2005

Asynchronous random Boolean network model based on elementary cellular automata rule 126

Mihaela Teodora Matache
University of Nebraska at Omaha, dvelcsov@unomaha.edu

Jack Heidel
University of Nebraska at Omaha, jheidel@unomaha.edu

Asynchronous random Boolean network model based on elementary cellular automata

Mihaela T. Matache*
Jack Heidel

Department of Mathematics
University of Nebraska at Omaha
Omaha, NE 68182-0243, USA
*dmatache@mail.unomaha.edu

Abstract This paper considers a simple Boolean network with N nodes, each node's state at time t being determined by a certain number k of parent nodes, which is fixed for all nodes. The nodes, with randomly assigned neighborhoods, are updated based on various asynchronous schemes. We make use of a Boolean rule that is a generalization of rule 126 of elementary cellular automata. We provide formulae for the probability of finding a node in state 1 at a time t for the class of Asynchronous Random Boolean Networks (ARBN) in which only one node is updated at every time step, and for the class of Generalized ARBNs (GARBN) in which a random number of nodes can be updated at each time point. We use simulation methods to generate consecutive states of the network for both the real system and the models under the various schemes. The results match well. We study the dynamics of the models through sensitivity of the orbits to initial values, bifurcation diagrams, and fixed point analysis. We show, both theoretically and by example, that the ARBNs generate an ordered behavior regardless of the updating scheme used, whereas the GARBNs have behaviors that range from order to chaos depending on the type of random variable used to determine the number of nodes to be updated and the parameter combinations.

1. Introduction

Due to their convenient and easy to understand structure, Boolean networks have been used extensively as models for complex networks such as genetic or biochemical networks, networks in artificial life, biophysics, condensed matter and solid-state physics, or statistical mechanics. Originally introduced by Kauffman ([1], [2], [3]), the Boolean network models appeal to any situation in which the activity of the nodes of the network can be quantized to only two states, ON and OFF, and each node updates its state based on logical relationships with other nodes of the network. For example, most biological phenomena are often described in binary language such as "responsive and nonresponsive", "upregulated and downregulated", despite their manifestation in the continuous domain [4]. Although a Boolean

network model may represent a very simplified view of a network, it retains in most cases meaningful information that can be used to study the dynamics of the network and make inferences regarding the real system they model.

Boolean and random Boolean networks have been extensively considered and studied as models of genetic regulatory networks ([4], [5], [6], [7], [8], [9], [10], [11], [12], [13], [14]) with the goal of understanding the global network dynamics. Knowing the long-run behavior of such networks would allow one to identify steady-state behavior associated with tumors, and develop a methodology for altering this steady-state as means of therapy. Applications of synchronous Boolean networks to biochemical systems have been studied in [15], [16].

Cellular automata (CA) are a special case of Boolean networks, with various systems whose structure lies between the two. CA are dynamical systems which are discrete in space and time, operate on a uniform, regular lattice, and are characterized by "local" interactions. They provide models in computational and physical systems, in biological systems, such as pattern formation, and in ecology, for example modelling forest fires ([17], [18]). There has been a great interest in studying the dynamics of these systems in light of Wolfram's analysis of randomness in modeling nature, which categorizes the rules of elementary cellular automata (ECA) [19]. In this paper we analyze a random Boolean network whose dynamics are established by a generalization of ECA Rule 126.

It is known that related to condensed matter and solid-state physics, the dynamics of "spin-glasses" have been influential in the formulation of Kauffman's N/K models used in his random Boolean networks and other complex, adaptive systems ([3]). Such models yield insight into the dynamics of interactive systems through the changing of connectivity rules and the exploration of the ensuing emergent phenomena. So it is important to model the behavior of interconnected systems in terms of coupling between components and understanding the means for moving the system into and out of equilibrium states.

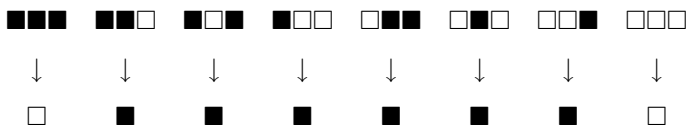
Understanding the dynamics of large interacting systems is one of the challenges of statistical mechanics. In such systems the nodes (units) have diverse functions and they are connected in random fashion to other nodes [20]. It is important to understand under what circumstances the systems self-organize, and how the dynamics is influenced by the way the elements are connected and interact. The study of scale-free networks by Barabasi and Albert ([20], [21], [22]) has created the framework for the study of systems in which the distribution of the node links obeys a power-law rule. These kinds of systems have been found in many real-world complex networks, such as the Internet, cellular metabolic networks, and research collaboration networks [23]. Although in this paper we assume that all nodes have a fixed number of parents, future work will include the study of similar systems in which the number of parents varies according to specified rules, such as power-law distributions.

One important aspect of all the studies mentioned above is that the networks are assumed to be synchronous, that is the nodes update their states at the same time. However, various authors have

observed that for many biological phenomena or cellular automata, including examples discussed above, asynchronous versions are more plausible models. For example, individual ants display aperiodic patterns of active and resting periods, while the colony as a whole may exhibit synchronized activity; asynchronous activity of the neurons in the brain could lead to some global patterns [24]. Studies of asynchronous random Boolean networks (ARBN) include properties of attractors of the ARBNs [25], role of the updating scheme of the nodes in the dynamics of the system and the emergence of modularity ([24], [26]), rhythmic and non-rhythmic attractors in ARBNs ([27], [28]), critical values in ARBNs [29], role of asynchrony in generating edge of chaos patterns in cellular automata [30]. In this paper we extend previous work on synchronous random Boolean networks governed by a generalization of ECA Rule 126 ([31], [32]) to the case of asynchronous updating.

Following Wolfram [19] it makes sense to think about three types of randomness in modeling nature. There may be randomness in the environment. Such phenomena are studied mathematically by, for example, Markov processes, probabilistic cellular automata [33] or probabilistic Boolean networks [4]. The second Wolfram category is randomness in initial conditions. A prominent example here are random Boolean networks as discussed by Kauffman [3]. Wolfram puts the phenomenon of deterministic chaos into this second group. The third group is comprised of intrinsic generators of randomness such as the elementary cellular automata rule 30 and rule 110.

In this paper we discuss a random Boolean network model which generalizes ECA rule 126 and therefore falls into Wolfram second type of generation of randomness. Rule 126 is most simply described as



where black is ON and white is OFF. Rule 126 falls into both of Wolfram's "legalistic" and "totalistic" groups of rules ([19], [32]). Rule 126 is useful as a conceptual model of (biological) cell growth and of a (chemical) catalytic process because the central site survives (or is born) unless the neighborhood is too poorly populated or too crowded, in which case it dies. Other ECA rules such as 22, 90, and 150 have similar interpretations ([32], [34], [35]). It is interesting that Rule 126 is both a very simple growth model and yet exhibits a quite sophisticated dynamic behavior.

The present paper uses an approach introduced by Andrecut and Ali [31], whereby the density function for the number of 1's in a network at time t, is shown to satisfy a simple first order difference equation. These authors then apply the familiar methods of bifurcation analysis, with respect to the neighborhood size k, to show the existence of chaos in their generalized Rule 126 model. A similar investigation of a different generalization of Rule 126 has been carried out by Boccara and Roger [36].

The scalar density function discussed here is exact as opposed to the probabilistic approximation in CA mean field theory ([19], [37]). Furthermore our theory can also be extended to all of the 32 legalistic rules by interpreting them as the simple growth rules discussed above. Rule 126 has the most sophisticated behavior in this way. For example the nontrivial legalistic and totalistic ECA rule 22 ([19], p. 263, or [32],) turns out to have a non-bifurcating density function when analyzed by the methods of this paper. This extension will be the subject of future work.

The model considered by Andrecut and Ali [31] is a simple Boolean network with N nodes, each node being influenced by exactly k other nodes at each step of the Boolean system. In other words each node has exactly k parents, selected randomly, so that the Boolean rule for each node is determined only by the state of the k parents. The number k is fixed and the nodes of the network are updated synchronously. Our emphasis in this paper is to extend that model by allowing an asynchronous update rule for the N nodes. There are various types of updating schemes in the literature such as the clock scheme ([38], [39]), the cyclic scheme ([30]), the random independent scheme ([25]), and the random order scheme ([25]). It has been shown ([24]) that properties of the models are changed by the particular update scheme chosen. At the same time the random Boolean networks have been classified by Gershenson [40]. According to this author the class of Asynchronous Random Boolean Networks (ARBN) incorporates all the cases in which at each time point a single node is selected in order to be updated. The node to be updated can be chosen at random or according to a deterministic rule based on the above mentioned updating schemes. He then generalizes the class of ARBN to the Generalized Asynchronous Random Boolean Networks (GARBN) defined as ARBNs which can update any number of nodes, picked at random, at each time step. In this paper we analyze the dynamics of ARBNs and GARBNs, for cellular automata rule 126, using various updating schemes. We provide a model for the probability $p(t+1)$ of finding a node in state 1 at time $t+1$ given $p(t)$, and study the dynamics of the networks through sensitivity of the orbits to initial values, bifurcation diagrams, and fixed point analysis.

In Section 2 we start with the study of the dynamics of ARBNs. We show that the formula for the probability of finding a node in state 1 does not depend on the updating scheme, only on the fact that exactly one node is updated at each time point. The formula is

$$p(t+1) = p(t) + \frac{1}{N}\left[1 - p(t) - p(t)^{k+1} - (1-p(t))^{k+1}\right]$$

where k is the number of parents of each node, and N is the size of the network. We show that ARBNs have a very ordered behavior under this model.

