ACMS Applied Math Seminar

Elizabeth Wolf

Thursday, October 1st
154 Hurley Hall
3:30- 4:30 PM

Computational Methods for Parameter Sensitivities of Stochastic Chemical Reaction Networks

Stochastic models are commonly used to simulate and analyze biochemical networks, in particular when the abundances of the constituent molecules are small and ordinary differential equations cease to provide a good description of system behavior. Example networks include the transcription and translation of DNA, and genetic switching. A common modeling choice is to use a continuous time Markov chain (CTMC). As solving analytically for the expectations of model quantities is usually intractable or impossible, one typically uses simulation methods to generate sample paths for analysis.

Even when biochemical knowledge suggests an appropriate model, parameter values are typically unknown and must be estimated experimentally. Therefore, parameter sensitivity estimation is a valuable tool as it provides a quantitative method for understanding how perturbations in model parameters affect different response functions of interest. We will discuss the three main classes of procedures for sensitivity estimation in this setting, and present a hybrid method that combines elements from each. We will also demonstrate that the hybrid method is quite efficient, particularly if one wishes to estimate the full gradient of parametric sensitivities.