Generalized Automata Networks

Marco Tomassini

Information Systems Department, University of Lausanne, Switzerland
marco.tomassini@unil.ch

Abstract. In this work standard lattice cellular automata and random Boolean networks are extended to a wider class of generalized automata networks having any graph topology as a support. Dynamical, computational, and problem solving capabilities of these automata networks are then discussed through selected examples, and put into perspective with respect to current and future research.

1 Introduction

Cellular automata (CA) have been widely used since their introduction by Ulam and Von Neumann at the beginning of the 1950s. They have turned out to be an extremely flexible and simple model for studying many phenomena in a large variety of fields. Indeed, it would be hard to name a single area of investigation where CA have not been used with some success. This can be seen in two recent books [6,33] in which the focus is either on CA's modeling capabilities [6], or on their intrinsic computational and pattern formation properties [33]. In Wolfram's book the claim is even more ambitious, since CA are seen as the computational model at the source of almost all natural phenomena. Without necessarily accepting such "grand" claims, it should be granted that CA are indeed an extremely useful model. The "secrets" of the wide applicability of CA models are to be found in their structural simplicity, the fact that they can approximate continuous fields by a simpler discrete model which is easier to understand and to implement numerically, and by their universal computational properties. Structural simplicity is apparent in the use of rules that act locally in a regular lattice, and universal computational properties of CA have been known for a long time [33].

On the whole, and although there are many variations on the central theme, CA have been seen in general as simple homogeneous automata laid out on a regular grid, interacting in a small geometrically regular neighborhood. On the other hand, in recent years there has been substantial research activity in the science of networks, motivated by a number of innovative results, both theoretical and applied. Starting from the seminal 1998 paper of Watts and Strogatz [31], networks have been recognized as a central model for the description of countless phenomena of scientific, social and technological interest. Typical examples include the Internet, the World Wide Web, social acquaintance networks, electric power supply networks, biological networks, and many more. The key idea is that most real networks, both in the natural world as well as in man-made structures, have mathematical properties that set them apart from regular lattices and random graphs, which were the two main topologies studied until then. Inspired by previous qualitative observations made by social scientists, Watts and Strogatz

S. El Yacoubi, B. Chopard, and S. Bandini (Eds.): ACRI 2006, LNCS 4173, pp. 14–28, 2006.

introduced an algorithmic construction for *small-world networks* [1] in which pairs of vertices are connected by short paths through the network. The existence of short paths between any pair of nodes has been found since then in real networks as diverse as the Internet, airline routes, the World Wide Web, neural, genetic, and metabolic networks, citation and collaboration networks, and many others [22] . The presence of short paths is also a property of standard random graphs as those constructed according to the Erdös-Rényi model [22], but what sets real networks apart from random graphs is a larger *clustering coefficient*, a measure that reflects the locality of a structure. The topological structure of a network has a marked influence on the dynamical processes that may take place on it, a point that has been strikingly demonstrated, for example, by the fault-tolerant properties of the Internet [2], and by the spreading of epidemics [23].

Regular lattices and random networks (which are also regular in a statistical sense) have been thoroughly studied in many disciplines. For instance, the dynamics of lattices and random networks of simple automata have received a great deal of attention [16,12,6,33]. Starting from the above facts, conceiving of irregular networks of automata does not take a large stretch of imagination and could prove useful. Due to their novelty, and in spite of their potential interest, there have been comparatively few studies of the computational and dynamical properties of automata networks. Notable exceptions are [26,30,24,27,28,19] which mainly deal with extensions of classical CA, and a few recent articles on Boolean automata networks [3,4,21,13].

My intention in the present work is twofold: first, to define in a systematic manner a wider class of CA built on top of general networks, and second, to review recent work on their dynamical and computational properties in the new environment. Thus, I shall first present a graph-theoretic unified view of automata networks, followed by examples taken from the fields of automata computation and dynamics, and random boolean networks. The automata considered will be static, in the sense that the supporting network topology does not change in time. However, this is not a good assumption for many systems either because faults dynamically affect nodes and links, or just because the nature of the interaction between network nodes is itself dynamical as in social networks of interacting agents. Here I shall deal briefly with the effect of network perturbations but not with intrinsically dynamical network systems.

2 Cellular and Networked Automata

Cellular Automata are dynamical systems in which space and time are discrete. A standard d-dimensional cellular automaton consists of a finite or infinite d-dimensional grid of cells, i.e. a regular lattice, each of which can take on a value from a finite, typically small, set of values Σ. The value of each cell at time step t is a function of the values of a small local neighborhood of cells at time $t-1$. The cells update their states simultaneously according to a given local rule. Asynchronous CA with a given sequential update order can also be considered (see section 6).

[1] Small-world network is a general term meaning that a graph that has this property has both a small diameter and a clustering coefficient that is larger than that of a corresponding random graph. Watts–Strogatz small-world networks are just one particular family of graphs that possess these properties.