Section 3 is dedicated to a discussion of fixed points and bifurcation that comes to explain the observed phenomena. In [32] the present authors extend the results of Andrecut and Ali [31], based on Elementary Cellular Automata Rule 126, to networks with varying sizes of parent neighborhoods. In this particular setting it is shown that "high connectivity can erase all chaotic behavior in a synchronous network" (quote

from an anonymous referee). The present paper, in a generalization of [31] to asynchronous networks, shows that high connectivity (i.e. letting $k \to \infty$) again swamps out chaos and periodicity and leaves only stable fixed points. This regularity is shown to be quite general with exceptions occurring only for a small number of neighborhood distributions.

In Section 4 we extend the study to GARBNs using several different random number generators for the number x_t of nodes to be updated at each time point t. The recursive formula for the probability of a node being in state 1 is very similar to the one for ARBNs, except for the random term x_t. The formula is

$$p(t+1) = p(t) + \frac{x_t}{N}\left(1 - p(t) - (1-p(t))^{k+1} - p(t)^{k+1}\right).$$

We show that the random generator of x_t has an impact on the behavior of the system which can pass from chaos to order or vice versa with transition phases of various lengths depending on the underlying parameters.

2. Asynchronous Random Boolean Networks

Consider a network with N nodes. Each node c_n, $n = 0, 1, 2, \ldots, N-1$ can take on only two values 1 or 0. Often this is interpreted as a system in which each node can be either ON or OFF. At each time point t the system can be in one of the 2^N possible states. If all the nodes update their value at the same time the network is synchronous, otherwise it is asynchronous. The evolution of the nodes from time t to time $t+1$ is given by a Boolean rule which is considered the same for all nodes. Each node c_n is assigned a random "neighborhood" of parents, whose values at time t influence the value of c_n at time $t+1$ through the following Boolean rule. If c_n and all its parents have the same value at time t (that is they are all either 0 or 1), then $c_n(t+1) = 0$, otherwise $c_n(t+1) = 1$. This generalizes rule 126 of cellular automata ([19], [32]). The parents of a node are chosen randomly from the remaining $N-1$ nodes and do not change thereafter. More precisely, if a node has k parents, then a set of k nodes is chosen from the remaining $N-1$ nodes with probability $\frac{1}{\binom{N-1}{k}}$.

This model is a description of a random Boolean cellular automaton. The system is described by the number of parents of each node. Observe that the quantity

$$N_1(t) := \sum_{n=0}^{N-1} c_n(t)$$

gives the number of nodes that are in state 1 at time t. The concentration of nodes in state 1 is given by $\frac{1}{N}\sum_{n=0}^{N-1} c_n(t)$. We are interested in finding the probability $p(t+1)$ that a node is in state 1 at time $t+1$. In [31] it is shown that $p(t+1)$ is given by

$$p(t+1) = 1 - p(t)^{k+1} - (1-p(t))^{k+1}$$

where $k \geq 1$ is the number of parents of each node. (Note: we take the liberty to provide the formula with $k+1$ rather than k as it is misprinted in [31]).

We extend this result by allowing an asynchronous update rule for the N nodes. There are various types of updating schemes in the literature such as the clock scheme ([38], [39]), the cyclic scheme ([30]), the random independent scheme ([25]), and the random order scheme ([25]). It has been shown ([24]) that properties of the models are changed by the particular update scheme chosen. Based on the various possible updating schemes the random Boolean networks have been classified by Gershenson [40]. According to him the class of Asynchronous Random Boolean Networks (ARBN) incorporates all the cases in which at each time point a single node is selected in order to be updated. This case encompasses all the previously mentioned updating schemes with the exception of the clock scheme. The node to be updated can be chosen at random or according to a deterministic rule. Gershenson ([40]) also generalizes the class of ARBN to the Generalized Asynchronous Random Boolean Networks (GARBN) defined as ARBNs which can update any number of nodes, picked at random, at each time step. This case incorporates the previously mentioned clock scheme. In what follows we will start by looking at ARBNs using the cyclic updating scheme. As we shall see, the model provided for this case can be generalized to the entire ARBN class. Next we will focus on GARBNs using various random generators for the number of nodes to be updated at each time point.

We start with the cyclic scheme in which at each time step t only one node is updated. To simplify the first look at the problem we fix the updating order to be the following: at time t we update the node $t \, mod \, N$. Thus the nodes are updated in order from 0 to $N-1$ every N time steps. Observe that from time t to time $t+1$ only one node may change its state, so the total number of nodes that are in state 1 at time $t+1$ cannot differ with more than one unit from $N_1(t)$. This means that for large N, $p(t+1)$ and $p(t)$ are approximately the same. It would be of interest to look at $p(t+T)$, the probability of finding a node in state 1 after T iterations of the system, where T is large enough so that all nodes have been updated at least once.

Denote by $N_0(t)$ the number of nodes that are 0 at time t. Then $N_1(t)+N_0(t) = N$. We are interested in how node $t \, mod \, N$ changes from time t to time $t+1$ in order to determine $N_1(t+1), N_0(t+1)$. Observe that node $t \, mod \, N$ is in state 1 at time t with probability $p(t)$ and in state 0 with probability $1-p(t)$. If node $t \, mod \, N$ is 0 at time t then the number of nodes that change from 0 to 1 at time $t+1$ is $N^0_{0\to 1}(t) = 1-(1-p(t))^k$ given that only the node $t \, mod \, N$ could change and that would happen only if all the parents of this node are 0 as well. Similarly, the number of nodes that remain 0 is $N^0_{0\to 0}(t) = N_0(t)-1+(1-p(t))^k$, the number of nodes that change from 1 to 0 is $N^0_{1\to 0}(t) = 0$, and the number of nodes that remain 1 is $N^0_{1\to 1}(t) = N_1(t)$. Similarly, if the node $t \, mod \, N$ is 1 at time t we obtain the corresponding number of nodes $N^1_{0\to 1}(t) = 0, N^1_{0\to 0}(t) = N_0(t), N^1_{1\to 0}(t) = p(t)^k, N^1_{1\to 1}(t) = N_1(t) - 1 + (1-p(t)^k) = N_1(t) - p(t)^k$.

Thus we may write the formulas for the number of nodes that either change or remain in the same state from time t to time $t+1$ as follows:

$$N_{0\to 1}(t) = (1-p(t))(1-(1-p(t))^k) = 1-p(t)-(1-p(t))^{k+1}$$

$$N_{0\to 0}(t) = (N_0(t)-1+(1-p(t))^k)(1-p(t)) + N_0(t)p(t) = N_0(t)-1+p(t)+(1-p(t))^{k+1}$$

$$N_{1\to 0}(t) = p(t)^k p(t) = p(t)^{k+1}$$

$$N_{1\to 1}(t) = N_1(t)(1-p(t)) + (N_1(t)-p(t)^k)p(t) = N_1(t)-p(t)^{k+1}$$

One can easily check that $N_{0\to 1}(t)+N_{0\to 0}(t)+N_{1\to 0}(t)+N_{1\to 1}(t) = N$. We include for comparison the formulas obtained in [31] for the same quantities, following a synchronous updating rule: $N_{0\to 1}(t) = N_0(t)(1-(1-p(t))^k), N_{0\to 0}(t) = N_0(t)(1-p(t))^k, N_{1\to 0}(t) = N_1(t)p(t)^k, N_{1\to 1}(t) = N_1(t)(1-p(t)^k)$.

We can write now that

$$N_1(t+1) = N_{0\to 1}(t)+N_{1\to 1}(t) = N_1(t) + \left[1-p(t)-p(t)^{k+1}-(1-p(t))^{k+1}\right],$$

$$N_0(t+1) = N_{0\to 0}(t)+N_{1\to 0}(t) = N_0(t) - \left[1-p(t)-p(t)^{k+1}-(1-p(t))^{k+1}\right].$$

As a consequence, the probability of finding a node in state 1 at time $t+1$ is given by

$$p(t+1) = \frac{N_1(t+1)}{N} = p(t) + \frac{1}{N}\left[1-p(t)-p(t)^{k+1}-(1-p(t))^{k+1}\right]. \tag{1}$$

Note that if all the nodes are 0 at time t, then $p(t)=0$ so $p(t+1)=0$, which is to be expected since by the Boolean rule all the nodes stay 0 at time $t+1$. Similarly, if all the nodes are 1 at time t, $p(t+1) = \frac{N-1}{N}$ by the formula, as well as by the Boolean rule.

To study the behavior of this model we construct the map

$$f(p) = p + \frac{1}{N}(1-p-p^{k+1}-(1-p)^{k+1})$$

and observe that $p(t+T) = f^T(p(t))$, where f^T represents $f\circ f\circ\cdots\circ f$, T times.

Observe that the updating scheme given by $t\, mod\, N$ has not been explicitly used in generating the model, only the fact that at a given time point exactly one node is updated. Thus, the model is suitable for any scheme in which the nodes are updated one by one in a certain order, fixed or random. The most common schemes in this category are the random order scheme and the interlaced order scheme ([30]). According to the fixed random order scheme, a permutation of the first N natural numbers is performed. The nodes are updated by repeating this order every N time steps ([30]). In the case of a more general random order scheme a new permutation is selected every N time steps ([25]). Another version of the random order scheme assumes that at each time point t a uniform number u between 1 and N is generated and the u-th node is updated ([30]). For the interlaced order scheme, an integer number $C>0$ relatively prime to N is generated and at time t the $(Ct)\, mod\, N$ node is updated. In other words, every other C-th node is updated at consecutive time points.

