

I still remember advice I received four years ago from my advisor, the head of my major. Loosely, he told me I'd be a fool not to consider research as a viable career opportunity. These words were music to the ears of a scared, first-year student at a large university who had been bitten by the science bug. This one conversation was the single most transformative moment in my college career, and I will always be grateful to my advisor. Following his advice, I went out and found a lab on campus to be my home away from home and began exploring the wonderful world of evolutionary biology.

I landed in the Moore lab in Bayesian Phylogenetics, and it has been an amazing place to work. I was in the lab for three years as an undergraduate, and I am several months in to a yearlong position as a research technician. In my time in the lab, I have assisted conservation efforts, performed meta-analyses, and studied trait evolution in damselfishes and across the entirety of Metazoa. I have learned how to use simulation to my advantage, how to implement bioinformatic techniques to pipe large amounts of data through numerous programs for analysis, and carefully assess the performance of Markov chain Monte Carlo, the vehicle by which we perform most analyses. I have even been given the chance to mentor a high school student.

I have participated in scientific research outside of the Moore lab. I assisted researchers from the University of Washington and Michigan State University in studying the genetics of adaptation and speciation in monkeyflowers. The project revisited the divergence between the bee-pollinated *Mimulus lewisii* and the hummingbird-pollinated *Mimulus cardinalis*. Professor Toby Bradshaw of the University of Washington had isolated three quantitative trait loci (QTL) thought to have been related to a change from bee pollination (considered ancestral) to hummingbird pollination (considered derived). He and his lab had bred a line of *M. lewisii* with one of each of these QTLs introgressed. Our task was to take these plants to the field, with a control line of purebred *M. lewisii*, and assess the impact of each QTL on pollination by observing pollinator visitation. Despite unforeseen circumstances preventing the collection of usable data, the experience was highly satisfying and affirmed my passion for research science.

My first year in the Moore lab, I had been assisting postdoctorate research fellow Luke Mahler with conservation reports and collection of primary literature on *Anolis* lizards. When I returned from the *Mimulus* fieldwork, I took my familiarity with searching the scientific literature and considered a new question: is diversification (speciation minus extinction) slowing down across the tree of life? My first task was determining what previous studies had reported. I was shocked to find that, while several recent studies were theorizing about the causes of diversification-rate decreases, few had done any work to establish that it was actually slowing in any significant number of lineages. I amassed over 200 studies, all of which had cited one, or both, of the two most popular methods for testing phylogenies for diversification-rate decreases. A survey of these studies revealed that no good answer would come from simply summarizing previous findings. Some studies had misapplied methods. Many had analyzed the same phylogeny multiple times, usually with conflicting results. Few of the studies that used the more complicated method had used it as intended. What we needed to do, we found, was to reanalyze the studies' phylogenies ourselves. Very few studies made their phylogenies available online, so we had to solicit the data ourselves.

For several months, I spearheaded an effort to collect the phylogenies from my list of studies. I had help from Dr. Moore, and from Michael May, Dr. Moore's graduate student. We

found that there was a discrepancy among responses to our solicitations: people responded more to Dr. Moore than to either Michael or myself, and people responded more to me than to Michael. These discrepancies were especially unexpected because we all used the same solicitation procedure, even using the same form letters when initiating contact. We also found that there was a surprisingly low rate of successful retrieval of the data we needed. Our experience led us to write a paper on the availability of phylogenetic data. When we looked at the data more carefully, we found that the Joint Data Archiving Policy (JDAP) had a noticeable positive effect on data archival rates, as did the strength of a journal's archival policy. From this experience soliciting data, I learned that persistence is important, and that if you look for it, you can always find a silver lining. There were two silver linings in this case, the efficacy of JDAP and our ability to make something useful out of a frustrating experience, namely a paper (cited eight times) calling for better archival practices and evaluating what does and does not work.

Despite the low rate of retrieval, our solicitations allowed us to obtain a sufficient amount of data for me to continue with my project. Between the phylogenies we collected, and those obtained from an earlier meta-analysis on a similar topic, we ended up with over 300 phylogenies to analyze, and I was able to present preliminary findings at the Botany 2014 conference. Though this meta-analysis is ambitious, it is far from the only ambitious project in which I have been involved. When my lab took on interns, I was given the responsibility of mentoring one, a high school student named Audrey. Audrey's project was to be a continuation of the paper we wrote on data sharing, looking at whether there is a correlation between the reproducibility of results and the sharing of data. Her task was to gather the data necessary to reproduce nearly 100 phylogenies, 50 from studies that shared data, 50 from studies that did not. My task was to automate for her the process of turning that information into 100 trees, as doing each individually would be impossible on her deadline. I was able to successfully automate the production of 100 trees, and her project was completed on time. Given the rushed nature of the project, the pipeline was somewhat incomplete. But I have continued to revise it, making it significantly more useful.