Formally, a cellular automaton A is a quadruple

$$A = (\Sigma, U, d, f),$$

where Σ is a finite set of states, U is the cellular neighborhood, $d \in Z^+$ is the dimension of A, and f is the local cellular interaction rule, also referred to as the transition function.

Given the position of a cell, $\mathbf{i}$, $\mathbf{i} \in Z^d$, in a regular d-dimensional uniform lattice, or grid (i.e., $\mathbf{i}$ is an integer vector in a d-dimensional space), its *neighborhood* U is defined by:

$$U_{\mathbf{i}} = \{\mathbf{i}, \mathbf{i} + \mathbf{r}_1, \mathbf{i} + \mathbf{r}_2, \ldots, \mathbf{i} + \mathbf{r}_{n-1}\},$$

where n is a fixed parameter that determines the neighborhood size, and $\mathbf{r}_j$ is a fixed vector in the d-dimensional space.

The *local transition rule* f

$$f : \Sigma^n \rightarrow \Sigma,$$

maps the state $s_{\mathbf{i}} \in \Sigma$ of a given cell $\mathbf{i}$ into another state from the set Σ, as a function of the states of the cells in the neighborhood $U_{\mathbf{i}}$. In uniform CA f is identical for all cells, whereas in non-uniform ones f may differ between different cells, i.e., f depends on $\mathbf{i}$, $f_{\mathbf{i}}$.

For a finite-size CA of size N (such as those treated herein) a *configuration* of the grid at time t is defined as

$$C(t) = (s_{\mathbf{0}}(t), s_{\mathbf{1}}(t), \ldots, s_{\mathbf{N-1}}(t)),$$

where $s_{\mathbf{i}}(t) \in \Sigma$ is the state of cell $\mathbf{i}$ at time t. The progression of the CA in time is then given by the iteration of the *global mapping*, also called *evolution operator* Φ

$$\Phi : C(t) \rightarrow C(t+1), \qquad t = 0, 1, \ldots$$

through the simultaneous application in each cell of the local transition rule f. The global dynamics of the CA can be described as a directed graph, referred to as the CA's *phase space*.

For one-dimensional CA with two possible states per cell f is a function $f : \{0,1\}^n \rightarrow \{0,1\}$, and the neighborhood size n is usually taken to be $n = 2r + 1$ such that:

$$s_i(t+1) = f(s_{i-r}(t), ..., s_i(t), ..., s_{i+r}(t)),$$

where $r \in Z^+$ is a parameter, known as the *radius*, representing the standard one-dimensional cellular neighborhood. The domain of f is the set of all 2^n n-tuples. For finite-size grids, spatially periodic boundary conditions are frequently assumed, resulting in a circular grid for one-dimensional systems and a torus for two dimensional ones; formally, this implies that cellular indices are computed modulus N.

To visualize the behavior of a one-dimensional CA one can use a two-dimensional space-time diagram, where the horizontal axis depicts the configuration $C(t)$ at a certain time t and the vertical axis depicts successive time steps, with time increasing down the page (for example, see Fig. 1).

We now extend the previous concepts to *Generalized Automata Networks* (GAN). With respect to standard CA, the most important change concerns the network topology: whilst in CA this topology is a d-dimensional regular lattice, GAN can be built on any connected graph. Let $G = (V, E)$ be a graph, where V is a set of vertices and E is a set of edges. E is a binary relation on V; it is either *symmetric* if the edge is unordered, as in undirected graphs, or it is an *ordered* pair, as in directed graphs. Both cases arise in GAN. With these definitions, a GAN on V is a quadruple $(G, \Sigma, U, \{f_i | i \in V\})$. The only change with respect to lattice synchronous CA is in the local transition function f which now depends on the *degree* k_i of vertex i, i.e. the number of neighbors can be different for different $i \in V$. This can be formalized as: $f_i : \Sigma^{k_i} \to \Sigma$. As in the case of CA, non-uniform GAN can be defined by allowing f_i to depend not only on the degree k_i of vertex i, but also on the position of i in the graph G. Likewise, asynchronous GAN can be defined by explicitly stating a sequence of vertex updates, including random sequences. In this paper I deal with binary, i.e. $\Sigma = \{0, 1\}$, uniform and non-uniform, synchronous and partially asynchronous GAN.

3 Small-World and Scale-Free Graphs

In this section I shall describe the main network types that will be used or referred to in the sequel. Although the following material is well known, I include a succint description for the sake of completeness so as to make the paper more self-contained. The reader is referred to the original works for more details.

The Watts–Strogatz Model. Following Watts and Strogatz [31], a small-world graph can be constructed starting from a regular ring of N nodes in which each node has k neighbors ($k \ll N$) by simply systematically going through successive nodes and "rewiring" each link with a certain probability β. When an edge is deleted, it is replaced by an edge to a randomly chosen node. If rewiring an edge would lead to a duplicate edge, the graph is left unchanged. This procedure will create a number of links, called *shortcuts*, that join distant parts of the lattice. Shortcuts are the hallmark of small worlds. While the average path length[2] between nodes scales logarithmically with the number of nodes in a random graph, in Watts-Strogatz graphs it scales approximately linearly for low rewiring probability but goes down very quickly and tends towards the random graph limit as β increases. This is due to the progressive appearance of shortcut edges between distant parts of the graph, which obviously contract the path lengths between many vertices. However, small world graphs typically have a higher clustering coefficient[3] than random graphs, and a degree distribution $P(k)$ close to Poissonian.

