Research and Teaching Statements

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1 Research Overview

In my research I use mathematical and computational tools to solve problems in genetics and evolutionary biology. My background includes formal training in both biology and pure and applied mathematics. This dual-path training has given me a comprehensive set of techniques that allows me to find and use the best method for solving new biological problems, crafting elegant solutions that encompass the appropriate level of complexity.

Building on my research experience in behavioral ecology, statistical genetics, and population genetics, I am currently examining the evolution of genetic networks, genome structure, and developmental regulation. This focus has developed during the past several years of my association with the University of Oregon, where I have been an active member of the NSF-funded IGERT program in Evolution, Development, and Genomics. My current research is funded by an NIH NRSA fellowship and promises to be an area of increasing interest.

2 Previous Research

Behavioral Ecology

Traditional models of male display assume that display traits are made once, last forever, and have a fixed cost. I have created game theoretic models of male display that incorporates the timing of signaling costs and the effects of aging. This work shows that signaling is generally more "honest" among older males, which is a novel explanation for the observed female preference for older mates (**Figure 1**). Because the amount of future reproduction available decreases as individuals age, the optimal signaling strategy shifts to higher levels of signaling for all males. However, the relationship between quality and signal changes as males age so that a tighter relationship between male quality and signal exists in older age groups.

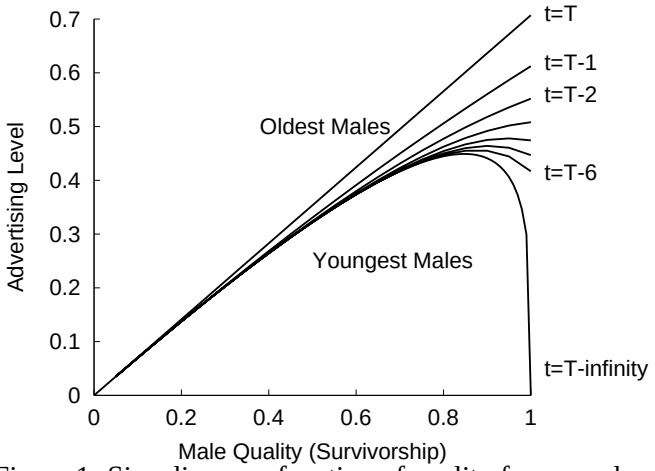

Figure 1: Signaling as a function of quality for several age classes. In older age classes signaling increases with quality.

Statistical Genetics

I have worked with colleagues in molecular genetics to understand the functional relationship between gene products at the synapse of *C. elegans*. I designed a maximum likelihood method to test for genetic interactions between partially recessive mutations at known loci. The estimates of the genetic interactions were obtained from an analytical model, but a computational approach was required to define confidence intervals and conduct hypothesis testing. By applying this method we were able to both verify known physical interactions (validating the method), and infer novel interactions between gene products.

Population Genetics

My research in population genetics has included studies of sexual selection, sex allocation, genetic dynamics in stochastic environments, and virulence evolution. A major theme of my research is concerned with the interaction between sexual selection and adaptation in both space and time. I have shown that the mating system can have a large influence on whether populations survive climate change and affect the rate of adaptation to novel conditions. Further, sexual selection can enhance the ability of a species to achieve local adaptation and maintain genetic variation along a spatial gradient. This creates a feedback cycle that strengthens selection for female mating preferences and local adaptation simultaneously. By focusing on the dynamics of adaptation and mating system evolution, I have shown that speciation is not necessarily the most likely response to spatial variation, but rather that sexual selection can maintain both local adaptation and gene flow simultaneously.

I am generally interested in the role that stochasticity plays in adaptive evolution and the creation of neutral genetic variance. As biologists we often attempt to predict the outcome of evolution as though it were a deterministic process, despite the fact that it is inherently stochastic. A more valid view of adaptive evolution embraces its inherent uncertainty, focusing on the relative probability of observing different adaptive states. I have taken this approach by studying trait evolution both when individuals face random variance in their ability to reproduce and when whole populations face random environmental variance. For the case of individual variance, I have derived both methods to bound the fixation probability of a novel allele, as well as diffusion approximations to calculate fixation probabilities. This method represents an important improvement on previous methods, as is shown by its ability to predict simulation results (**Figure 2**). I have applied this method to sex allocation in finite populations and have shown that allocation to the more risky sex will be reduced, a pattern observed in plants with risky pollination syndromes.

