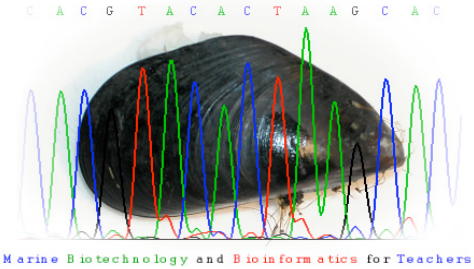

MARINE BIOTECHNOLOGY & BIOINFORMATICS FOR TEACHERS
MOSS LANDING MARINE LABS NSF ITEST GRANT
TEACHER LESSON PLAN FOR CLASSROOM USE
CREATING REALTIONSHIP TREES

Title of Lesson: CREATING RELATIONSHIP TREES

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Background
This lesson is an extension of a lesson already in use by biology teachers which teaches students about the practice of evolutionary biology. Students are familiar with the evidences that scientists work with to uncover evolutionary relationships among organisms. In the past, students would examine skeletons and create a cladogram based on similarities in forelimb structure of 7 different animals: bat, cat, frog, human, perch, rat and pigeon. This lesson keeps that component, but also adds DNA analysis and use of CLUSTAL to build trees so that students appreciate the importance of collecting DNA evidence in the science of evolutionary biology. This is a multi-day lesson, due to the fact that students will need instruction in order to use the bioinformatics necessary for the lesson.

Description of Audience: This biotechnology/bioinformatics activity is designed for use by high school students.

State Standards: This biotechnology/bioinformatics activity fulfills the following State of Illinois Science Standards:

- **12.A.4c** Describe processes by which organisms change over time using evidence from comparative anatomy and physiology, embryology, the fossil record, genetics and biochemistry.
- **13.A.4c** Describe how scientific knowledge, explanations and technological designs may change with new information over time
- **13.A.5c** Explain the strengths, weaknesses and uses of research methodologies including observational studies, controlled laboratory experiments, computer modeling and statistical studies.
- **13.B.5b** Analyze and describe the processes and effects of scientific and technological breakthroughs.

National Standards: This biotechnology/bioinformatics activity fulfills the following National Science Standards:

- *** List standard(s) here ***
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STEM Connection. What careers are tied to this activity? Specifically highlight the career connections.

Technology Integration. This lesson requires that students collect DNA sequences from BLAST and then analyze homology using CLUSTAL. Students also create a relationship tree in CLUSTAL.

Goals(s):

- Students will discover relationships between various vertebrates
- Students will compare relationships based on skeletal analysis with relationships generated by DNA analysis

- Students will learn how to use computer bioinformatics related to DNA analysis

Learning Objective(s)

- Students will be able to use bioinformatics
- Students will be able to analyze cladograms

Purpose/Rationale

This lesson is being taught in this manner so that students use deductive reasoning skills in order to build a cladogram from skeletal structure analysis. Students will then confirm or revise their cladograms based on DNA sequence data. Students will understand the role of DNA analysis in evolutionary biology, and see first-hand how technology is changing our understanding in this field.

Materials/Resources

In order to complete this lesson, the following materials are needed:

- Skeletons of various vertebrates (bat, cat, frog, human, perch, rat and pigeon)
- Computers with access to the internet (for using BLAST) and CLUSTAL

Prior Teacher Preparation

In order to teach this lesson, the teacher must research gene homologies for each of the species being used and correctly identify what genes can be used for DNA analysis. This also requires that the teacher create a tree, to make sure they've chosen the correct genes for analysis. The teacher would have to prepare a lesson on how to use BLAST and CLUSTAL so that students are familiar with how to use these applications before trying to apply them to this lesson.

