

Procedure for Phylogenetic tree experiment:

1. Install Phylip from <http://evolution.gs.washington.edu/phylip/getme.html>.
2. Get Treeview from <http://taxonomy.zoology.gla.ac.uk/rod/treeview.html> and Clustal from <http://www.clustal.org/download/current/>. For the latter, go for the file named clustalx-2.1-win.msi (size 4.7 MB).
3. Obtain the mRNA data of rohu, gonius, kontius, fimbriatus and bata from <http://www.ncbi.nlm.nih.gov/>
4. Keep the data in a single .txt file, say *rohu.txt*.
5. Open ClustalX > File > Load sequences> *rohu.txt*.
6. Alignment > Output Format options > PHYLIP format
7. Alignment > Do complete alignment > (Create the PHYLIP file)
8. Copy the PHYLIP file (*rohu.phy* in this case) to the phylip-3.69/exe folder and rename the file to 'infile' (without .txt, .phy or any other extension)
9. Open seqboot.exe > Create the 'outfile'.
10. Rename the *infile* into *barking_doggie* and rename *outfile* as *infile*.
11. Open dnaphars.exe > Press M > Press D> Enter the no. of data sets (5 in this case) > Enter seed (1/3/5/7/9) > Enter no. of time it should juggle (say 345) > Return. One can also modify number of trees to save.
12. dnaphars.exe modifies *outfile* and yields another file named *outtree*. Rename *outtree* into *intree* and *outfile* into *outfile2*.
13. Open consense.exe> Y > Return
14. Open treeview and drag the file named *outtree* into it.
15. The tree is ready!