The Barabási–Albert Model. Albert and Barabási were the first to realize that real networks grow incrementally and that their evolving topology is determined by the way in which new nodes are added to the network. They proposed an extremely simple model based on these ideas [1]. One starts with a small *clique* of m_0 nodes. At each

[2] The average path length L of a graph is the average value of all pairs shortest paths.

[3] The clustering coefficient C of a node is a measure of the probability that two nodes that are its neighbors are also neighbors among themselves. The average $\langle C \rangle$ is the average of the Cs of all nodes in the graph.

successive time step a new node is added such that its $m \leq m_0$ edges link it to m nodes already in the graph. When choosing the nodes to which the new nodes connect, it is assumed that the probability π that a new node will be connected to node i depends on the current degree k_i of i. This is called the *preferential attachment* rule. Nodes with already many links are more likely to be chosen than those that have few. The probability $\pi(k_i)$ of node i to be chosen is given by:

$$\pi(k_i) = \frac{k_i}{\sum_j k_j},$$

where the sum is over all nodes already in the graph. The model evolves into a stationary network with power-law probability distribution for the vertex degree $P(k) \sim k^{-\gamma}$, with $\gamma \sim 3$, which justifies the name *scale-free*. As for Watts–Strogatz small-worlds, scale-free graphs have short average path length and clustering coefficients that are higher than those of the corresponding random graphs with comparable number of vertices and edges.

The Barabási–Albert model is by no means the only way for constructing scale-free graphs. For example, the BA incremental construction introduces historical correlations, due to the non-equilibrium dynamics of the construction process, and also degree correlations to some extent. Other constructions, such as the configuration model, may produce uncorrelated scale-free graphs. It is also possible to build scale-free graphs with a given degree distribution function, i.e. with an exponent $\gamma \neq 3$. Here these distictions are not crucial, although the reader is referred to the specialized literature for details (see [22] and references therein).

4 Dynamics and Pattern Formation in GAN

In a recent work, Marr and Hütt [19] have investigated the connection between network topology and the corresponding impact on network dynamics for binary GAN in a systematic manner. The tools of their analysis were similar to those employed by Wolfram [32] in his study of the emerging spatio-temporal patterns in one-dimensional CA. Although there are other, more rigorous classifications, Wolfram four-classes system, together with Langton's λ parameter [18] are still useful to understand the dynamical behavior of those CA, and an analogous of this classification was used in [19].

Marr and Hütt studied Watts–Strogatz small-world graphs, Barabási–Albert scale-free graphs, and random networks. They defined two main classes of binary GAN $\Omega_1(\kappa)$ and $\Omega_2(\kappa)$, each depending on a single parameter κ. This parameter takes into account the fact that in CA the transition function is defined for a constant number of neighbors while, by definition, this is not the case in GAN. In the first class λ remain constant, while in the second one it varies with κ.

Marr and Hütt showed by numerical simulation that the pattern formation capability of binary GAN strongly depends on the topology of the underlying network and that there are marked differences between GAN belonging to the two classes. By using temporal entropies, they found that in Watts–Strogatz small worlds increasing the rewiring probability progressively destroys local collective behavior, and beyond the small-world regime long-range correlations disappear. In Barabási–Albert scale-free

graphs, variation of the degree correlations through rewiring without changing the degree distribution, leads to an inhomogeneous distribution in word entropy of the time series for the symbolic dynamics of individual nodes. From that point of view, nodes with low degree have a far greater entropy than their regular graph counterparts. On average, however, the word entropy is similar to that of CA. There are many other interesting considerations in the paper of Marr and Hütt for which we do not have space here; the reader is referred to the original work for details.

5 Collective Tasks on GAN: Density and Synchronization

The density and the synchronization tasks are prototypical distributed computational problems for binary CA. The design, evolution, and performance evaluation of one-dimensional CA that approximately perform those tasks has a long history; an excellent review appears in [7]. The tasks are briefly described below.

The density Task. The density task for a finite one-dimensional CA of size N is defined as follows. Let $C(0)$ be the *initial configuration* of the CA, i.e. the sequence of bits that represents the state of each automaton at time 0, and let ρ_0 be the fraction of 1s in the initial configuration. The task is to determine whether ρ_0 is greater than or less than $1/2$. If $\rho_0 > 1/2$ then the CA must relax to a fixed-point configuration of all 1's, otherwise it must relax to a fixed-point configuration of all 0's, after a number of time steps of the order of the grid size N. Here N is set to 149, the value that has been customarily used in research on the density task (taking N odd avoids the case where $\rho_0 = 0.5$ for which the problem is undefined).

