

# Package ‘methylock’

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**Type** Package

**Title** Methylock - DNA methylation-based clocks

**Version** 1.2.0

**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

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**Depends** R (>= 4.1.0), methylockData, 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/methylock>

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

**VignetteBuilder** knitr

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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 column - 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

*DNAM age estimation using different DNA methylation clocks.*


---

**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 dlpc" 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<sub>m</sub>GA clock data from methylclockData*

---

**Description**

Loads DNA<sub>m</sub>GA clock data from methylclockData

**Usage**

```
load_DNAmGA_Clocks_data()
```

**Value**

void

**Examples**

```
load_DNAm_Clocks_data()
```

---

```
load_DNAm_Clocks_data
```

*Loads DNA<sub>m</sub> clock data from methylclockData*

---

**Description**

Loads DNA<sub>m</sub> 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 github : <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](mailto:juanr.gonzalez@isglobal.org)>

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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)
```

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