

# Package ‘AlphaBeta’

January 10, 2025

**Type** Package

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

**Version** 1.21.0

## 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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**Author** Yadollah Shahryary Dizaji [cre, aut],  
Frank Johannes [aut],  
Rashmi Hazarika [aut]

**Maintainer** Yadollah Shahryary Dizaji <shahryary@gmail.com>

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ABneutral	<i>Run Model with no selection (ABneutral)</i>
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## 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$Pdata
p0uu_in <- inFile$tmp00
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$Pdata
p0uu_in <- inFile$tmppp0
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",
  intract = 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$Pdata
p0uu_in <- inFile$tmppp0
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$Pdata
p0uu_in <- inFile$tmp0
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: >= 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)
```

**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)
```

---

<code>plotPedigree</code>	<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 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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