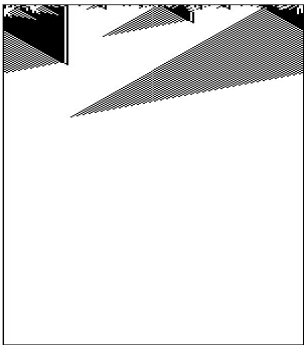

Fig. 1. The density task. Cell states are represented horizontally (black stands for 1). Time increases down the page. The initial density of ones is 0.416.

This computation is trivial for a computer with a central control: just scanning the array and adding up the number of, say, 1 bits will provide the answer in $O(N)$ time. However, it is nontrivial for a small radius one-dimensional CA since such an automaton can only transfer information at finite speed relying on local information exclusively, while density is a global property of the configuration of states. An example is given in

Fig. 1. It has been shown that the density task cannot be solved perfectly by a uniform, two-state CA with finite radius [17], although a slightly modified version of the task allows perfect solution by such an automaton [5], or by a combination of automata [11].

The *performance* of a CA rule on the density task is defined as the fraction of correct classifications over $n = 10^4$ randomly chosen initial configurations (ICs). ICs are sampled according to a binomial distribution among the 2^N possible binary strings i.e., each bit is independently drawn with probability $1/2$ of being 0. Clearly, this distribution is strongly peaked around $\rho_0 = 1/2$ and thus makes a difficult case for the CA to classify. The best CA found to date either by evolutionary computation or by hand have performances around 0.8 [7].

Using his small-world construction, and thus relaxing the regular lattice constraint, Watts [30] has been able to obtain GAN with performance around 0.85, with the same mean connectivity $\langle k \rangle$ as in the regular CA case. Moreover, given that different nodes may have now different degrees, Watts used a simple majority rule [4] as a transition function, a rule that cannot classify density in a regular CA. In [27] it was shown that such high-performance GAN can be obtained automatically and easily with a simple evolutionary algorithm, starting from either regular or completely random graphs.

The Synchronization Task. The one-dimensional synchronization task was introduced in [9]. In this task the CA, given an arbitrary initial configuration $C(0)$, must reach a final configuration, within $m \simeq 2N$ time steps, that oscillates between all 0s and all 1s on successive time steps, i.e. if $C(m)$ is such a final configuration, and (say) $C(m) = \{0\}^n$, one has $C(m+2k+1) = \{1\}^n$, and $C(m+2k) = \{0\}^n$, $k = 0, 1, \ldots$. Figure 2 depicts the space-time diagram of a CA that solves the task for the given initial configuration.

As with the density task, synchronization also comprises a non-trivial computation for a small-radius CA, and it is thus extremely difficult to come up with CA rules that, when applied synchronously to the whole lattice produce a stable attractor of oscillating all 0s and all 1s configurations. Das et al. were able to automatically evolve very good ring CA rules of radius three for the task by using genetic algorithms [9]. Sipper did the same for quasi-uniform CA, i.e. CA with a few different rules instead of just one [25], attaining excellent performance for radius-one CA. The performance of a CA on this task is evaluated by running it on randomly generated initial configurations, uniformly distributed over densities in the range $[0, 1]$, with the CA being run for $M \simeq 2N$ time steps. Performance values close to 1 have been obtained.

Task Performance on Watts–Strogatz Networks. Figure 3 shows that GAN obtained by artificial evolution of the network topology without including any preconceived design issue, yield high-performance automata networks in the same class of those constructed by Watts and better than ring CA for the density task. The simple majority rule was used at each node. In these figures ϕ is the fraction of shortcuts in the graph; thus $\phi = 0$ corresponds to the ring case while $\phi = 1$ approaches the random graph case.

The results for the synchronization task (not reported here) are similar [28]. Thus, relaxing the regularity condition of the network, one can easily obtain GAN that are at

[4] The majority rules attributes to the central cell the state of the majority of neighbors, including the cell itself. In case of tie, the state is chosen uniformly at random.

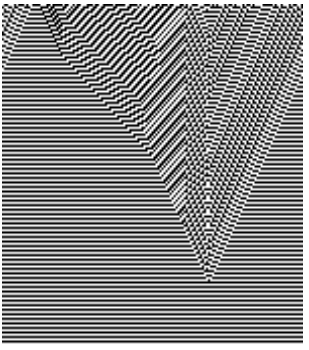

Fig. 2. A one-dimensional CA correctly performing the synchronization task

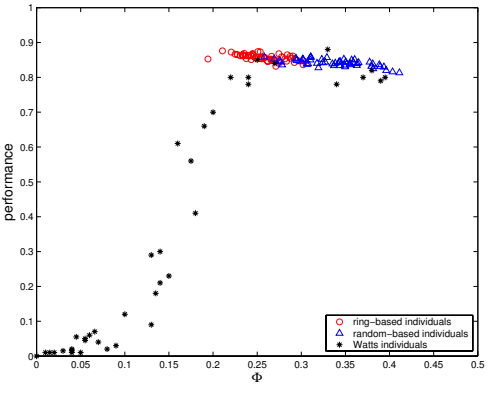

Fig. 3. Density task. The ϕ - performance values of the 50 best individuals found by evolution starting from rings and random graphs. For comparison, Watt's results (redrawn from [30])are also plotted.

least as good as the best designed or evolved CA for the tasks, with a similar average number of neighbors. Besides, if instead of using the simple majority rule the local transition function f was made itself to evolve, results would probably be even better. In fact, in a recent work Mesot and Teuscher [21] shown that randomly interconnected boolean automata using arbitrary boolean functions at the nodes (see section 6) can perform the synchronization and density task with high performance.

