

Package ‘methylclock’

November 14, 2025

Type Package

Title Methylclock - DNA methylation-based clocks

Version 1.17.0

Description This package allows to estimate chronological and gestational DNA methylation (DNAm) age as well as biological age using different methylation clocks.
Chronological DNAm age (in years) : Horvath's clock, Hannum's clock, BNN, Horvath's skin+blood clock, PedBE clock and Wu's clock.
Gestational DNAm age : Knight's clock, Bohlin's clock, Mayne's clock and Lee's clocks.
Biological DNAm clocks : Levine's clock and Telomere Length's clock.

biocViews DNAMethylation, BiologicalQuestion, Preprocessing, StatisticalMethod, Normalization

License MIT + file LICENSE

Depends R (>= 4.1.0), methylclockData, devtools, quadprog

Imports Rcpp (>= 1.0.6), ExperimentHub, dplyr, impute, PerformanceAnalytics, Biobase, ggpmisc, tidyverse, ggplot2, ggpubr, minfi, tibble, RPMM, stats, graphics, tidyr, gridExtra, preprocessCore, dynamicTreeCut, planet

Suggests BiocStyle, knitr, GEOquery, rmarkdown

LinkingTo Rcpp

Encoding UTF-8

RoxygenNote 7.1.2

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

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

VignetteBuilder knitr

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

git_branch devel

git_last_commit 33c0153

git_last_commit_date 2025-10-29

Repository Bioconductor 3.23

Date/Publication 2025-11-13

Author Dolors Pelegri-Siso [aut, cre] (ORCID: <https://orcid.org/0000-0002-5993-3003>),
Juan R. Gonzalez [aut] (ORCID: <https://orcid.org/0000-0003-3267-2146>)

Maintainer Dolors Pelegri-Siso <dolors.pelegri@isglobal.org>

Contents

checkClocks	2
checkClocksGA	3
commonClockCpgs	4
DNAmAge	4
DNAmGA	6
getCellTypeReference	7
load_DNAmGA_Clocks_data	8
load_DNAm_Clocks_data	8
meffilEstimateCellCountsFromBetas	9
meffilListCellTypeReferences	10
methylock	10
plotCorClocks	11
plotDNAmAge	12
progress_data	13
progress_vars	13
Index	15

checkClocks	<i>Check wheter input data contains the required CpGs for the implemented clocks.</i>
-------------	---

Description

Check wheter input data contains the required CpGs for the implemented clocks.

Usage

checkClocks(x, ...)

Arguments

- x data.frame or tibble (Individual in columns, CpGs in rows, CpG names in first colum - i.e. Horvath’s format), ExpressionSet or GenomicRatioSet. A matrix is also possible having the CpG names in the rownames.
- ... other parameters

Details

To be supplied

Value

a list with the different clocks when there are more than 80 the required CpGs

Examples

```
TestDataset <- get_TestDataset()
checkClocks(TestDataset)
```

checkClocksGA	<i>Check wheter input data contains the required CpGs for the implemented clocks for Gestational Age.</i>
---------------	---

Description

Check wheter input data contains the required CpGs for the implemented clocks for Gestational Age.

Usage

```
checkClocksGA(x, ...)
```

Arguments

x	data.frame or tibble (Individual in columns, CpGs in rows, CpG names in first colum - i.e. Horvath's format), ExpressionSet or GenomicRatioSet. A matrix is also possible having the CpG names in the rownames.
...	other parameters

Details

To be supplied

Value

a list with the different GA clocks when there are more than 80

Examples

```
TestDataset <- get_TestDataset()
checkClocksGA(TestDataset)
```

commonClockCpgs	<i>Get common CpGs</i>
-----------------	------------------------

Description

Show the required CpGs contained on input data for the implemented clocks

Usage

```
commonClockCpgs(object, clock)
```

Arguments

object	resulting object from checkClocks functions
clock	string with the implemented clock, possible values are : "Knight", "Bohlin", "Mayne" and "Lee", "Horvath", "Hannum", "Levine", "skinHorvath", "PedBE", "Wu" and "TL"

Value

The common CpGs between input data and defined GA clock

Examples

```
TestDataset <- get_TestDataset()
cpgs.missing.GA <- checkClocksGA(TestDataset)
cpgs.missing <- checkClocks(TestDataset)
commonClockCpgs(cpgs.missing.GA, "Bohlin")
commonClockCpgs(cpgs.missing, "Hannum")
```

DNAmAge	<i>DNAm age estimation using different DNA methylation clocks.</i>
---------	--

Description

DNAm age estimation using different DNA methylation clocks.

