

Bayesian inference for stochastic kinetic models via a diffusion approximation

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Abstract

In order to perform analysis on a stochastic biochemical network model, it is essential that each network parameter (rate constant) is obtained. Such inferences are typically required to allow predictive in silico experiments. One approach is to replace the underlying model by a diffusion approximation so that a noise term represents intrinsic stochastic behaviour and the model is identified using discrete-time (and often incomplete) data that is subject to error. Unfortunately, likelihood based inference can be problematic as closed form transition densities of nonlinear diffusions are rarely available. A widely used solution involves the introduction of latent data points between every pair of observations to allow an Euler-Maruyama approximation of the true transition densities to become accurate. We propose some efficient Markov chain Monte Carlo (MCMC) methods that can then be used to sample the posterior distribution of latent data and kinetic rate constants.