

Advanced Stochastic Numerical Methods for Systems and Synthetic Biology

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Abstract:

Using complementary approaches, systems and synthetic biology study how interacting genetic components can work together to create programmatic dynamical behaviors, such as pattern formation, temporal ordering of gene expression, and environmentally responsive systems. In synthetic biology, the goal is to engineer new dynamical behaviors, such as bacterial edge detection or tumor-invading bacteria, by combining both natural and synthetic genetic parts together. In order to reliably engineer these systems, we need a quantitative understanding of the interactions between the genetic parts and numerical methods that determine the best ways to combine them together.

In this talk, we review our recent work on hybrid and approximate stochastic numerical methods for the stochastic simulation of biochemical networks. Specifically, we will discuss describing stochastic chemical kinetic systems as hybrid jump/continuous Markov processes and applying probabilistic steady-state approximations to arbitrary reaction networks. These methods can determine the kinetic or thermodynamic parameters of a collection of parts that can yield a desired behavior, such as oscillations or bistability. However, to connect these parameters to an actual DNA sequence, additional numerical methods are required. We briefly discuss an accurate sequence-dependent method of estimating the efficiency of bacterial ribosome binding sites using a thermodynamic model, which can be used to optimize the flux of a biosynthetic pathway or to tune a genetic circuit for optimal input-output behavior.

About the Speaker:

Howard Salis received his doctorate in Chemical Engineering from the University of Minnesota in 2007. He is currently a postdoctoral fellow at UC San Francisco, where he uses a combined experimental-computational approach to rationally engineering biological systems.
