

## Introduction to Phylogenetic Trees

A phylogenetic tree is a visual representation of the relationship between the organisms being considered for making the tree. It depends mainly on two different parameters. First, the data that is used to make the tree and second the method by which it is made. The data can be from morphology, protein sequence, DNA sequence or a combination of them. Today, we are going to use DNA sequences. The other factor is the method in which a tree is made. There are many different statistical models and hundreds of programmes to build a tree and today we are going to use a programme called Mr. Bayes which uses Bayesian statistics to make a tree.

### What will you need?

Download the following programmes: Mr. Bayes, Treeview or Fig Tree. Mr. Bayes is a phylogenetic programme by which you are going to make the tree. Treeview or Fig Tree are programmes by which you will visualize the tree and save it for printing. The DNA sequence alignment to be used is the file that you submitted previously after selecting the taxa of your choice.

### Converting your file:

1. Mr. Bayes likes DNA alignment in a particular format called nexus format (.nex).
2. You can use this online tool to convert your fasta format DNA alignment files into a .nex format:
3. <https://www.sing-group.org/ALTER/>
4. Save the output file as your\_file.nex and put it in the same folder as Mr. Bayes.

### Running a phylogenetic tree:

1. Locate the your\_file.nex file and put it in the same folder as Mr. Bayes (this is very important).
2. Click on the mrbayes\_x86 icon. Mr. Bayes window will appear.
3. Type exe your\_file.nex. Mr. Bayes will now process the file.
4. At the Mr. Bayes> prompt, type lset nst=6 rates=invgamma
5. At the Mr. Bayes> prompt, type mcmc ngen=1000000 samplefreq=1000 printfreq=1000 diagnfreq=10000.
6. The analysis will start and Mr. Bayes will print a bunch of files in the same folder. Do not delete these files!
7. When it is done it will ask whether to continue with the analysis. Type no.
8. Type sump.
9. Type sumt.
10. Mr. Bayes will now show you the phylogenetic file.
11. Visualize the tree with the posterior probabilities. These are numbers in each node. They tell you how statistically robust your analysis has been.

### Visualizing a Phylogenetic tree:

1. Open Treeview (or Fig Tree). File>Open and select your\_file.nex.con.tre file from the Mr. Bayes folder.
2. In Treeview go to Tree>Define outgroup. A window will appear. Select pig from the ingroup list and put it in the outgroup list. Click OK.

**Please submit:**

1. the .con.tre file (the file used to visualize the tree)
2. The screen-capture of your cladogram
3. The final edited tree copied into a ppt file.
4. In the ppt please provide the posterior probabilities for each node, the name of the taxa used (e.g. H. sapiens) and not just the accession numbers, the outgroup taxa and the scale.
5. label the heading of the ppt with your roll number and the common name of your chosen ingroup.
6. Marks will be given (out of 10) based on how easy is it to read your phylogenetic tree.
7. Please submit it by the assigned date.