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Evolutionary Stability of Bacterial Persister Cells

We model the switching process of bacteria between antibiotic dormant features and normal active replication using an integro-reaction-diffusion-advection partial differential equation (PDEs). The PDE captures the impacts of epigenetic inheritance of metabolic state by implementing a non-local term that models a birth jump process. We prove the well-posedness of the non-local PDE model followed by the corresponding stability analysis of the positive steady-state solutions. Of primary interest is an extension of the model to a wider scenario of biological evolution by examining the evolutionarily stable strategies (ESSs) of persister cells. The idea is that genetic mutations will occasionally occur, and these mutations can alter any of the parameters describing the persister cell dynamics. As a first step we prove that, in a finite dimensional version of the model, the ESS strain is one that optimizes resource consumption irrespective of its pattern of dormancy. The next step will be to apply semigroup methods to the infinite dimensional system.