

# Package ‘AlphaBeta’

July 16, 2025

**Type** Package

**Title** Computational inference of epimutation rates and spectra from high-throughput DNA methylation data in plants

**Version** 1.22.0

## Description

AlphaBeta is a computational method for estimating epimutation rates and spectra from high-throughput DNA methylation data in plants.

The method has been specifically designed to:

1. analyze 'germline' epimutations in the context of multi-generational mutation accumulation lines (MA-lines).
2. analyze 'somatic' epimutations in the context of plant development and aging.

**License** GPL-3

**Depends** R (>= 3.6.0)

**Imports** dplyr (>= 0.7), data.table (>= 1.10), stringr (>= 1.3), utils (>= 3.6.0), gtools (>= 3.8.0), optimx (>= 2018-7.10), expm (>= 0.999-4), stats (>= 3.6), BiocParallel (>= 1.18), igraph (>= 1.2.4), graphics (>= 3.6), ggplot2 (>= 3.2), grDevices (>= 3.6), plotly (>= 4.9)

**Encoding** UTF-8

**LazyData** false

**LazyLoad** yes

**VignetteBuilder** knitr

**RoxygenNote** 7.1.0

**Suggests** knitr, rmarkdown

**biocViews** Epigenetics, FunctionalGenomics, Genetics, MathematicalBiology

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|           |                                                |
|-----------|------------------------------------------------|
| ABneutral | <i>Run Model with no selection (ABneutral)</i> |
|-----------|------------------------------------------------|

---

Description

This model assumes that heritable gains and losses in cytosine methylation are selectively neutral.

Usage

ABneutral(pedigree.data, p0uu, eqp, eqp.weight, Nstarts, out.dir, out.name)

Arguments

- pedigree.data pedigree data.
- p0uu initial proportion of unmethylated cytosines.
- eqp equilibrium proportion of unmethylated cytosines.
- eqp.weight weight assigned to equilibrium function.
- Nstarts iterations for non linear LSQ optimization.
- out.dir output directory.
- out.name output file name.

**Value**

ABneutral RData file.

**Examples**

```
#Get some toy data
inFile <- readRDS(system.file("extdata/dm/", "output.rds", package="AlphaBeta"))
pedigree <- inFile$Pdata
p0uu_in <- inFile$tmpp0
eqp.weight <- 1
Nstarts <- 2
out.name <- "CG_global_estimates_ABneutral"
out <- ABneutral(pedigree.data = pedigree,
                 p0uu=p0uu_in,
                 eqp=p0uu_in,
                 eqp.weight=eqp.weight,
                 Nstarts=Nstarts,
                 out.dir=getwd(),
                 out.name=out.name)

summary(out)
```

---

ABneutralSOMA

*Model with no selection (outneutral)*


---

**Description**

This model assumes that somatically heritable gains and losses in cytosine methylation are selectively neutral.

**Usage**

```
ABneutralSOMA(pedigree.data, p0uu, eqp, eqp.weight, Nstarts, out.dir, out.name)
```

**Arguments**

|               |                                                   |
|---------------|---------------------------------------------------|
| pedigree.data | pedigree data.                                    |
| p0uu          | initial proportion of unmethylated cytosines.     |
| eqp           | equilibrium proportion of unmethylated cytosines. |
| eqp.weight    | weight assigned to equilibrium function.          |
| Nstarts       | iterations for non linear LSQ optimization.       |
| out.dir       | output directory.                                 |
| out.name      | output file name.                                 |

**Value**

ABneutralSoma RData file.

**Examples**

```
#Get some toy data
inFile <- readRDS(system.file("extdata/soma/", "outputSoma.rds", package="AlphaBeta"))
pedigree <- inFile$Pdata
p0uu_in <- inFile$tmp0
eqp.weight <- 0.001
Nstarts <- 2
out.name <- "ABneutralSOMA_CG_estimates"
out <- ABneutralSOMA(pedigree.data = pedigree,
                     p0uu=p0uu_in,
                     eqp=p0uu_in,
                     eqp.weight=eqp.weight,
                     Nstarts=Nstarts,
                     out.dir=getwd(),
                     out.name=out.name)

summary(out)
```

---

ABnull

*Run model that considers no accumulation of epimutations (ABnull)*

---

**Description**

Run model that considers no accumulation of epimutations (ABnull)

**Usage**

```
ABnull(pedigree.data, out.dir, out.name)
```

**Arguments**

|               |                                                    |
|---------------|----------------------------------------------------|
| pedigree.data | Generation table name, you can find sample file in |
| out.dir       | outputdirectory                                    |
| out.name      | name of file                                       |

**Value**

ABnull RData file.

