

Asymptotic and Multiscale Analysis of Stochastic Biological Systems

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Title: Large deviations for fully-coupled switching diffusion systems

Abstract: We consider a multiscale system where the dynamics of a slow-moving diffusion is modulated by a rapidly oscillating finite state space pure jump Markov process. Such systems arise naturally in many contexts, including cellular processes; for example in genetic networks, protein production is controlled by genes rapidly switching between active and inactive states. Typically, the fast process reaches its quasi-equilibrium state at much shorter time scales. This allows approximation of the trajectories of the slow moving diffusion by averaging out its coefficients with respect to the local equilibrium distribution of the fast component. This is known as averaging principle, which can yield significant reduction in model complexity. The objective of this talk is to understand deviation of the system from the limiting averaged one through large deviation analysis, which, in particular, sheds light on quality of such model simplifications.

John Fricks (Arizona State University, US)

Title: Integrating nanoscale kinetics into motor-cargo transport systems using semi-Markov processes

Abstract: Intracellular transport is driven by molecular motors, typically kinesin and dynein, which convert ATP into mechanical forces, stepping along microtubules. Multiple motors are attached to a single cargo and interact with one another through this attachment. In this talk, a semi-Markov framework will be presented as a way to integrate the nanoscale kinetics of the motors into a stochastic model of motor-driven cargo. Understanding recent experiments of artificial cargos with a fixed number of kinesin and/or dynein motors will be a particular focus for this presentation.

Daniel Linder (Augusta University, US)

Title: Statistical inference in stochastic reaction networks

Abstract: Statistical inference, or model calibration, is a notoriously challenging problem of great value. In this talk I will present work we have done in terms of parameter estimation and network learning from data in these models. I will also talk about recent work we have done that is closely related to likelihood free MCMC, but which is more efficient in terms of information content and computational complexity than ad hoc ABC methods. I will wrap up with an example of the methodologies presented on historical plague outbreak data at Eyam, England 1665-1666.

Wasiur R. KhudaBukhsh (The Ohio State University, US)

Title: Survival dynamical systems for the population-level analysis of epidemics

Abstract: Motivated by the classical Susceptible-Infected-Recovered (SIR) epidemic models proposed by Kermack and Mckendrick, we consider a class of stochastic compartmental dynamical systems with a notion of partial ordering among the compartments. We call such systems uni-directional Mass Transfer Models (MTMs). We show that there is a natural way of interpreting a uni-directional MTM as a Survival Dynamical System (SDS) that is described in terms of survival functions instead of population counts. This SDS interpretation allows us to employ tools from survival analysis to address various issues with data collection and statistical inference of unidirectional MTMs. In particular, we propose and numerically validate a statistical inference procedure based on SDS-likelihoods. We use the SIR model as a running example to illustrate the ideas. (Joint work with Boseung Choi, Eben Kenah, and Gzregorz Rempala)