Stochastic multi-scale models of cell populations

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Abstract.

Stochastic multi-scale models of cell population: The remit of population dynamics is the study of how individuals of different types interact, compete for existing resources and evolve to adapt to changing conditions. Many biomedical problems t within this framework: The competition between normal and malignant cells in cancer for space and resources; The interaction between the cells of the immune system and infected cells in viral infections; Evolution of drug resistance. The aim of this work is to illustrate how concepts and techniques from mathematical population dynamics can be used to address and shed some light on a number of issues relevant in different biomedical contexts

In order to formulate our stochastic model of the intracellular scale, in particular, the coupling between extra-cellular oxygen levels and progression through the cell-cycle,we will re-formulate our model as a Markov process in terms of a Master Equation. The resulting model, a continuity equation for a multi-dimensional probability density, will be analysed using the asymptotic methods similar to those used by Maier & Stein, i.e. large N, WKB asymptotics. An alternative approach is to treat the progression through the cell-cycle and other intracellular processes as first-passage problems.

This (sub-)model will provide the proliferation rate of the cells as a function of the extracellular oxygen. This information will then be used within the cellular scale as a parameter (i.e. the oxygen-dependent birth rate) in the Master Equation describing the dynamics of the cellular phase.

A mathematical model of a population composed by different types of individuals keeps track of the evolution in time and space of the number or density of each one of the species as a function of a number of parameters: birth and death rates, metabolic rates, mutation rates, etc.