

**Exercise 1:** Explore with simulated data how robust posterior probabilities given by BEAST are against misspecification of priors, substitution models and relaxed-clock models.

**Exercise 2:** The files QuantTraitsA.csv, QuantTraitsB.csv, and QuantTraitsC.csv contain datasets of quantitative traits for species whose phylogeny is given in the file QuantTraits\_Tree.txt. Do you find evidence for selection and/or for correlated evolution of some of the traits?

**Exercise 3:** Write a computer program or an R script that reads a tree in newick format and simulates the evolution of quantitative traits along the branches of the tree. The output should be the values of the traits at the tips of the tree.

**Exercise 4:** Simulate trees from several prior distributions and let sequences evolve along the trees. Estimate the trees from the data by maximum-likelihood methods and apply bootstrap with PHYLIP and/or RAxML. Repeat this many times and explore whether the bootstrap support values are good approximations of the probabilities that branches are correct.