The reason for the above discussion on ARBN updating schemes is to show how many cases are encompassed by the model (1).

It is useful to provide some simulations to see how well does the model match the real system. The simulations that follow in this paper have been obtained by running Matlab and Maple programs. Although we present only a few graphs in this paper, the conclusions have been drawn from numerous simulations run by the authors. In general we present only typical graphs.

We restrict our attention to the $t \, mod \, N$ cyclic scheme. The graphs are similar in other cases of ARBNs as expected. The graphs in Figure 1 represent simulations of the model and the actual Boolean system for the case of $N = 128$ with $k = 32$. There are 9 different graphs representing iterations of the system and the model, namely we graph $p(t + iteration)$ versus $p(t)$ for $iteration = 2^i, i = 0, 1, 2, \ldots, 8$. We can deduce the behavior of the system and the model for other cases from these graphs, since all the other simulations obtained by the authors for various parameter combinations are quite similar to those in Figure 1.

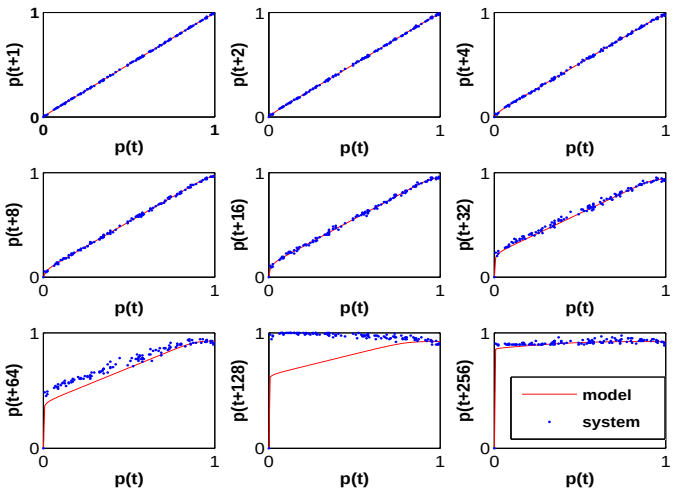


FIGURE 1. Iterations of the system and the model for ARBNs, with $N = 128$ and $k = 32$. We plot some of the first 256 iterations of the system and the model as specified in the labels. We observe the perfect match for the first 32 iterations followed by a transition phase in which the system and the model do not match perfectly for iterations up to approximately 256 when the model and the system reach a steady behavior with a very good match.

We make the following observations. There is an excellent match between the model and the system for iterations that go up to order $2^5 - 2^7$ depending on the situation. For higher number of iterations the match is also good, and both the system and the model settle around a certain value of $p(t)$ suggesting that no matter what the initial conditions are, in the long run there is either an absorbing state or cycles

of states that differ only slightly in terms of the number of nodes that are 1. That is, in the long run, the probability of finding a node in state 1 is approximately the same regardless of the initial state of the system. We observe also that the model has a slower rate of convergence towards this probability than the system in the range of $2^5 - 2^7$ iterations, so there is a transient phase in which the model is not a perfect match for the system. This behavior is observed to be independent of the number of nodes or parents of a node, however the transient phase holds for a longer time period for higher values of the number of parents k, and occurs later as the number of nodes increases. Theoretical justification for these remarks is provided in the next section.

We note that the graphs are very close to the first diagonal for the first few iterates, as the number of nodes in state 1 does not change more than one from one time point to the next.

The situation suggested by the previous graphs is clarified even more by the sensitivity of the orbits to the initial values for the model. We fix the parameters N and k and choose two initial values $p(0)$ and $q(0)$ as starting points for the orbits. We iterate many times the equation of the model and compute $p(t)$ and $q(t)$ for each time point t. Then we plot the error $E(t) = |p(t) - q(t)|$ versus t. Figure 2 shows the case of $N = 128$ and $k = 4$. This graph is typical and very similar for any other combinations of parameters considered in the experiments, including small or large values for both N and k. We observe that the error converges to zero at a faster rate for smaller values of k and a slower rate for larger values of k for a fixed N. Also, as N increases the behavior is the same, but in general the convergence rates are slower. For the three graphs in the figure $p(0) - q(0) = 0.5, 0.01, 0.0001$ respectively. We see that it does not matter how far apart the initial values are, since the error will eventually converge to zero.

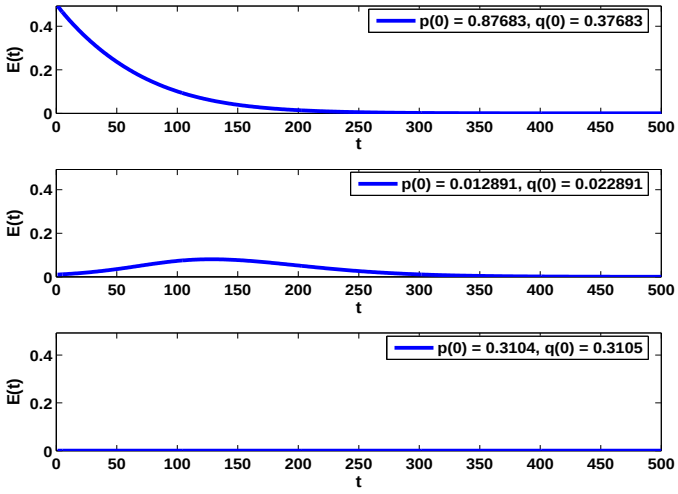


FIGURE 2. Error plot for the ARBN model with $N = 128$ and $k = 4$. In each graph we plot the error $E(t) = |p(t) - q(t)|$ versus t. We start with initial values $p(0)$ and $q(0)$ that are $0.5, 0.01$, and 0.0001 apart respectively. The error converges to zero in all cases.

In order to clarify even more the situation suggested by the sensitivity of the orbits to the initial values, we construct bifurcation diagrams with integer values for the parameter k. We fix the number of nodes $N = 512$ in Figure 3, and we iterate the function $f(p)$ a number of times for various initial values of p and plot the iterations $N/2, N, 2N$, and $5N$. We observe that there is a transient period for reduced number of iterations, but after significant iterations the bifurcation map converges to a value that gets closer and closer to 1 as N and k increase. Thus in the long run, the system exhibits a very ordered behavior.

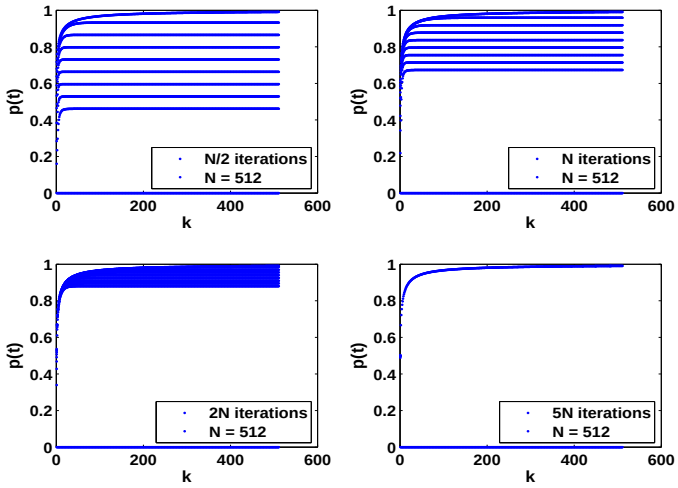


FIGURE 3. Bifurcation diagram for the ARBN model, with $N = 512$. The model is iterated a number of times, as specified in each graph, before plotting the values of $p(t)$, to understand how the transient phase behaves. We observe the ordered behavior of the system.

Finally, to end the analysis of the above updating cyclic scheme we look at the map

$$f(p) = p + \frac{1}{N}(1 - p - p^{k+1} - (1 - p)^{k+1})$$

and find its fixed points, that is we solve the equation $f(p) = p$. This leads to the equation in p

$$1 - p - p^{k+1} - (1 - p)^{k+1} = 0.$$

It is clear that if $k \to \infty$ in the above equation, we obtain $p = 1$. Also, $p = 0$ is obviously a fixed point of the map. Figure 4 shows this fact.

3. Digression on Fixed Points and Bifurcation

The map

$$f(p) = p + \frac{1}{N}(1 - p - p^{k+1} - (1 - p)^{k+1})$$

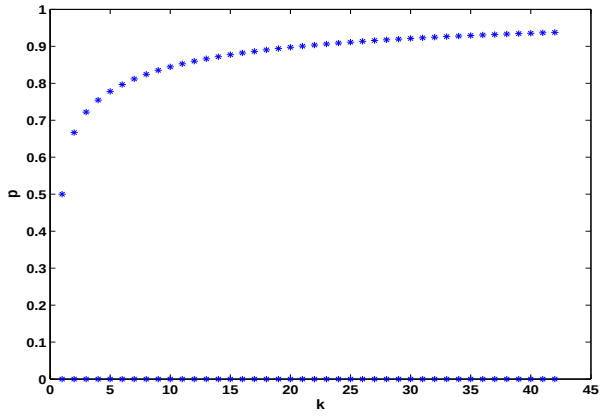


FIGURE 4. Fixed points for the ARBN model $f(p) = p + \frac{1}{N}(1 - p - p^{k+1} - (1 - p)^{k+1})$. The fixed points converge to 1 as k increases.

from the ARBN scheme has the characteristic shape for all positive integers N, k as the first iteration of Figure 5.

