AlphaBeta

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2019-07-24

Contents

1 Introduction

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.

Heritable changes in cytosine methylation can arise stochastically in plant genomes independently of DNA sequence alterations. These so-called 'spontaneous epimutations' appear to be a byproduct of imperfect DNA methylation maintenance during mitotic and meitotic cell divisions.

Accurate estimates of the rate and spectrum of these stochastic events are necessary to be able to quantify how epimutational processes shape methylome diversity in the context of plant evolution, development and aging.

Here we describe AlphaBeta, a computational method for estimating epimutation rates and spectra from pedigree-based high-throughput DNA methylation data in plants.

The method requires that the topology of the pedigree is known, which is typically the case in the construction of mutation accumulation lines (MA-lines) in sexually or clonally reproducing plant species.

However, the method also works for inferring somatic epimutations in long-lived perrenials, such as trees, using leaf methylomes and coring data as input. In this case, AlphaBeta treats the tree branching structure as an intra-organismal phylogeny of somatic lineages that carry information about the epimutational history of each branch.

2 Preparing Files

NOTE In this tutorial we are reading methylome files from the methimpute package:

You can find more information here: Methimpute package

2.1 Generation file

A file containing the list of filenames should be provided for generation of a divergence matrix and calculation of methylation proportions.

```
# SAMPLE FILE
generation.fn <- system.file("extdata", "generations.fn", package = "AlphaBeta")
file <- fread(generation.fn)
head(file)
```

```
                               filename generation lineage
  1:     data/methylome_Col_G0-merged.txt         G0
  2:  data/methylome_Col_G1_L2-merged.txt         G1      L2
  3:  data/methylome_Col_G4_L8-merged.txt         G4      L8
  4: data/methylome_Col_G11_L2-merged.txt        G11      L2
```

2.2 Generate divergence matrix

Estimating epimutation rates from high-throughput DNA methylation data. Generation of divergence matrix and calculation of methylation levels.

```
dMatrix(genTable = generation.fn, cytosine = "CG", posteriorMaxFilter = 0.99)
```

```
# Sample output from dMatrix function
head(fread("AB-dMatrix-CG-0.99.csv"))
```

```
    pair.1 pair.2 D.value
  1:     G0  G1-L2 0.01366
  2:     G0  G4-L8 0.01412
```

```
3:     G0 G11-L2 0.00806
4:  G1-L2  G4-L8 0.03265
5:  G1-L2 G11-L2 0.00473
6:  G4-L8 G11-L2 0.00904
```

2.3 Generate methylation proportions

```
rc.meth.lvl(genTable = generation.fn, cytosine = "CG", posteriorMaxFilter = 0.99,
    nThread = 4)
```

```
# Sample output from proportions function
head(fread(system.file("extdata/dm", "AB-methprop-CG-0.99.csv",
    package = "AlphaBeta")))
```

```
     Sample_name context rc.meth.lvls
1:    G3_26_r1      CG    0.2542201
2:    G3_87_r1      CG    0.2522355
3:    G3_87_r2      CG    0.2524761
4:  G31_109_r1      CG    0.2482041
5:  G31_109_r2      CG    0.2654014
6:  G31_119_r1      CG    0.2623544
```

2.4 Information about Sample file.

This file containing information on generation times and pedigree lineages

```
# Sample file
head(fread(system.file("extdata/dm", "sampleInfo.csv", package = "AlphaBeta")))
```

```
         Sample Generation Lineage
1:   G3_26_r1          3      26
2:   G3_87_r1          3      87
3:   G3_87_r2          3      87
4: G31_109_r1         31     109
5: G31_109_r2         31     109
6: G31_119_r1         31     119
```

2.5 File containing lineage branch points

```
# Sample file
head(fread(system.file("extdata/dm", "branchPoints.csv", package = "AlphaBeta")))
```

```
    BP Generation Lineage
1:  1          0    none
2:  2          2      87
3:  3         30     109
4:  4         30     119
5:  5         30      29
6:  6         30      39
```

3 Germline epimutations

Models ABneutral, ABselectMM and ABselectUU can be used to estimate the rate of spontaneous epimutations from pedigree-based high-throughput DNA methylation data. The models are generally designed for pedigree data arising from selfing diploid species.

