

Package ‘AlphaBeta’

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Type Package

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

Version 1.18.0

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

Maintainer Yadollah Shahryary Dizaji <shahryary@gmail.com>

Contents

ABneutral	2
ABneutralSOMA	3
ABnull	4
ABplot	5
ABselectMM	6
ABselectMMSOMA	7
ABselectUU	8
ABselectUUSOMA	9
BOOTmodel	10
buildPedigree	11
dMatrix	12
FtestRSS	12
plotPedigree	13
rc.meth.lvl	14

Index	15
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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$Pdata
p0uu_in <- inFile$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$Pdata
p0uu_in <- inFile$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: >= 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)
```

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 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)
```

Index

ABneutral, [2](#)
ABneutralSOMA, [3](#)
ABnull, [4](#)
ABplot, [5](#)
ABselectMM, [6](#)
ABselectMMSOMA, [7](#)
ABselectUU, [8](#)
ABselectUUSOMA, [9](#)

BOOTmodel, [10](#)
buildPedigree, [11](#)

dMatrix, [12](#)

FtestRSS, [12](#)

plotPedigree, [13](#)

rc.meth.lvl, [14](#)