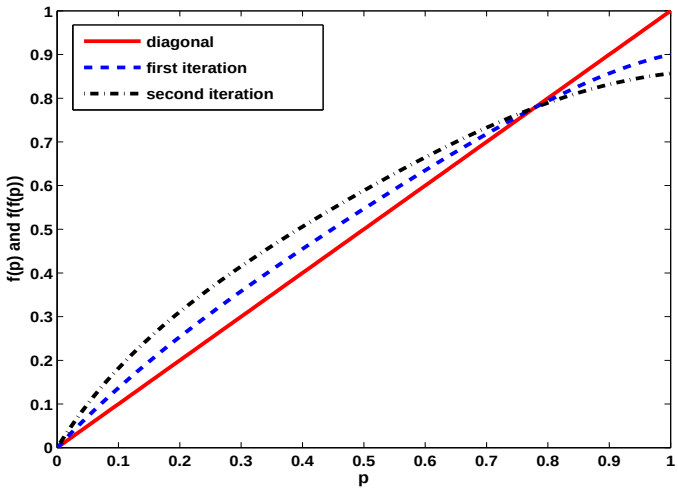


FIGURE 5. Plot of the first two iterations of the map $f(p) = p + \frac{1}{N}(1 - p - p^{k+1} - (1 - p)^{k+1})$ in the case $N = 10, k = 5$.

A so called cobweb stability diagram [41] shows immediately that the nonzero fixed point at $p \cong 0.8$ is stable on the p interval $(0, 1]$. The general theory of one dimensional maps then shows that there are no nontrivial period 2 or higher period orbits. This, of course is also indicated in the second iteration graph of the same map, as in Figure 5. In Figure 6 we show the collection of the first 30 iterations to clarify even more this situation, for $N = 10, k = 5$. We observe that the behavior is similar for larger values of N, and even for a larger number of iterations when transient phases have passed.

Thus the ARBN scheme exhibits no bifurcations to high order periodic orbits.

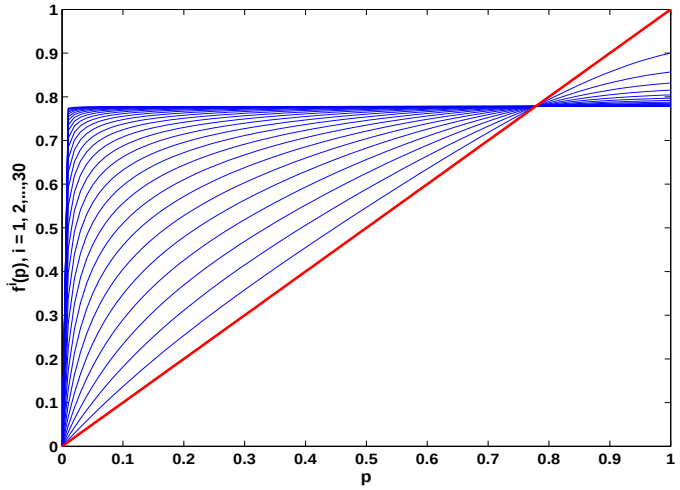


FIGURE 6. Plot of the first 30 iterations of the map $f(p) = p + \frac{1}{N}(1-p-p^{k+1}-(1-p)^{k+1})$ in the case $N = 10, k = 5$.

For future reference (the GARBN scheme), we now generalize the following discussion by considering

$$f(p) = p + \alpha(1 - p - p^{k+1} - (1-p)^{k+1}). \tag{2}$$

Then we find that

$$f'(p) = 1 - \alpha - \alpha(k+1)p^k + \alpha(k+1)(1-p)^k.$$

Since a bifurcation from a fixed point to a period two point occurs only when $f'(p) = -1$ at a fixed point, we then set $f'(p) = -1$ in the above equation to get

$$\alpha + \alpha(k+1)p^k - \alpha(k+1)(1-p)^k = 2$$

or

$$\alpha = \frac{2}{1 + (k+1)p^k - (k+1)(1-p)^k}. \tag{3}$$

Thus the value of α where a bifurcation occurs depends on both p and k. However the fixed point condition

$$p + p^{k+1} + (1-p)^{k+1} = 1 \tag{4}$$

means that p is a function of k. This means that α is also a function of k and in fact we get the graph in Figure 7.

As a matter of fact, by denoting $g(p) = f(f(p))$ and solving the system of equations $g(p) = p$, $g\prime(p) = -1$ we are able to obtain the value of α where the second set of bifurcations occur, for period 4 cycles. In Figure 8 we graph α versus k for the period 2 and 4 cycles for comparison. Due to the complicated computations for solving the system of equations we restricted our attention to values of k from 1 to 6 .

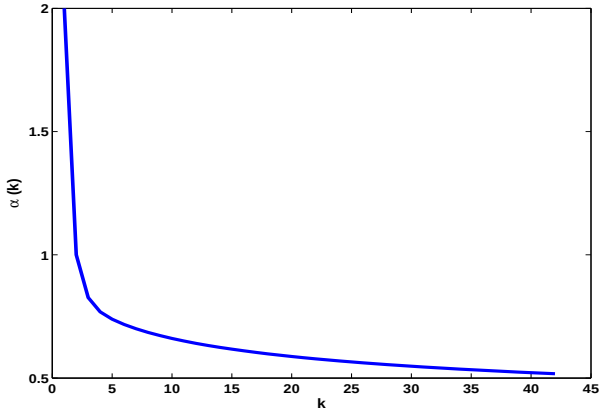


FIGURE 7. Plot of the $\alpha = \frac{2}{1+(k+1)p^k-(k+1)(1-p)^k}$ as a function of k, where $p + p^{k+1} + (1-p)^{k+1} = 1$. The function approaches zero as k increases.

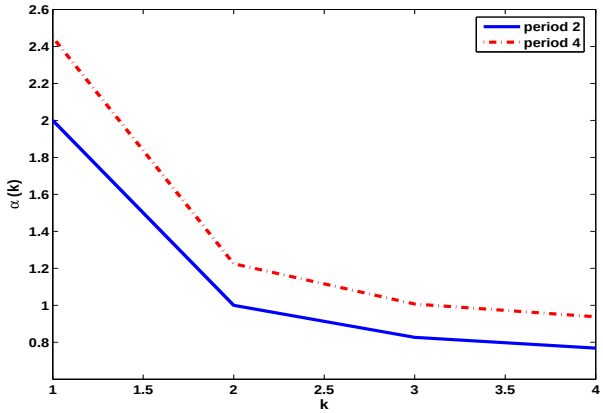


FIGURE 8. Plot of the $\alpha = \frac{2}{1+(k+1)p^k-(k+1)(1-p)^k}$ as a function of k, for period 2 and period 4 cycles.

It is interesting to look at some three dimensional bifurcation diagrams for p as a function of α and k. The system is iterated 100 times to obtain the graphs in Figures 9-12. Similar results occur for more than 100 iterations. Figures 9-10 show slices along α, whereas Figures 11-12 show slices along k. We observe that the more complex behavior occurs for generally large values of α. At the same time, as k increases the complex behavior occurs for smaller and smaller values of α.

We now show that the function $\alpha(k)$ defined in (3) under the condition (4) satisfies the inequality $\alpha(k) \geq \frac{1}{k}$. This will allow us to prove that there are only stable fixed points for the cyclic scheme. First observe that (4) is equivalent to

$$(1-p)^k = 1 - \frac{p^{k+1}}{1-p}$$

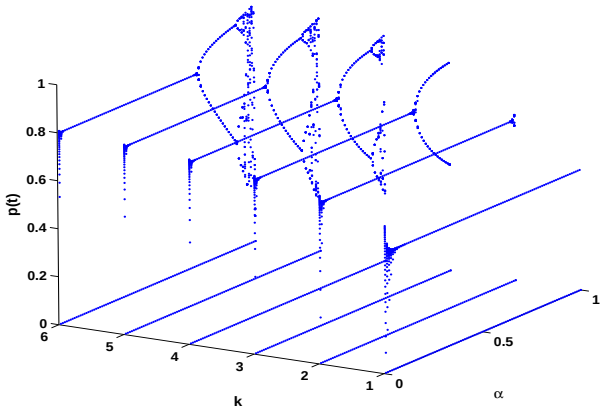


FIGURE 9. Bifurcation surface of p as a function of k and α. The slices correspond to a few k values (1 through 6) and the bifurcations occur along α. We observe that the complex behavior occurs for larger values of k and for smaller values of α as k increases.

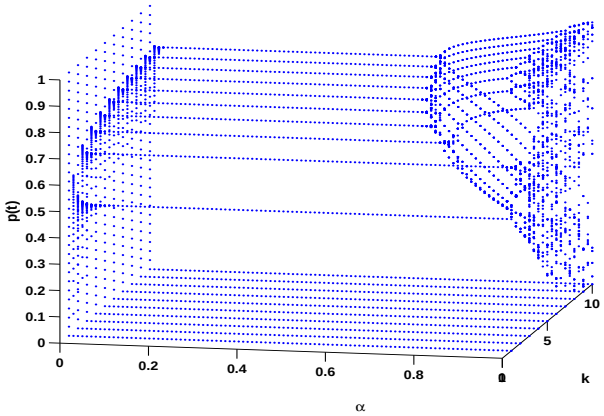


FIGURE 10. Bifurcation surface of p as a function of k and α. The slices correspond to k values and the bifurcations occur along α. This is a different view of the previous figure to show that the values of α for which the bifurcations occur move towards zero as k increases.

where p cannot be equal to 1 since 1 does not satisfy (4). Using this one can see that the inequality $\alpha(k) \geq \frac{1}{k}$ is equivalent to

$$2k \geq 1 + (k+1)p^k - (k+1)\left(1 - \frac{p^{k+1}}{1-p}\right) \Leftrightarrow \frac{3k}{k+1} \geq \frac{p^k}{1-p}.$$

Thus it is enough to show that this last inequality holds. We have the following result.

