Stochastic Modeling of Chemical Reactions in Biology

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Abstract: Inherent fluctuations play a crucial role in biological and biophysical systems, particularly when the system involves species with low copy numbers. In this talk, I will present my recent work on the stochastic modeling of chemical reaction networks. The first part of the talk will focus on enzyme kinetics, where we use a continuous-time Markov chain model to describe the temporal evolution of system dynamics across different time scales. We apply a multiscale approximation method to simplify the model while preserving its key features.
In the second part, I will discuss two models that exhibit switching behavior, where molecular copy numbers oscillate between two or more distinct states. While both models show switching among multiple states, their underlying mechanisms differ significantly. By employing stochastic simulations and classification techniques, we analyze both models and compare their dynamics to assess whether they are distinguishable from one another.