The primate mtDNA Nexus file contains sequence data from monkeys and apes. Following the instructions below you will perform a phylogenetic analysis to evaluate who the closest relative of humans is. The analysis will contain a maximum likelihood phylogenetic tree search, bootstrapping of the phylogeny using maximum likelihood and a Bayesian tree inference to estimate the posterior probability of the relationship between humans and their closest relative. Lastly, a statistical test will be performed to evaluate whether one or several phylogenetic hypotheses are significantly better than others.

Execute the nexus file in PAUP after you downloaded it to an appropriate folder in your home directory on the server. You may want to run the following commands in a screen sessions since they may take some time to run (select Y if PAUP asks you to quit despite unsaved trees being discarded).

$ paup primate-mtDNA-interleaved.nex

Who is the closest relative to humans in the best likelihood tree?

$ figtree Primates.ML.tree.nex

The majority rule consensus tree for 100 bootstrap replicates is contained in Primates.ML.BootStrap.tree.nex). Open the tree in figtree, display the bootstrap values on the nodes or branches. Who is the closest relative to humans in the majority rule consensus tree? What is the bootstrap support for this relationship?

PAUP also performed an SH test to evaluate whether some trees are not good explanations of the data. The constraint trees depicting different relationships between humans and other apes are contained in Primates.ML.Constraints.tree.tre.

Which hypotheses of who the closest relative of humans is are being tested by the SH test? Open the treefile with the constraint trees in figtree to check (note that you can click through the trees in the tree file using the arrow keys at the top of the figtree window).

Open the log file with less Primates.ML.Constraints.log and scroll all the way to the bottom. Which trees cannot be rejected by the SH test as being good explanations of the data? Which relationships do these trees depict when it comes to humans' closest relative?

Now run the Bayesian analysis using MrBayes:

$ mb -i primate-mtDNA-interleaved.nex

When asked if you want to continue the analysis choose no (type n and hit enter). Exit MrBayes by typing quit.

Who is the closest relative of humans according to the Bayesian analysis? What is the posterior probability of this relationship? Open the Bayesian tree with figtree to answer these questions - primate-mtDNA-interleaved.nex.con.tre

Lastly, for both the Bayesian and maximum likelihood analysis a model of evolution ad to be specified. Earlier, PAUP executed the pertinent files from modeltest for you (you may not have realized that this was happening). Run modeltest as specified below.

$ mrmodeltest2 < mrmodel.scores > mrmodel.out

Use less to open mrmodel.out which contains the results of the model testing procedure. Which model was chosen to be the best according to the hierarchial likelihood ration (hlrt) test and which model was chosen according to the Akaike Information Criterion (AIC)?

Open the primates nexus file primate-mtDNA-interleaved.nex with less and check which model was implemented for the likelihood analysis in PAUP and which model was implemented for the Bayesian analysis in MrBayes. Which model was chosen, the one favoried by the hlrt or by the AIC?