Task Performance on Scale-Free Networks. In [8] Albert and Barabási type networks (see section 3) were constructed to be used as support for CA computations with $\langle k \rangle = \{6, 12\}$. Results depicted in Figure 4 show that performance on the density task of CA mapped on scale-free networks are above 0.7 for networks with a smaller m_0, the size of the initial kernel. When a certain threshold is reached (m_0 about 14 for $\langle k \rangle = 6$ and 35 for $\langle k \rangle = 12$), performances drop dramatically. This means that the more the structure of the scale-free network become star-like, with a unique oversized cluster and only small satellites weakly connected ($m \rightarrow 1$), the information circulates with

more difficulties. Results for scale-free graphs built using the configuration model are comparable. One can thus conclude that scale-free network topologies are less suitable than Watts–Strogatz small worlds as a substrate for the density task. The results are even worse than those obtained in rings [7] using specialized rules.

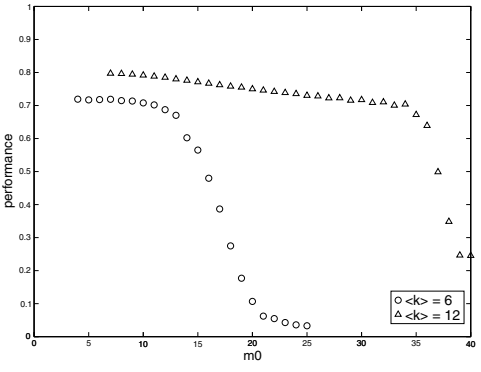

Fig. 4. Performance vs m_0 of scale-free networks (built on the Albert and Barabási model) on the density task. The circles represent the performance of networks with an average connection $\langle k \rangle = 6$ and triangles $\langle k \rangle = 12$.

The relative unsuitability of scale-free nets for collective task solving is confirmed by the numerical study of their behavior under noise for the density task. Using a probabilistic fault model, it appears that Watts–Strogatz type networks are much more robust than scale-free ones, as they tolerate a higher amount of errors without compromising task performance too much [8]. This is a surprising result, given that scale-free networks are notoriously very robust under random node or link failure [2]. Needless to say, Watts–Strogatz small worlds also have much better faul-tolerance capabilities than rings for the same task.

6 Generalized Boolean Networks

Random Boolean Networks (RBN) are directed GAN that have been introduced by Kauffman more than thirty years ago in a landmark paper [15] as a highly simplified model of genetic regulatory networks. In a RBN with N nodes, a node represents a gene and is modeled as an on-off device, meaning that a gene is expressed if it is on (1), and it is not otherwise (0). Each gene receives K randomly chosen inputs from other genes. Initially, one of the possible Boolean functions of K inputs is assigned at random to each gene. The network dynamics is discrete and synchronous: at each time step all nodes simultaneously examine their inputs, evaluate their Boolean functions, and find themselves in their new states at the next time step. Over time, the system travels through its phase space, until a point or cyclic attractor is reached whence either it will remain in that point attractor forever, or it will cycle through the states of the periodic attractor. Since the system is finite and deterministic, this will happen at most after 2^N time steps.

This extremely simple and abstract model has been studied in detail by analysis and by computer simulations of statistical ensembles of networks and it has been shown to be capable of extremely interesting dynamical behavior. We summarize the main results here (a full description is found in [16]).

First of all, it has been found that, as some parameters are varied such as K, or the probability p of expressing a gene, i.e. of switching on the corresponding node's state, the RBN can go through a phase transition. Indeed, for every value of p, there is a critical value of connectivity K such that for values of K below this critical value the system is in the ordered regime, while for values of K above this limit the system is said to be in the chaotic regime. In classical RBN $K = 1$ corresponds to the ordered regime, $K = 2$ is critical, and $K \geq 3$ means that the system is in the chaotic phase. Kauffman found that for $K = 2$ the size distribution of perturbations in the networks is a power law with finite cutoff that scales as the square root of N. Thus perturbations remain localized and do not percolate through the system. The mean cycle length scales at most linearly with N for $K = 2$. Kauffman's suggestion is that cell types correspond to attractors in the RBN phase space, and only those attractors that are short and stable under perturbations will be of biological interest. Thus, according to Kauffman, $K = 2$ RBN lying at the edge between the ordered phase and the chaotic phase can be seen as abstract models of genetic regulatory networks.

