Teaching notes for phylogenetic tree module

**Course Information**

Department: Biology

Level: Introductory Undergraduate Course

Course Type: Lecture + Lab

Students: Non-majors and/or majors

**Learning Goals**

After completing these exercises, we expect students to be able to:

* Define the key concepts that underlie phylogenetic trees
* Distinguish between a rooted and an unrooted tree
* Construct phylogenic trees and networks
* Analyze and interpret phylogenetic trees and networks
* Generate hypotheses related to phylogeny using phylogenetic trees

**Teaching Notes**

This module was designed to introduce introductory biology level students to phylogenetic trees and networks. More specifically, it uses phylogeny of bacteriophages as an example and was created to supplement bioinformatic analysis performed as part of the SEA-PHAGES program. The module is general enough however that any introductory biology course may benefit from its use.

The overview and exercise 1 introduce students to the importance of data analysis and the role of phylogenetic trees, basic vocabulary of phylogenetic trees, different methods used to produce trees and the concept of bootstrapping to confirm predictions made from trees. We suggest assigning the overview and Exercise 1 together as homework that can be discussed the following class period or as an exercise to be done in class. Exercises 2 and 3 lead students through the process of gathering fasta sequences to analyze using the maximum likelihood and neighbor-joining methods using two freely available phylogeny programs. In these exercises cytochrome c protein sequences are gathered and used by students to create trees and networks, which they are then asked to interpret. These skill building exercises are meant to prepare students for analyzing bacteriophage data in Exercise 4. Each of these exercises may be completed as homework or in class. We suggest introducing the concepts and tools to student in class, having them complete the exercises for homework and having students work in groups to discuss their findings and correct any misconceptions during the following class period.

Exercise 4 involves phylogenetic analysis of bacteriophages to predict relationships between phages. This exercise can be used in a variety of ways. We have provided the complete file containing the fasta sequences which can be used directly to create phylogenetic trees. However, we suggest having students gather the data themselves so that they are able to use this knowledge to explore further questions about bacteriophage biology. Each student may be assigned to gather all of the sequences and create a file themselves, though this activity is time intensive. We suggest having students each gather several of the sequences to add to a class document, which can then be used by each student in the class to produce trees. Gathering the fasta sequences can be assigned as homework or done as a class.

Producing trees and networks for Exercise 4 is relatively straight forward, but interpretation of the data is more time intensive. We suggest assigning tree production and answering the corresponding questions for homework, and during the following class period have students discuss their responses in small groups. Ultimately, having students hypothesize in small groups or individually how they can use these skills to investigate other biological questions will reinforce the concept of phylogenetic trees.