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Deterministic and Stochastic Density-Dependent Population Process in Chemostat Model

The well-known mathematical model of a chemostat is an explicit resource model to analyse the competitive density-dependent population process. It has been given broad applications in microbiology. In our model, a chemostat model with Monod kinetics, two species and single limiting resource is given. These species are defined as quasi-neutral when they require the same resource concentration at equilibrium. The deterministic model is used to derive a stochastic model by assuming the birth and deaths follow a Poisson process. With the consideration of infinity volume V(in units of volume of cell), we pass the discrete model to a continuous limit. Several limit theorems are presented in our model to approximate and characterize the Markov process.

We will present the deterministic model approximated by the Law of Large Numbers, and analyse the stability of its equilibrium state. After the process approaches the neighbourhood of the equilibrium state, it will behave approximately as a diffusion process along with the equilibrium state. With the help of Central Limited Theorem, Ito's formula and Thomas Kurtz's weak convergence theorem, when the initial condition is in longer-scale, rigorous proofs will be presented for the diffusion approximation maps onto deterministic trajectory. To get this diffusion approximation, the derivatives of projection map will be calculated, which part is based on Dr. Todd Parsons's work.

The calculation of Fixation probability and extinction times is a consequence of the above diffusion approximation result, driven by the formulation of infinitesimal generator A of the diffusion process, with the form of $Af(p) = b(p)\frac{df}{dp} + \frac{1}{2}a(p)\frac{d^2f}{dp^2}$ and initial relative abundance of one species, p. We will present the results for the fixation of this species, mean first absorption time, and the expected time to fixation in the function set of f.

Lastly, we verify our approximations by comparison with exact numerical computations, and we investigate the accuracy of our approximations at small population size over a range of parameters.