RBN are interesting in their own as complex dynamical systems and have been throughly studied as such using the concepts and tools of statistical mechanics. However, I believe that the original view of Kauffman, namely that these models may be useful for understanding real cell regulatory networks, is still a valid one, provided that the model is updated to take into account present knowledge about the topology of real gene regulatory networks, and the timing of events, without loosing its attractive simplicity. In the following I shall describe a couple of ways in which the Kauffman model could be modified in order to take into account a number of experimental observations that were not available at the time (more details of the model can be found in [13]).

The Network Model. Kauffman's RBN model rests on three main assumptions:

- The nodes implement Boolean functions and their state is either on or off;
- The nodes that affect a given node in the network are randomly chosen and are a fixed number;
- The dynamics of the network is synchronous in time.

The binary state simplification could seem extreme but actually it represents quite well "threshold phenomena" in which variables of interest suddenly change their state, such as neurons firing or genes being switched on or off.

Random networks with fixed connectivity degree were a logical generic choice in the beginning, since the exact couplings in networks were generally unknown. Today it is more open to criticism since it does not correspond to what we know about the topology of biological networks. In fact, many biological networks, including genetic regulatory networks, seem to be of the scale-free type or of a hierarchical type (see [29] and references therein) but not random, according to present data. For scale-free networks, this means that the degree distribution function $P(k)$ is a power law $P(k) \sim k^{-\gamma}$, usually with $2 < \gamma < 3$, instead of a Poisson distribution as in a random graph, or a delta

distribution as in a classical RBN. Thus the low connectivity suggested by Kauffman for candidate stable systems is not found in such networks, where a wide range of degrees is present instead. The consequences for the dynamics may be important, since in scale-free graphs there are many nodes with low degree and a low, but not vanishing, number of highly connected nodes. Along this line, M. Aldana has recently presented a detailed analysis of Boolean networks with scale-free topology [3]. He definened a phase space diagram for boolean networks, including the phase transition from ordered to chaotic dynamics, as a function of the power law exponent γ. He also made exhaustive simulations for several relatively small values of N, the network size.

The model of [13] has in common with Aldana's the scale-free topology of the networks, although the graphs are constructed in a different way. But, in contrast to Aldana's, a suitable semi-synchronous dynamics is defined for the system, instead of using the customary synchronous update.

As sais above, according to present data many biological networks, including genetic regulatory networks, show a scale-free output distribution $P_{out}(k)$ and a Poissonian input distribution $P_{in}(k)$ [29]. The networks used in Giacobini's et al. work [13] have been generated according to a mixed generalized/poisson random graph : first a sequence of N out-degrees that satisfies a power-law distribution with exponent γ is assigned to N nodes; then, every out-going edge is assigned as input to one of the N nodes chosen at random (excluding self-connections). The resulting networks have a scale-free distribution of the output degrees and a Poisson distribution of the input degrees.

Synchronous, Asynchronous and Semi-Synchronous Network Dynamics. Standard RBN update their state synchronously. This assumption simplifies the analysis, but it is open to discussion if the network has to be biologically plausible. In particular, for genetic regulatory networks, this is certainly not the case, as many recent experimental observations tend to prove. Rather, genes seem to be expressed in different parts of the network at different times, according to a strict sequence (see, for instance, [10]). Thus a kind of serial, asynchronous update sequence seems to be needed. Asynchronous dynamics must nevertheless be further qualified, since there are many ways for serially updating the nodes of the network.

Several researchers have investigated the effect of asynchronous updating on classical RBN dynamics in recent years [14,20]. Harvey and Bossomayer studied the effect of asynchronous updating on some statistical properties of network ensembles, such as cycle length and number of cycles. They used un update sequence in which the next cell to be updated is chosen at random with uniform probability and with replacement. [14]. They found that many features that arise in synchronous RBN do not exist, or are different in non-deterministic asynchronous RBN. Thus, while point attractors do persist, there are no true cyclic attractors, only so-called loose ones and states can be in more than one basin of attraction. Also, the average number of attractors is very different from the synchronous case: even for $K = 2$ or $K = 3$, which are the values that characterize systems at the edge of chaos, there is no correspondence between the two dynamics. Mesot and Teuscher [20] studied the critical behavior of asynchronous RBN and concluded that they do not have a critical connectivity value analogous to synchronous RBN and they behave, in general, very differently from the latter, thus confirming the findings of [14].

Considering the above reults and what is known experimentally from microarray data about the timing of events in genetic networks it seems that neither fully synchronous nor completely random asynchronous network dynamics are suitable models. Synchronous update is implausible because events do not happen all at once, while completely random dynamics does not agree with experimental data on gene activation sequences and the model does not show stable cyclic attractors of the right size. Thus, the activation/update sequence in a RBN should be in some way related to the topology of the network. A topology-driven semi-synchronous update method, called *Cascade Update* (CU) has been proposed in [13]. Such an update scheme is certainly not a faithful model for true biological gene activation sequences which are clearly not the same for different regulatory networks. But the scheme is closer to biological reality than previously proposed ones namely, fully synchronous and various asynchronous policies.

