

Figures for RevBayes Molecular Dating Tutorial

I. Exercise 1: The global clock molecular model

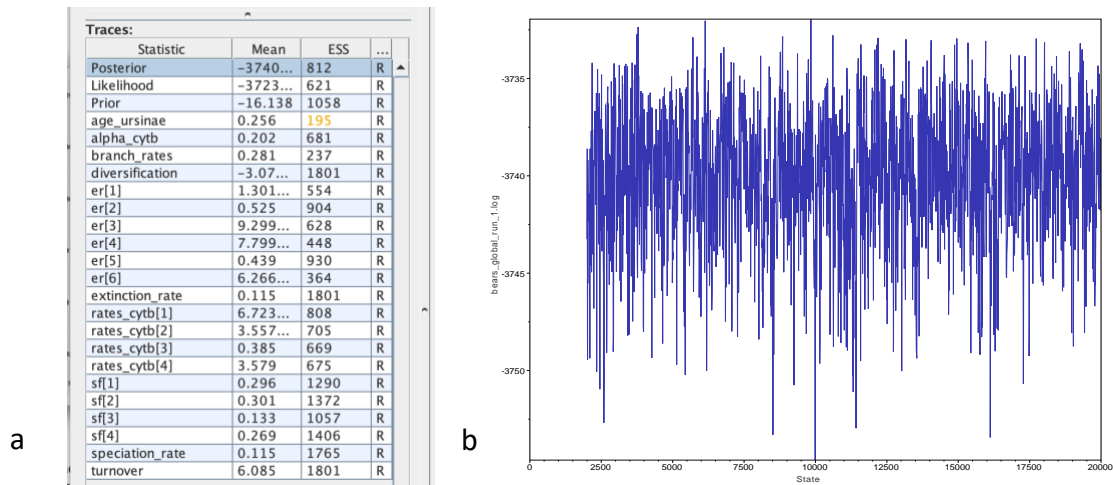


Figure 1. Graph and table showing the convergence and mixing of the MCMC analysis, used to construct a global-clock model of the phylogenetic relationship between Ursid species. Figure made using Tracer. a. For all but one parameter (age_ursinae) the effective sample size (ESS) of the Markov chain is above 200 indicating decent mixing. b shows the posterior probability sampled across all 20,000 cycles of the Markov chain.

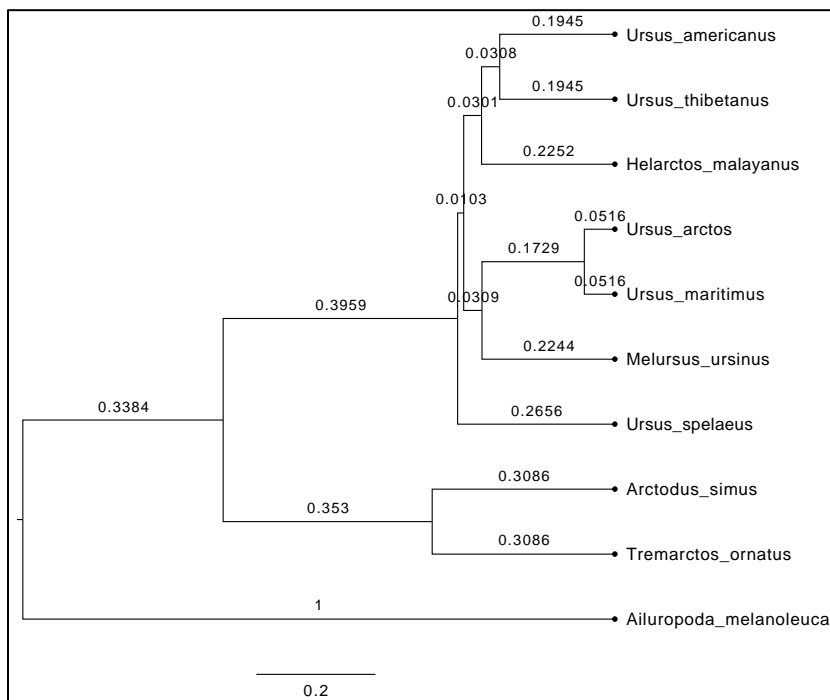


Figure 2. Tree showing the phylogenetic relationship among extant species of family Ursidae (bears), made using a strict molecular clock model. Figure made using FigTree.

