Marine Biological Laboratory (MBL) Summer Workshop on Molecular Evolution, Woods Hole, MA
Summary Report for NASA Astrobiology Institute – Early Career Scientist Award Program

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The MBL Workshop on Molecular Evolution was very well organized and the curriculum was helpful to my career interests in Precambrian paleobiology. The organizers made the course as comprehensive as possible; in many cases, the faculty (Peter Beerli, David Swofford, Paul Lewis, John Huelsenbeck, Mark Holder, Laura Kubatko, etc.) conducted lectures on theory and assisted the in lab demonstrations of the software they had written for the phylogenetic community.

John Huelsenbeck conducts a lecture on Bayesian methods of phylogenetic analysis.

I had a number of specific objectives that I wanted to accomplish throughout the course. Generally speaking, I wanted to gain sufficient knowledge of Bayesian theory to understand how phylogenetic models are constructed. Specifically, I wanted to learn how to manipulate multi-gene phylogeny models created in BEAST to incorporate 1.5 billion year old fossils that I have discovered in rocks of the Belt

Supergroup of Montana. These fossils are exceedingly rare, having been found in only a handful of locations worldwide, and they may provide critical information about how, when and why early eukaryotes evolved. Tying together molecular clock models and fossil data is important because there are very few constraints on early eukaryotic evolution; what little data we have from this period of time underpins models that can produce highly variable results, so it is important to understand, and to properly justify, how the fossils are interpreted and incorporated into such models. I left this workshop with the basic knowledge needed to understand, manipulate and generate BEAST models. These models may assist the evaluation of various possible taxonomic assignments of the fossils, which may in turn help to constrain the nature of the original organisms and their relation to subsequent organisms that became extremely complex. By the end of the course, I had completed all of the objectives that I had outlined for the course, and had even gained sufficient knowledge to apply genomics data to another research project that I am working on to evaluate organismal complexity over time.

I would highly recommend this course for other early career scientists working with the NASA Astrobiology Institute on problems related to molecular evolution, phylogeny or the interaction and history of biological innovations at multiple levels as recorded in genetic sequences. The course organizers go to great lengths to tailor the curriculum to the particular research objectives of the attendees. There is an effective balance between teaching of background theory (required for more creative uses of existing applications) and use of particular software applications that have been developed to analyze phylogenyr related data. Additionally, and perhaps most importantly, there is ample time devoted to oner onr one discussion between students and faculty regarding the research questions that the students are investigating. I believe anyone attending this course with similar objectives will be similarly impressed. Participating in this workshop can serve as an effective means of advancing many of NAI's organizational objectives regarding the use of phylogenetic models to understand the history and evolution of life on Earth.