

# Package ‘AlphaBeta’

July 25, 2025

**Type** Package

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

**Version** 1.23.0

## 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)

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**LazyLoad** yes

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## Contents

|                          |           |
|--------------------------|-----------|
| ABneutral . . . . .      | 2         |
| ABneutralSOMA . . . . .  | 3         |
| ABnull . . . . .         | 4         |
| ABplot . . . . .         | 5         |
| ABselectMM . . . . .     | 6         |
| ABselectMMSOMA . . . . . | 7         |
| ABselectUU . . . . .     | 8         |
| ABselectUUSOMA . . . . . | 9         |
| BOOTmodel . . . . .      | 10        |
| buildPedigree . . . . .  | 10        |
| dMatrix . . . . .        | 11        |
| FtestRSS . . . . .       | 12        |
| plotPedigree . . . . .   | 12        |
| rc.meth.lvl . . . . .    | 13        |
| <b>Index</b>             | <b>15</b> |

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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) |
| interact        | 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$Pdata
p0uu_in <- inFile$tmpp0
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$Pdata
p0uu_in <- inFile$tmpp0
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$Pdata
p0uu_in <- inFile$tmpp0
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$Pdata
p0uu_in <- inFile$tmpp0
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 | <i>Comparison of different models and selection of best model</i> |
|----------|-------------------------------------------------------------------|

---

Description

Comparison of different models and selection of best model

Usage

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

Arguments

pedigree.select                      pedigree model.  
pedigree.null      ABnull pedigree.

Value

result of Ftest.

Examples

```
## Get some toy data
file1 <- system.file("extdata/models/", "ABneutral_CG_global_estimates.Rdata", package="AlphaBeta")
file2 <- system.file("extdata/models/", "ABnull_CG_global_estimates.Rdata", package="AlphaBeta")
out <- FtestRSS(pedigree.select=file1,
                pedigree.null=file2)
```

---

|              |                      |
|--------------|----------------------|
| plotPedigree | <i>Plot Pedigree</i> |
|--------------|----------------------|

---

Description

Plotting Pedigree tree

**Usage**

```
plotPedigree(
  nodelist,
  edgelist,
  sampling.design,
  out.pdf = NULL,
  output.dir = NULL,
  plot.width = 11,
  plot.height = 8,
  vertex.label = NULL,
  vertex.size = 12,
  aspect.ratio = 2.5
)
```

**Arguments**

|                 |                                                                                                             |
|-----------------|-------------------------------------------------------------------------------------------------------------|
| nodelist        | input file containing information on generation times and pedigree lineages "ext-data" called "nodelist.fn" |
| edgelist        | input file containing edges "edgelist.fn"                                                                   |
| sampling.design | "progenitor.intermediate"; "sibling"; "progenitor.endpoint"; "tree"                                         |
| out.pdf         | output file name                                                                                            |
| output.dir      | output directory                                                                                            |
| plot.width      | plotting with                                                                                               |
| 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.lv1

---

*Calculating rc.Meth.lv1*


---

**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)
```

# Index

ABneutral, [2](#)  
ABneutralSOMA, [3](#)  
ABnull, [4](#)  
ABplot, [5](#)  
ABselectMM, [6](#)  
ABselectMMSOMA, [7](#)  
ABselectUU, [8](#)  
ABselectUUSOMA, [9](#)  
  
BOOTmodel, [10](#)  
buildPedigree, [10](#)  
  
dMatrix, [11](#)  
  
FtestRSS, [12](#)  
  
plotPedigree, [12](#)  
  
rc.meth.lvl, [13](#)