

8. January 2013

**Exercise 1:** Simulate several datasets for trees with five taxa  $\{A,B,C,D,E\}$  that is nearly, but not exactly ultrametric. Assume that the taxa  $\{A,B,C\}$  are known to form a monophyletic group because they have some morphological traits that  $\{D,E\}$  do not have. A fossil is found and dated with high precision that has the same morphological traits as  $\{A,B,C\}$ . We neglect the possibility that D or E stem from species that once had these morphological traits but lost them. Feed your simulated data and the fossil information into BEAST and check how precisely BEAST can date the inner nodes in the tree.

**Exercise 2:** Assume that 10000 trees haven been MCMC-sampled from the posterior distribution for a given data set. To summarize these trees we would like to show a single tree that has all branches that appear in more than 5000 of the sampled trees (as splits of the taxa sets). Proof that this is always possible or give a counter-example.

**Exercise 3:** Perform simulation studies to examine how robust posterior probabilities given by BEAST are against misspecification of priors, substitution models and relaxed-clock models.

**Exercise 4:** We flip a coin 1000 times to test whether it is fair. If we apply Bayesian inference with a uniform prior on  $[0, 1]$  for the probability  $p$  that the coin shows “head”, how probable is it that we estimate the probability of  $\{p > 0.5\}$  to be higher than 90% or lower than 10%?

**Exercise 5:** Repeat Exercise 1 with TreeTime instead of Beast:

[http://evol.bio.lmu.de/\\_statgen/software/treetime/](http://evol.bio.lmu.de/_statgen/software/treetime/)