Abstract:

Many processes in cell biology process information and enact responses by modulating the concentrations of biological molecules. Such modulations serve functions ranging from encoding and transmitting information about external stimuli to regulating internal metabolic states. To understand how such processes operate requires gaining insights into the basic mechanisms by which biochemical species interact and respond to internal and external perturbations. One approach is to model the biochemical species concentrations through the van Kampen Linear Noise Equations, which account for the change in biochemical concentrations from reactions and account for fluctuations in concentrations. For many systems, the Linear Noise Equations exhibit dynamical stiffness as a consequence of the chemical reactions occurring at significantly different rates. This presents challenges in the analysis of the kinetics and in performing efficient numerical simulations. To deal with this source of dynamical stiffness and to obtain reduced models more amenable to analysis, we present a systematic procedure for obtaining effective stochastic dynamics for the chemical species having relatively slow characteristic time scales while eliminating representations of the chemical species having relatively fast characteristic time scales. To demonstrate the applicability of this multiscale technique in the context of Linear Noise Equations, the reduction is applied to models of gene regulatory networks. Results are presented which compare numerical results for the full system to the reduced descriptions. The presented stochastic reduction procedures provide a systematic way to obtain reduced approximations of Linear Noise Equations.