II. Exercise 2: The uncorrelated exponential relaxed clock model

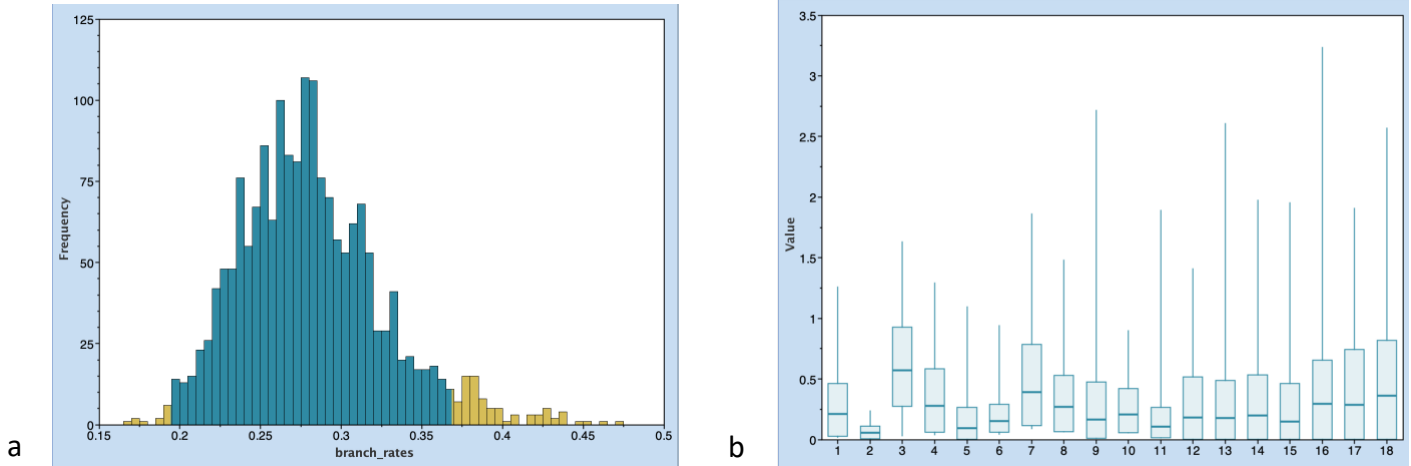


Figure 3. Comparison of output for global molecular clock model and uncorrelated relaxed exponential molecular clock models. A. shows the substitution rate parameter for the global clock model (branch_mean), while b shows the varying substitution rate for the uncorrelated exponential relaxed clock model (branch_rates_mean).