3.1 Calculate divergence times

Divergence time (delta t) is calculated as follows: delta t = t1 + t2 - 2*t0, where t1 is the time of sample 1 (in generations), t2 is the time of sample 2 (in generations) and t0 is the time (in generations) of the most recent common founder of samples 1 and 2.

To calculate divergence times of the pedigree should be provided in the form of 4 files as shown below.

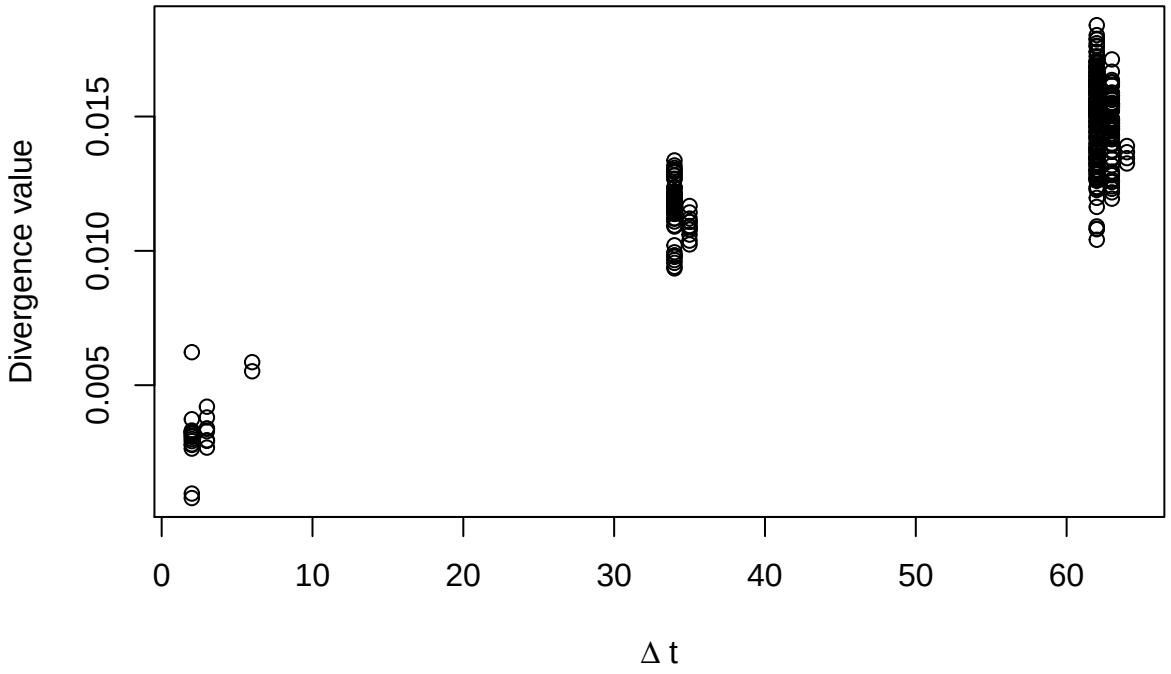
```
props.name <- read.table(system.file("extdata/dm", "AB-methprop-CG-0.99.csv",
    package = "AlphaBeta"), sep = "\t", header = TRUE)
sample.info <- read.table(system.file("extdata/dm", "sampleInfo.csv",
    package = "AlphaBeta"), sep = "\t", header = TRUE)
branch.points <- read.table(system.file("extdata/dm", "branchPoints.csv",
    package = "AlphaBeta"), sep = "\t", header = TRUE)
dmatrix <- read.table(system.file("extdata/dm", "AB-dMatrix-CG-0.99.csv",
    package = "AlphaBeta"), sep = "\t", header = TRUE)
context <- "CG"
```

calculate divergence times of the pedigree:

```
pedigree <- convertDMATRIX(sample.info = sample.info, branch.points = branch.points,
    dmatrix = dmatrix, design = "sibling")
head(pedigree)
```

```
      time0 time1 time2     D.value
 [1,]     0     3     3 0.005516667
 [2,]     0     3     3 0.005856857
 [3,]     0     3    31 0.011792749
 [4,]     0     3    31 0.009345341
 [5,]     0     3    31 0.010905316
 [6,]     0     3    31 0.011464732
```