Proposition 1 *Let $k \in \mathbf{N}$, $k > 0$. If $p \in [0,1]$ and $p + p^{k+1} + (1-p)^{k+1} = 1$ then*

$$\frac{3k}{k+1} \geq \frac{p^k}{1-p}.$$

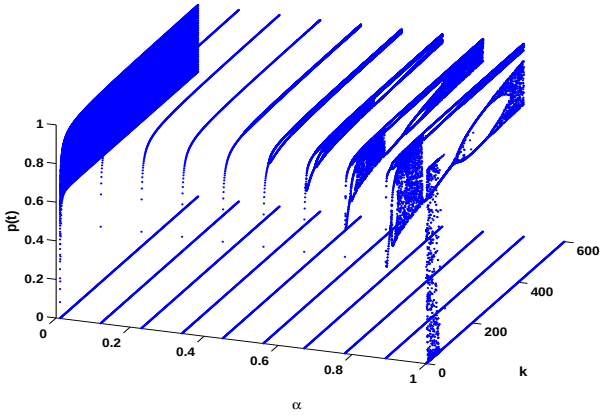


FIGURE 11. Bifurcation surface of p as a function of k and α. The slices correspond to α values and the bifurcations occur along k. We observe the more complex behavior for larger α.

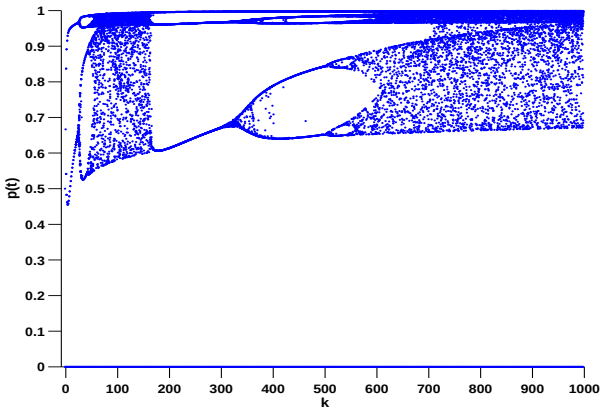


FIGURE 12. Bifurcation diagram for p as a function of k for $\alpha = 0.9$. This is a zoom in on a slice of the previous figure.

Proof Clearly $p \neq 1$ since 1 does not satisfy the hypothesis. The only value in $[0, \frac{1}{2})$ that satisfies the hypothesis is $p = 0$ for $k \geq 2$. Observe that for $k = 1$ the hypothesis is equivalent to $p^2 + (1-p)^2 = 1 - p$ which has roots 0 and $\frac{1}{2}$. We claim that for $k > 1$ the only value that satisfies the equation is 0.

Clearly 0 satisfies the equation for all k. If $0 < p < \frac{1}{2}$ then $0 < p < 1$ and $0 < 1 - p < 1$ so one has

$$p^{k+1} + (1-p)^{k+1} < p^k + (1-p)^k < \cdots < p^2 + (1-p)^2.$$

Now $p^2 + (1-p)^2 < 1 - p$ since this is equivalent to $2p^2 < p \Leftrightarrow p < \frac{1}{2}$ which is true. Thus for $k = 2, 3, \ldots$ there is only one value of p satisfying $p + p^{k+1} + (1-p)^{k+1} = 1$ and situated in $[0, \frac{1}{2}]$, namely $p = 0$.

Now we show that even more is true. There is a unique p in $[\frac{1}{2}, 1]$ satisfying $p + p^{k+1} + (1-p)^{k+1} = 1$, and actually $\frac{2}{3} < p < 1$. Indeed, define the function $\phi(x) = x^{k+1} + (1-x)^{k+1} + x - 1$. Its derivative is $\phi\prime(x) = (k+1)[x^k - (1-x)^k] + 1 > 0$ if $x \geq \frac{1}{2}$. This is because if $x \geq \frac{1}{2}$ then $x > 1 - x$, so $\phi\prime(x) \geq 1 > 0$. Thus ϕ is strictly increasing on $[\frac{1}{2}, 1]$ so it can have at most one root. But $\phi(1) = 1 > 0$ and $\phi(\frac{2}{3}) = \frac{2^{k+1}+1-3^k}{3^{k+1}} < 0$. This last fact is true since $\frac{2^{k+1}+1-3^k}{3^{k+1}} < 0 \Leftrightarrow 1 < 3^k - 2^{k+1}$ which is true for $k = 2, 3, \ldots$. So ϕ being continuous and strictly increasing there is a unique root $p \in (\frac{2}{3}, 1)$.

Now, since p is a root of $p + p^{k+1} + (1-p)^{k+1} = 1$ we have that $p^{k+1} = (1-p)[1 - (1-p)^k]$ so

$$\frac{p^k}{1-p} = \frac{1-(1-p)^k}{p} < \frac{1}{p} < \frac{3}{2} = \frac{3 \cdot 1}{1+1} \leq \frac{3k}{k+1} \quad \text{for} \quad k = 2, 3, \ldots.$$

Thus

$$\frac{p^k}{1-p} \leq \frac{3k}{k+1}$$

so the result is proven.

■

We can now completely resolve the behavior of fixed points for ARBN updating.

Theorem 1 *For the cyclic scheme $\alpha = \frac{1}{N}$ there are only stable fixed points, i.e. no period doubling bifurcations.*

Proof Note that we always have $k \leq N$ and thus $\alpha = \frac{1}{N} \leq \frac{1}{k}$. Since it has been shown above that $\alpha > \frac{1}{k}$ for $\alpha(k)$ representing a k value of fixed point bifurcation, then no such point can exist.

■

Now we turn our attention to the GARBN scheme.

Theorem 2 *When a fixed number of two or more nodes update at once, so that $\alpha = \frac{2}{N}, \frac{3}{N}$, etc. then there can only be stable fixed points for sufficiently large k, i.e. any periodicity or chaos disappear as $k \to \infty$.*

In order to start the proof we need a few lemmas.

Lemma 1 *The stable fixed point p_k satisfies $p_k \to 1$ as $k \to \infty$.*

Proof This is a consequence of a lim sup, lim inf argument in the fixed point condition

$$p_k + p_k^{k+1} + (1-p_k)^{k+1} = 1.$$

For example suppose there is a sequence of p_k's, $p_{k_1}, p_{k_2}, \ldots$ such that $p_{k_n} \to \epsilon < 1$ as $n \to \infty$. Then ${p_{k_n}}^{kn} \to 0$ and $(1-p_{k_n})^{k_n+1} \to 0$ as $n \to \infty$ which is a contradiction.

■

Lemma 2 $p_k^{k+1} \to 0$ *and* $(1-p_k)^{k+1} \to 0$ *as* $k \to \infty$.

Lemma 3 $p_k^k \to 0$ *as* $k \to \infty$.

Lemma 4 $(1-p_k)^k \to 0$ *as* $k \to \infty$.

Proof Suppose $\limsup_{k\to\infty}(1-p_k)^k = \epsilon > 0$. Then $\limsup_{k\to\infty}(1-p_k) = \limsup_{k\to\infty}\epsilon^{\frac{1}{k}} = 1$, which is a contradiction.

■

Proof of Theorem 2 We assume $\alpha = \frac{2}{N}$ since the other cases are similar. Again it follows immediately that since $k \leq N$ we have $\alpha = \frac{2}{N} \leq \frac{2}{k}$. But now suppose that

$$\frac{2}{k} = \alpha(k) = \frac{2}{1+(k+1)p_k^k - (k+1)(1-p_k)^k}.$$

Then

$$1+(k+1)p_k^k - (k+1)(1-p_k)^k = k$$

or

$$p_k^k - (1-p_k)^k = \frac{k-1}{k+1}.$$

But the left hand side converges to 0 as $k \to \infty$ while the right hand side converges to 1 as $k \to \infty$. This is a contradiction.

■

4. Generalized Asynchronous Random Boolean Networks

In this section we describe a mathematical model for a GARBN. One familiar updating scheme for GARBNs is the clock scheme ([24], [38], [39]). This scheme allows more than one node to be updated at each time step, by assigning a timer to each node and setting the period of each timer at random. Observe that although the periods of timers are chosen at random, they are fixed from the very beginning and do not change thereafter. Thus the number of nodes to be updated at each time point is fixed. We provide a more general view by allowing a random number of nodes to be updated at each time point. We use the same Boolean rule as in section 2, and the same notation. We will focus on a few probability distributions to generate the number of nodes to be updated at each time point.