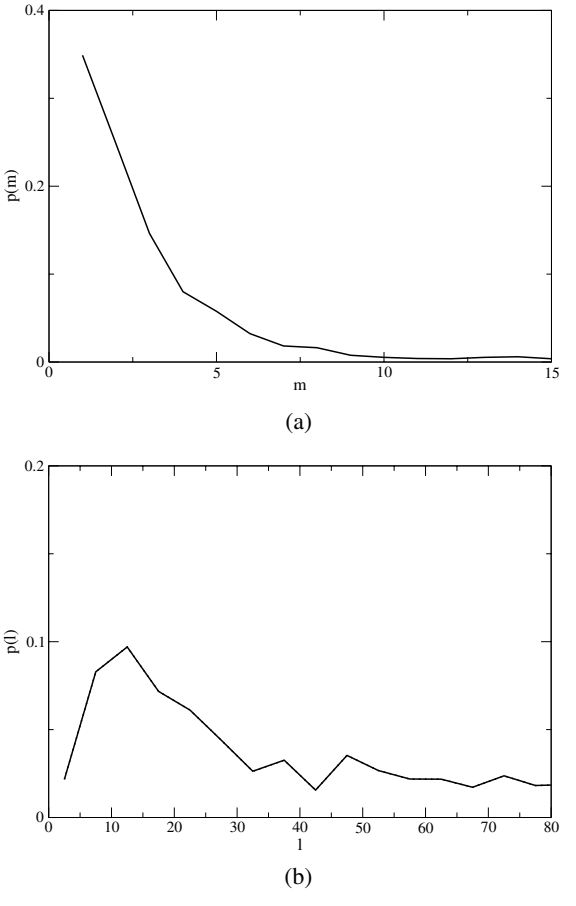

Fig. 5. probability distributions of the number of different attractors (a), and of the length of the attractors (b) for network realizations having $N = 50$ nodes evolving using cascade update

The CU consists in an asynchronous sequence of synchronously updated blocks of nodes. At the beginning of the evolution of the network, a node, say i, is randomly chosen and updated. Then, in the next time step, the block of the nodes to whom i projects is synchronously updated. The process continues, updating at each time step a new block formed by all the nodes in the network to which the nodes updated in the previous time step project. This scheme is deterministic: once the first node is chosen, the sequence of all the successive updates is unique and will reach a cycle, since the dynamical system is finite. As a consequence, the attractors of the dynamics cannot be loose attractors, they have to be true point or cyclic ones.

The results found in [13] by extensive numerical simulation covering Aldana's ordered regime, edge of chaos, and chaotic phase confirm that the behavior of the network model is biologically plausible, showing cyclic attractors of reasonable length. This can be seen in Fig. 5 where average results are reported for a network size $N = 50$ and a power lae exponent $\gamma = 2.48$ which places the system at the edge between the ordered and the chaotic phase. This intermediate regime, the analogous of Kauffman's $K = 2$, is the one where perturbations remain localized, according to Aldana, and thus the system enjoys the necessary stability.

7 Conclusions

Relaxing the regularity constraints in cellular automata gives rise to generalized automata networks (GAN). Although in this way the systems become more complex to describe ant to analyze, they also show a richer set of dynamical behaviors. Here we have reviewed a number of those GAN, ranging from networks for collective task solving, to biological-like Boolean GAN. It has been seen that GAN have better problem solving capabilities than CA, while at the same time offering superior fault-tolerance behavior, except in the scale-free case, which is rather fragile from this point of view. As models of biological regulatory networks, GAN are more credible than customary RBN. They correctly describe the observed network topologies, and their dynamics is also on the right track qualitatively. GAN have been known for a number of years now, but they are still mostly unexplored. The review presented here and the work cited is only a first step toward their characterization.

Acknowledgments. Financial support for this research by the Swiss National Science Fundation under contarct 200021-107419 is gratefully acknowledged.

References

1. R. Albert and A.-L. Barabási. Statistical mechanics of complex networks. *Reviews of Modern Physics*, 74:47–97, 2002.
2. R. Albert, H. Jeong, and L. Barabási. Error and attack tolerance of complex networks. *Nature*, 406:378–382, 2000.
3. M. Aldana. Boolean dynamics of networks with scale-free topology. *Physica D*, 185:45–66, 2003.
4. L. A. N. Amaral, A. Díaz-Guilera, A. Moreira, A. L. Goldberger, and L. A. Lipsitz. Emergence of complex dynamics in a simple model of signaling networks. *Proc. Nat. Acad. Sci. USA*, 101(44):15551–15555, 2004.

