

Title: Bayesian Modeling of Evolutionary Dynamics

Speaker: Dr. Mandev Gill, Columbia University

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Abstract: Phylogenetic inference can enhance our understanding of the dynamics of viruses (and other measurably evolving populations) by providing a framework to elucidate the interaction of evolutionary, epidemiological, immunological, and ecological processes. We introduce new statistical tools based on the foundation of Bayesian phylogenetics to help realize this potential. First, we focus on the effective population size, an abstract quantity that characterizes a population's genetic diversity and is of fundamental importance in population genetics, conservation biology, and infectious disease epidemiology. We present a flexible nonparametric Bayesian framework to infer the effective population size as a function of time directly from molecular sequence data. Our model is based on the coalescent, a stochastic process that relates phylogenetic trees to population dynamics. Notably, our framework incorporates data from multiple genetic loci to achieve improved inference of population dynamics. A central goal in reconstructing the effective population size is to ascertain its association with potential driving factors and epidemiological indices. To this end, we discuss an extension of our effective population size inference model that incorporates external time-varying covariates. Integrating covariates into the framework enables modeling of associations between the effective population size and related factors while accounting for uncertainty in population histories that is ignored by post hoc analyses. Furthermore, it can yield improved estimates of population dynamics. Finally, we turn to phylogenetic trait evolution. Understanding the processes that give rise to quantitative measurements associated with molecular sequence data is crucial in comparative studies of phenotypic traits as well as in phylogeographic analyses that reconstruct the spatiotemporal spread of viruses. A popular, yet restrictive approach is to model such processes as standard Brownian diffusion acting on a phylogenetic tree. We relax a major restriction by introducing a nontrivial estimable mean into the process. Importantly, we implement a relaxed directional random walk model that accommodates variation of directional trends along the branches of a phylogenetic tree while preserving model identifiability. This flexibility allows us to uncover a clearer, more detailed picture of trait evolution dynamics.