Lab 8 R Source Code

Code:

```r
#
# Shawn Schwartz, 2019
# EEB C174 UCLA Spring 2019
# Lab 8 HW - BAMM and FiSSE
#

rm(list=ls())

#imports
library(BAMMtools)
library(coda)

cwd <- "~/Developer/EEB-C174-Labs/Lab8/cetacean_BAMM"
setwd(cwd)

tree <- read.tree("whaleTree.tre")
tree <- ladderize(tree)
plot(x = tree, cex = 0.2, no.margin = T)
axisPhylo()

#check bamm assumptions
is.ultrametric(tree)
is.binary(tree)
min(tree$edge.length) > 0


#generate bamm control file
# estimate priors and create control files
priors <- setBAMMpriors(phy = tree, traits = "whaleSize.txt",
    outfile = NULL)
generateControlFile(file = "cetacean_bamm_controlfile.txt", type =
    "trait", params = list(
  treefile = "whaleTree.tre",
  traitfile = "whaleSize.txt",
  seed = sample(1:1000000, 1),
  overwrite = "0",
  expectedNumberOfShifts = "2",
  betaInitPrior = as.numeric(priors["betaInitPrior"]),
```

```
37    betaShiftPrior = as.numeric(priors["betaShiftPrior"]),
38    numberOfGenerations = "120000000",
39    mcmcWriteFreq = "30000",
40    eventDataWriteFreq = "30000",
41    printFreq = "15000",
42    acceptanceResetFreq = "30000",
43    outName = "cetacean_bamm_homework",
44    numberOfChains = "8"
45  ))
46
47  edata <- getEventData(tree, eventdata = "2_expected_shifts/
       cetacean_bamm_homework_event_data.txt", burnin = 0.1, type = "
       trait")
48  summary(edata)
49
50  #### Assess MCMC convergence ####
51  mcmcout <- read.csv("2_expected_shifts/cetacean_bamm_homework_mcmc
       _out.txt")
52  plot(mcmcout$logLik ~ mcmcout$generation)
53
54  #### Test for convergence of the MCMC chains with the coda package
        for R ####
55  burnstart <- floor(0.1 * nrow(mcmcout))
56  postburn <- mcmcout[burnstart:nrow(mcmcout), ]
57  effectiveSize(postburn$N_shifts)
58  effectiveSize(postburn$logLik)
59
60  #### Analysis of rate shifts ####
61  plotPrior("2_expected_shifts/cetacean_bamm_homework_mcmc_out.txt",
        expectedNumberOfShifts = 2)
62  s <- plot.bammdata(edata, labels = T, font = 3, cex = 0.1,
       logcolor = T)
63  title(main = "Mean phenotypic rate", sub = "time before present")
64  addBAMMlegend(s, location = "left", nTicks = 1)
65  axisPhylo()
66
67  css <- credibleShiftSet(edata, expectedNumberOfShifts = 30,
       threshold = 5, set.limit = 0.95)
68  css$number.distinct
69  summary(css)
70
71  sss <- plot.credibleshiftset(css, border = F, logcolor = T)
```

```
72
73  plot.new()
74  best <- getBestShiftConfiguration(edata, expectedNumberOfShifts =
        2)
75
76  ss <- plot.bammdata(best, labels = T, font = 3, cex = 0.1,
        logcolor = T)
77  title(main = "Best shift configuration", sub = "time before
        present")
78  addBAMMlegend(ss, location = "left", nTicks = 1)
79  addBAMMshifts(best, cex = 3, pch = 1)
80  axisPhylo()
81
82  ##### scaled branch lengths #####
83  par(font = 1)
84  marg_probs <- marginalShiftProbsTree(edata)
85  plot.phylo(marg_probs, cex = 0.45, no.margin = T)
86  title(sub = "Marginal shift probability")
87  add.scale.bar(x = 0.5, y = 0.5, font = 1)
88
89
90  ##### rate through time analysis #####
91  par(font = 1)
92  plotRateThroughTime(edata,
93                      ratetype = "auto",
94                      avgCol = "black", intervalCol = "gray80",
                        intervals = c(0.05, 0.95), opacity = 1)
95
96  ##### FiSSE #####
97  library(phangorn)
98  library(diversitree)
99  library(ape)
100
101 source("traitDependent_functions.R")
102
103 diet <- read.csv(file = "whaleDiet.csv", stringsAsFactors = F)
104 generalist <- diet$generalist
105 names(generalist) <- diet$species
106 generalist <- generalist[tree$tip.label]
107 colvec <- rep("white", length(generalist))
108 colvec[generalist == 1] <- "black"
109 plot.phylo(tree, show.tip.label = F, cex = 0.4, no.margin = T)
```

```
110  tiplabels (pch = 21, bg = colvec, cex = 0.8)
111  add.scale.bar(x = 0.5, y = 0.5, font = 1)
112  title(sub = "time before present (my)")
113
114  res <- FISSE.binary(tree, generalist)
115  res
116
117  # two-tailed pvalue is obtained as
118  pval_2tailed <- min(res$pval, 1 - res$pval) * 2
119  pval_2tailed
120
121  #two planel plot for lab report
122  par(mfrow = c(1,2))
123  par(mar=c(5, 1.0, 2, 0.0))
124  #plotPrior("2_expected_shifts/cetacean_bamm_homework_mcmc_out.txt
         ", expectedNumberOfShifts = 2)
125  s <- plot.bammdata(edata, labels = T, font = 3, cex = 0.5,
         logcolor = T)
126  title(main = "Mean phenotypic rate", sub = "time before present (
         my)")
127  addBAMMlegend(s, location = "left", nTicks = 1)
128  axisPhylo()
129
130  par(font = 1)
131  marg_probs <- marginalShiftProbsTree(edata)
132  plot.phylo(marg_probs, cex = 0.5, no.margin = F)
133  title(main = "Marginal shift probability")
134  add.scale.bar(x = 0.75, y = 0.5, font = 1)
135
136
137  library(geiger)
138  library(apTreeshape)
139  library(phytools)
140
141  ltt.plot(tree, log = "y")
142  lines(c(0, 1), c(log(2), log(100)), lty = "dashed", lwd = 2, col =
         "red")
143  gammaStat(tree)
```