

Posterior Inference over Nonlinear Differential Equations via Hamiltonian Monte Carlo on the Riemann Manifold with Application to Biochemical System Modeling

M.A. Girolami
University of Glasgow

Abstract

Formally characterising uncertainty in systems of differential equations within a statistical inferential framework is something which mathematicians and statisticians have only very recently started to consider. There is great motivation within the area of Computational Systems Biology to fully define and propagate all sources of uncertainty in model-based reasoning regarding the biochemical mechanisms initiating and regulating fundamental biological processes. The Bayesian methodology provides one such inferential framework, however, whilst beautifully elegant in principle the computational statistical challenges associated with its practical instantiation are formidable. This talk presents two contributions in addressing such challenges, the first presents a statistically and computationally efficient Markov Chain Monte Carlo Sampler for systems of nonlinear differential equations by the introduction of auxiliary functional processes into the overall model. The second contribution defines a non-separable Hamiltonian defined on the Riemann manifold and an explicit time reversible symplectic integrator is developed which provides a means of performing Hybrid Monte Carlo on the manifold defined by the nonlinear dynamic system described by the system of equations. Convergence to the stationary distribution in cases of, for example, time-delayed differential equations describing mRNA translocation from nucleus to cytosol is improved four-hundred fold, additional biochemical pathway examples will be presented.

Professor M.A. Girolami F.I.E.T.
EPSRC Advanced Research Fellow
Department of Computing Science
Sir Alwyn Williams Building, Room 302
University of Glasgow
Glasgow, G12 8QQ
Scotland UK