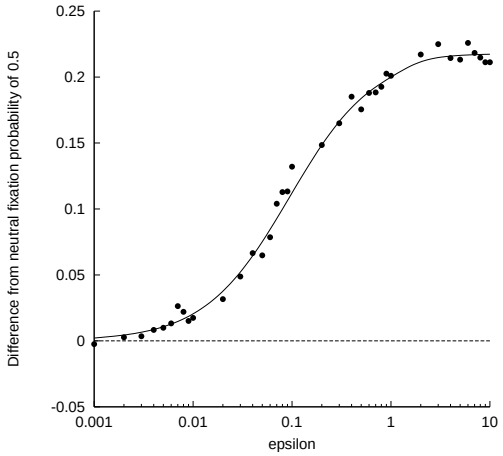

Figure 2: The curve represents the predicted fixation probability from the diffusion approximation while the dots represent observed fixation probability from simulations.

3 Current Research

Canalization and Genetic Networks

One of the central themes of organismal biology is the functional integration of the organism as a whole. Changes in one part or system of an organism are likely to have cascading effects through its other systems and impact seemingly unrelated functions. These cascading effects make the organism susceptible to perturbations in the environment or in the genome. On the other hand, regulatory interactions among different systemic elements allow the organism to lessen the impact of these cascading effects through buffering, feedback, and compensation. Genetic canalization can be defined as the evolutionary reduction in the effect of perturbations on the output of a genetic network.

I have developed a general framework for studying the strength of selection on canalization. The simple result is that selection on canalization is at most equal to the fitness load minus the per gene mutation rate ($L - \mu$). For load induced by mutation alone, canalization is only favored when the number of interacting genes is large, as is the case for heat shock proteins. However, the fitness load induced by both spatial and temporal variance can be large, providing ample selection for canalization even when only a few genes are involved. This implies that ecological processes play an important role in shaping genetic interactions and genomic structure.

Evolutionary Ecology of Virulence Evolution

Virulence evolution is an intrinsically complex problem because it includes several interacting partners, hierarchical spatial structure, and selection at multiple levels. The dynamics of virulence evolution cannot be modeled with standard evolutionarily stable strategy techniques because of both within host dynamics and the effects of timing in transmission. My recent work with Troy Day has created a general framework to study virulence dynamics that includes within host population genetics. We modeled both super-infection and within host mutation using the same technique and were able to show that within host mutation generally leads to an increase in virulence.

I am expanding on this theme to consider models that involve both host population dynamics and virulence evolution. Because the selective pressure on increasing virulence depends on host population size, changes in virulence caused by mutation and super-infection will lead to changes in host population size. This can lead to a kind of feedback loop, not unlike mutational meltdown, that causes an open ended increase in virulence. This theory could explain the existence of highly virulent pathogens that become locally extinct.

The Micro-Evolution of Regulatory Control

The regulatory control of genes involved in development has recently received increased attention due to experimental advances. One of the striking features is that positive regulation occurs at a broad level while inhibitory regulation is more important in determining where genes are expressed. I am currently developing models that include both population genetics and developmental dynamics to investigate the micro-evolution of regulatory control during development. My preliminary results suggest that positive regulation of spatial expression can only evolve by major changes, while inhibition control can evolve by small steps. This suggests that the present patterns of genetic control evolved because of historical constraints rather than due to the system level properties of control structures.

The Evolution of Gene Families

Most evolutionary models of gene duplication focus on events that occur after a duplication has become fixed in the population, and largely ignore the role of natural selection in setting up the conditions that are favorable to gene duplication. This has created a paradox where gene duplicates and gene families evolve more commonly than the neutral approach predicts. I have derived a population genetic model that include selection before, during, and after duplication to examine the role that natural selection plays in the evolution of gene families. My main result is that the divergence and specialization that creates gene families usually begins when the gene is present as a single copy. This divergence creates strong selection for duplication, in most cases leading to a smooth evolutionary birth of a gene family before duplication (**Figure 3**).

