Name:

Comparative Genomics

Divergence Time Estimation Lab

Why are we linking the site model but not the tree and clock models?

In this lab, we applied the HKY substitution model to each partition. How would you determine if this was optimal given the data?

Is the clock model implemented here likely the best possible one to use given this data? Explain.

The prior for the single calibration used in this lab is a normal distribution with a mean of 6 million years. Is this setting ideal for node calibration, and what better alternatives might there be? Explain your answer based on the “Rocks and Clocks” paper and the lecture for Phylogenomics 2.

For this lab, we first run the MCMC using 1,000,000 generations. Did this result in quality estimates of the posterior distribution for all parameters? What is your reasoning? How did you improve the sampling from the MCMC? Follow the instructions from the Tutorial PDF and the lecture for Phylogenomics 2.

According to the Tracer analysis of the primate-mtDNA\_long.log, what is the mean estimate and 95% highest posterior density from the posterior for the tree height? How do you interpret this number?

What is the mean and 95% highest posterior density for the mrca.human-chimp (the most recent common ancestor for human-chimp)? How do you interpret this estimate?

Select all four mutation rates by clicking the first mutation rate (mutationRate.noncoding), then holding Shift and clicking the last mutation rate (mutationRate.3rdpos). Select the Marginal Prob Distribution tab on the right to view the four distributions together. What does viewing the marginal probability distributions for all of these allow us to say about the estimated mutation rates for each of these partitions?

Use FigTree to edit your phylogenetic tree (primate.MCC.tree) from BEAST2 according to the instructions in the tutorial. Export the edited tree as a pdf and attach it to this assignment.

Use FigTree to click on ‘Node Labels’ and display ‘Node ages’. How does the node age for the root of the tree compare to the estimated Tree Height?

What is the mean and 95% HPD for the common ancestor of the great apes (which encompass human and orangutan, or *Pongo*)?

According to the data, what is the time to most recent common ancestor of apes and old world monkeys?