A comparison of Bayesian inference techniques applied to systems biology models

Ian Vernon[1*], Michael Goldstein[1], & Darren J. Wilkinson[2]

[1] Department of Mathematical Sciences, University of Durham
[2] School of Mathematics & Statistics, Newcastle University

Traditionally, chemical reaction networks have been modelled by sets of ODE's. However, for intracellular reaction networks, especially those concerning gene transcription, the discrete number of molecules involved and the inherently stochastic behaviour of the network both become important. These networks can be accurately modelled by stochastic processes (namely continuous-time Markov processes), that possess many unknown rate constants representing all the various reactions involved.

The goal of this work is to perform Bayesian inference on these rate parameters using the available data which is often incomplete, measured infrequently and has substantial measurement error. We apply a new approach to the problem of inference based on Bayes Linear emulation methods, and compare this with various MCMC schemes. Our approach treats the simulation of the network as a Stochastic Computer Model and utilises various techniques for callibrating computer models when the input parameter space (the space of rate constants) is large.