My results suggest that the creation of gene families is not caused by relaxed selection following duplication events, but rather by selection for genetic specialization within an organism. When divergence occurs at a single

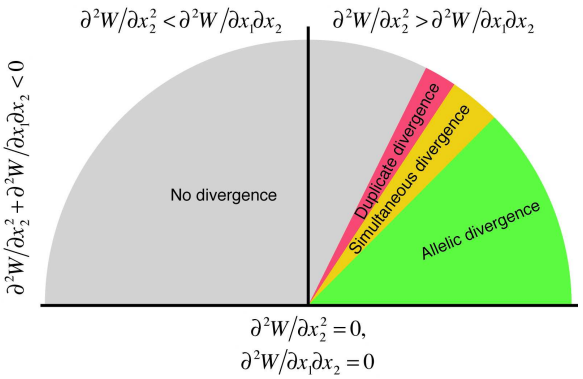

Figure 3: In the green region, selection for genetic specialization causes allelic divergence at a single locus. In the yellow region, divergence and duplication occur simultaneously. Only in the small red region does divergence occur after a gene duplication is fixed in the population.

locus, heterozygote advantage is created. Once heterozygote advantage has evolved, there is selection for gene duplication through a form of canalization. Because natural selection plays a prominent role in this theory it can help to explain why so many gene duplicates are maintained over evolutionary time.

4 Teaching Experience and Interests

Teaching Experience

I have gained valuable teaching experience over the past 10 years, ranging from guiding field courses to lecturing in the math department and from one-on-one tutoring to lecturing for large classes. My role has included that of guest lecturer, teaching assistant, and solo instructor.

As a graduate student I acted as a teaching assistant for a wide variety of classes, including ecology, mathematical biology, and several field courses. In addition to acting as a teaching assistant, I also had the opportunity to give lectures for many of these classes. As a lecturer, I discovered that one of the many hang-ups students face in introductory ecology is applying mathematical knowledge to specific problems. For example, students often have trouble understanding differential equations describing population growth because calculus courses typically only teach how to integrate functions only in abstract terms.

While completing my graduate studies, I tutored advanced placement high school students in physics, calculus, and biology. This brought home the conceptual difficulties inexperienced students have, difficulties that must be addressed to successfully teach ecology and evolutionary biology. Both at university and in preparatory programs, I found it helpful to provide physical analogies to processes students come into contact with in their everyday lives, such as driving a car or draining a bath tub. Once I translated the concepts into those terms, the students understand the concepts much more readily.

My first year in graduate school was also the first year that my advisor, Fred Adler, taught his course “Mathematics for Life Scientists.” I acted as TA during this first year, and later took part in researching and designing “problem sets” for his book *Modeling the Dynamics of Life*. As I worked through the problem sets with Dr. Adler, I learned how to break down even the most complex problems, like pressure regulation in the human eye, into manageable parts that students can work through. Acting as a TA for this class was a unique experience as it offers an alternate pathway for undergraduates to learn calculus: students learn calculus from examples in biology. When these students are later asked to apply calculus in biology classes, they are more prepared than students with a traditional calculus background. I anticipate applying these lessons to a modeling course for biologists at the undergraduate/graduate level.

Teaching Philosophy and Goals

As an instructor, my main goal is to clarify the conceptual underpinnings of biological phenomenon. While I find this type of teaching particularly effective in subjects that are primarily conceptual in nature, such as ecology and evolution, experimental design and statistics, and theoretical biology, I believe it is an excellent way to introduce students to biology.

Often, introductory courses give students the impression that biology is mostly a descriptive science, filled with lists of species, names of structures, and associations between molecules. While it is true that understanding biology requires an expanded vocabulary and concept base, the courses that most excite students are often inspired by current research that is focused on understanding patterns and phenomena at a conceptual level.

My main teaching method is this: I take a problem and break it down into components, describing each component as simply as possible. Once the students have a good grasp on the new information, I teach them to see the individual components as part of an interactive system. This method helps to guide students to a deeper understanding of biological processes as a whole and gives me the opportunity to introduce students at an early stage to the conceptual nature of biology. I can actually show them that working their way up the learning curve will indeed lead to more exciting studies.

I believe that avid interest on the part of both the instructor and the student is a necessary ingredient to successful learning. Like many instructors, I find much personal satisfaction in watching my students succeed in their studies. The students’ enthusiasm as they discover new ideas renews my own interest in the topic at hand and inevitably leads to an increase in my own knowledge.