

# Abstract

This work examines the dynamics of a multitype Moran model, which sustains a constant population size over time, with a specific focus on the Gerrish-Lenski mutation regime. In this regime, beneficial mutations occur at a rate of  $\frac{\lambda}{\log N}$ . Typically, there is a finite number of contending mutations alongside a single resident type and these mutations compete for fixation, a phenomenon known as clonal interference.

The primary objective is to analytically study and simulate a multitype Moran model with strong selection that encompasses these interactions. We introduce and define the Poissonian Interacting Trajectories (PIT) and we will show that the PIT arises as the scaling limit of the rescaled logarithmic sizes of the contending mutant families and also that this is only driven by a Poisson point process. The thesis delves into the mathematical foundations necessary to determine the speed of adaptation, examining the conditions required for its existence and the impact of various fitness distributions. Moreover, we discuss the Gerrish-Lenski heuristic as a method to estimate the speed of adaptation. The thesis also addresses the challenges encountered during the simulation of these models using the IBMPopSim package, providing practical insights into the computational costs and implementation difficulties.