

Marine Biotechnology and Bioinformatics

for Teachers

Using Molecular Homologies to Predict Evolutionary Relationships

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Abstract

This interactive tutorial exposes students to the power and relevance of common web-based bioinformatics resources (NCBI, Crn3D, Clustal, etc.). Through a student-centered and individually paced lesson involving the use of web databases and molecular alignment software, students research a particular protein sequence in several organisms and then experience first-hand how our growing knowledge of molecular data coupled with advancements in computer technology can enhance our understanding of evolutionary relationships between seemingly unrelated organisms.

Background

The central dogma of molecular biology, that information in all living organisms translates from DNA to mRNA to protein is a central concept taught in all high-school Biology classes. Since the discovery of DNA as the universal genetic code in all life, the past 50 years have been spent sequencing genomes and accumulating information concerning the underlying codes of countless proteins in a plethora of organisms. Comparisons of DNA and protein sequences have armed scientists with a new method to categorize organisms by their degree of similarity at the molecular level. Web databases of molecular information as well as web-based alignment software are readily available and commonly used in the research world. This lesson was designed to introduce students to these tools and reinforce their knowledge of molecular genetics as a foundation for understanding how evolution can be used as a lens to comprehend the unity and diversity of life.

Instructional Objectives

- Expose students to web-based bioinformatics resources and technology (NCBI, Crn3D, ClustalW)
- Demonstrate how similarities between organisms at the molecular level can be used to infer evolutionary relationships
- Allow students to visualize and manipulate the 3D structure of a protein
- Reinforce the connection between protein structure and function

Teacher and Student Preparation

Prior to this lesson,

Teachers should:

- Test out all websites to make sure they are still accessible. (NCBI is a dynamic database and searches that students conduct may not always result in the same hits as indicated in the directions.)
- Develop a general familiarity with how databases work, so they are prepared to help students troubleshoot.

Students should:

- Have a basic understanding of the central dogma of molecular biology (protein structure, amino acid codes, relationship of protein structure to protein function)
- Have general knowledge of classification schemes and how to interpret a phylogenetic tree

Materials and Resources

The following resources are needed to implement this lesson:

- Access to computers with internet (ideally, one per student) and the following web resources:
 - NCBI (<http://www.ncbi.nlm.nih.gov/>) - Used to find protein sequences and protein structure files
 - ClustalW (<http://align.genome.jp/>) - Used to align protein sequences and construct phylogenetic trees
 - Crn3D (available at NCBI website) - 3D protein viewer used to visualize and manipulate protein files

Time: if each student has access to a computer, completing the assignment (and accompanying worksheet) should take no longer than one 40-50 minute class period.

Assessment

As students explored the websites and completed the guided tutorial, they answered questions that assessed their understanding of and ability to analyze the data they were collecting. The questions were intentionally designed to also connect the activity with prior knowledge. At a few points in the exercise, they were required to print out evidence of their progress. They were also asked to reflect on possible research or clinical applications of the technology they were using.

Upon completing this lesson, after the students feel proficient at navigating these bioinformatics resources, teachers could further enhance this lesson by assigning students to investigate a different protein of interest.

Conclusion

This lesson successfully accomplished its objective as a simple and user-friendly introduction to bioinformatics. Overall, students enjoyed the self-paced, hands-on aspect of the activity, and several commented on the eye-opening realization that Biology could connect to computer technology. Upon navigating the websites, several students were intrigued by the multitude of web-based resources available to analyze molecular data. In terms of implementation, I was pleasantly surprised by my students' technological literacy; they were rather adept at navigating websites and following directions.

In the future, to enhance this lesson, I would encourage creativity and personal investment by asking students to formulate and subsequently answer their own question of interest after becoming familiar with the bioinformatics resources.

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Method



NCBI is used to search for various protein sequences from various organisms.



After several realized sequences have been compiled, ClustalW, a web-based program, is used to align the sequences based on their similarities and measure how different each aligned word appeared to form the others.



A "bootstrap" value can also be calculated to graphically display predicted evolutionary relationships.



Crn3D is a protein viewing program designed to view and manipulate the various protein files. It can also be used to examine the structure and function of individual regions in the protein being studied.