Colloquium

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Analysis and Simulation of Biochemical Reaction Networks

Abstract: Intracellular processes can be mapped to biochemical reaction networks using experimental data. In principle, the classical chemical master equation (CME) provides a framework for mathematical modelling of reaction networks. However, a great challenge we meet is how we analyze and simulate this equation. The famous Gillespie stiochastic simulation algorithm solves the computation issue of a single stochastic trajectory but not the joint probability distribution. The analysis and simulation of the CME is a long-term standing question. In this talk, I will introduce two novel formulations for the CME, which can be applied to the analysis and simulation of any biochemical reaction networks. Using these formulations, one can not only find analytical solution to the CME but also develop highly efficient algorithms.