Package: AlphaBeta (via r-universe)

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Type Package

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

Version 1.26.0

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)

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Contents

`ABneutral` *Run Model with no selection (ABneutral)*

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$Pdata
p0uu_in <- inFile$tmpp0
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 intarctive plot. (useing 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` *Run model with selection against spontaneous gain of methylation (ABselectMM)*

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` *Model with selection against spontaneous gain of methylation (outselectMM)*

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` *Run model with selection against spontaneous loss of methylation (ABselectUU)*

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` *Model with selection against spontaneous loss of methylation (outselectUU)*

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 "extdata" 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` *Plot Pedigree*

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 "extdata" 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 vertix
`vertex.size`	size of vertix
`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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