This is a manual step for inspecting the divergence data and removing outlier samples (if any):



Read in the proportions data:

```
outliers <- "none"
dmatrix <- dmatrix[which(dmatrix[, 1] != outliers), ]
dmatrix <- dmatrix[which(dmatrix[, 2] != outliers), ]
pedigree <- pedigree[c(as.numeric(rownames(dmatrix))), ]

props <- props.name[which(as.character(props.name[, 2]) == context),
```

```
    ]
props <- props.name[which(!is.element(props.name[, 1], outliers) ==
    TRUE), ]
```

Calculate initial proportions of unmethylated cytosines after removal of outliers:

```
p0uu_in <- 1 - mean(as.numeric(as.character(props[, 3])))
p0uu_in
```

```
[1] 0.7435074
```

3.2 Run Models

3.2.1 Run Model with no selection (ABneutral)

This model assumes that heritable gains and losses in cytosine methylation are selectively neutral.

```
# output directory
output.data.dir <- paste0(getwd(), "/")

output <- ABneutral(pedigree.data = pedigree, p0uu = p0uu_in,
    eqp = p0uu_in, eqp.weight = 1, Nstarts = 2, out.dir = output.data.dir,
    out.name = "CG_global_estimates_ABneutral")
```

```
  Progress:  0.5
  Progress:  1
```

NOTE: it is recommended to use at least 50 Nstarts to achieve best solutions

Showing summary output of only output:

```
summary(output)
```

```
                   Length Class      Mode
  estimates           20   data.frame list
  estimates.flagged   20   data.frame list
  pedigree          2457   -none-     numeric
  settings             2   data.frame list
  model                1   -none-     character
  for.fit.plot       315   -none-     numeric
```

```
head(output$pedigree)
```

```
      time0 time1 time2     div.obs delta.t div.pred residual
  [1,]     0     3     3 0.005516667       6       NA       NA
  [2,]     0     3     3 0.005856857       6       NA       NA
  [3,]     0     3    31 0.011792749      34       NA       NA
  [4,]     0     3    31 0.009345341      34       NA       NA
  [5,]     0     3    31 0.010905316      34       NA       NA
  [6,]     0     3    31 0.011464732      34       NA       NA
```

3.2.2 Run model with selection against spontaneous gain of methylation (ABselectMM)

This model assumes that heritable losses of cytosine methylation are under negative selection. The selection parameter is estimated.

```
output <- ABselectMM(pedigree.data = pedigree, p0uu = p0uu_in,
    eqp = p0uu_in, eqp.weight = 1, Nstarts = 2, out.dir = output.data.dir,
    out.name = "CG_global_estimates_ABselectMM")
```

```
  Progress:  0.5
  Progress:  1
```

```
summary(output)
```

```
                   Length Class      Mode
  estimates           22   data.frame list
  estimates.flagged   22   data.frame list
  pedigree          2457   -none-     numeric
  settings             2   data.frame list
  model                1   -none-     character
  for.fit.plot       315   -none-     numeric
```

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

This model assumes that heritable gains of cytosine methylation are under negative selection. The selection parameter is estimated.

```
output <- ABselectUU(pedigree.data = pedigree, p0uu = p0uu_in,
    eqp = p0uu_in, eqp.weight = 1, Nstarts = 2, out.dir = output.data.dir,
    out.name = "CG_global_estimates_ABselectUU")
```

```
  Progress:  0.5
  Progress:  1
```

```
summary(output)
```

```
                   Length Class      Mode
  estimates           22   data.frame list
  estimates.flagged   22   data.frame list
  pedigree          2457   -none-     numeric
  settings             2   data.frame list
  model                1   -none-     character
  for.fit.plot       315   -none-     numeric
```

