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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`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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