Bayesian Inference for Systems Biological Models via a Diffusion Approximation

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Abstract

As post-genomic biology becomes more predictive, the ability to infer rate parameters (known as reverse-engineering) of biochemical networks will become increasingly important. One approach is to replace the underlying model by a diffusion approximation 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. Markov chain Monte Carlo (MCMC) methods can then be used to sample the posterior distribution of latent data and model parameters; however, naive schemes suffer from a mixing problem that worsens with the degree of augmentation. A reparameterisation is therefore implemented to overcome this difficulty and the methodology is applied to a simple prokaryotic auto-regulatory gene network.