Modelling approach for cells in a chemostat

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Abstract

The first difficulty for the modelling of biological problems is in choosing the type of model which is appropriate for the problem (stochastic or determinisic model, discreet or continuous model,...). In this talk, I will present a variety of models for cells modelling and the links between them.

At a microscopic scale, that is the scale of individuals, it is more judicious to describe the population by an individual based model (IBM). These models describe the behavior of each individual and can represent the stochasticity of the population. It is also a good way to discuss with biologists; in fact these models are constructed describing the biological mechanisms by basic rules before the description by mathematical equations.
When the number of individuals in the population is very large, these models can however be very costly to compute. It is then important to link IBMs with other models. Under suitable assumptions, we can obtain the convergence of IBMs, in large population size, toward deterministic partial differential equations (PDEs) models, which correspond to the macroscopic model associated to the microscopic one. At an intermediate scale we can also derive stochastic PDEs by central limit theorems. These models are easier to compute than IBM, but still represent stochasticity of the population.

I will present the links between these models through convergence theorems for growth-fragmentation chemostat models and I will propose a modelling approach based on these mathematical results as well as numerical simulations.
Finally, I will present how to derive results on the PDE, like variations of the main eigenvalue w.r.t. model parameters, through probabilistic methods using the stochastic microscopic interpretation. I will apply these results to an adaptive dynamics model of chemostat.

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