An introduction to stochastic reaction networks

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Abstract: Models of cellular processes are often represented with networks that describe the interactions between the constituent molecules. If the counts of the molecular “species" are low, then these systems are most often modeled stochastically using a continuous-time Markov chain. These stochastic reaction networks can be quite complex. However, hidden within the complexity there are sometimes underlying structures that, if properly quantified, give great insight into the dynamical or stationary behavior of the system. In this talk, I will begin with an introduction to the basic mathematical model and then provide a broad overview of research in this direction. I will detail some of the main results in the field, and I will present some open problems that people are actively working on. I plan to make this talk accessible to graduate students, though having some knowledge of continuous-time Markov chains would be helpful.

Speaker

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