A PROJECTION METHOD FOR SOLVING THE CHEMICAL MASTER EQUATION

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Abstract. The mathematical framework of the chemical master equation (CME) uses a Markov chain to model the biochemical reactions that are taking place within a biological cell. Computing the probability distribution of this Markov chain allows us to track the composition of molecules inside the cell over time, with important practical applications in a number of areas such as molecular biology or medicine. However the CME is typically difficult to solve, since the state space involved can be very large or even countably infinite. This study investigates a numerical method based on the stochastic simulation algorithm (SSA) to address this challenge. Supported by NSF Grant 1320849

Extended Abstract

Models of cellular processes promise great benefits in important fields such as molecular biology or medicine. Within a cell , some key regulatory molecules exist only in small numbers, in which case it becomes appropriate to formulate the models in a discrete and stochastic setting. The mathematical framework that underpins this is a continuous-time, discrete-state, Markov process, and computing its probability distribution amounts to solving the chemical master equation (CME).

While promising many insights, the CME is difficult to solve, especially for large models. Consequently, researchers often resort to simulating trajectories, using most notably Gillespie's stochastic simulation algorithm (SSA) [2] or its improved variants, e.g., [1]. A direct approach to the CME was the catalyst of the finite state projection (FSP) algorithm of Munsky and Khammash [3] that truncated the state space to a more tractable size. The efficiency of the method depends on how well one selects the truncated state space.

We prototype a SSA-driven reduction that builds on the principle that the CME aims at computing a probability vector $\boldsymbol{p} = (p_1, \ldots, p_n)^T \in [0,1]^n$, with components that sum to one, $\sum_{i=1}^{n} p_i = 1$. For very large problems, $n \gg 1$, the probability sum condition implies that some of the components must necessarily be zero or negligible, Dropping those negligible components allows us to reduce the size dramatically. We tested the SSA-driven projection which is a central element, and early results are quite promising.

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References

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