

Abstract Submitted
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Control of Stochastic Master Equation Models of Genetic Regulatory Networks by Approximating Their Average Behavior MEHMET UMUT CAGLAR, RANADIP PAL, Texas Tech — The central dogma of molecular biology states that “information cannot be transferred back from protein to either protein or nucleic acid.” However, this assumption is not exactly correct in most of the cases. There are a lot of feedback loops and interactions between different levels of systems. These types of interactions are hard to analyze due to the lack of data in the cellular level and probabilistic nature of interactions. Probabilistic models like Stochastic Master Equation (SME) or deterministic models like differential equations (DE) can be used to analyze these types of interactions. SME models based on chemical master equation (CME) can provide detailed representation of genetic regulatory system, but their use is restricted by the large data requirements and computational costs of calculations. The differential equations models on the other hand, have low calculation costs and much more adequate to generate control procedures on the system; but they are not adequate to investigate the probabilistic nature of interactions. In this work the success of the mapping between SME and DE is analyzed, and the success of a control policy generated by DE model with respect to SME model is examined. Index Terms— Stochastic Master Equation models, Differential Equation Models, Control Policy Design, Systems biology

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