**Examples**

```
#Get some toy data
inFile <- readRDS(system.file("extdata/dm/", "output.rds", package="AlphaBeta"))
pedigree <- inFile$Pdata
out.name <- "CG_global_estimates_ABnull"
out <- ABnull(pedigree.data = pedigree,
              out.dir=getwd(),
              out.name=out.name)

summary(out)
```

ABplot

*Plotting estimates***Description**

Plotting Estimating epimutation

**Usage**

```
ABplot(
  pedigree.names,
  output.dir,
  out.name,
  alpha = 0.5,
  geom.point.size = 2,
  geom.line.size = 0.9,
  plot.height = 8,
  plot.width = 11,
  plot.type = "both",
  lsq.line = "theory",
  interact = FALSE
)
```

**Arguments**

|                 |                         |
|-----------------|-------------------------|
| pedigree.names  | Models output AB*.Rdata |
| output.dir      | output directory        |
| out.name        | filename                |
| alpha           | ggplot parameters       |
| geom.point.size | ggplot parameters       |
| geom.line.size  | ggplot parameters       |
| plot.height     | ggplot parameters       |

|            |                                               |
|------------|-----------------------------------------------|
| plot.width | ggplot parameters                             |
| plot.type  | type of plot (data.only, fit.only, both)      |
| lsq.line   | Least Square Regression line (theory or pred) |
| intract    | to see interactive plot. (using plotly)       |

**Value**

plot

**Examples**

```
# Get some toy data
file <- system.file("extdata/dm/", "Col_CG_global_estimates_ABneutral.Rdata", package="AlphaBeta")
ABplot(pedigree.names=file, output.dir=getwd(), out.name="ABneutral")
```

---

|            |                                                                                      |
|------------|--------------------------------------------------------------------------------------|
| ABselectMM | <i>Run model with selection against spontaneous gain of methylation (ABselectMM)</i> |
|------------|--------------------------------------------------------------------------------------|

---

**Description**

This model assumes that heritable losses of cytosine methylation are under negative selection.

**Usage**

```
ABselectMM(pedigree.data, p0uu, eqp, eqp.weight, Nstarts, out.dir, out.name)
```

**Arguments**

|               |                                                   |
|---------------|---------------------------------------------------|
| pedigree.data | pedigree data.                                    |
| p0uu          | initial proportion of unmethylated cytosines.     |
| eqp           | equilibrium proportion of unmethylated cytosines. |
| eqp.weight    | nweight assigned to equilibrium function.         |
| Nstarts       | iterations for non linear LSQ optimization.       |
| out.dir       | output directory.                                 |
| out.name      | output file name.                                 |

**Value**

ABselectMM RData file.

## Examples

```
#Get some toy data
inFile <- readRDS(system.file("extdata/dm/", "output.rds", package="AlphaBeta"))
pedigree <- inFile$Pdata
p0uu_in <- inFile$tmp0
eqp.weight <- 1
Nstarts <- 2
out.name <- "CG_global_estimates_ABselectMM"
out <- ABselectMM(pedigree.data = pedigree,
                  p0uu=p0uu_in,
                  eqp=p0uu_in,
                  eqp.weight=eqp.weight,
                  Nstarts=Nstarts,
                  out.dir=getwd(),
                  out.name=out.name)

summary(out)
```

---

|                |                                                                                   |
|----------------|-----------------------------------------------------------------------------------|
| ABselectMMSOMA | <i>Model with selection against spontaneous gain of methylation (outselectMM)</i> |
|----------------|-----------------------------------------------------------------------------------|

---

## Description

This model assumes that somatically heritable gains of cytosine methylation are under negative selection.

## Usage

```
ABselectMMSOMA(
  pedigree.data,
  p0uu,
  eqp,
  eqp.weight,
  Nstarts,
  out.dir,
  out.name
)
```

## Arguments

|               |                                                   |
|---------------|---------------------------------------------------|
| pedigree.data | pedigree data.                                    |
| p0uu          | initial proportion of unmethylated cytosines.     |
| eqp           | equilibrium proportion of unmethylated cytosines. |
| eqp.weight    | weight assigned to equilibrium function.          |
| Nstarts       | iterations for non linear LSQ optimization.       |

out.dir            output directory.  
 out.name         output file name.

### Value

ABneutralSoma RData file.

