

MCMC Sampling for Diffusion Processes

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Abstract

It is well known that likelihood inference for arbitrary nonlinear diffusion processes observed at discrete times is problematic since closed form transition densities are rarely available. One widely used solution adopts the treatment of Pedersen (1995) and 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. In recent literature, Markov chain Monte Carlo (MCMC) methods have been used to sample the posterior distribution of latent data and model parameters; however, naive schemes suffer from a mixing problem, highlighted by Roberts and Stramer (2001), that worsens with the degree of augmentation. We will consider some recently developed MCMC schemes that are not adversely affected by the amount of augmentation. The methodology will be illustrated by estimating parameters governing the diffusion approximations of some interesting systems biological models.

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References

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