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A constrained multiscale approach to modelling biochemical systems

It is well known that intrinsic noise can play a significant role in biological systems. Stochastic descriptions of these types of systems give far more accurate representations of the true dynamics. Exact methods for the stochastic simulation of these systems exist, but can be very computationally expensive, particularly in the presence of multiple timescales. Many different methods exist for reducing the system to one which is only concerned with the slowly evolving variables.

In this talk we introduce the Conditional SSA (CSSA), a method for sampling directly from the conditional distribution on the fast variables, given a value for the slow variables. Using this, we go on to describe the Constrained Multiscale Algorithm (CMA), which uses simulations of the CSSA to estimate the drift and diffusion terms of the effective dynamics of the slow variables. We show how this approach can give accurate estimates for quantities of interest, such as average period of oscillation in biological processes. This is joint work with Radek Erban and Kostas Zygalakis (Oxford), and Ioannis Kevrekidis (Princeton).