

## Assignment 8

1. Write code to do Bayesian MCMC analysis of phylogeny under the Jukes Cantor substitution model. The only parameters in this model are the tree and the branch lengths. Assume an  $\text{Exp}(10)$  prior on each individual branch length and use a uniform prior on all possible bifurcating tree topologies. To sample from the posterior, use the LOCAL update mechanism; it changes both the branch lengths and (potentially) the tree topology. The LOCAL update mechanism is described in the notes for lecture 13. Use your previous code to calculate the likelihood ratio of the new to the old tree; note that you do not have to optimize the branch lengths since the branch lengths are specified for the new and the old tree. Thus, it is sufficient to use the likelihood downpass algorithm. Write new code to calculate the prior ratio and the Hastings ratio, and combine all pieces into a complete MCMC sampler of the Bayesian posterior.