Self-Consistent Proteomic Field Theory of Stochastic Gene Switches ALEKSANDRA M. WALCZAK, UCSD, MASAKI SASAI, Nagoya University, PETER G. WOLYNES, UCSD — The need for a computationally efficient treatment of genetic networks and cascades, which, while acknowledging their stochastic character, at the same time allows us to gain a better and deeper understanding of the global attractor structure is widely recognized. Even treating the building blocks of these systems, genetic switches, generally requires some approximations. We propose a powerful generically applicable method, a self-consistent proteomic field approximation in which the mean influence of the proteomic cloud created by one gene on the action of another is computed self-consistently [1]. The stochastic nature of protein synthesis and degradation, and DNA binding events are treated stochastically and on equal footing. For a large class of problems, in which the output proteins of one gene influence other genes, the probability distributions may be determined exactly without any further assumptions within the self-consistent proteomic field approximation. We compare the results for various versions of a toggle switch composed of two mutually repressing genes to solutions of deterministic rate equations and find that when proteins are produced in bursts, the deterministic approach can fail dramatically.
1. Walczak, A.M., Sasai, M., Wolynes P.G., Self Consistent Proteomic Field Theory of Stochastic Gene Switches, to be published in Biophysical Journal

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