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Parameter Inference in Biochemical Reaction Networks

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Systems biologists seek to understand the higher-level organizational properties that a proposed system exhibits from the interactions of its many lower level components. It is then typically beneficial to learn, in a statistical sense, the nature of these interactions from experimental data; this is sometimes called reverse engineering. In this talk, I will discuss some methods for learning the kinetic parameters from trajectories of certain stochastic systems, measured at discrete time points. I will also discuss estimating the system topology, or network structure, with an algebraic statistical technique. Finally, I will discuss some ongoing work aimed at improving both parameter estimation and system topology estimation.