At time t we generate x_t, the number of nodes to be updated at time t, according to a given discrete random variable X with values $1, 2, \ldots, N$. Then we select the x_t nodes randomly (that is any collection of x_t nodes has the same probability of being chosen). Observe that now we can write $N_1(t) = N_1^u(t) + N_1^s(t)$ where $N_1^u(t)$ is the number of nodes in state 1 to be updated at time t, and $N_1^s(t)$ is the number of nodes in state 1 that do not change at time t and therefore will be in state 1 at time $t+1$ as well. Similarly,

we can write a formula for $N_0(t) = N_0^u(t) + N_0^s(t)$. Thus $N_1^u(t) + N_0^u(t) = x_t$. Observe that if $p(t)$ is the probability of finding a node in state 1 at time t, then $N_1^u(t) = x_t p(t)$ and $N_0^u(t) = x_t(1-p(t))$, and consequently $N_1^s(t) = N_1(t) - x_t p(t)$, $N_0^s(t) = N_0(t) - x_t(1-p(t))$. Given these quantities we can write the formulae for the number of nodes that change or not from time t to time $t+1$ as follows.

$$\begin{aligned} N_{0\to 1}(t) &= x_t(1-p(t))(1-(1-p(t))^k) \\ N_{1\to 0}(t) &= x_t p(t)^{k+1} \\ N_{0\to 0}(t) &= N_0(t) - x_t(1-p(t)) + x_t(1-p(t)^{k+1} \\ N_{1\to 1}(t) &= N_1(t) - x_t p(t)^{k+1} \end{aligned}$$

The sum of all these quantities is N as expected. Then the probability of finding a node in state 1 at time $t+1$ is

$$p(t+1) = \frac{N_{0\to 1}(t) + N_{1\to 1}(t)}{N} = p(t) + \frac{x_t}{N}\left(1 - p(t) - (1-p(t))^{k+1} - p(t)^{k+1}\right). \tag{5}$$

If all the nodes are 0 at time t, then $p(t) = 0$ so $p(t+1) = 0$, which is to be expected since by the Boolean rule all the nodes stay 0 at time $t+1$. Similarly, if all the nodes are 1 at time t, $p(t+1) = 1 - \frac{x_t}{N}$ by the formula, as well as by the Boolean rule. Observe that in this last case if x_t is close to 0, $p(t+1)$ is close to 1, and if x_t is close to N, $p(t+1)$ is close to 0. Therefore the actual shape of a graph of $p(t+1)$ versus $p(t)$ could be quite diverse.

Thus we want to study the behavior of the maps

$$f_t(p) = p + \frac{x_t}{N}\left(1 - p - (1-p)^{k+1} - p^{k+1}\right) \qquad t = 1, 2, 3, \ldots.$$

Observe that although the formula (5) is very similar to the formula for the cyclic scheme (1), there is a basic difference between them. The formula for the GARBNs depends on x_t which may change at each time point t, thus the iterations of the model do not represent simple compositions of a map f with itself.

Simulations of iterations of the system and the model show that the model is in general a good approximation for the Boolean system with a possible transitional phase as in the case of the cyclic scheme. We provide in Figures 13-14 some simulations in which the values x_t are generated according to the discrete uniform distribution on $\{1, 2, 3, \ldots, N\}$ with $N = 256, k = 128$ (Figure 13), and the binomial distribution with number of trials $N = 128$, probability of a success 0.9, and $k = 64$ (Figure 14). Other distributions have also been studied such as negative binomial, Poisson, power law on $\{1, 2, 3, \ldots, N\}$ for various parameters. The results for these distributions are similar to Figure 1 for the cyclic scheme.

A few comments are in order. A general feature is that the model is a good approximation for the system. In some cases there is a transition phase, but after enough iterations the model and the system become close regardless of the underlying distribution of x_t. The only distribution for which it could potentially take a long time to reach a steady state is the binomial distribution with a large probability

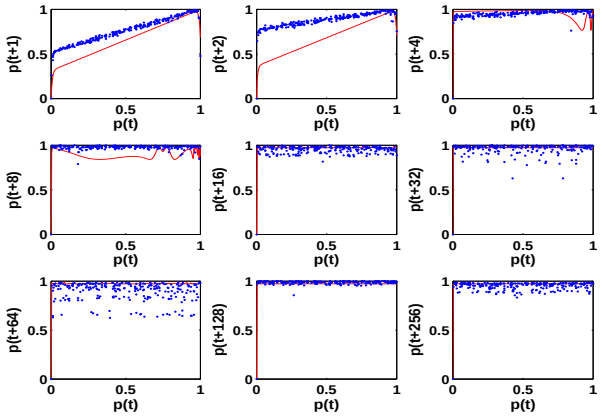


FIGURE 13. Iterations of the GARBN system and model for the case when x_t is discrete uniform on $\{1, 2, \ldots N\}$, $N = 256, k = 128$. We plot some of the first 256 iterations of the system and the model as specified in the labels. After about 2^5 iterations the model reaches a steady range of values for $p(t)$. There is a transient phase in which the model and the system do not match perfectly, but after several iterations, the match becomes quite clear. This figure is typical for the case of the uniform distribution.

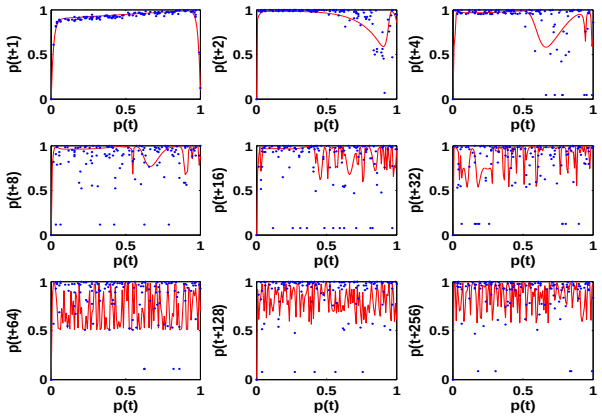


FIGURE 14. Iterations of the GARBN system and model for the case when x_t is binomial with number of trials $N = 128$ and probability of a success 0.9. Here the number of parents is $k = 64$. We plot some of the first 256 iterations of the system and the model as specified in the labels. It is clear that in this case the model does not seem to converge to a fixed value of $p(t)$, but rather oscillates in a certain range of values of $p(t)$. On the other hand the system does not settle either. This kind of situation occurs for large values of the probability of a success. Note that the mean value of the distribution, 115.2, is almost as large as N.

of a success (Figure 14). In this case the system may not reach a steady state behavior for the amount of iterations considered. Another common feature is that $p(t)$ approaches a value p as $t \to \infty$ for the model in most cases (exceptions were observed for the uniform distribution and the binomial distribution), which suggests that the system is reaching an equilibrium with the probability of finding a node in state 1 close to p. Again this is a feature encountered in the cases under study, with the comment that in the case of the binomial distribution, the values $p(t)$ do not settle into a value, but oscillate within an interval of values. The value of p has a wide range depending on the distribution and on the parameters of the distribution and the number of parents k. In general, the larger the number of parents k, the larger the probability p. The rate of convergence toward the probability p may differ from one case to another. But it is observed that if the number of nodes x_t to be updated at times t is large (that is a significant number of nodes is updated at most time points), the convergence is faster.

To complete these observations, we note that the iteration graphs can have various shapes for various distributions, especially during the transition phase.

Since the model is a good match for the system, we can use it to understand the behavior of the system under various scenarios. To do this we present again a study of the sensitivity of the orbits to initial values, bifurcation diagrams, and fixed point analysis.

The study of the sensitivity of the orbits to initial values shows that for the cases when x_t is obtained from the Poisson, negative binomial, or power law distributions, the error converges to zero rather fast. It is observed that as the number of nodes N increases the rate of convergence decreases, and as the number of parents k increases for a fixed N, the rate of convergence increases too. Intuitively this makes sense since the more nodes are in the network the more time seems to be needed to reach a steady state. At the same time, for a fixed N, if the nodes have more parents, then the node interaction is more elaborate and speeds up the process of reaching a steady behavior.

The case of x_t from a discrete uniform distribution on $\{1, 2, \ldots, N\}$ shows that if the number of nodes N is relatively small, the error converges to zero fast. When N is large, the error converges to zero faster for smaller values of k, but in most cases, depending on initial conditions, does settle only after many iterations, as shown in Figure 15.

Finally, in case x_t is from a binomial distribution, for small probabilities of success, the error converges to zero. Otherwise, the simulations performed show that the error may or may not converge to zero. Even for a relatively small number of nodes with small or large number of parents, or for large number of nodes with small number of parents, the error may not converge to zero.

We make the observation that the study of the error is related to the analysis of the robustness of the system, indicating how sensitive the system is to perturbations. The error plot in this paper is an analog of the Hamming distance analysis of other authors ([42]). The Hamming distance gives the proportion of nodes that are different in two states of the network.

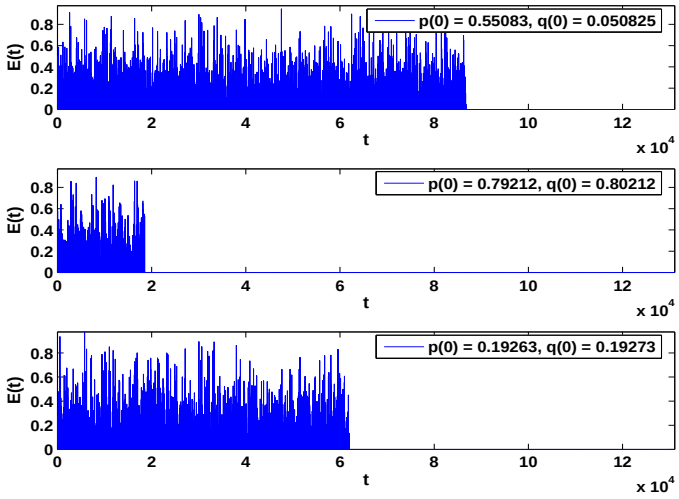


FIGURE 15. Error plot for the GARBN model in the case when x_t is a discrete uniform distribution on $\{1, 2, \ldots, N\}$, $N = 4096, k = 2048$. The error settles to zero after many iterations.

