

BOOLEAN FUNCTIONS AND DISCRETE DYNAMICS: ANALYTIC AND BIOLOGICAL APPLICATION

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Abstract

Modeling complex gene interacting systems as Boolean networks lead to a significant simplification of computational investigation. This can be achieved by discretization of the expression level to ON or OFF states and classifying the interactions to inhibitory and activating. In this respect, Boolean functions are responsible for the evolution of the binary elements of the Boolean networks. In this thesis, we investigate the mostly used Boolean functions in modeling gene regulatory networks. Moreover, we introduce a new type of function with strong inhibitory, namely the veto function. Our computational and analytic studies on the verity of the networks capable of constructing the same State Transition Graph, lead to define a new concept, namely the “degeneracy” of Boolean functions. We further derive analytically the sensitivity of the Boolean functions to perturbations. It turns out that the veto function forms the most robust dynamics. Furthermore, we verify the applicability of veto function to model the yeast cell cycle networks. In particular, we show that in an intracellular signal transduction network [Helikar et al, PNAS (2008)], the functions with veto are over-represented by a factor exceeding the over-representation of threshold functions and canalizing functions in the same system. The statistics of the connections of the functional networks are studied in detail. Finally, we look at a different scale of biological phenomena using a binary model. We propose a simple correlation-based model to describe the pattern formation of Fly eye. Specifically, we model two different procedures of Fly eye formation, and provide a generic approach for Fly eye simulation.