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Simplifying Mathematical Models of Biochemical Systems

Modeling the intermolecular reactions taking place in a single cell is a key problem in computational biology. Biochemical reaction systems usually involve species in both low and large molecular numbers. Therefore, the noise due to the presence of small population numbers may be significant and thus stochastic models are required for an accurate description of the system dynamics. Often, the biochemical reaction systems arising in applications consist of many species interacting through many reaction channels. Also, the dynamics of such systems is typically non-linear and presents multiple time-scales. Thus, the stochastic mathematical models of biochemical systems can be quite complex and thus difficult to analyze. In this talk we present a method to reduce a stochastic continuous model of biochemical systems, the Chemical Langevin Equation, while preserving the overall behavior. The method is tested on several examples of practical interest. (Joint work with my student, Samaneh Gholami)