The bifurcation diagrams support the behavior observed so far. For the uniform distribution the bifurcation diagram suggests that the system may reach a more ordered behavior after many iterations as shown in Figure 16, where $N = 512$.

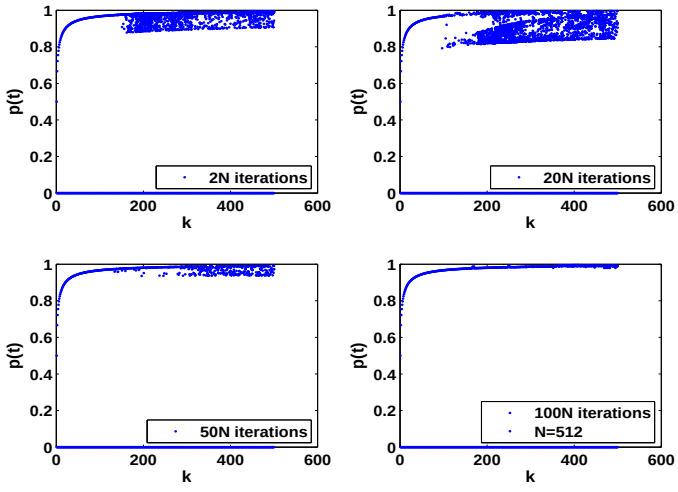


FIGURE 16. Bifurcation diagram for the GARBN model where x_t is from a uniform distribution on $\{1, 2, \ldots, N\}$, $N = 512$. We observe that after $20N$ iterations the diagram suggests a chaotic behavior, but in the long run it settles in an ordered behavior.

We note that the bifurcation diagram in Figure 16 is typical also for the case of a binomial distribution with a probability of success small or medium. For probability of a success relatively close to 1, the

bifurcation diagrams suggest a chaotic behavior for larger values of k, as in Figure 17. We note that the graphs are similar for a much larger number of iterations.

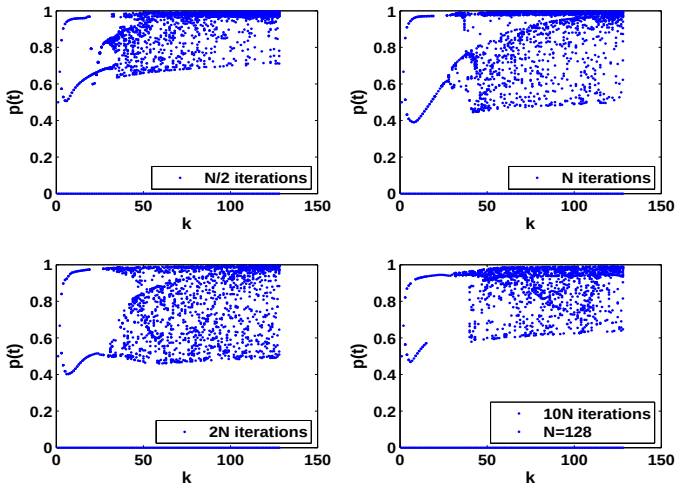


FIGURE 17. Bifurcation diagram for the GARBN model where x_t is from a binomial distribution with $N = 128$ trials and probability of a success 0.9. For certain values of the parameter k the system can exhibit order, for other values it can exhibit chaos. The mean value, 115.2, is large.

For the Poisson, negative binomial, and power law distributions, the bifurcation diagrams are similar to the one in Figure 3 for the ARBN, with the observations that the ordered behavior could be reached sooner or later, depending on the parameters.

Observe that the fixed points of the map

$$f(p) = p + \frac{x_t}{N}(1 - p - p^{k+1} - (1-p)^{k+1})$$

are the same as in the case of the cyclic scheme since the factor x_t does not change the equation which gives the fixed points, therefore Figure 4 is valid also in this case.

In conclusion, when random parameters dictate the evolution of the system, its behavior can be quite diverse, ranging from order to chaos.

Now we look more closely at the map

$$f_t(p) = p + \frac{x_t}{N}(1 - p - p^{k+1} - (1-p)^{k+1})$$

in which x_t is the value of a random variable X taking values in $\{1, 2, \ldots, N\}$. The shape of this map is dependent on the random term and can exhibit a variety of features. We study the iterations of this map using the following random variables: discrete uniform, continuous uniform, Poisson, binomial, negative binomial, power law, exponential, chi-square, and normal. As observed, we have extended our study from just discrete random variables to both discrete and continuous, thus allowing also fractional values for

x_t, for a more in depth analysis. In each case, the parameters of the distributions are selected so that the probability of generating values outside the interval $[1, N]$ is practically zero.

It is observed that in many cases the behavior is not very complex, and there is a sometimes slow, but clear tendency to a steady state. In the cases of the following distributions: uniform, Poisson, binomial with small probability of success, negative binomial, power law, exponential, chi-square with small number of degrees of freedom, and normal with small mean, the iteration graphs are approximately similar to those in Figure 6, with the observation that sometimes the iterations may exhibit some degree of complexity which vanishes after a short while. However, in the other cases, namely the chi-square with larger number of degrees of freedom, binomial with large probability of success, or normal with large mean distributions, the iterations suggest either "distributional periodicity" (Figure 18) or "distributional chaos" (Figure 19). Figures 18-19 are from a binomial distribution, but the other two cases mentioned previously produce graphs similar to those in Figure 18. The behavior is similar even after a much larger number of iterations of the model.

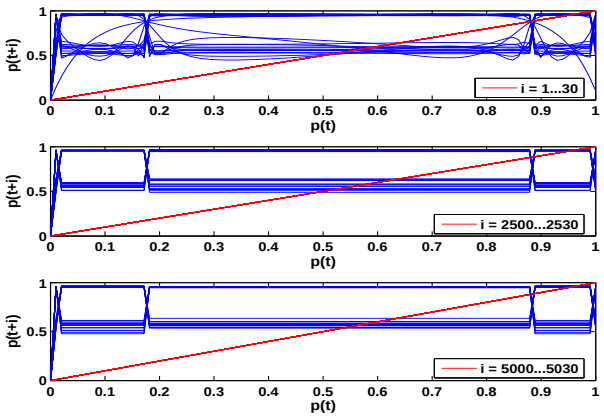


FIGURE 18. Plot of the iterations $1-30$, $2500-2530$, and $5000-5030$ of the map $f(p) = p + \frac{x_t}{N}(1-p-p^{k+1}-(1-p)^{k+1})$ in the case $N = 1024, k = 16$. Here x_t are values of a binomial distribution with number of trials $N = 1024$ and probability of success in a trial $\theta = 0.9$.

Observe that the complex behavior exhibited by the iterations of the model, such as in the case of the binomial distribution with probability of success 0.9 corresponds mainly to large values of x_t. In terms of the network, this means that a large number of nodes are updated at each time point. The larger the number of nodes updated, the more complex the behavior and the slower a potential steady state is reached. Observe that a large number of nodes updated at each time point brings the system closer to a synchronous random Boolean network which can exhibit chaos [31]. In fact, if one allows $\alpha \to 1$ in (2) the resulting function represents exactly the corresponding one obtained in [31] for synchronous networks. This emphasizes previous results showing that asynchrony could simplify the behavior of the

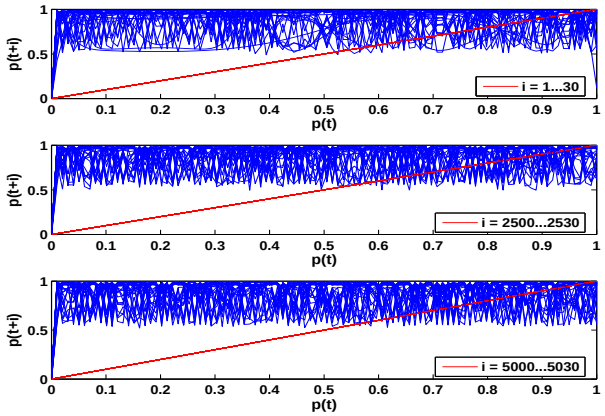


FIGURE 19. Plot of the iterations $1-30$, $2500-2530$, and $5000-5030$ of the map $f(p) = p + \frac{x_t}{N}(1-p-p^{k+1}-(1-p)^{k+1})$ in the case $N = 1024, k = 64$. Here x_t are values of a binomial distribution with number of trials $N = 1024$ and probability of success in a trial $\theta = 0.9$.

system in some cases, while synchrony can generate a more sophisticated behavior [25]. At the same time it becomes clear that randomness or noise in the system can generate various types of dynamics, emphasizing previous remarks [30].

The above discussion with distributions generalizes the observed behavior of the map

$$f(p) = p + \alpha(1-p-p^{k+1}-(1-p)^{k+1})$$

studied in Section 3, because the constant α, $0 < \alpha < 1$, can be interpreted as the mean value of the distribution divided by N.

5. Conclusions

In this paper we consider a Boolean network with N nodes, each node having k parents. We use a unique Boolean rule for all the nodes, which generalizes rule 126 of cellular automata. We study the behavior of the system in the case of Asynchronous Random Boolean Networks (ARBNs) and Generalized Asynchronous Random Boolean Networks (GARBNs) providing a model for the probability of a node being in state 1. We use the model to describe the system behavior through error plots, bifurcation diagrams and fixed point analysis. We show that the ARBN scheme generates an ordered behavior, while the GARBN scheme generates mainly order but possibly chaos depending on the distributions used to generate the number of nodes to be updated at each time point, as well as the parameters of these distributions.

