



Bayesian Evolutionary Analysis Sampling Trees  
Version v2.4.1, 2002-2016

BEAST XML File: primate-mtDNA-bMT.xml

Choose File...

default: only write new log files

Random number seed: 1985

Thread pool size: Automatic

☐ Use BEAGLE library if available:

Prefer use of: CPU

Prefer precision: Double

☐ Show list of available BEAGLE resources and Quit

BEAGLE is a high-performance phylogenetic library that can make use of additional computational resources such as graphics boards. It must be downloaded and installed independently of BEAST:

<http://beagle-lib.googlecode.com/>

Quit

Run