Multiscale Methods for Modelling Intracellular Processes

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I will discuss mathematical and computational methods for spatio-temporal modelling in molecular and cell biology, including all-atom and coarse-grained molecular dynamics (MD), Brownian dynamics (BD), stochastic reaction-diffusion models and macroscopic mean-field equations. Microscopic (BD, MD) models are based on the simulation of trajectories of individual molecules and their localized interactions (for example, reactions). Mesoscopic (lattice-based) stochastic reaction-diffusion approaches divide the computational domain into a finite number of compartments and simulate the time evolution of the numbers of molecules in each compartment, while macroscopic models are often written in terms of mean-field reaction-diffusion partial differential equations for spatially varying concentrations.

In the first part of my talk, I will discuss connections between these different modelling frameworks. I will consider chemical reactions both at a surface and in the bulk, summarizing our results reported in [1, 2, 3, 4]. In the second part of my talk, I will discuss the development, analysis and applications of multiscale methods for spatio-temporal modelling of intracellular processes, which use (detailed) BD or MD simulations in localized regions of particular interest (in which accuracy and microscopic details are important) and a (less-detailed) coarser model in other regions in which accuracy may be traded for simulation efficiency [5, 6, 7]. I will discuss error analysis and convergence properties of the developed multiscale methods [8, 9], their software implementation [10] and applications of these multiscale methodologies to modelling of intracellular calcium dynamics [11], actin dynamics [12, 13] and DNA dynamics [14]. I will also discuss the development of multiscale methods which couple MD and coarser stochastic models in the same dynamic simulation [15, 16].

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