3.2.4 Run model that considers no accumulation of epimutations (ABnull)

This is the null model of no accumulation.

```
output <- ABnull(pedigree.data = pedigree, out.dir = output.data.dir,
    out.name = "CG_global_estimates_ABnull")

summary(output)
```

```
                   Length Class  Mode
  estimates           1   -none- numeric
  estimates.flagged   0   -none- NULL
  pedigree          2457   -none- numeric
  settings             0   -none- NULL
  model                1   -none- character
  for.fit.plot      1755   -none- numeric
```

3.3 Comparison of different models and selection of best model

3.3.1 Testing ABneutral vs. ABnull

```
file1 <- system.file("extdata/models/", "CG_global_estimates_ABneutral.Rdata",
    package = "AlphaBeta")
file2 <- system.file("extdata/models/", "CG_global_estimates_ABnull.Rdata",
    package = "AlphaBeta")

out <- FtestRSS(pedigree.select = file1, pedigree.null = file2)
```

```
out$Ftest
```

```
          RSS_F          RSS_R           df_F           df_R         Fvalue         pvalue
   7.084342e-04   4.124786e-03   3.460000e+02   3.500000e+02   4.171374e+02 6.260446e-131
```

3.3.2 Testing ABselectMM vs.ABneutral

```
file1 <- system.file("extdata/models/", "CG_global_estimates_ABselectMM.Rdata",
    package = "AlphaBeta")
file2 <- system.file("extdata/models/", "CG_global_estimates_ABnull.Rdata",
    package = "AlphaBeta")

out <- FtestRSS(pedigree.select = file1, pedigree.null = file2)

out$Ftest
```

```
          RSS_F          RSS_R           df_F           df_R         Fvalue         pvalue
   6.507729e-04   4.124786e-03   3.460000e+02   3.500000e+02   4.617618e+02 2.662626e-137
```

3.3.3 Testing ABselectUU vs.ABneutral

```
file1 <- system.file("extdata/models/", "CG_global_estimates_ABselectUU.Rdata",
    package = "AlphaBeta")
file2 <- system.file("extdata/models/", "CG_global_estimates_ABnull.Rdata",
    package = "AlphaBeta")

out <- FtestRSS(pedigree.select = file1, pedigree.null = file2)

out$Ftest
```

```
          RSS_F          RSS_R           df_F           df_R         Fvalue         pvalue
   6.509786e-04   4.124786e-03   3.460000e+02   3.500000e+02   4.615886e+02 2.812040e-137
```

3.4 Bootstrap analysis with the best model

i.e ABneutral in our case

```
inputModel <- system.file("extdata/models/", "CG_global_estimates_ABneutral.Rdata",
    package = "AlphaBeta")

# Bootstrapping models CG
output.data.dir <- paste0(getwd(), "/")

Boutput <- BOOTmodel(pedigree.data = inputModel, Nboot = 2, out.dir = output.data.dir,
    out.name = "Boot_CG_global_estimates_ABneutral")
```

```
  Bootstrap interation:  0.5
  Bootstrap interation:  1
```

```
summary(Boutput)
```

```
                 Length Class      Mode
  standard.errors 24     -none-     numeric
  boot.base       20     data.frame list
  settings         2     data.frame list
  N.boots          1     -none-     numeric
  N.good.boots     1     -none-     numeric
  boot.results    19     data.frame list
```

```
  model            1     -none-     character
```

```
Boutput$standard.errors
```

```
                     SE         2.5%        97.5%
  alpha      7.046629e-06 0.0001036593 0.0001131264
  beta       2.049553e-05 0.0003009681 0.0003285039
  beta/alpha 3.190467e-04 2.9034362083 2.9038625925
  weight     5.920888e-03 0.0195117894 0.0274665199
  intercept  1.036692e-04 0.0021763607 0.0023156405
  PrMMinf    4.186762e-05 0.2558201867 0.2558764360
  PrUMinf    4.186143e-05 0.0006162034 0.0006724444
  PrUUinf    6.187976e-09 0.7435073606 0.7435073689
```