This pipeline has been helpful in other contexts. Recently, several researchers came to my lab data for a variety of reproductive traits, many theoretical predictions, and a question: had these traits evolved in a correlated fashion? They had no tree, and in talking to them, it became clear that we had expertise that could greatly enrich their work, availing ourselves of the best and most rigorous available phylogenetic methods. Using a provided list of species names and synonyms, I devised a way to obtain all information from GenBank about available sequence data for the project. Inferring a phylogeny was significantly easier using my automation scripts, but nevertheless it was an intense struggle. The sequences diverged so long ago (some billion years in the past) that phylogenetic inference programs had serious problems analyzing the dataset. With advice from Dr. Moore and from Michael, I kept pushing, and we recently finished our phylogeny and using it to analyze the evolution of the reproductive traits. Though I am unfamiliar with the biology at hand, it has been intensely rewarding to see the excitement of our collaborators as we unravel the evolutionary answers to their questions. Together, we are able to ask questions with strong biological relevance on a scale previously unheard of and without compromising the validity of our results. Our collaborators have every expectation that this will be a landmark study, and I am thrilled that I was able to help it happen.

My interest in science has been stimulated almost constantly for the past three years; I pushed the boundaries of my own knowledge and helped push the boundaries of the scientific community's knowledge. I have found both these to be almost addictive. Each time I unravel the workings of a model, or use that model to address unanswered questions, I experience a profound joy, and each setback along the way only amplifies the satisfaction. I want more than anything else to continue pushing the boundaries of knowledge, which is why I have set my sights on graduate school. I want to get a PhD and continue research at a world-class university not unlike the University of California, Davis. I know that there is a lot of work required to pursue my dreams, but I know that I will persevere, and that the skills and knowledge I acquire in graduate school, and the papers I publish there, will prepare me for post-doctorate positions and, eventually, a professorship.

I am also motivated by a profound gratitude and desire to give back. I have been given a lot since I came to college. My advisor gave me the gift of confidence. Dr. Moore has given me many opportunities to learn and acquire skills at advanced levels, and to participate in meaningful projects in critical ways. These are gifts that I wish to pay forward. I want to teach undergraduates and be as approachable as possible, so that they will come to me for advice. I want to help them navigate their own futures as I had help navigating mine. I intend to one day maintain an active research lab of my own, and to populate it with motivated students, both graduates and undergraduates.

I want to bridge the theoretical and empirical sides of evolutionary biology. Not just because both are stimulating and enjoyable, but because the quality of research done in both areas is dependent on collaboration and dialog. Without theoreticians and mathematicians, it is difficult to truly understand our confidence in our work, and to develop ideas in ways that are broadly applicable and testable. Without empiricists, we risk pointless theorizing and developing ways to answer questions no one cares about. Dialog between the Moore lab and empiricists has led not just to a large study on reproductive evolution, but to the realization that current trait-evolution models are insufficient for answering questions posed by many empiricists. If people continue to provide this bridge, the entire field of evolutionary biology profits. I want to go a step further and develop a research program with both empirical and theoretical aspects.

Without communication between model-developers and model-users, disaster can strike. Like I saw with the relatively simple models for diversification rates, it is easy to misapply or misuse a model. And as phylogenetic models get increasingly sophisticated, it becomes increasingly easy to misuse them. To prevent this, there are a variety of strategies that model-developers have used. They put on workshops, write blogs, teach courses (to undergraduate and graduate students alike), and keep their work visible at conferences. I hope to be able to do all of these things in my career. I would also like to try something new. I would like to host frequent, at least monthly, open problem-solving sessions online. I imagine these sessions lasting a few hours utilizing something like Google Hangouts. I would include experienced model-users and model-developers available to help me properly advise attendees. The help could range from simple, like "how do I specify model X in program Y?" to more complex, like, "how do I address this question?" I would make a special effort to reach out to graduate students, who can more easily slip through the cracks. I would also welcome advanced undergraduates to sit in, which would allow them to develop their own understanding of how to do research.