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Efficient adaptive uniformisation for the analysis of biochemical reaction networks

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A common modelling technique to include stochastic effects in biochemical reaction networks is the use of discrete-state continuous time Markov chains. Analytic results for the resulting systems are rare and one often has to rely on stochastic simulation approaches to quantitatively probe their dynamics. Many conventional simulation methods, however, become prohibitively slow if the system is characterised by multiple different time scales, i.e. for stiff systems.

In this contribution we consider the application of adaptive uniformisation techniques which can significantly reduce the number of simulation trajectories needed to estimate summary statistics of the reaction network. By making the uniformisation rate adaptive, rather than fixed, this method can efficiently deal with multiple scales in the dynamics of reaction networks.

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