Product form stationary distributions of stochastic reaction networks with non-mass action kinetics, and application to constrained averaging of multiscale systems

Simon Cotter, University of Manchester

In many applications in cell biology, the inherent underlying stochasticity and discrete nature of individual reactions can play a very important part in the dynamics. The stochastic simulation algorithm has been around since the 1970s, which allows us to simulate trajectories from these systems, by simulating in turn each reaction, giving us a Markov jump process. However, in multiscale systems, where there are some reactions which are occurring many times on a timescale for which others are unlikely to happen at all, this approach can be computationally intractable. Several approaches exist for the efficient approximation of the dynamics of the "slow" reactions, some of which rely on the "quasi-steady state assumption" (QSSA). In this talk, we will present the Constrained Multiscale Algorithm. This method requires us to find the stationary distribution of stochastic reaction network with non-mass action kinetics in order to estimate the effective slow rates in the system. We will present a new result stating the analytical form of these distributions, which allow us to use these highly accurate multiscale approximations without the need for costly stochastic simulations or approximations. We will then present some results comparing the resulting approximations of the effective dynamics with those arising from the QSSA.