4 Somatic epimutations

Models ABneutralSOMA, ABselectMMSOMA and ABselectUUSOMA can be used to estimate the rate of spontaneous epimutations from pedigree-based high-throughput DNA methylation data. The models are generally designed for pedigree data arising from clonally or asexually propagated diploid species. The models can also be applied to long-lived perrenials, such as trees, using leaf methylomes and coring data as input. In this case, the tree branching structure is treated as an intra-organismal pedigree (or phylogeny) of somatic lineages.

4.1 Loading data and generation of pedigree

```
props.name <- read.table(system.file("extdata/soma/", "AB-methprop-CG-0.99.csv",
    package = "AlphaBeta"), sep = "\t", header = TRUE, stringsAsFactors = FALSE)
sample.info <- read.table(system.file("extdata/soma/", "sampleInfo.csv",
    package = "AlphaBeta"), sep = "\t", header = TRUE, stringsAsFactors = FALSE)
dmatrix <- read.table(system.file("extdata/soma/", "AB-dMatrix-CG-0.99.csv",
    package = "AlphaBeta"), sep = "\t", header = TRUE, stringsAsFactors = FALSE)
```

4.2 Generate pedigree from the input files

```
pedigree.out <- makePHYLO(tall = 330, pedigree = dmatrix, sample.info = sample.info)
pedigree.out <- pedigree.out[[1]]
head(pedigree.out)
```

```
       time0 time1 time2     D.value
  [1,]     0   297   287 0.003796614
  [2,]     0   297   324 0.003974756
  [3,]     0   327   287 0.003995156
  [4,]     0   297   287 0.004040671
  [5,]     0   328   287 0.004046553
  [6,]     0   328   287 0.004048672
```

4.3 Calculate the proportion of unmethylated cytosines

```
p0uu_in <- mean(props[, 3])
p0uu_in
```

```
  [1] 0.2564926
```

4.4 Run Models

4.4.1 Run Model with no selection (ABneutralSOMA)

This model assumes that somatically heritable gains and losses in cytosine methylation are selectively neutral.

```
outneutral <- ABneutralSOMA(pedigree.data = pedigree.out, p0uu = p0uu_in,
    eqp = p0uu_in, eqp.weight = 0.001, Nstarts = 2, out.dir = output.data.dir,
    out.name = "ABneutralSOMA_CG_estimates")
```

```
  Progress:  0.5
  Progress:  1
```

```
summary(outneutral)
```

```
                   Length Class      Mode
  estimates           20   data.frame list
  estimates.flagged   20   data.frame list
  pedigree           196   -none-     numeric
  settings             2   data.frame list
  model                1   -none-     character
  for.fit.plot      3275   -none-     numeric
```

```
head(outneutral$pedigree)
```

```
      time0 time1 time2     div.obs delta.t    div.pred      residual
  [1,]     0   297   287 0.003796614     584 0.004009969 -2.133546e-04
  [2,]     0   297   324 0.003974756     621 0.004124751 -1.499947e-04
  [3,]     0   327   287 0.003995156     614 0.004103042 -1.078861e-04
  [4,]     0   297   287 0.004040671     584 0.004009969  3.070237e-05
  [5,]     0   328   287 0.004046553     615 0.004106144 -5.959125e-05
  [6,]     0   328   287 0.004048672     615 0.004106144 -5.747225e-05
```

4.4.2 Run model with selection against spontaneous gain of methylation (ABselectMMSOMA)

This model assumes that somatically heritable losses of cytosine methylation are under negative selection. The selection parameter is estimated.

```
outselectMM <- ABselectMMSOMA(pedigree.data = pedigree.out, p0uu = p0uu_in,
    eqp = p0uu_in, eqp.weight = 0.001, Nstarts = 2, out.dir = output.data.dir,
    out.name = "ABselectMMSOMA_CG_estimates")
```

```
  Progress:  0.5
  Progress:  1
```

```
summary(outselectMM)
```

```
                   Length Class      Mode
  estimates           22   data.frame list
  estimates.flagged   22   data.frame list
  pedigree           196   -none-     numeric
  settings             2   data.frame list
  model                1   -none-     character
  for.fit.plot      3275   -none-     numeric
```

