1. A phylogenetic tree was constructed using the tree construction program MrBayes. The evolutionary model was set to the Generalized Time Reversible (GTR) which allows base pairs to be present at different frequencies and transitions and transversions are equally possible. This program utilizes the Markov chain Monte Carlo method which is based on Bayesian statistics. The priori information used to asses the (if the new tree is better than the previous) after every 1000 generations over 20,000 generations. The tree was then visualized in FigTree and rerooting the tree with the lemur as the outgroup as it is more evolutionary divergent from the rest of the primates while still being relatively closely related.
2. The phylogenetic tree contains 2 distinctive clades, one which contains macaques (old world monkeys?) and the other contains ape species. Within the ape clade, humans are most related to chimpanzees, and are most distantly related to gibbons. Maccas are most closely related to *M. mulatta* and most distantly related to *M. sylvanus*. Gibbons are most closely related to the macaques and *M. sylvanus*  is most closely related to the apes. Samiri is more related to these two clades than tarsus.
3. One thing that I found interesting is that Gorillas are more closely related to chimps and humans than orangutans are. Just visually looking at them, I would think orangutans were more closely related. Using these phylogenetic trees you can estimate how long ago these divergence happen