

## **Abstracts of Additional Major Workshops Presented at the 28<sup>th</sup> ABLÉ Conference**

### **Fossil Leaves and Paleoclimates**

*Mark E. Lyford* (University of Wyoming)

This laboratory is designed to engage students in a problem solving activity that models how inferences are developed in science. Specifically, students are presented with a future scenario in which an entrepreneur wishes to develop a dinosaur theme park, populating it with the Cretaceous dinosaurs he grew up loving (DNA technology has advanced enough to make this possible). He is using DNA preserved in bones excavated from a site in Wyoming. To determine what sort of climatic region he should buy land for his preserve, he has hired the students to infer what sort of climatic regime these dinosaurs would have lived in. The only clue is that there is a bed of fossil leaves adjacent to the dig site that is of the same age as the bones. Ultimately, the students will develop a relationship for estimating mean annual temperature of the site based on the characteristics of modern leaves. To get to this point, the instructor plays a central role in guiding students through a series of questions. Some groups will pursue a line of study that does not result in a good method of estimation, whereas other groups will. Once the class has agreed on the best method for estimating mean annual temperature, they use this means of estimation on the fossil leaf assemblage to determine the mean annual temperature of the site during Cretaceous times. This activity highlights the investigative nature of science, demonstrates how inferences can be made, and outlines some limitations of science based on assumptions that have to be made at times.

### **EvoBeaker simulation software for teaching micro and macro evolutionary biology**

*Eli Meir* (SimBiotic Software; also Massachusetts Institute of Technology)

EvoBeaker is a new computer program written by SimBiotic Software, collaborating with Jon Herron (co-author of Evolutionary Analysis) and Joel Kingsolver (UNC Chapel Hill) for teaching evolutionary biology at the undergraduate level. EvoBeaker includes six laboratories covering topics from the assumptions behind natural selection to evolutionary trees to Hardy-Weinberg equilibrium, at levels suitable for both introductory and non-majors biology as well as intro evolution classes. The labs are inquiry-based and use real examples, with a similar philosophy to the EcoBeaker ecology program. In this workshop, participants will run through 2 of the introductory biology-level laboratories, and we will present results from the extensive assessment we did on those labs. We'll also demonstrate the other 4 labs in the program, and talk about the modeling engine and our future plans for the next version.

### **Bioinformatics for Beginners**

*Steven Caruso and Lark Claassen* (University of Maryland Baltimore County)

Bioinformatics is a relatively new sub-discipline of biology that will have a major impact on our student's lives in their roles as consumers, as practitioners in medical fields, and as biologists. However, the field requires an advanced understanding of molecular biology, enzymology, and

computer science that makes it accessible only to advanced students who have taken the necessary pre-requisite courses. In this workshop we present our approach to making bioinformatics available to a broader cross-section of our student population. In our curriculum the field of bioinformatics is introduced to biology majors and non-majors who enroll in two one-semester laboratory courses: an introductory biology course that serves a mixture of allied health-, biology/biochemistry-, and non-majors; and a sophomore-level genetics and molecular biology course taken by biology/biochemistry majors and by pre-medical students. In the introductory lab, students learn about the history of bioinformatics and the types of information available in four of the databases accessible from the NCBI website. A capstone project allows them to apply what they have learned to a phenotype or disease that runs in their own family. In the genetics and molecular biology lab students sequence the 16s rRNA gene from an unknown bacterial culture and then send the resulting sample to a sequencing lab for analysis. In a second session, students receive the chromatogram of the 16s rRNA sequence they submitted, which they must then edit using Gene Tool Lite. Students then use the BLAST program on the National Center for Biotechnology Information website to search for homologies to sequences already submitted to Genbank, and thus identify the species of their unknown bacteria. This lab can also be performed in a shortened “dry” version in which students are provided the chromatograms and perform the second session only. In this laboratory workshop, participants will have an opportunity to do portions of the exercise performed in the genetics and molecular biology course, including the bench work required to sequence the 16s rRNA gene of an unknown bacterium and the computer work editing the resulting chromatogram.