**Bioinformatics Lab 7**

**RAxML, MrBayes, and BEAST2**

**Week 8**

**Methods and Results:**

The program I used was BEAST2, which is a program to run a Bayesian Evolutionary analysis. I had to first install BEAST2, then I used the instructions on how to run BEAST2 to conduct the Bayesian Tree analysis. The general steps were to first create an XML file to run the tree analysis. Before creating the XML file, I needed to adjust different parameters of the data before running the tree analysis.

After importing the primate data to BEAUTI, the partitions needed to be linked to the clock model and tree. Then a substitution model was set, this is used to create the best fit in terms of data without having to “estimate the parameters”. Then I had to set a clock model, which is used to estimate where two or more life forms diverged. Afterwards I set the priors or parameters for the XML file such as adding a calibration node and MCMC option.

There are a total of 1001 trees, but I only saved one of the trees for me to annotate on this document. The tree shows an evolutionary separation from Homo sapiens/ Pan to M. mulatta. The orange circles are nodes, which represent species that share the most recent common ancestor. The red circle is the root node, which is rooted, represents the common ancestor that all the species in the phylogeny share. Then of course all the species on the ends represent the tips of the tree.

I think this is interesting, because they show the clear evolutionary separation between, homo sapiens and M.mulatta. This is useful if say I want to learn more about a fungus such as Aspergillus fumigatus. There are still some genes that need to be understood in this fungus. So, using the phylogeny tree, I could compare what fungus is closely related to Aspergillus and compare the two in terms of how similar they are. Hopefully that will tell us something about Aspergillus and its pathogenicity.

