

Lab 7 Cetacean BAMM Control File Source

Code:

```
1 # BAMM configuration file for speciation/extinction analysis
2 # =====
3 #
4 # Format
5 # -----
6 #
7 #     - Each option is specified as: option_name = option_value
8 #     - Comments start with # and go to the end of the line
9 #     - True is specified with "1" and False with "0"
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12 #
13 # #####
14 #
15
16 # GENERAL SETUP AND DATA INPUT
17 # #####
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modeltype = speciationextinction
Specify "speciationextinction" or "trait" analysis

treefile = whaleTree.tre
File name of the phylogenetic tree to be analyzed

runInfoFilename = run_info.txt
File name to output general information about this run

sampleFromPriorOnly = 0
Whether to perform analysis sampling from prior only (no
 likelihoods computed)

runMCMC = 1
Whether to perform the MCMC simulation. If runMCMC = 0, the
 program will only
check whether the data file can be read and the initial
 likelihood computed

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32 loadEventData = 0
33 # Whether to load a previous event data file
34
35 eventDataInfile = event_data_in.txt
36 # File name of the event data file to load, used only if
    loadEventData = 1
37
38 initializeModel = 1
39 # Whether to initialize (but not run) the MCMC. If initializeModel
    = 0, the
40 # program will only ensure that the data files (e.g., treefile)
    can be read
41
42 useGlobalSamplingProbability = 1
43 # Whether to use a "global" sampling probability. If False (0),
    expects a file
44 # name for species-specific sampling probabilities (see
    sampleProbsFilename)
45
46 globalSamplingFraction = 0.8
47 # The sampling probability. If useGlobalSamplingProbability = 0,
    this is ignored
48 # and BAMM looks for a file name with species-specific sampling
    fractions
49
50 sampleProbsFilename = sample_probs.txt
51 # File name containing species-specific sampling fractions
52
53 seed = 2831993
54 # Seed for the random number generator.
55 # If not specified (or is -1), a seed is obtained from the system
    clock
56
57 overwrite = 0
58 # If True (1), the program will overwrite any output files in the
    current
59 # directory (if present)
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63 # PRIORS
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65
66 expectedNumberOfShifts = 1
67 # prior on the number of shifts in diversification
68 # Suggested values:
69 #     expectedNumberOfShifts = 1.0 for small trees (< 500 tips)
70 #     expectedNumberOfShifts = 10 or even 50 for large trees (> 5000
    tips)
71
72 lambdaInitPrior = 2.07443033285194
73 # Prior (rate parameter of exponential) on the initial lambda
    value for rate
74 # regimes
75
76 lambdaShiftPrior = 0.0312201302653702
77 # Prior (std dev of normal) on lambda shift parameter for rate
    regimes
78 # You cannot adjust the mean of this distribution (fixed at zero,
    which is
79 # equal to a constant rate diversification process)
80
81 muInitPrior = 2.07443033285194
82 # Prior (rate parameter of exponential) on extinction rates
83
84 lambdaIsTimeVariablePrior = 1
85 # Prior (probability) of the time mode being time-variable (vs.
    time-constant)
86
87
88 #
#####

89 # MCMC SIMULATION SETTINGS & OUTPUT OPTIONS
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#####

91
92 numberOfGenerations = 5000000
93 # Number of generations to perform MCMC simulation
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mcmcOutfile = mcmc_out.txt
# File name for the MCMC output, which only includes summary
  information about
# MCMC simulation (e.g., log-likelihoods, log-prior, number of
  processes)

mcmcWriteFreq = 1000
# Frequency in which to write the MCMC output to a file

eventDataOutfile = event_data.txt
# The raw event data (these are the main results). ALL of the
  results are
# contained in this file, and all branch-specific speciation rates
  , shift
# positions, marginal distributions etc can be reconstructed from
  this output.
# See R package BAMMtools for working with this output

eventDataWriteFreq = 1000
# Frequency in which to write the event data to a file

printFreq = 1000
# Frequency in which to print MCMC status to the screen

acceptanceResetFreq = 1000
# Frequency in which to reset the acceptance rate calculation
# The acceptance rate is output to both the MCMC data file and the
  screen

outName = whaleBAMMhomeworkoutput
# Optional name that will be prefixed on all output files (
  separated with "_")