Usage

```
DNAmAge(
  x,
  clocks = "all",
  toBetas = FALSE,
  fastImp = FALSE,
  normalize = FALSE,
  age,
```

```

    cell.count = TRUE,
    cell.count.reference = "blood gse35069 complete",
    min.perc = 0.8,
    ...
)

```

Arguments

<code>x</code>	data.frame (Individual in columns, CpGs in rows, CpG names in first column - i.e. Horvath's format), matrix (individuals in columns and CpGs in rows having CpG names in the rownames), ExpressionSet or GenomicRatioSet.
<code>clocks</code>	the methods used for estimating DNAmAge. Currently "Horvath", "Hannum", "Levine", "BNN", "skinHorvath", "PedBE", "Wu", "TL", "BLUP", "EN" and "all" are available. Default is "all" and all clocks are estimated.
<code>toBetas</code>	Should data be transformed to beta values? Default is FALSE. If TRUE, it implies data are M values.
<code>fastImp</code>	Is fast imputation performed if necessary? (see details). Default is FALSE
<code>normalize</code>	Is Horvath's normalization performed? By default is FALSE
<code>age</code>	individual's chronological age.
<code>cell.count</code>	Are cell counts estimated? Default is TRUE.
<code>cell.count.reference</code>	Used when 'cell.count' is TRUE. Default is "blood gse35069 complete". See 'meffil::meffil.list.cell.count.references()' for possible values.
<code>min.perc</code>	Indicates the minimum coincidence percentage required between CpGs in or dataframe <code>x</code> and CpGs in clock coefficients to perform the calculation. If <code>min.perc</code> is too low, the estimated gestational DNAm age can be poor
<code>...</code>	Other arguments to be passed through impute package

Details

Imputation is performed when having missing data. Fast imputation is performed by ... what about imputing only when CpGs for the clock are missing?

Value

The estimated chronological and biological mDNA age

Examples

```

MethylationData <- get_MethylationDataExample()
age.example55 <- DNAmAge(MethylationData)

```

DNAmGA	<i>Gestational DNAm age estimation using different DNA methylation clocks.</i>
--------	--

Description

Gestational DNAm age estimation using different DNA methylation clocks.

Usage

```
DNAmGA(
  x,
  toBetas = FALSE,
  fastImp = FALSE,
  normalize = FALSE,
  age,
  cell.count = TRUE,
  cell.count.reference = "andrews and bakulski cord blood",
  min.perc = 0.8,
  ...
)
```

Arguments

x	data.frame (Individual in columns, CpGs in rows, CpG names in first column - i.e. Horvath's format), matrix (individuals in columns and CpGs in rows having CpG names in the rownames), ExpressionSet or GenomicRatioSet.
toBetas	Should data be transformed to beta values? Default is FALSE. If TRUE, it implies data are M values.
fastImp	Is fast imputation performed if necessary? (see details). Default is FALSE
normalize	Is Horvath's normalization performed? By default is FALSE
age	individual's chronological age. Required to compute gestational age difference output
cell.count	Are cell counts estimated? Default is TRUE.
cell.count.reference	Used when 'cell.count' is TRUE. Default is "blood gse35069 complete". See 'meffil::meffil.list.cell.count.references()' for possible values.
min.perc	Indicates the minimum coincidence percentage required between CpGs in or dataframe x and CpGs in clock coefficients to perform the calculation. If min.perc is too low, the estimated gestational DNAm age can be poor
...	Other arguments to be passed through impute package

Details

Imputation is performed when having missing data. Fast imputation is performed by ... what about imputing only when CpGs for the clock are missing?

Value

the estimated gestational DNAm age

Examples

```
TestDataset <- get_TestDataset()
TestDataset[1:5, ]
ga.test <- DNAmGA(TestDataset)
```

getCellTypeReference *Get cell type reference*

Description

Get cell type reference

Usage

```
getCellTypeReference(name)
```

Arguments

name	string with predefined 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", "guintivano dlpfc" or "saliva gse48472"
------	--

Details

ORIGINAL AUTHOR: Matthew Suderman at github : <https://github.com/perishky/meffil> The original meffilListCellTypeReferences and getCellTypeReference function from meffil v1.0.0

Value

name and reference.globals

Examples

```
name <- "andrews and bakulski cord blood"
getCellTypeReference(name)
```

`load_DNAmGA_Clocks_data`*Loads DNA_mGA clock data from methylclockData*

Description

Loads DNA_mGA clock data from methylclockData

Usage`load_DNAmGA_Clocks_data()`**Value**

void

Examples`load_DNAm_Clocks_data()`

`load_DNAm_Clocks_data` *Loads DNA_m clock data from methylclockData*

Description

Loads DNA_m clock data from methylclockData

Usage`load_DNAm_Clocks_data()`**Value**

void

Examples`load_DNAm_Clocks_data()`

`meffilEstimateCellCountsFromBetas`*Estimate cell counts for a beta matrix from a reference*

Description

Estimate cell type ratios from methylation profiles of purified cell populations (Infinium Human-Methylation450 BeadChip).

Usage

```
meffilEstimateCellCountsFromBetas(beta, cellTypeReference, verbose = FALSE)
```

Arguments

<code>beta</code>	Matrix of Illumina 450K methylation levels (rows = CpG sites, columns = subjects).
<code>cellTypeReference</code>	Character string name of the cell type reference to use for estimating cell counts. See <code>meffilListCellTypeReferences()</code> for a list of available references. New references can be created using
<code>verbose</code>	If TRUE, then status messages are printed during execution (Default: FALSE).

