

**Usage**

```
get_coefPedBE()
```

**Value**

`coefPedBE` dataset

**Examples**

```
get_coefPedBE()
```

---

|              |                 |
|--------------|-----------------|
| get_coefSkin | <i>coefSkin</i> |
|--------------|-----------------|

---

**Description**

get\_coefSkin returns the Horvath's skin+blood clock coefficients

**Usage**

```
get_coefSkin()
```

**Value**

coefSkin dataset

**Examples**

```
get_coefSkin()
```

---

|            |               |
|------------|---------------|
| get_coefTL | <i>coefTL</i> |
|------------|---------------|

---

**Description**

get\_coefTL returns the Telomere Length clock coefficients

**Usage**

```
get_coefTL()
```

**Value**

coefTL dataset

**Examples**

```
get_coefTL()
```

---

|            |           |
|------------|-----------|
| get_coefWu | <i>Wu</i> |
|------------|-----------|

---

**Description**

get\_coefWu returns the Wu's clock coefficients

**Usage**

```
get_coefWu()
```

**Value**

Wu dataset

**Examples**

```
get_coefWu()
```

---

|             |                |
|-------------|----------------|
| get_cpgs_bn | <i>cpgs_bn</i> |
|-------------|----------------|

---

**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 |
|----------------|------------|

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## 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 Sliker 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()
```

---

|                              |                    |
|------------------------------|--------------------|
| <code>get_TestDataset</code> | <i>TestDataset</i> |
|------------------------------|--------------------|

---

**Description**

`get_TestDataset` returns `TestDataset`

**Usage**

`get_TestDataset()`

**Value**

`TestDataset` dataset

**Examples**

`get_TestDataset()`

# Index

`get_coefBLUP`, [2](#)  
`get_coefBohlin`, [3](#)  
`get_coefEN`, [3](#)  
`get_coefEPIC`, [4](#)  
`get_coefHannum`, [4](#)  
`get_coefHorvath`, [5](#)  
`get_coefKnightGA`, [5](#)  
`get_coefLeeGA`, [6](#)  
`get_coefLevine`, [6](#)  
`get_coefMayneGA`, [7](#)  
`get_coefPedBE`, [7](#)  
`get_coefSkin`, [8](#)  
`get_coefTL`, [8](#)  
`get_coefWu`, [9](#)  
`get_cpgs_bn`, [9](#)  
`get_MethylationDataExample`, [10](#)  
`get_probeAnnotation21kdatMethUsed`, [10](#)  
`get_references`, [11](#)  
`get_TestDataset`, [12](#)