Abstract

Through this work, we aim to characterize and explore the fixation probability (the probability that a mutant attains a 100 percent frequency in the given population) of a mutant which has been placed in a population which evolves following a stochastic process where birth and death occur independently with different rates. The population follows regulated growth where the per capita growth rate decreases as the population approaches a stable equilibrium.

The simulation work is done by implementing a Gillespie algorithm, where we have an initial population of 90 residents and one mutant, and time steps are chosen according to a Poisson process. At each time step, one of the four possible 'reactions' (resident birth, resident death, mutant birth and mutant death) takes place whose probabilities of occurrence have been predefined as parameters in the simulation. The code is run for a time length of 100 units, and the trajectory is simulated for 1000 iterations.

We look at the number of trajectories in which the mutant survives at the end of a time duration whose length is 100 units. This is our estimate for the fixation probability of the mutant for that set of parameters. Then this value is plotted for different values of the mutant birth rate and we find that the analytical prediction derived by Marrec et. al. (2020) which assumes a constant population size does a good job at predicting the fixation probability for this simulation.

Next we look at the predictions while changing the function that regulates the population size. We look at four different functions, namely logistic, Richards, Blumberg and Gompertz. We add correction factors to our predictions to account for sources of error and make a better match between the simulated data and the analytical predictions.

We also note that the predictions consistently underestimate fixation probability at small selection advantages. We delve into the reasons why this could be so and look for ways to incorporate this into our predictions. Lastly we look at a scenario when the selection is applied to death rates rather than birth rates and once again compare it to the generalized analytical predictions. Here again, we look at lacunae in our predictions, reasons behind them and ways to correct them.