5. M. S. Capcarrère, M. Sipper, and M. Tomassini. Two-state, r=1 cellular automaton that classifies density. *Physical Review Letters*, 77(24):4969–4971, December 1996.
6. B. Chopard and M. Droz. *Cellular Automata Modeling of Physical Systems*. Cambridge University Press, Cambridge, UK, 1998.
7. J. P. Crutchfield, M. Mitchell, and R. Das. Evolutionary design of collective computation in cellular automata. In J. P. Crutchfield and P. Schuster, editors, *Evolutionary Dynamics: Exploring the Interplay of Selection, Accident, Neutrality, and Function*, pages 361–411. Oxford University Press, Oxford, UK, 2003.
8. C. Darabos, M. Giacobini, and M. Tomassini. Scale-free automata networks are not robust in a collective computational task. Lecture Notes in Computer Science. Springer, Berlin, 2006. this volume.
9. R. Das, M. Mitchell, and J. P. Crutchfield. A genetic algorithm discovers particle-based computation in cellular automata. In Y. Davidor, H.-P. Schwefel, and R. Männer, editors, *Parallel Problem Solving from Nature- PPSN III*, volume 866 of *Lecture Notes in Computer Science*, pages 344–353, Heidelberg, 1994. Springer-Verlag.
10. E. H. Davidson and et al. A genomic regulatory network for development. *Science*, 295:1669–1678, March1 2002.
11. H. Fukś. Solution of the density classification problem with two cellular automata rules. *Physical Review E*, 55(3):2081–2084, 1997.
12. M. Garzon. *Models of Massive Parallelism: Analysis of Cellular Automata and Neural Networks*. Springer-Verlag, Berlin, 1995.
13. M. Giacobini, M. Tomassini, P. De Los Rios, and E. Pestelacci. Dynamics of scale-free semi-synchronous boolean networks. In L. M. Rocha et al., editor, *Artificial Life X*, pages 1–7, Cambridge, Massachusetts, 2006. The MIT Press.
14. I. Harvey and T. Bossomaier. Time out of joint: attractors in asynchronous random boolean networks. In P. Husbands and I. Harvey, editors, *Proceedings of the Fourth European Conference on Artificial Life*, pages 67–75, Cambridge, MA, 1997. The MIT Press.
15. S. A. Kauffman. Metabolic stability and epigenesis in randomly constructed genetic nets. *Journal of Theoretical Biology*, 22:437–467, 1969.
16. S. A. Kauffman. *The Origins of Order*. Oxford University Press, New York, 1993.
17. M. Land and R. K. Belew. No perfect two-state cellular automata for density classification exists. *Physical Review Letters*, 74(25):5148–5150, June 1995.
18. C. G. Langton. Computation at the edge of chaos: Phase transitions and emergent computation. *Physica D*, 42:12–37, 1990.
19. C. Marr and M.-T.Hütt. Topology regulates pattern formation capacity of binary cellular automata on graphs. *Physica A*, 354:641–662, 2005.
20. B. Mesot and C. Teuscher. Critical values in asynchronous random boolean networks. In W. Banzhaf, editor, *Advances in Artificial Life, ECAL2003*, volume 2801 of *Lecture Notes in Artificial Intelligence*, pages 367–376, Berlin, 2003. Springer.
21. B. Mesot and C. Teuscher. Deducing local rules for solving global tasks with random Boolean networks. *Physica D*, 211:88–106, 2005.
22. M. E. J. Newman. The structure and function of complex networks. *SIAM Review*, 45:167–256, 2003.
23. R. Pastor-Satorras and A. Vespignani. Epidemic spreading in scale-free networks. *Phy. Rev. Lett.*, 86:3200–3203, 2001.
24. R. Serra and M. Villani. Perturbing the regular topology of cellular automata: implications for the dynamics. In S. Bandini, B. Chopard, and M. Tomassini, editors, *Cellular Automata, ACRI 2002*, volume 2493 of *Lecture Notes in Computer Science*, pages 168–177. Springer-Verlag, Heidelberg, 2002.
25. M. Sipper. *Evolution of Parallel Cellular Machines: The Cellular Programming Approach*. Springer-Verlag, Heidelberg, 1997.

26. M. Sipper and E. Ruppin. Co-evolving architectures for cellular machines. *Physica D*, 99:428–441, 1997.
27. M. Tomassini, M. Giacobini, and C. Darabos. Evolution of small-world networks of automata for computation. In X. Yao et al., editor, *Parallel Problem Solving from Nature - PPSN VIII*, volume 3242 of *Lecture Notes in Computer Science*, pages 672–681. Springer Verlag, Berlin, 2004.
28. M. Tomassini, M. Giacobini, and C. Darabos. Evolution and dynamics of small-world cellular automata. *Complex Systems*, 15:261–284, 2005.
29. A. Vázquez, R. Dobrin, D. Sergi, J.-P. Eckmann, Z. N. Oltvai, and A.-L. Barabàsi. The topological relationships between the large-scale attributes and local interactions patterns of complex networks. *Proc. Natl. Acad. Sci USA*, 101(52):17940–17945, 2004.
30. D. J. Watts. *Small worlds: The Dynamics of Networks between Order and Randomness*. Princeton University Press, Princeton NJ, 1999.
31. D. J. Watts and S. H. Strogatz. Collective dynamics of 'small-world' networks. *Nature*, 393:440–442, 1998.
32. S. Wolfram. Universality and complexity in cellular automata. *Physica D*, 10:1–35, 1984.
33. S. Wolfram. *A New Kind of Science*. Wolfram Media, 2002.