

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 1.21.0

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)

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LazyLoad yes

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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$Pdata
p0uu_in <- inFile$tmp0
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 Fttest.

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 <- FttestRSS(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)
```

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