

Abstract Submitted
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A stochastic moment based approach of the biochemical reaction networks MICHAEL VLYSIDIS, YIANNIS KAZNESSIS, Univ of Minnesota - Twin Cities — Biological systems are wonderfully complex. In order to gain a better understanding on how the complexity dictates the biological functions, it is important to investigate the underlying dynamic interactions of the biomolecular components. These interactions are governed by random events and thus stochastic models are needed to gain fundamental insight. However, stochastic models tend to be more difficult to fit to experimental data and are computationally demanding. We have developed a closure scheme method that calculates the stationary probability distribution of stochastic biochemical reaction networks. The method postulates that only a finite number of probability moments is necessary to capture all of the system's information, which can be achieved by maximizing the information entropy of the system. We attempt to provide useful information about the mesoscopic behavior of biochemical reaction networks with the help of the aforementioned closure scheme method. For our analysis, we study the Schlögl model reaction network, a simple single component system that can exhibit bistability. Finally, we wonder whether the maximization of entropy can be a general criterion for establishing non-equilibrium steady state of biochemical reacting systems.

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