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HW 7: Methods and Results

BEAST2 was used to create a phylogenetic tree. First, BEAUti2 was used to import the multiple sequence alignment data of the primate mtDNA. This program helped to set the parameters for the evolutionary analysis. Then we used the HYK substitution model and the clock model to set a time frame of the evolutionary histories of the DNA sequences. The output from this program was a XML file, which was ran in BEAST2 to analyze it. TreeAnnotator was used to summarize the trees and find the best tree for the data. Finally, FigTree visualized the phylogenetic tree.

The ouput from FigTree provided a phylogenetic tree of the primate mtDNA sequences. It was found that Homo sapiens are more closely related to Chimpanzee, and they both have a closely related ancestor to Gorillas. Lemur catta and Tarius syrichta are the least related and are only related by the root ancestor to the rest of the primates that were recorded for this phylogenetic tree.

This analysis is interesting for comparing what we are closely related to as Homo sapiens. This analysis also shows the probability of this phylogenetic tree being correctly made with the values close to 1 or 1. Using programs like this are important for identifying closely related species and their connections of their ancestors throughout evolutionary time. Analyses like this one comparing primates to humans allows us to understand our own evolutionary history and connections to organisms on Earth better.