

Pre-Lab

Audience

This lab is appropriate for High School (grades 10 and above); AP Biology (completed or currently enrolled) is a suggested pre-requisite.

Important terms

Here are some important terms you may already be familiar with or could look up and links to some resources to review before watching the presentation.

- Multiple sequence alignment
- Conserved (sequence)/sequence conservation
- Phylogenetic tree
- Neighbor joining phylogenetic tree
- Bootstrapping (statistical method)
- Maximum likelihood phylogenetic tree

Bioinformatics Lab Computer Setup

To follow along with this laboratory you will need:

- 1. Access to an up-to-date web browser such as Chrome or Firefox.
- 2. (Optional) We suggest getting a DNA Subway account through CyVerse. To get an account, go to https://user.cyverse.org/

Resources

Teaching the Process of Molecular Phylogeny and Systematics: A Multi-Part Inquiry-Based Exercise: https://www.ncbi.nlm.nih.gov/pmc/articles/PMC2995769/pdf/cbe513.pdf

Teaching Tree-Thinking to Undergraduate Biology Students http://evolution.berkeley.edu/UToL/meisel10.pdf



Laboratory Questions

These questions can be completed using the **Companion packet: Using DNA Subway to Analyze DNA Barcoding Sequences (Pages 22-29)** and by watching the video.

- 1. Looking at the sequence conservation histogram, are some regions in the barcode more conserved or less conserved than other regions?
- 2. How would you describe the relationships in your tree (i.e. what two species are the most closely related, followed by next most closely related species, etc.)?
- 3. How should you view relationships with low bootstrap support (i.e. bootstrap value < 70)?
- 4. When we add one of the insects in the reference data group, we see several of them that have the word fly in their name (e.g. Mayfly, Scorpionfly, etc.). True flies are members of the order Diptera. Are all the species with the term "fly" in their common name members of Diptera based on your tree?
- 5. Given the BLAST results and the phylogenetic tree, what identifications do you propose for the 4 mosquito samples?