

My research is in probability theory, applied to models from evolution and ecology. Such models arise in the exploration of how diversity is created, maintained, or lost in organismal systems, particularly through processes incorporating spatial and/or social structure. In these investigations I use a wide variety of tools from probability theory and stochastic processes to study related processes, especially the embedded genealogical processes, and to explore mathematical and statistical models that yield results of mathematical interest and are of practical use to biologists.

For instance, in work with Steve Evans, we have provided a complete description of the temporal dynamics of the time back to the most recent common ancestor for certain continuous-state branching processes, and are working towards a Ewens-type sampling formula. Continuous-state branching processes (CSBPs) are scaling limits of branching processes, model populations with few constraints on reproduction – for instance, a population undergoing range expansion, or the initial spread of an advantageous allele. CSBPs have been extensively studied and generalized in the probabilistic literature since their introduction by Feller in 1931, but they have received remarkably little attention in the mathematical population genetics literature, which has focused on the Wright-Fisher model. These investigations have led to a complete description of a much wider class of stochastic processes and identification of a family of semigroups that are possibly a stable analogue of the Bessel processes.

I am also investigating properties of the random network of biparental ancestry of sexual organisms. Recording the identity of both parents of each organism (rather than only the parent that contributed a particular gene) yields a super-genealogy that contains the genealogies of all inherited traits. Incorporation of a spatial component can yield important information about the spread of neutral genetic material. Despite widespread interest, there have so far been few serious studies on the subject. In work with Steve Evans, Montgomery Slatkin, and Erick Matsen, we are investigating the use dual processes to describe the dynamics, including both a smoothing process and a process on symmetric polynomials.

Another promising area of research is in the application of particle systems and Markov chains on finite graphs to models of selection and adaptive evolution. Martin Nowak introduced a framework he termed “evolutionary graph theory”, which seeks to characterize the effect of graph structure (representing spatial and/or social structure of stable populations) on the likelihood and speed of the spread of fitter types across the graph. We hope to give a local description of this effect in certain models of random graphs, and extend the analysis to more general fitness distributions, and have results in both those directions. This work is in collaboration with Shankar Bhamidi and Lee Worden.

Finally, it is commonly observed that different traits, particularly maternally versus biparentally inherited traits, introgress differently between hybridizing species. Various explanations for this are given in the literature. I am using numerical simulations of hybrid zone dynamics to investigate possible neutral causes, in collaboration with Abby Moore, Ricardo Pereira, Sean Schofield, and Sonal Singhal, advanced graduate students in various disciplines of biology. The goal of this project is not only to produce interesting numerical results, but also to illuminate promising directions for mathematical investigation.

In my future work, I will continue to investigate theoretical issues in these veins in close collaboration with biologists, and to use those investigations to produce and analyze interesting stochastic models as well as statistics, software, or hypotheses of practical use to biologists. I find that collaboration with scientists directly engaged in the study of natural systems is highly rewarding, as they can provide a vital perspective on the interesting or essential features of a system, and are familiar with the questions of practical import within their discipline. Questions from evolution and genetics have inspired a great deal of good mathematics, and I aim to continue that tradition.

The training that I bring to these problems includes a wide range of mathematical tools, including work on discrete diffusions, and study of coalescent theory, superprocesses, mixing of Markov chains, two-dimensional conformally invariant models from statistical physics, and partial differential equations. I have also consistently kept contact with the current trends in diverse areas of biology, as well as continuing my interests in statistical physics. Finally, and invaluablely, I am an instinctive naturalist, taking time to learn as much local natural history as I can to better observe the traces of the constantly evolving natural world that surrounds us.