4.4.3 Run model with selection against spontaneous loss of methylation (ABselectUUSOMA)

This model assumes that somatically heritable gains of cytosine methylation are under negative selection. The selection parameter is estimated.

```
outselectUU <- ABselectUUSOMA(pedigree.data = pedigree.out, p0uu = p0uu_in,
    eqp = p0uu_in, eqp.weight = 0.001, Nstarts = 2, out.dir = output.data.dir,
    out.name = "ABselectUUSOMA_CG_estimates")
```

```
  Progress:  0.5
  Progress:  1
```

```
summary(outselectUU)
```

```
                   Length Class      Mode
  estimates           22   data.frame list
  estimates.flagged   22   data.frame list
  pedigree           196   -none-     numeric
  settings             2   data.frame list
  model                1   -none-     character
  for.fit.plot      3275   -none-     numeric
```

5 R session info

```
sessionInfo()
```

```
  R version 3.6.1 (2019-07-05)
  Platform: x86_64-pc-linux-gnu (64-bit)
  Running under: Ubuntu 18.04.2 LTS

  Matrix products: default
  BLAS:   /usr/lib/x86_64-linux-gnu/openblas/libblas.so.3
  LAPACK: /usr/lib/x86_64-linux-gnu/libopenblasp-r0.2.20.so

  locale:
   [1] LC_CTYPE=en_US.UTF-8       LC_NUMERIC=C               LC_TIME=en_US.UTF-8
   [4] LC_COLLATE=C               LC_MONETARY=en_US.UTF-8    LC_MESSAGES=en_US.UTF-8
   [7] LC_PAPER=en_US.UTF-8       LC_NAME=C                  LC_ADDRESS=C
  [10] LC_TELEPHONE=C             LC_MEASUREMENT=en_US.UTF-8 LC_IDENTIFICATION=C

  attached base packages:
  [1] stats     graphics  grDevices utils     datasets  methods   base

  other attached packages:
  [1] data.table_1.12.2 AlphaBeta_0.99.1

  loaded via a namespace (and not attached):
   [1] Rcpp_1.0.1          formatR_1.7         compiler_3.6.1      pillar_1.4.1
   [5] iterators_1.0.10    prettyunits_1.0.2   remotes_2.1.0       tools_3.6.1
   [9] testthat_2.1.1      digest_0.6.19       pkgbuild_1.0.3      pkgload_1.0.2
  [13] evaluate_0.14       lattice_0.20-38     memoise_1.1.0       tibble_2.1.3
  [17] pkgconfig_2.0.2     rlang_0.4.0         Matrix_1.2-17       foreach_1.4.4
  [21] cli_1.1.0           rstudioapi_0.10     commonmark_1.7      yaml_2.2.0
  [25] parallel_3.6.1      expm_0.999-4        xfun_0.8            knitr_1.23
  [29] withr_2.1.2         stringr_1.4.0       dplyr_0.8.1         roxygen2_6.1.1
  [33] xml2_1.2.0          gtools_3.8.1        desc_1.2.0          fs_1.3.1
  [37] devtools_2.1.0      grid_3.6.1          rprojroot_1.3-2     tidyselect_0.2.5
  [41] glue_1.3.1          R6_2.4.0            processx_3.3.1      rmarkdown_1.13
  [45] sessioninfo_1.1.1   callr_3.2.0         purrr_0.3.2         magrittr_1.5
  [49] htmltools_0.3.6     codetools_0.2-16    backports_1.1.4     ps_1.3.0
  [53] usethis_1.5.0       assertthat_0.2.1    numDeriv_2016.8-1.1 optimx_2018-7.10
  [57] stringi_1.4.3       doParallel_1.0.14   crayon_1.3.4
```