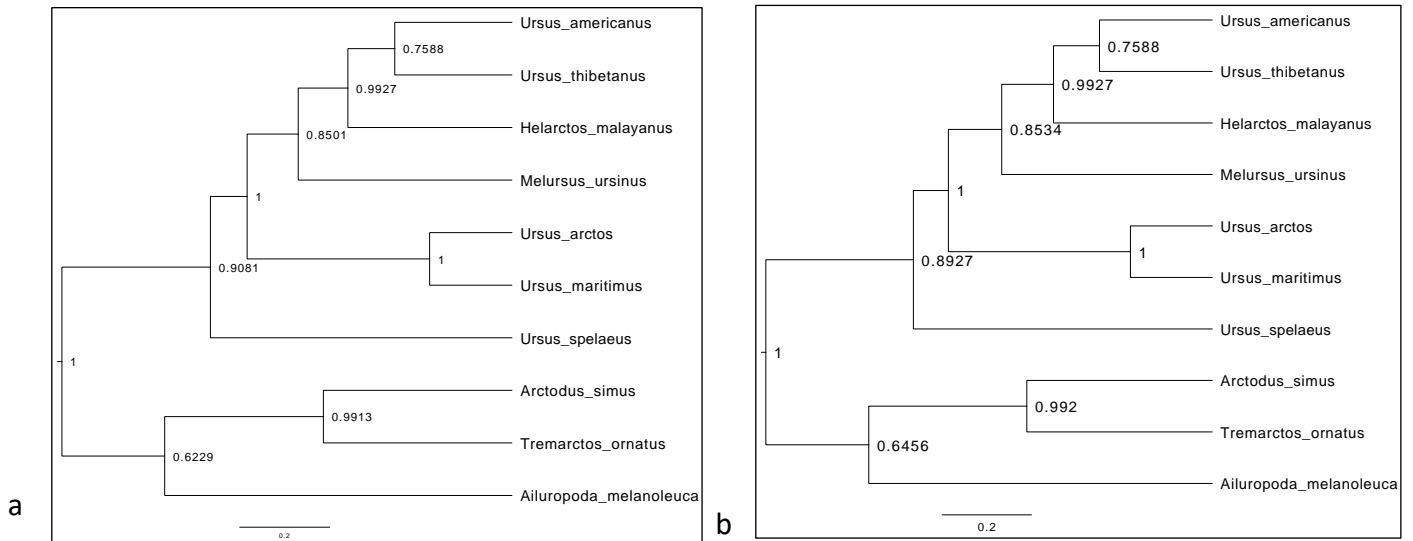


Figure 4. Tree showing the phylogenetic relationship among extant species of family Ursidae (bears), made using an (a) uncorrelated exponential relaxed clock model and (b) an uncorrelated lognormal relaxed clock model. Posterior probabilities are shown at each node. Although the topology of the tree is the same for the two models, the posterior probabilities differ among nodes and among models. Figures made using FigTree.

III. Exercise 3: Estimating speciation times using node dating

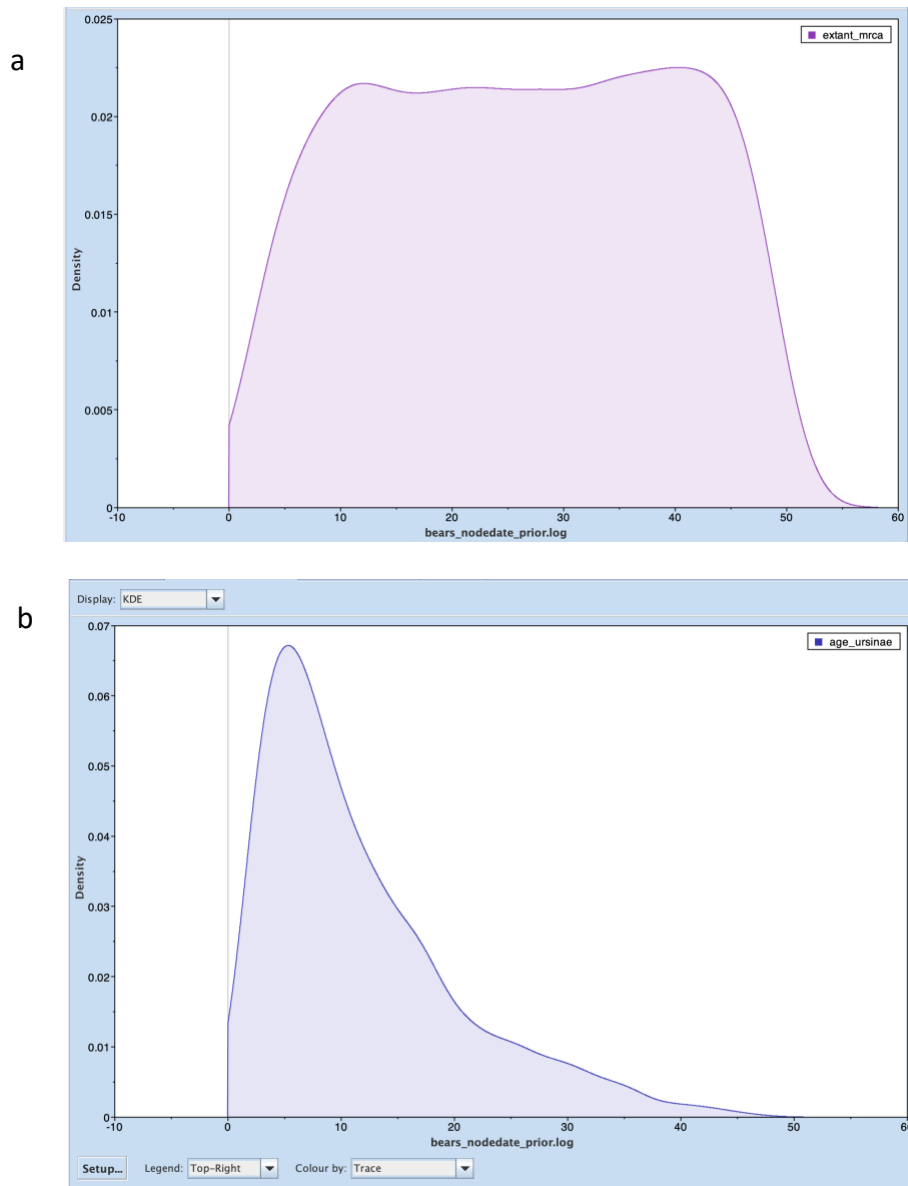


Figure 5. Examining the output of Ursidae molecular dating, made by incorporating temporal information of fossils and using a prior. a. shows the marginal estimates for the age of the root and b. shows the marginal estimates of the age of Ursinae. Figure made using Tracer.