Modern Numerical Methods for Continuous Time Markov Chains of High-Dimensions

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The aim of the talk is to present modern methods for computing large Continuous Time Markov Chains (CTMC) which arise in Biology. These modern methods have theoretically and experimentally overcome key obstacles of dimension and computation inherent in high dimensional CTMC [1,2,3].

Continuous Time Markov Chains (CTMC) are a key tool in describing discretely interacting biological systems. Biological processes such as RNA transcription, signalling cascades and catalysis are key examples where the system is being driven by independent inhomogeneous Poisson processes. Researchers have used realisation based simulation methods, such as the Stochastic Simulation Algorithm (SSA), for in-silico observations of these systems. Even though simulations are cheap and quick to implement, it has been shown that they do not always guarantee the capture of critical features such as bi-modality, without multiple realisations. In this talk, we will be presenting the Optimal Finite State Projection method, proposed by Sunkara and Hegland [1] and the Hybrid method proposed by Jahnke and Schütte independently [2,3]. For the two methods, we will discuss their respective error bounds and computation times for particular examples.

References

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