Stochastic modelling and Bayesian inference for biochemical network dynamics

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Abstract

This talk will provide an overview of computationally intensive methods for stochastic modelling and Bayesian inference for problems in computational systems biology. Particular emphasis will be placed on the problem of inferring the rate constants of mechanistic stochastic biochemical network models using high-resolution time course data, such as that obtained from single-cell fluorescence microscopy studies. The computational difficulties associated with "exact" methods make approximate techniques attractive. There are many possible approaches to approximation, including methods based on diffusion approximations, and methods exploiting stochastic model "emulators". Other important inferential problems will also be considered, such as inferring dynamic network connectivity from time course microarray data.