

Package ‘methylockData’

April 13, 2022

Title Data for methylock 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 dlpc 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 1.2.0

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

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

biocViews SpecimenSource, ExperimentHub, Tissue, OrganismData, Homo_sapiens_Data

Imports ExperimentHubData, ExperimentHub, utils

Suggests knitr, rmarkdown

License MIT + file LICENSE

NeedsCompilation no

Encoding UTF-8

RoxygenNote 7.1.1

VignetteBuilder knitr

git_url <https://git.bioconductor.org/packages/methylockData>

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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()
```

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	<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()
```

get_coefLeeGA	<i>coefLeeGA</i>
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Description

get_coefLeeGA returns the Lee's Gestational Age clock coefficients

Usage

```
get_coefLeeGA()
```

Value

coefLeeGA dataset

Examples

```
get_coefLeeGA()
```

<code>get_coefLevine</code>	<i>coefLevine</i>
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Description

`get_coefLevine` returns the Levine's clock coefficients

Usage

`get_coefLevine()`

Value

`coefLevine` dataset

Examples

`get_coefLevine()`

<code>get_coefMayneGA</code>	<i>coefMayneGA</i>
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Description

`get_coefMayneGA` returns the Mayne's clock coefficients

Usage

`get_coefMayneGA()`

Value

`coefMayneGA` dataset

Examples

`get_coefMayneGA()`

get_coefPedBE	<i>coefPedBE</i>
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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>
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Description

get_coefSkin returns the Horvath's skin+blood clock coefficients

Usage

```
get_coefSkin()
```

Value

coefSkin dataset

Examples

```
get_coefSkin()
```

<code>get_coefTL</code>	<i>coefTL</i>
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Description

`get_coefTL` returns the Telomere Length clock coefficients

Usage

`get_coefTL()`

Value

coefTL dataset

Examples

`get_coefTL()`

<code>get_coefWu</code>	<i>Wu</i>
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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 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>
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Description

`get_TestDataset` returns `TestDataset`

Usage

```
get_TestDataset()
```

Value

`TestDataset` dataset

Examples

```
get_TestDataset()
```

references.rda	'references' data
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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

```
data("references")
```

Format

A list with different data frame.

blood gse35069 complete methylation profiles from @reinius2012differential for purified blood cell types. It includes CD4T, CD8T, Mono,

blood gse35069 methylation profiles from @reinius2012differential for purified blood cell types. It includes CD4T, CD8T, Mono, Bcell, NK and Gran.

blood gse35069 chen methylation profiles from @chen2017epigenome blood cell types. It includes CD4T, CD8T, Mono, Bcell, NK, Neu and Eos.

andrews and bakulski cord blood Cord blood reference from @bakulski2016dna. It includes Bcell, CD4T, CD8T, Gran, Mono, NK and nRBC.

cord blood gse68456 Cord blood methylation profiles from @de2015nucleated. 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 @sliker2013identification. It includes Buccal, CD4T, CD8T, Mono, Bcell, NK, Gran.

Examples

```
data(references)
## maybe str(references) ; plot(references) ...
```

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