

Lab 8 Cetacean BAMM Trait Control File Source

Code:

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1
2 # BAMM configuration file for phenotypic analysis
3 # =====
4 #
5 # Format
6 # -----
7 #
8 #     - Each option is specified as: option_name = option_value
9 #     - Comments start with # and go to the end of the line
10 #     - True is specified with "1" and False with "0"
11
12
13 #
14 # #####
15 #
16
17 # GENERAL SETUP AND DATA INPUT
18 # #####
19
20
21 modeltype = trait
22 # Specify "speciationextinction" or "trait" analysis
23
24
25 treefile = whaleTree.tre
26 # File name of the phylogenetic tree to be analyzed
27
28
29 traitfile = whaleSize.txt
30 # File name of the phenotypic traits file
31
32
33 runInfoFilename = run_info.txt
34 # File name to output general information about this run
35
36
37 sampleFromPriorOnly = 0
38 # Whether to perform analysis sampling from prior only (no
39   likelihoods computed)
40
41
42 runMCMC = 1
43 # Whether to perform the MCMC simulation. If runMCMC = 0, the
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    program will only
34 # check whether the data file can be read and the initial
    likelihood computed
35
36 loadEventData = 0
37 # Whether to load a previous event data file
38
39 eventDataInfile = event_data_in.txt
40 # File name of the event data file to load, used only if
    loadEventData = 1
41
42 initializeModel = 1
43 # Whether to initialize (but not run) the MCMC. If initializeModel
    = 0, the
44 # program will only ensure that the data files (e.g., treefile)
    can be read
45
46 seed = 439537
47 # Seed for the random number generator.
48 # If not specified (or is -1), a seed is obtained from the system
    clock
49
50 overwrite = 0
51 # If True (1), the program will overwrite any output files in the
    current
52 # directory (if present)
53
54
55 #
    #####

56 # PRIORS
57 #
    #####

58
59 expectedNumberOfShifts = 2
60 # prior on the number of shifts in diversification
61 # Suggested values:
62 #     expectedNumberOfShifts = 1.0 for small trees (< 500 tips)
63 #     expectedNumberOfShifts = 10 or even 50 for large trees (> 5000
    tips)
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betaInitPrior = 86.8468913729087
# Prior (rate parameter of exponential) on the initial
# phenotypic evolutionary rate associated with regimes

betaShiftPrior = 0.0312201302645236
# Prior (std dev of normal) on the rate-change parameter
# You cannot adjust the mean of this distribution (fixed at zero,
  which is
# equal to a constant rate diversification process)

useObservedMinMaxAsTraitPriors = 1
# If True (1), will put a uniform prior density on the
  distribution
# of ancestral character states, with upper and lower bounds
  determined
# by the min and max of the observed data

traitPriorMin = 0
# User-defined minimum value for the uniform density on the
  distribution of
# ancestral character states. Only used if
  useObservedMinMaxAsTraitPriors = 0.

traitPriorMax = 0
# User-defined maximum value for the uniform density on the
  distribution of
# ancestral character states. Only used if
  useObservedMinMaxAsTraitPriors = 0.

betaIsTimeVariablePrior = 1
# Prior (probability) of the time mode being time-variable (vs.
  time-constant)

#####

# MCMC SIMULATION SETTINGS & OUTPUT OPTIONS
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```
numberOfGenerations = 120000000
# Number of generations to perform MCMC simulation

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 = 30000
# 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 = 30000
# Frequency in which to write the event data to a file

printFreq = 15000
# Frequency in which to print MCMC status to the screen

acceptanceResetFreq = 30000
# Frequency in which to reset the acceptance rate calculation
# The acceptance rate is output to both the MCMC data file and the
  screen

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

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127 # OPERATORS: MCMC SCALING OPERATORS
128 #
    #####

129
130 updateBetaInitScale = 1
131 # Scale operator for proportional shrinking-expanding move to
    update
132 # initial phenotypic rate for rate regimes
133
134 updateBetaShiftScale = 1
135 # Scale operator for sliding window move to update initial
    phenotypic rate
136
137 updateNodeStateScale = 1
138 # Scale operator for sliding window move to update ancestral
    states
139 # at internal nodes
140
141 updateEventLocationScale = 0.05
142 # Scale parameter for updating LOCAL moves of events on the tree
143 # This defines the width of the sliding window proposal
144
145 updateEventRateScale = 4.0
146 # Scale parameter (proportional shrinking/expanding) for updating
147 # the rate parameter of the Poisson process
148
149
150 #
    #####

151 # OPERATORS: MCMC MOVE FREQUENCIES
152 #
    #####

153
154 updateRateEventNumber = 1
155 # Relative frequency of MCMC moves that change the number of
    events
156
157 updateRateEventPosition = 1
158 # Relative frequency of MCMC moves that change the location of an
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    event
159 # on the tree
160
161 updateRateEventRate = 1
162 # Relative frequency of MCMC moves that change the rate at which
    events occur
163
164 updateRateBeta0 = 1
165 # Relative frequency of MCMC moves that change the initial
    phenotypic rate
166 # associated with an event
167
168 updateRateBetaShift = 1
169 # Relative frequency of MCMC moves that change the exponential
    shift parameter
170 # of the phenotypic rate associated with an event
171
172 updateRateNodeState = 25
173 # Relative frequency of MCMC moves that update the value of
    ancestral
174 # character states. You have as many ancestral states as you have
175 # internal nodes in your tree, so there are a lot of parameters:
176 # you should update this much more often than you update the event
    -associated
177 # parameters.
178
179 updateRateBetaTimeMode = 0
180 # Relative frequency of MCMC moves that flip the time mode
181 # (time-constant <=> time-variable)
182
183 localGlobalMoveRatio = 10.0
184 # Ratio of local to global moves of events
185
186
187 #
    #####

188 # INITIAL PARAMETER VALUES
189 #
    #####

190
```

```
191 betaInit = 0.5
192 # Initial value of the phenotypic evolutionary process at the root
    of the tree
193
194 betaShiftInit = 0
195 # Initial value of the exponential change parameter for the
    phenotypic
196 # evolutionary process at the root of the tree. A value of zero
    implies
197 # time-constant rates
198
199 initialNumberEvents = 0
200 # Initial number of non-root processes
201
202
203 #
    #####

204 # METROPOLIS COUPLED MCMC
205 #
    #####

206
207 numberOfChains = 8
208 # Number of Markov chains to run
209
210 deltaT = 0.1
211 # Temperature increment parameter. This value should be > 0
212 # The temperature for the i-th chain is calculated as 1 / [1 +
    deltaT * (i - 1)]
213
214 swapPeriod = 1000
215 # Number of generations in which to propose a chain swap
216
217 chainSwapFileName = chain_swap.txt
218 # File name in which to output data about each chain swap proposal
    .
219 # The format of each line is [generation],[rank_1],[rank_2],[swap_
    accepted]
220 # where [generation] is the generation in which the swap proposal
    was made,
221 # [rank_1] and [rank_2] are the chains that were chosen, and [swap
```

```
222  # _accepted is whether the swap was made. The cold chain has a rank of 1.
```