# If commented out, no prefix will be used

#####

# OPERATORS: MCMC SCALING OPERATORS
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126

127 updateLambdaInitScale = 2.0

128 # Scale parameter for updating the initial speciation rate for
each process

129

130 updateLambdaShiftScale = 0.1

131 # Scale parameter for the exponential change parameter for
speciation

132

133 updateMuInitScale = 2.0

134 # Scale parameter for updating initial extinction rate for each
process

135

136 updateEventLocationScale = 0.05

137 # Scale parameter for updating LOCAL moves of events on the tree
138 # This defines the width of the sliding window proposal

139

140 updateEventRateScale = 4.0

141 # Scale parameter (proportional shrinking/expanding) for updating
142 # the rate parameter of the Poisson process

143

144

145 #

#####

146 # OPERATORS: MCMC MOVE FREQUENCIES

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#####

148

149 updateRateEventNumber = 0.1

150 # Relative frequency of MCMC moves that change the number of
events

151

152 updateRateEventPosition = 1

153 # Relative frequency of MCMC moves that change the location of an
event on the

154 # tree

155

156 updateRateEventRate = 1

157 # Relative frequency of MCMC moves that change the rate at which

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    events occur
158
159 updateRateLambda0 = 1
160 # Relative frequency of MCMC moves that change the initial
    speciation rate
161 # associated with an event
162
163 updateRateLambdaShift = 1
164 # Relative frequency of MCMC moves that change the exponential
    shift parameter
165 # of the speciation rate associated with an event
166
167 updateRateMu0 = 1
168 # Relative frequency of MCMC moves that change the extinction rate
    for a given
169 # event
170
171 updateRateLambdaTimeMode = 0
172 # Relative frequency of MCMC moves that flip the time mode
173 # (time-constant <=> time-variable)
174
175 localGlobalMoveRatio = 10.0
176 # Ratio of local to global moves of events
177
178
179 #
    #####

180 # INITIAL PARAMETER VALUES
181 #
    #####

182
183 lambdaInit0 = 0.032
184 # Initial speciation rate (at the root of the tree)
185
186 lambdaShift0 = 0
187 # Initial shift parameter for the root process
188
189 muInit0 = 0.005
190 # Initial value of extinction (at the root)
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192 initialNumberEvents = 0
193 # Initial number of non-root processes
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197 # METROPOLIS COUPLED MCMC
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199
200 numberOfChains = 4
201 # Number of Markov chains to run
202
203 deltaT = 0.01
204 # Temperature increment parameter. This value should be > 0
205 # The temperature for the i-th chain is computed as 1 / [1 +
    deltaT * (i - 1)]
206
207 swapPeriod = 1000
208 # Number of generations in which to propose a chain swap
209
210 chainSwapFileName = chain_swap.txt
211 # File name in which to output data about each chain swap proposal
    .
212 # The format of each line is [generation],[rank_1],[rank_2],[swap_
    _accepted]
213 # where [generation] is the generation in which the swap proposal
    was made,
214 # [rank_1] and [rank_2] are the chains that were chosen, and [swap
    _accepted] is
215 # whether the swap was made. The cold chain has a rank of 1.
216
217
218 #
#####

219 # NUMERICAL AND OTHER PARAMETERS
220 #
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```

```
221
222 minCladeSizeForShift = 1
223 # Allows you to constrain location of possible rate-change events
    to occur
224 # only on branches with at least this many descendant tips. A
    value of 1
225 # allows shifts to occur on all branches.
226
227 segLength = 0.02
228 # Controls the "grain" of the likelihood calculations.
    Approximates the
229 # continuous-time change in diversification rates by breaking each
    branch into
230 # a constant-rate diversification segments, with each segment
    given a length
231 # determined by segLength. segLength is in units of the root-to-
    tip distance of
232 # the tree. So, if the segLength parameter is 0.01, and the crown
    age of your
233 # tree is 50, the "step size" of the constant rate approximation
    will be 0.5.
234 # If the value is greater than the branch length (e.g., you have a
    branch of
235 # length < 0.5 in the preceding example) BAMM will not break the
    branch into
236 # segments but use the mean rate across the entire branch.
```