3-Step Procedure

#1 Introduction

- Prior knowledge that students would have to have in order to complete this lesson include DNA structure, Mutations, Species homology, Evolution, BLAST, CLUSTAL
- Student misconceptions include the idea that different species have entirely different genomes. Students don't always realize how much of the genome is conserved over time, especially genes necessary for overall functioning of the cell. By analyzing a highly conserved gene and a highly variable gene, students will be forced to re-evaluate this misconception.
- Review what was learned in prior lessons – including: 1) DNA structure, in particular, nitrogenous base sequences 2) Mechanisms of mutation 3) Natural selection and speciation 4) Cladogram analysis 5) Homologous structures. Then introduce content and vocabulary necessary for today's lesson: 1) lesson on using BLAST to find gene sequences 2) lesson on using CLUSTAL to align sequences and create trees.
- The teacher will need to use a laptop and LCD projector to model how to use the bioinformatics applications necessary for this activity. teaching charts, video clips, books, presentation software, instructional software, articles, tapes, overhead projector, handouts, models, etc. to accent instruction.
- Students will individually create an initial cladogram based on analysis of skeletal structures. The entire class will discuss possible evolutionary relationships based on the homologous structures that they've seen in the different skeletons. Students will work in pairs in order to BLAST the genes and use CLUSTAL to align the sequences and create an evolutionary tree. Students will then work individually to compare their tree with the computer generated tree and write an essay discussing the similarities and differences between the two.

#2 Exploration

1) Students will be asked to describe the relationship between the selected species. Students are using deductive reasoning to propose a hypothesis for evolutionary relationships.
2) The class will discuss individual hypotheses.
3) Students will then be asked to look at skeletons of the selected species. The teacher will need to review forearm bond structure so that students can accurately describe and identify the bones that they see.

4) Students will draw the forearms of the different species; color-coding the bones so that they can compare bones of each species.
5) Students will then use these drawings to create a cladogram. Students should already be familiar with creating cladograms from previous lessons, however, teacher may need to review
6) The class will discuss these initial cladograms.
7) Students will be given a lesson in using BLAST to aquire gene sequences.
8) Students will be given a lesson on using CLUSTAL to align those sequences and create cladograms.
9) Students will then be given the names of two genes: a highly conserved gene and a highly variable gene.
10) Students are asked to BLAST those genes and align in CLUSTAL to create evolutionary trees.
11) Students will then compare what they have found with CLUSTAL to the initial cladogram they created and write an essay describing if they are similar or different and why.
12) Teacher should lead a class discussion about why they were given two genes to analyze and how they aligned between the different species.

#3 Application

- How can the student apply what was learned today in his/her experience?
- How can the value of this lesson be made relevant in their lives?
- How can interest be extended?
- What is a good follow-up activity to reinforce concepts learned today?
- Provide relevant homework, class work, parent-involvement activity, research assignment…
- Career Connection**.** At this point write a paragraph describing careers in bioinformatics and biotechnology related to this activity. Describe how this activity contributes to students' understanding of science careers. You may also choose to list specific careers related to this activity.

Assessment

- Students will be assessed using their computer generated trees. Students will also be assessed based on the conclusion essay they have prepared.
- Students will be given a homework assignment (the whales & hippos activity) where they will be able to prove that they can apply the bioinformatics to other situations.
- Students are placed in groups of 2 so that students who are having a hard time will be paired with those who better understand the material. Directions will be provided orally and written to students and students will also be given a flow chart with a pictorial representation of directions for those students who are visual learners.
- Extension of the lesson will include student research of a gene of their choice. They will be asked to pick three species they believe are closely related to each other and pick a gene to sequence, creating a tree for those species.

Please include several copies of students' work, ideas, journals, and completed lab sheets. Include copies of any text pages you used as well as any handouts, lab sheets, and workbook pages.

Teachers' Self Evaluation

Reflect on strengths and weaknesses of the lesson as taught.

- Describe individual student responses to techniques used. How did they react?
- Discuss student "thinking" and ideas.
- Include samples of students answers on lab sheet or journal entry (photocopy is fine).
- Ask students for a brief evaluation of lesson. Include their responses.
- Discuss fulfilled and unfulfilled expectations. Any surprises?
- In retrospect, how would you modify this lesson?