Details

ORIGINAL AUTHOR: Matthew Suderman The original `meffil.list.cellTypeReferences` and `get.cellTypeReference` function from `meffil` v1.0.0 downloaded from github : <https://github.com/perishky/meffil>

Value

A matrix of cell count estimates.

Results should be nearly identical to `minfi::estimateCellCounts()`

`betas`

Examples

```
cell.count.reference <- "andrews and bakulski cord blood"
TestDataset <- get_TestDataset()
cpgs <- t(as.matrix(TestDataset[, -1]))
colnames(cpgs) <- TestDataset$CpGName
meffilEstimateCellCountsFromBetas(t(cpgs), cell.count.reference)
```

`meffilListCellTypeReferences`*List of available cell type references*

Description

List of available cell type references

Usage

```
meffilListCellTypeReferences()
```

Details

ORIGINAL AUTHOR: Matthew Suderman The original `meffilListCellTypeReferences` and `getCellTypeReference` function from `meffil` v1.0.0 at githug : <https://github.com/perishky/meffil>

Value

a list with reference globals

Examples

```
meffilListCellTypeReferences()
```

`methylock`*methylock*

Description

Package to estimate DNA methylation age (DNAmAge) using different methylation clocks.

Author(s)

Juan R Gonzalez <juanr.gonzalez@isglobal.org>

plotCorClocks	<i>Plot correlation among DNAm clockx</i>
---------------	---

Description

Plot correlation among DNAm clockx

Usage

```
plotCorClocks(x, ...)
```

Arguments

x	a tibble or data.frame with the different DNAm clocks
...	other arguments to be passs through function 'chart.Correlation' from 'PerformanceAnalytics' package

Details

To be supplied

Value

Plot with Correlation Clocks

Examples

```
library(Biobase)
library(GEOquery)

dd <- GEOquery::getGEO("GSE109446")
gse109446 <- dd[[1]]
controls <- Biobase::pData(gse109446)$`diagnosis:ch1` == "control"
gse <- gse109446[, controls]
age <- as.numeric(Biobase::pData(gse)$`age:ch1`)
age.gse <- DNAmAge(gse, age = age)
plotCorClocks(age.gse)
```

plotDNAMAge	<i>Plot DNAM age estimation vs chronological age.</i>
-------------	---

Description

Plot DNAM age estimation vs chronological age.

Usage

```
plotDNAMAge(x, y, tit = "Horvath's method", clock = "chronological", ...)
```

Arguments

x	DNAM age estimation
y	Chronological age
tit	Plot title. Default is "Horvath's method".
clock	Type of clock 'chronological' or 'GA', default 'chronological'
...	Other plot parameters for ggplot

Value

Plot with estimated DNAMAge

Examples

```
library(tidyverse)

path <- system.file("extdata", package = "methylock")
covariates <- read_csv(file.path(
  path,
  "SampleAnnotationExample55.csv"
))
age <- covariates$Age
MethylationData <- get_MethylationDataExample()

age.example55 <- DNAMAge(MethylationData)
plotDNAMAge(age.example55$Horvath, age)
```

progress_data	<i>PROGRESS cohort data</i>
---------------	-----------------------------

Description

The PROGRESS cohort data is available in the additional file 8 of : Knight, A.K., Craig, J.M., Theda, C. et al. An epigenetic clock for gestational age at birth based on blood methylation data. Genome Biol 17, 206 (2016). <https://doi.org/10.1186/s13059-016-1068-z>

Usage

```
data(progress_data)
```

Format

A data frame with 148 obs. and 151 variables

Details

A dataset containing data from the PROGRESS (Programming Research in Obesity, Growth, Environment and Social Stressors) cohort

Examples

```
data(progress_data)
```

progress_vars	<i>PROGRESS cohort variables</i>
---------------	----------------------------------

Description

The PROGRESS cohort data is available in the additional file 8 of : Knight, A.K., Craig, J.M., Theda, C. et al. An epigenetic clock for gestational age at birth based on blood methylation data. Genome Biol 17, 206 (2016). <https://doi.org/10.1186/s13059-016-1068-z>

Usage

```
data(progress_vars)
```

Format

A data frame with 150 obs. and 3 variables

Details

A dataset containing data from the PROGRESS (Programming Research in Obesity, Growth, Environment and Social Stressors) cohort

Examples

```
data(progress_vars)
```

Index

* **datasets**

progress_data, [13](#)

progress_vars, [13](#)

checkClocks, [2](#)

checkClocksGA, [3](#)

commonClockCpgs, [4](#)

DNAMAge, [4](#)

DNAMGA, [6](#)

getCellTypeReference, [7](#)

load_DNAM_Clocks_data, [8](#)

load_DNAMGA_Clocks_data, [8](#)

meffilEstimateCellCountsFromBetas, [9](#)

meffilListCellTypeReferences, [9](#), [10](#)

methylock, [10](#)

minfi::estimateCellCounts(), [9](#)

plotCorClocks, [11](#)

plotDNAMAge, [12](#)

progress_data, [13](#)

progress_vars, [13](#)