## Teaching Notes

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**Course Information**

Department: Biology

Level: **Upper Undergraduate**

Course type: **Lab and Lecture**

Students: **Majors**

Approximate Number of Students: 15

**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**: Similarity in Developmental Biology – A Bioinformatics Exercise Using Myostatin

**Files associated**: (i.e., 1.Teaching Notes, 2. Student Handout, 3. Class Hand-Outs from Kleinschmit et al. (2019), 4. Diagram TGF-beta Signal Transduction Pathway, 5. Summative Worksheet (Bioinformatics\_BIO 434 Worksheet), 6. Worksheet Answer Key.

**Learning Goals for your modified module:**

* Explain how a scoring matrix can be used as a quantitative assessment to identify similar proteins or protein domains.
* Interpret the meaning of E values with regards to sequence similarity.
* Explain how similarity is used to perform a BLAST search.
* Explain the BLAST search algorithm.
* Retrieve and interpret the results of a BLAST search.
* Make predictions based on bioinformatic data (and sequence similarities).
* Explain why model organisms are relevant for the study of human development and disease
* Given the consequence of a mutation in a highly conserved protein in a model organism, students should be able to predict the effect of the same mutation in humans.

**Teaching Notes**

The submitted materials were based on Kleinschmit, A., et al., 2019. Sequence Similarity: An inquiry based and "under the hood" approach for incorporating molecular sequence alignment in introductory undergraduate biology courses. *CourseSource.* <https://doi.org/10.24918/cs.2019.5>

Modifications

I used the material above as an outline and made changes according to my specific learning objectives and lecture material for my Developmental Biology course. A summary of those modifications follows.

The background given in the Student Hand-out is specific to my gene of interest – myostatin – and linked to previous lecture material on the effects of a myostatin mutation in the mouse. My student learning objectives incorporate both biological- and bioinformatic-based objectives. I focused on using bioinformatics as a tool for biology, rather than the gained knowledge of precisely how the bioinformatic analysis worked.

Regarding the computational procedures, I edited them for my particular protein, myostatin, rather than histone proteins, and compared the mouse (*Mus musculus*) to humans, rather than to the chimpanzee (Pan troglodytes). This modification allowed me to tie our lab exercise in with my lecture and to demonstrate how mice might be used as models to study human disease. I also added instructions for screen capture using the Mac – Grab tool.

Implementation of the Activity

The exercise occurred during a laboratory session, using 1 of our 3 hours. The lab session was preceded weeks earlier, by lecture material covering gene expression, protein production and the phenotypic effects of a mouse myostatin mutation.

The students worked in groups, but were encouraged to navigate through the exercise and NCBI website for themselves. The instructor roamed the room answering questions as they arose. Most students in this class had little to no exposure to NCBI or bioinformatics tools, so everything including navigation and evaluation of the NCBI website was new. The students had trouble navigating the NCBI website. The website contains a vast amount of information on a single page, which could be a little over whelming. Adding select screen shots indicating where the buttons for navigation and the pertinent information reside would be helpful. Additionally, when using a 3-amino acid query word, if only 2 /3 amino acids were represented, some students would use this to calculate their similarity score, not realizing that all 3 of the 3 amino acids in our example were to be used to find a match with their sample sequences. Making the instructions more clear and reinforcing what not to do (don’t use 2/3 amino acids for the search), would help to minimize this challenge.

It helped to inform the students prior to our exercise of why we were learning bioinformatics – that we need more students to think about computational methods to solve biological problems, especially those who can decipher ”Big Data” sets. I also hoped that the exercise would allow the students to “think outside of the box” regarding different methods to resolve research questions, and I wanted to relate the exercise to some of my own research, using NextGeneration sequencing to identify microbial communities. This field is new to me and I shared the challenges and necessity of using bioinformatics to decipher the information from my sequencing experiments. Overall, the students enjoyed this exercise, and were interested to learn more about what questions could be answered with bioinformatics.

Future Modifications

In future iterations of this exercise, when the students are asked to calculate similarity scores, I would ask them to submit their BLOSUM-62 calculation to ensure that they could calculate this score, rather than simply asking them a question about which sequences were more or less similar and why.

Preparation

Even though this exercise occurred during a laboratory session, there is no wet laboratory preparation for this exercise. For those well-versed in bioinformatics, its associated analysis and language, modifying the exercise should take a minimal amount of time. However, for those like myself who are not yet well-versed in bioinformatics, the modification of this activity took a lot of time. Additionally, I needed to run through the Kleinschmit (2019) exercise a few times to understand where my students might have problems, to learn the language associated with bioinformatics and to anticipate questions and have answers ready for my students.