Stochastic Methods in Evolutionary Biology

**Project Description:** Advanced mathematical modeling and computational methods are key elements in many research topics of current interest in evolutionary biology. Probabilistic and statistical approaches are essential, as the fundamental evolutionary forces in nature are regulated by random mechanisms which act over millions of years. Today we see the signatures of reproduction, mutation, selection, recombination, and migration as statistical patterns of variation in sequence and genome data.

Stochastic models have played an important role in population genetics for many decades. The Wright-Fisher reproduction model and diffusion processes obtained under scaling of time and population size provide a solid theoretical framework. More recently, methods based on random coalescent processes, which trace the evolutionary dynamics backwards in time towards a common ancestor in the “tree of life”, have proven to be extremely useful. In phylogenetics, branching processes and random tree models are being used to improve our understanding of how species are interrelated.

This project will contribute to resolving some of the many remaining challenges in evolutionary biology modeling and data analysis. An ongoing study focuses on time-dependent estimates of molecular evolutionary rates, and the implications of time-dependence for inferences of adaptive evolution. A second ongoing project is devoted to modeling trait-dependent evolution on a random species tree. A unifying aspect of the current projects is the mathematical study of $dN/dS$, the ratio of nonsynonymous and synonymous substitutions, a widely used measure in evolutionary genetic studies to investigate the extent to which selection modulates gene sequence evolution.

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Recent publications and preprints related to the project:


Figure 1: Sample illustration, Tahir et. al. Estimated phylogeny of Geraniaceae plant species family. Outcrossing species in blue, selfing species in red.