

Abstract Submitted
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Exploring information transmission in gene networks using stochastic simulation and machine learning¹ KYEMYUNG PARK², Maryland Biophysics Program, University of Maryland - College Park, THORSTEN PRÜSTEL, YONG LU, MANIKANDAN NARAYANAN, ANDREW MARTINS, JOHN TSANG, Laboratory of Systems Biology, National Institute of Allergy and Infectious Diseases, National Institutes of Health — How gene regulatory networks operate robustly despite environmental fluctuations and biochemical noise is a fundamental question in biology. Mathematically the stochastic dynamics of a gene regulatory network can be modeled using chemical master equation (CME), but nonlinearity and other challenges render analytical solutions of CMEs difficult to attain. While approaches of approximation and stochastic simulation have been devised for simple models, obtaining a more global picture of a systems behaviors in high-dimensional parameter space without simplifying the system substantially remains a major challenge. Here we present a new framework for understanding and predicting the behaviors of gene regulatory networks in the context of information transmission among genes. Our approach uses stochastic simulation of the network followed by machine learning of the mapping between model parameters and network phenotypes such as information transmission behavior. We also devised ways to visualize high-dimensional phase spaces in intuitive and informative manners. We applied our approach to several gene regulatory circuit motifs, including both feedback and feedforward loops, to reveal underexplored aspects of their operational behaviors.

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