## Teaching Notes

### By *William Tapprich*

*wtapprich@unomaha.edu*

**Course Information**

Department: **Biology**

Level: **Upper Undergraduate**

Course type: **Lecture**

Students: **Majors**

Approximate Number of Students: **30**

**Module Information**

**Original Module Name**: Sequence Similarity: An inquiry based and "under the hood" approach for incorporating molecular sequence alignment in introductory undergraduate biology courses

**Link to Original**: <https://qubeshub.org/qubesresources/publications/56/5>

**Adapted Module Name**: Exploring Ebola Virus

**Files associated**:

* Teaching Notes
* Exercises 1-3, streamlined to remove questions to worksheets.
* Worksheets to accompany exercises 1-3
* New Ebola inquiry exercise 4 and worksheet
* Answer sheets for all exercises

**Learning Goals for your modified module:**

**Kleinschmit Resource Learning Goals (all apply)**

* Define similarity in a non-biological and biological sense.
* Quantify the similarity between two sequences.
* Explain how a substitution matrix is used to quantify similarity.
* Calculate amino acid similarity scores using various matrices.
* Explain how similarity is used to perform a BLAST search.
* Explain the BLAST search algorithm.
* Evaluate the results of a BLAST search.
* Create a dissimilarly matrix and multiple sequence alignment.
* Create a phylogram based on similarity of amino acid sequences.
* Distinguish between a rooted and unrooted phylogenetic tree.

**Tapprich Ebola Inquiry Exercise Adaptation Learning Goals**

* Apply bioinformatics skills to conduct inquiry of Ebola virus phylogenetic relationships
* Analyze phylogenetic tree of Ebola strains to guide vaccine development
* Develop new research questions and hypotheses for the exploration of Ebola virus

**Teaching Notes**

 This adaptation was developed and implemented in Spring semester 2019 in a senior level virology course. The lecture course focuses on molecular virology. There were 33 students in the course. They have varied experience with bioinformatics, but all have completed an introductory biology laboratory that includes a simple sequence alignment and ORF finding. There is an accompanying virology laboratory, taught as a CURE, that is not required. The 18 students taking the laboratory receive extensive bioinformatics experience including *de novo* sequence assembly, BLAST, and genome annotation.

The adaptation was meant to give all students bioinformatics experience. The first three exercises of the Kleinschmit resource were assigned without extensive modification. Since the students are advanced, the exercises were assigned as homework, one exercise per week for three weeks. In the adaptation of the three exercises, the questions were separated into worksheets that students turned in for credit. The worksheets were assigned 10 points per exercise, accounting for approximately 20% of the in-class activity points for the course.

Approximately 30 minutes of in-class time during each of the three weeks was devoted to discussion and completion of the exercise worksheets. Students were allowed to work in groups or on their own. Most students worked in groups. Most students came to class with the worksheets complete and used the time to discuss their answers with colleagues. There were a fair number of students that had misconceptions and needed the in-class time to correct their responses. Several students asked me questions directly. This was helpful for identifying misconceptions and roadblocks. I brought the entire class together to address these issues when they occurred. For students at this level, 30 minutes of class time was sufficient to address concepts, demonstrate tools and correct misconceptions.

The open-ended Ebola inquiry exercise (fourth exercise, also assigned 10 points) was developed specifically for the virology course. It explores the phylogenetic relationship between Ebola virus strains. It addresses the hypothesis that the ongoing 2018-2019 Ebola outbreak in the Democratic Republic of Congo (DRC) is caused by a known viral strain rather than a new strain. This information is important for vaccine development. Using skills acquired from working the first three exercises, students are asked to address the hypothesis on their own given reference sequences for the viral glycoprotein (GP) from all of the known viral strains as well as four sequences from individuals infected in the ongoing DRC outbreak. Again, 30 minutes of class time was reserved for completion of this exercise, but nearly all students had already completed the worksheet successfully and the time was spent discussing the implications of the results.

I will implement the resource in virology again next year unless I am able to migrate the resource to our introductory biology series. I believe the resource is better as an introductory experience. If successful, I will implement Kleinschmit exercises 1 and 2 in our first semester course and Kleinschmit exercise 3 in our second semester course. Also in the second semester course, I would offer the open-ended inquiry exercises, including this Ebola exercise as a menu of options for students.