### Examples

```
#Get some toy data
inFile <- readRDS(system.file("extdata/soma/", "outputSoma.rds", package="AlphaBeta"))
pedigree <- inFile$Pdata
p0uu_in <- inFile$tmp0
eqp.weight <- 0.001
Nstarts <- 2
out.name <- "ABselectMMSOMA_CG_estimates"
out <- ABselectMMSOMA(pedigree.data = pedigree,
                      p0uu=p0uu_in,
                      eqp=p0uu_in,
                      eqp.weight=eqp.weight,
                      Nstarts=Nstarts,
                      out.dir=getwd(),
                      out.name=out.name)

summary(out)
```

---

|            |                                                                                      |
|------------|--------------------------------------------------------------------------------------|
| ABselectUU | <i>Run model with selection against spontaneous loss of methylation (ABselectUU)</i> |
|------------|--------------------------------------------------------------------------------------|

---

### Description

This model assumes that heritable gains of cytosine methylation are under negative selection.

### Usage

```
ABselectUU(pedigree.data, p0uu, eqp, eqp.weight, Nstarts, out.dir, out.name)
```

### Arguments

pedigree.data    pedigree data.  
 p0uu            initial proportion of unmethylated cytosines.  
 eqp             equilibrium proportion of unmethylated cytosines.  
 eqp.weight      weight assigned to equilibrium function.  
 Nstarts         iterations for non linear LSQ optimization.  
 out.dir         output directory.  
 out.name        output file name.



**Value**

ABselectMM RData file.

**Examples**

```
#Get some toy data
inFile <- readRDS(system.file("extdata/dm/", "output.rds", package="AlphaBeta"))
pedigree <- inFile$Pdata
p0uu_in <- inFile$tmp0
eqp.weight <- 1
Nstarts <- 2
out.name <- "CG_global_estimates_ABselectUU"
out3 <- ABselectUU(pedigree.data = pedigree,
                   p0uu=p0uu_in,
                   eqp=p0uu_in,
                   eqp.weight=eqp.weight,
                   Nstarts=Nstarts,
                   out.dir=getwd(),
                   out.name=out.name)

summary(out3)
```

---

|                |                                                                                   |
|----------------|-----------------------------------------------------------------------------------|
| ABselectUUSOMA | <i>Model with selection against spontaneous loss of methylation (outselectUU)</i> |
|----------------|-----------------------------------------------------------------------------------|

---

**Description**

This model assumes that somatically heritable gains of cytosine methylation are under negative selection.

**Usage**

```
ABselectUUSOMA(
  pedigree.data,
  p0uu,
  eqp,
  eqp.weight,
  Nstarts,
  out.dir,
  out.name
)
```

**Arguments**

pedigree.data    pedigree data.  
p0uu              initial proportion of unmethylated cytosines.

|            |                                                   |
|------------|---------------------------------------------------|
| eqp        | equilibrium proportion of unmethylated cytosines. |
| eqp.weight | weight assigned to equilibrium function.          |
| Nstarts    | iterations for non linear LSQ optimization.       |
| out.dir    | output directory.                                 |
| out.name   | output file name.                                 |

**Value**

ABneutralSoma RData file.

**Examples**

```
#Get some toy data
inFile <- readRDS(system.file("extdata/soma/", "outputSoma.rds", package="AlphaBeta"))
pedigree <- inFile$Pdata
p0uu_in <- inFile$tmppp0
eqp.weight <- 0.001
Nstarts <- 2
out.name <- "ABselectUUSOMA_CG_estimates"
out <- ABselectUUSOMA(pedigree.data = pedigree,
                      p0uu=p0uu_in,
                      eqp=p0uu_in,
                      eqp.weight=eqp.weight,
                      Nstarts=Nstarts,
                      out.dir=getwd(),
                      out.name=out.name)

summary(out)
```

---

 BOOTmodel

*Bootstrap analysis with the best model*


---

**Description**

Bootstrap analysis with the best model

**Usage**

```
BOOTmodel(pedigree.data, Nboot, out.dir, out.name)
```

**Arguments**

|               |                   |
|---------------|-------------------|
| pedigree.data | pedigree data.    |
| Nboot         | number of boot.   |
| out.dir       | output directory. |
| out.name      | output file name. |

**Value**

bootstrap result.

