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Attractor-Based Obstructions to Growth in Homogeneous Cyclic Boolean Automata

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Abstract

We consider a synchronous Boolean organism consisting of N cells arranged in a circle, where each cell initially takes on an independently chosen Boolean value. During the lifetime of the organism, each cell updates its own value by responding to the presence (or absence) of diversity amongst its two neighbours' values. We show that if all cells eventually take a value of 0 (irrespective of their initial values) then the organism necessarily has a cell count that is a power of 2. In addition, the converse is also proved: if the number of cells in the organism is a proper power of 2, then no matter what the initial values of the cells are, eventually all cells take on a value of 0 and then cease to change further. We argue that such an absence of structure in the dynamical properties of the organism implies a lack of adaptiveness, and so is evolutionarily disadvantageous. It follows that as the organism doubles in size (say from m to 2m) it will necessarily encounter an intermediate size that is a proper power of 2, and suffers from low adaptiveness. Finally we show, through computational experiments, that one way an organism can grow to more than twice its size and still avoid passing through intermediate sizes that lack structural dynamics, is for the organism to depart from assumptions of homogeneity at the cellular level.

Keywords: Attractor-based obstructions; Cyclic boolean automata; Synchronous boolean; Robustness

Introduction

The subject of cellular automata has received much attention since John Von Neumann's seminal work [1] on the dynamics of a grid of cells which evolve in discrete time steps according to rules based on their neighbor's values (e.g., see the surveys in ref. [2,3]). Conway's Game of Life [4], perhaps the most famous example of cellular automata, consists of an infinite two-dimensional orthogonal grid of Boolean cells whose values are synchronously updated 1. Cellular automata are frequently studied by considering their collective dynamics. Wolfram [5], for example, examined the complexity of finding "Garden of Eden States" (i.e., states that are unreachable from any other state), as well as determining whether a network can reach a state in which all cells have value 1 (i.e., a question that is now known as the "All-Ones Problem"). Both these problems generally become computationally infeasible for all but the smallest one-dimensional networks [6].

A random graph model for automata was introduced by Stuart Kauffman in the course of his research on gene regulatory networks. These so-called "NK networks" [7] consist of *N* cells, each of which is connected to a randomly chosen subset of K cells. Kauffman and others considered self-organization and the spontaneous emergence of order [8] in NK and related networks. Consensus is a particular form of emergent order that has received particular attention, especially in the context of social systems. Miller considered consensus in the standing ovation problem as a means to examine behavior in social networks using computational models [9]. Arenas surveys network structures which lead to emergent features and reports on the implications of consensus emergence in a variety of settings [10]. In his work, the community structures of networks (i.e., clusters of densely interconnected cells, between which connections are sparse) play a crucial role. Ball describes how many natural systems rely on characteristics akin to community structure in order to reach a level of consensus robustly in the presence of noise [11]. Consensus problems are closely related to our research since both seeks to understand dynamical systems which move towards uniformity irrespective of initial conditions [12], and to identify the social network properties that lead to stasis and uniformity [13].

The organisms we consider in this paper are discrete Boolean cellular automata of the NK type, though we restrict ourselves to K=2 [14] and require that the cells be connected deterministically to form a circle. Such cyclic networks have received considerable attention themselves [6]. Like most prior research, we too (at least initially) consider only cellular automata that are homogenous at the cellular level, that is, cyclic networks in which all cells operate according to an identical update rule. For simplicity, we only consider networks in which cells synchronously update their values–recent progress in sequential dynamical systems [15-17] has shown that the behavior of more general asynchronous systems with small temporal variations can be examined by "equivalent" synchronous systems [18].

Where the All Ones Problem asks if the state in which all cells have value 1 is reachable from any other state, here we seek to determine if there is a state that is reachable from every other state. The networks we will consider are so simple as to lack community substructures, and yet always reach consensus regardless of noise. This is possible because (as we shall prove) their dynamics exhibit a single unique attractor. This work extends earlier results on thermal robustness and attractor density in synchronously updated cyclic Boolean networks [19].

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dynamics of homogeneous cyclic organisms of size N=2,...,20 cells, using software developed previously [8]. In these homogeneous organisms, each cell synchronously determines its successive states by computing the $\oplus$ of the value of its neighbors. From observations of these computationally simulated dynamics, we conjectured that if the number of cells in an organism is a proper power of 2, then the organism has exactly one attractor, which has length 1 and consists of the state where all cells have a value of 0. We then formally proved this statement as well as its converse: that if regardless of its initial state the organism always ends up in the same size 1 attractor, then the number of cells in the organism is a proper power of 2. Some of the evidence for this now-proven "if and only if" relationship is rendered in Figures 14, 15 and 16 versus Figures 7 and 8.

Since the act of incrementing the size of an organism until it reaches double its size necessarily requires traversing a number that is a proper power of 2, any organism that grows to more than twice its original size will necessarily encounter a stage in which it has minimal adaptivity and maximal robustness. If the organism seeks to always maintain "intermediate" values of adaptivity and robustness as it grows, then alternative growth patterns that exhibit more than one attractor at powers of 2 sizes will be evolutionarily advantageous. The alternative growth pattern we explore experimentally in this work, is one in which the organism departs from cellular homogeneity to a minimal extent—allowing a single constituent cell to apply a rule that is different from XOR. Through experiments, we show that at sizes that are powers of 2, such minimally heterogeneous organisms avoid manifesting the low adaptivity that is provably exhibited in homogenous organisms. We conclude that cellular differentiation is one way an organism can avoid low adaptivity configurations that would otherwise necessarily be encountered during organism growth. It follows that if there is evolutionary pressure selecting for adaptivity, then the phenomenon of organism growth may express this pressure as a drive towards cellular differentiation and the progression from homogeneity towards heterogeneity. Figures 10-13 show the dynamics graphs of minimally heterogeneous organisms of sizes 2, 4, 8, and 16 respectively, and have increasing numbers of attractors. These figures are placed side by side with the dynamics graphs of homogeneous organism of the same size, to further illustrate their contrasting dynamics.

Future work will entail simulation of more complex growth patterns, beyond merely homogeneous and minimally heterogeneous growth. One pattern we plan to explore is probabilistic cellular differentiation during growth. Future work needs to look at both larger and more diverse organisms, but for larger organisms exhaustive simulation is computationally intractable, requiring advances in random sampling and estimation theory. By considering dynamics data from a more diverse and larger range of systems, it may be possible to identify other evolutionary pressures (beyond cell differentiation) and meta-phenomena that arise as organisms attempt to maintain a balance between adaptivity and robustness during growth.

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