## Teaching Notes

### By *Selene Nikaido*

*nikaido@ucmo.edu*

**Course Information**

Department: School of Natural Sciences, Biology Program

Level: **Lower/Upper Undergraduate** (select one) Upper undergraduate

Course type: **Lab/Lecture/Both** (other, please describe) (select one) Both

Students: **Majors/Non-majors** (select one) Majors (mostly)

Number of Students: 12

**Module Information**

Original Module Name: Databases

Link to Original: <https://qubeshub.org/qubesresources/publications/855/1>

[Adapted Module Name: (if applicable). Link to Adapted Module]

Modified Module Name: Databases: A Study of Influenza

Files associated: (ie. Class Worksheet, Summative Quiz, Lecture Powerpoint, etc)

Class worksheet

Modification Learning Goals:

* Search a database
* Understand evolutionary relationships
* Determine how mutations relate to protein primary structure
* Learn about Influenza genome and how it can change
* Investigate an Influenza pandemic (2009)

**Teaching Notes**

*(Think about what you would like to read about this activity if you came back to it in 2 years)*

Suggestions for this section (not all required, and extras always welcome):

* What did you change and why? I used a combination of the Accession Numbers and Annotation Exercises as models and introduced a completely different topic on Influenza. I did this for several reasons. First, it was an exercise I had developed some time ago. Second, my students are not in microbiology, and Influenza pandemic is something of general interest. Third, in an earlier version of this exercise, I generated a crude phylogenetic tree. In the submitted, modified version, I allow students to create their own tree and use bioinformatics tools directly. Lastly, it provides some variety to the collection.
* How did the activity go? I did not introduce this exercise to students this semester. However, my experience with an earlier version had these outcomes.
  + What went well and why? The students were able to finish the exercise by answering questions within a 2-hour laboratory period. With help, they were able to interpret a phylogenetic tree.
  + What went wrong and why? Students were not asked to work with bioinformatics tools. Concepts of molecular evolution may not have sunk in.
* What was the prep like?
  + How much time went into prep? No prep is needed as this is a dry lab. Instructor may have to go through the websites as they change quite often.
  + Did you have to do any prep (i.e. grow cultures, grow seeds, order supplies) ahead of implementation? n/a
* Would you do this activity again?
  + What would you change in the future? I would like to beta test this exercise with advanced students (ones who completed Genetics) and then with Genetics students.
* What do you wish you’d known before you ran the activity? Students must have some understanding of how viruses replicate, molecular evolution, and connection between RNA and proteins.
* Is there anything else you would like to make note of? Before running through any bioinformatics exercise, you MUST review the website to make sure screens look the same. Novices often do not adjust well when you say something is in this corner when they are not.
* How does this activity fit in your overall course curriculum? I would like to expose students to some products of bioinformatics, but the courses are not bioinformatics courses. Instead, my courses are genetics and molecular biology courses. Hence, the exercises have more of a biology emphasis.
* In what ways, if any, did you modify your teaching practice with this activity? n/a