## Teaching Notes

### By *Ami N. Erickson, Ph.D.*

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**Course Information**

Course Name: BIOL 2023 Plant and Fungal Biology

Department: Natural Sciences

Level: **Lower - Undergraduate**

Course type: **Hybrid: Online lecture & Face-to-face Lab**

Students: **Majors**

Approximate Number of Students: 6

**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**: Bioinformatics: Investigating Sequence Similarity – A Plant Biology Approach

**Files associated**: Class Worksheet and Query sequence handout

**Learning Goals for your modified module:**

* Apply concepts in genetics and molecular biology to the evaluation of evolutionary relationships.
* Understand the role of bioinformatics in modern science.
* Relate their ability to calculate an amino acid similarity score using a substitution matrix to the powerful, bioinformatics tools available online.
* Recognize that angiosperms and moss and much more closely related to each other than angiosperms and yeast (fungi).

**Teaching Notes**

For this exercise, I utilized most of exercise 1 and 2 from Adam Klenschmit’s publication. The primary change that I made was to replace the comparison in exercise 2 of the chimpanzee and human with two comparisons: one between Arabidopsis and a moss species; the other between Arabidopsis and yeast. I also removed the “One Fish, Two Fish” example to shorten the exercise.

The week prior to completing this activity, students conducted a morphological comparison between bryophytes, vascular – seedless plants, angiosperms and gymnosperms. They had also read associated textbook chapters and discussed a paper about the evolution of land plants (de Vries and Archibald, 2018). Prior to this unit, the class had reviewed genetics and basic molecular biology concepts.

The activity was completed during a 3 hour lab session in a computer lab, and the activity was a little long for the time allotted.

Overall, I think the implementation of the exercise was successful, and I will use it in future classes. Changes that I will make will include assigning the second sequence alignment activity in exercise 2 as homework after the lab. I also will spend more time at the end of the lab, discussing the results that the students obtained.

For the unit exam, I included the following question to determine if the students could apply the concepts that they used in this lab. This was a take-home exam. Next time, I will assign the sequence alignment activity from exercise 2 as a homework assignment and include this question as part of that assignment.

1. Short Answer: Given the following query sequence with the hi-lighted query word and the comparison sequences, which protein sequence is most homologous to the query? Identify the similarity scores. Based on the organisms to which the protein belongs, do your results support their evolutionary relationship to each other? Explain.

    Query: >NP\_001170028.1 cytochrome c [Zea mays]

MASFSEAPPGNPKAGEKIFKTKCAQCHTVDKGAGHKQGPNLNGLFGRQ

    Comparison Sequences:

1. >NP\_173697.1 CYTOCHROME C-1 [Arabidopsis thaliana]

MASFDEAPPGNAKAGEKIFRTKCAQCHTVEAGAGHKQGPNLNGLFGRQ

2. >XP\_026597107.1 Cytochrome c [Candida viswanathii] (Saccharomycetes)

MPAPYEKGSEKKGATLFKTRCLQCHTVEKGGPHKVGPNLHGVFGRKSGLA

In the future, I do plan to extend this activity into a phylogenetic mapping activity involving more plant and related organisms.

Assigned Article:

De Vries, Jan and Archibald, John M. 2018. Plant Evolution: Landmarks on the Path to Terrestrial Life. New Phytologist. Vol 217: 1428 – 1434. <https://nph.onlinelibrary.wiley.com/doi/full/10.1111/nph.14975>