**Examples**

```
## Get some toy data
inFile <- system.file("extdata/models/", "ABneutral_CG_global_estimates.Rdata", package="AlphaBeta")
Nboot <- 4
out.name <- "Boot_CG_global_estimates_ABneutral"
Bout <- BOOTmodel(pedigree.data=inFile,
                  Nboot=Nboot,
                  out.dir=getwd(),
                  out.name=out.name)

summary(Bout)
```

---

buildPedigree

*Building Pedigree*

---

**Description**

calculate divergence times of the pedigree

**Usage**

```
buildPedigree(nodelist, edgelist, cytosine = "CG", posteriorMaxFilter = 0.99)
```

**Arguments**

|                    |                                                                                                             |
|--------------------|-------------------------------------------------------------------------------------------------------------|
| nodelist           | input file containing information on generation times and pedigree lineages "ext-data" called "nodelist.fn" |
| edgelist           | input file containing edges                                                                                 |
| cytosine           | Type of cytosine (CHH/CHG/CG)                                                                               |
| posteriorMaxFilter | Filter value, based on posteriorMax                                                                         |

**Value**

generating divergence matrices file.

**Examples**

```
# Get some toy data
file <- system.file("extdata/dm/", "nodelist.fn", package="AlphaBeta")
df<-read.csv(file)
df$filename <- gsub("^", paste0(dirname(dirname(file)), "/"), df$filename )
write.csv(df, file = paste0(dirname(file), "/", "tmp_nodelist.fn"), row.names=FALSE, quote=FALSE)
file <- system.file("extdata/dm/", "tmp_nodelist.fn", package="AlphaBeta")
file2 <- system.file("extdata/dm/", "edgelist.fn", package="AlphaBeta")
buildPedigree(nodelist = file, edgelist=file2, cytosine="CG", posteriorMaxFilter=0.99)
```

---

**dMatrix***Constructing D-Matrices*

---

**Description**

Estimating epimutation rates from high-throughput DNA methylation data

**Usage**

```
dMatrix(nodelist, cytosine, posteriorMaxFilter)
```

**Arguments**

nodelist            list of samples, you can find sample file in "extdata" called "nodelist.fn"  
 cytosine            Type of cytosine (CHH/CHG/CG)  
 posteriorMaxFilter            Filter value, based on posteriorMax ex:  $\geq 0.95$  or 0.99

**Value**

generating divergence matrices file.

**Examples**

```
# Get some toy data
file <- system.file("extdata/dm/", "nodelist.fn", package="AlphaBeta")
df<-read.csv(file)
df$filename<-sub("^",paste0(dirname(file),"/"),df$filename )
write.csv(df, file = paste0(dirname(file),"tmp_nodelist.fn"),row.names=FALSE,quote=FALSE)
file <- system.file("extdata/dm/", "tmp_nodelist.fn", package="AlphaBeta")
dMatrix(file, "CG", 0.99)
```

---

**FtestRSS***Comparison of different models and selection of best model*

---

**Description**

Comparison of different models and selection of best model

**Usage**

```
FtestRSS(pedigree.select, pedigree.null)
```



|              |                  |
|--------------|------------------|
| out.pdf      | output file name |
| output.dir   | output directory |
| plot.width   | plotting width   |
| plot.height  | plotting height  |
| vertex.label | label vertex     |
| vertex.size  | size of vertex   |
| aspect.ratio | aspect.ration    |

**Value**

plot pedigree matrices file.

**Examples**

```
# Get some toy data
file <- system.file("extdata/dm/", "nodelist.fn", package="AlphaBeta")
file2 <- system.file("extdata/dm/", "edgelist.fn", package="AlphaBeta")
plotPedigree(nodelist = file, edgelist=file2, sampling.design="sibling", vertex.label=TRUE,
  out.pdf="Plot", output.dir=getwd() )
```

rc.meth.lvl

*Calculating rc.Meth.lvl***Description**

Estimating epimutation rates from high-throughput DNA methylation data

**Usage**

```
rc.meth.lvl(nodelist, cytosine, posteriorMaxFilter)
```

**Arguments**

|                    |                                                                             |
|--------------------|-----------------------------------------------------------------------------|
| nodelist           | List of samples, you can find sample file in "extdata" called "nodelist.fn" |
| cytosine           | Type of cytosine (CHH/CHG/CG)                                               |
| posteriorMaxFilter | Filter value, based on posteriorMax                                         |

**Value**

rc meth lvl.

**Examples**

```
## Get some toy data
file <- system.file("extdata/dm/", "tmp_nodelist.fn", package="AlphaBeta")
rc.meth.lvl(file, "CG", 0.99)
```

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