
BEN BOLKER, McMaster University

Stochastic mutation-selection-drift models of parasite virulence evolution

Mathematical models of parasite evolution most often use a deterministic framework, where the only role of stochasticity is to provide raw material for adaptation via mutation. In an attempt to consider the diversity of parasite virulence from a broad perspective, and in particular to understand the broad range of virulence and the large number of low-virulence parasites found in natural communities, we explore a range of stochastic, discrete-population models. Our models incorporate mutation, drift, and selection; each distinct parasite strain differs in transmission, host clearance rate/virulence, or both. In the absence of a virulence-transmission tradeoff, we find as expected that parasites are strongly selected for increased transmission and decreased virulence, limited only by the effects of mutation and drift; smaller host populations have lower-transmission/lower-virulence parasites. We also observe a bimodal distribution of outcomes depending on the mean and standard deviation of the mutational spectrum.