

Abstract Submitted  
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**Comparison of Control Approaches in Genetic Regulatory Networks by Using Stochastic Master Equation Models, Probabilistic Boolean Network Models and Differential Equation Models and Estimated Error Analyzes** MEHMET UMUT CAGLAR, RANADIP PAL, Texas Tech University — 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 cell level data and probabilistic - nonlinear nature of interactions. Several models widely used to analyze and simulate these types of nonlinear interactions. Stochastic Master Equation (SME) models give probabilistic nature of the interactions in a detailed manner, with a high calculation cost. On the other hand Probabilistic Boolean Network (PBN) models give a coarse scale picture of the stochastic processes, with a less calculation cost. Differential Equation (DE) models give the time evolution of mean values of processes in a highly cost effective way. The understanding of the relations between the predictions of these models is important to understand the reliability of the simulations of genetic regulatory networks. In this work the success of the mapping between SME, PBN and DE models is analyzed and the accuracy and affectivity of the control policies generated by using PBN and DE models is compared.

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