## Exercise 1 Teaching Notes

### By ***Jennifer Katcher***

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**Course Information**

Department: Biology

Level: **Lower Undergraduate**

Course type: **Integrated lecture/lab**

Students: **Majors**

Number of Students: 24

**Module Information**

Original Module Name: Exercise/Module 1 – Similarity and Sequence Alignment

Link to Original:

Modified Module Name: Sequence Similarity: Introducing Biological Databases to Community College Biology Students

Files associated:

Google slides to introduce topic: <https://docs.google.com/presentation/d/1di-9RkzTsjy0UnSeDWSCctjfQZEUaP7PWK3-0h8_1vY/edit?usp=sharing>

Google doc with discussion questions that students completed in Zoom breakout rooms in groups of 3-4: <https://docs.google.com/document/d/1Je1ijNPBDjjA3vm8alEQTxSanR-V8SmiJj9zWBEutm4/edit?usp=sharing>

Students also received the original Exercise 1 document.

**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):

This introduction is the first time most students have seen or searched any kind of biological database. In previous semesters I had simply told students to “Do a BLAST search” and given them directions how. This exercise allows students to peek under the hood of a BLAST search, to see how the computer is selecting best matches.

Classes were virtual due to COVID-19. I chose to have the students work on this exercise in groups of 3-4 in Zoom breakout rooms. In the future I plan to have students work in groups in class for this first bioinformatics activity. Working in groups went well – it allowed students to compare ideas first before asking for help.

The intro with the vase and the Dr. Seuss-like quote lightened the mood and helped students to understand that they were comparing patterns. I initially demonstrated how to use the BLOSUM 62 substitution matrix. Students were confused that half of the matrix was blank but were easily guided through this.

It took longer for students to actually calculate similarity scores than I initially expected, and a number of students made mistakes initially. The most common mistake was that students only calculated scores for amino acid substitutions, not for all amino acids. Again, this was easily identified and corrected. The activity took about 45 min., all of which was done during class.

I was willing to give the students time to fumble around a bit with this activity because it was one of the few “hands-on” activities that they could easily do in a virtual environment. They learned by attempting to make calculations and learning from their mistakes. The iteration of aligning the query with two subject sequences was useful. Comparing their results with the Sequence Manipulation Suite website meant that students could check their work and determine if their calculations were correct.

There was no prep involved with using this activity beyond making the Google docs accessible to students.

In future semesters I plan to introduce the substitution matrix early in the semester when we discuss protein structure as part of introducing biological macromolecules. The matrix correlates well with comparing properties of amino acids (hydrophilic, hydrophobic, charged, etc.)