One possibility for future work consists on enlarging the class of random number generators for the number of nodes to be updated at each time point. Considering various stochastic processes as potential

random number generators would be of interest, including some processes such as Markov processes, Poisson processes, Brownian motion or fractional Brownian motion.

Further directions of investigation will include a generalization of the work in this paper to the case of a nonconstant number of parents studied by the authors in [32] under the assumption of a synchronous network. Various distributions of the number of parents could be considered, including power-law rules.

It would be interesting to analyze the given Boolean system and its behavior using asynchronous updating by finding potential critical values for the number of parents k, that is values of k for which the system is at "the edge between order and chaos". It has been shown [43] that for general synchronous Boolean networks the critical value is $k = 2$, while for a certain class of asynchronous Boolean networks such critical values do not exist [29]. It is important to understand how a certain approach toward identification of the dynamics of the system influence the final result. For example in [29] the authors do not find a phase transition (from order to chaos) for GARBN's due to the usage of the so-called annealed approximation method. On the other hand the author of [42] questions their findings due to a different approach using the normalized Hamming distance which suggests a phase transition for $1 < k < 3$ regardless of the updating scheme. Considering a more in-depth analysis of the Hamming distance of states obtained by small perturbations, to identify regions where the critical values may lay, is also a subject for future work.

The study of ARBNs and its variants is in its early stages. However, it has already been observed that many processes in natural or artificial networks, could be both asynchronous and ordered [26]. Asynchrony can happen at a local level, but the global system exhibits modularity. The authors of [26] propose the spotlight model in which the Boolean network is divided into modules, each module being associated to a regulator node which controls the updates of the module, depending on its own state. The amount of asynchronicity is obtained by altering the number of modules used. Applying the spotlight model to the work described in this paper could generate some interesting results.

Last, but not least, considering various Boolean rules for the nodes is of interest, since nodes of real systems usually do not behave according to a fixed rule. In this respect, the authors intend to extend the present work in the direction of cellular automata rule 22 ([19], [32]), as well as other legalistic and totalistic rules.

References

[1] Kauffman S.A., *Metabolic stability and epigenesis in randomly constructed genetic nets*, J. Theor. Biol., 22 (1969), p. 437-467.

[2] Glass K., Kauffman S.A., *The logical analysis if continuous, non-linear biochemical control networks*, J. Theor. Biol., 39 (1973), p. 103-129.

[3] Kauffman S.A., *The origins of order*, Oxford University Press, 1993, p. 173-235.

[4] Shmulevich I., Dougherty E.R., Zhang W., *From Boolean to Probabilistic Boolean Networks as Models of Genetic Regulatory Networks*, Proceedings of the IEEE, Vol. 90, 11 (2002), p. 1778-1792.

[5] Shmulevich I., Dougherty E.R., Kim S., Zhang W., *Probabilistic Boolean networks: a rule-based uncertainty model for gene regulatory networks*, Bioinformatics, Vol. 18, 2 (2002), p. 261-274.

[6] Shmulevich I., Dougherty E.R., Zhang W., *Control of stationary behavior in probabilistic Boolean networks by means of structural intervention*, Journal of Biological Systems, Vol. 10, 4 (2002), p. 431-445.

[7] Shmulevich I., Dougherty E.R., Zhang W., *Gene perturbation and intervention in probabilistic Boolean networks*, Bioinformatics, Vol. 18, 10 (2002), p. 1319-1331.

[8] Shmulevich I., Lähdesmäki H.Dougherty E.R., Astola J., Zhang W., *The role of certain Post classes in Boolean network models of genetic networks*, PNAS, Vol. 100, 19 (2003), p. 10734-10739.

[9] Shmulevich I., Kauffman S., *Activities and sensitivities in Boolean network models*, Physical Review Letters, Vol. 93, 4 (2004), 048701.

[10] Huang S., *Genomics, complexity and drug discovery: insights from Boolean network models of cellular regulation*, Pharmacogenomics, 2, 3 (2001), p. 203-222.

[11] Huang S., Ingber D.E., *Shape - dependent control of cell growth, differentiation, and apoptosis: switching between attractors in cell regulatory networks*, Experimental Cell Research, 261 (2000), p. 91-103.

[12] Silvescu A., Honavar V., *Temporal Boolean network models of genetic networks and their inference from gene expression time series*, Complex Systems, 13 (2001), p. 61-78.

[13] Gómez-Gardeńes J., Moreno Y., Floría L.M., *Modeling complex gene expression networks: steady, periodic and chaotic states*, Quantitative Biology, 39 (1973), p. 103-129.

[14] Kauffman S., Peterson C., Samuelsson B., Troein C., *Random Boolean network models and the yeast transcriptional network*, J. Theor. Biol., 22 (1969), p. 437-467.

[15] Heidel J., Maloney J., Farrow C., Rogers J.A., *Finding cycles in synchronous Boolean networks with applications to biochemical systems*, International Journal of Bifurcation and Chaos, 13 (2003), p. 535-552.

[16] Fox J.J., Hill C.C., *From topology to dynamics in biochemical networks*, Chaos, Vol. 11, 4 (2001), p. 809-815.

[17] Wuensche A., *Discrete Dynamical Networks and their Attractor Basins*, Complexity International, Vol. 6 (1999).

[18] Wuensche A., *Basins of Attraction in Network Dynamics: A Conceptual Framework for Biomolecular Networks*, Modularity in Development and Evolution, eds G.Schlosser and G.P.Wagner. Chicago University Press 2004, chapter 13, p. 288-311.

[19] Wolfram S., *A new kind of science*, Wolfram Media, Champaign, 2002, p. 51-114.

[20] Albert R., Barabasi A-L., *Dynamics of complex systems: scaling laws for the period of Boolean networks*, Physical Review Letters, 84, 24 (2000), p. 5660-5663.

[21] Albert R., Barabasi A-L., *Statistical mechanics of complex networks*, Rev. Mod. Phys., 74, 47 (2002), p. 47-97.

[22] Barabasi A-L., Albert R., *Emergence of scaling in random networks*, Science, 286, (1999), p. 509-512.

[23] Yuan B., Chen K., Wang B-H., *Growing directed networks: organization and dynamics*, arXiv:cond-mat/0408391 v1, (2004).

[24] Cornforth D., Green D.G., Newth D., Kirley M., *Do artificial ants march in step? Ordered asynchronous processes and modularity in biological systems* , Artificial Life VIII, MIT Press, 2002, p. 28-32.

[25] Harvey I., Bossomaier T., *Time out of joint: attactors in asynchronous random Boolean networks*, Proceedings of the Fourth European Conference on Artificial Life (ECAL97), MIT Press, 1997, p. 65-75.

[26] Cornforth, D., Green, D.G., Newth, D., Kirley, M.R., *Ordered asynchronous processes in natural and artificial systems*, P. Whigham et al. (eds). Proceedings of the 5th Australia-Japan Joint Workshop on Intelligent & Evolutionary Systems, The University of Otago, Dunedin, New Zealand, 2001, p. 105-112.

[27] Di Paolo E.A., *Rhythmic and non-rhythmic attractors in asynchronous random Boolean networks*, BioSystems, 59 (2001), p. 185-195.

[28] Di Paolo E.A., *Searching for rhythms in asynchronous random Boolean networks*, Proceedings of ALIFE7, (2001), p. 73-80.

[29] Mesot B., Teuscher C., *Critical Values in Asynchronous Boolean Networks*, Proceedings of the 7th European Conference on Artificial Life (ECAL), 2003.

[30] Kanada Y., *The effects of randomness in asynchronous 1D cellular automata*, Proceedings of ALIFE IV, 1994.

[31] Andrecut M., Ali M. K., *Chaos in a simple Boolean network*, International Journal of Modern Physics B, Vol. 15, 1 (2001), p. 17-23.

[32] Matache M.T., Heidel J., *A random Boolean network model exhibiting deterministic chaos*, Phys. Rev. E 69, 056214, 2004, 10 pages.

[33] Boccara N. *Modeling complex systems*, Springer Verlag NY (2004).

[34] Claussen J.C., Nagler J., Schuster H.G., *Sierpinski signal generates* $1/f^{\alpha}$ *spectra*, Phys. Rev. E, 70 (2004), 032101.

[35] Nagler J., Claussen J.C., $1/f^{\alpha}$ *spectra in elementary cellular automata and fractal signals*, arXiv:nlin.CG/041003.

[36] Boccara N., Roger M., *Period-doubling route to chaos for a global variable of a probabilistic automata network*, Journal of Physics A: Math. Gen, 25 (1992), p. L1009-L1014.

[37] Wolfram S., *Statistical mechanics of cellular automata*, Rev. Mod. Physics, 55 (1983), p. 601.

[38] Low S., Lapsley D., *Optimization flow control, i: Basic algorithm and convergence*, IEEE/ACM Transactions on Networking, 7(6), (1999), p. 861-875.

[39] Thomas R., ed., *Kinetic Logic: A Boolean approach to the analysis of complex regulatory systems*, Lecture Notes in Biomathematics, Springer Verlag, 29 (1979).

[40] Gershenson C., *Classification of Random Boolean Networks*, Artificial Life VIII, Standish, Abbass, Bedau (eds) (MIT Press), 2002, p. 1-8.

[41] Alligood K. T., Sauer T. D., Yorke J. A., *Chaos, An introduction to dynamical systems*, Springer-Verlag New York, 1997.

[42] Gershenson C., *Phase transitions in random Boolean networks with different updating schemes*, submitted to Physica D.

[43] Derrida B., Pomeau Y., *Random networks of automata: A simple annealed approximation*, Europhysics Letters, 1(2) (1986), p. 45-49.