

# Bioinformatics

## Lab 5

### Evolutionary Analysis and Phylogenetic Tree Construction

Software download site:

<https://www.megasoftware.net/>

Online manual:

[https://www.megasoftware.net/web\\_help\\_10/index.htm#t=First\\_Time\\_User.htm](https://www.megasoftware.net/web_help_10/index.htm#t=First_Time_User.htm)

Using MEGA software to perform

- (1) Evolutionary analysis – transition/transversion, distances, etc (for DNA only)
- (2) Construction of phylogenetic trees using different models (choose at least two methods to compare the trees for both DNA and proteins);
- (3) Rooting a tree (if possible, retrieve two or more outgroup sequences as a root to root your tree).
- (4) Bootstrap analysis of the tree. Compare the trees constructed using DNA with proteins.
- (5) Practice how to modify a tree such as labeling a node, generating a subtree, etc.

A few papers have trees – you may like to have a look at these papers:

[http://proteomics.yzu.edu/courses/BIOL4800\\_6900/ExtraReadings/MEN2007.pdf](http://proteomics.yzu.edu/courses/BIOL4800_6900/ExtraReadings/MEN2007.pdf)

[http://proteomics.yzu.edu/courses/BIOL4800\\_6900/ExtraReadings/Fungal\\_QA\\_phylogeny\\_CMB2021.pdf](http://proteomics.yzu.edu/courses/BIOL4800_6900/ExtraReadings/Fungal_QA_phylogeny_CMB2021.pdf)

[http://proteomics.yzu.edu/courses/BIOL4800\\_6900/ExtraReadings/fungal\\_ABC\\_protein.pdf](http://proteomics.yzu.edu/courses/BIOL4800_6900/ExtraReadings/fungal_ABC_protein.pdf)

[http://proteomics.yzu.edu/courses/BIOL4800\\_6900/ExtraReadings/Min\\_protease2018.pdf](http://proteomics.yzu.edu/courses/BIOL4800_6900/ExtraReadings/Min_protease2018.pdf)