RELAXATION IN THE RANDOM MAP MODEL*

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Properties of two sets of finite deterministic cellular automata are compared: the set of local homogeneous one-dimensional automata and the set of all possible automata (random map model). We investigate the following properties: relaxation time, number and length of limit cycles and the distribution of the size of bassins of attraction.

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1. Introduction

Cellular automata (CA) formalism is known [1, 2] to be a relatively new technique of computer simulation, with numerous existing and potential applications in various branches of technology and science. A good deal of problems of modern theoretical physics can be expressed within this formalism; in particular, our understanding of complexity [3], self-organization [4] and chaos [5] has been improved with the application of CA. Most generally, cellular automata can be divided into deterministic and probabilistic ones, but in this paper we shall not discuss probabilistic CA. Let us recall a standard definition of a deterministic cellular automaton as a triade: a discrete space (lattice), a set of its states and a rule of evolution of lattice states in discrete time. In most cases rules are local, i.e. they are defined as dependent on states of neighboring lattice cells. The language of CA is particularly useful when one intends to discuss the analogies between a physical process and a calculation [6]. Some general characteristics of both are hoped to be captured; then, asymptotic behaviour of complex physical processes could be simulated and foreseen, if their essential features are

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properly described in terms of simple rules of CA. It is appealing to recognize all possible results, which could be obtained at least within a limited family of CA. That is why people are interested in the problem of classification of rules [7]. Various schemes of classification of asymptotic states of CA have been proposed [7–13]. It is known, however, that in general case one cannot predict the future of a lattice before performing simulation [14].

The random map model [15] can be treated as a cellular automaton with randomly selected rule, defined on a whole lattice. This model is defined as a random mapping of a set of states onto itself; once the mapping is chosen, the trajectory is deterministic. This model is equivalent [16] to the Kauffman model [17] with maximal connectivity K ($K = N$), where K is the number of cells which influence a state of a given cell, and N is the number of lattice cells. The Kauffman model was introduced many years ago [18] to describe biological process of cell differentiation. It can be treated as a mixture of all possible cellular automata [19]. The random map model is even older (for a review see [20]) and it was taken as a reference model for the Kauffman model [16].

Recently, relaxation time t of an automaton was discussed [21] within the Kauffman model for the above mentioned case of $K = N$. The relaxation time of an automaton was defined as a number of time steps needed to reach a limit cycle (limit point). As the discussion was limited to finite systems, no other attractors were possible. Obviously, relaxation time depends on an initial state; then, we have to average over all possible initial states and over all possible mappings. A probability distribution $P(t)$ was proved [21] to be the same as the probability distribution $P(c)$ for the length c of limit cycles, *i.e.* for a given system $P(c) = P(t + 1)$. The distribution $P(c)$ was investigated analytically [15, 20] in the limit of infinite N. These results on $P(c)$ are valid for $P(t)$ as well.

Relaxation time of an automaton can be of interest because it is a simple analogue of a physical relaxation time, important feature of irreversible processes. The aim of this paper is to compare the distribution $P(t)$ obtained within the random map model with the same distribution obtained for more limited class of CA. The latter class is chosen to be one-dimensional, homogeneous CA, when rules are defined on three cells: a central one and its two nearest neighbours. This simple family of automata was investigated carefully by many authors ([1, 8, 11, 22] and references therein). Below we demonstrate that the definition of relaxation time allows to distinguish some subclasses within this well-known class of automata.

For the completeness of the comparison we investigate also some other quantities, namely the average number of attractors and the parameters of the distribution of the size of bassins of attraction. We believe that such analysis could be helpful also for other families of CA. In any case, the definition of a given family of CA is a constraint of the whole set of CA, which constitute the random map model. The comparison shows, then, the consequences of such a constraint.

2. The results

Average relaxation time $\langle t \rangle$ is calculated for two sets of CA: all possible mappings of the space of global lattice states onto itself, and all homogeneous local (LH1D) one-dimensional automata, defined on a ring of N cells (periodic boundary conditions). The former case is just the case of the random mapping model (RM). For this case, the distribution $P(t)$ depends on the number w of all possible states of lattice; the number of states of a cell is not determined. The latter LH1D family of CA is parametrized by N. To compare the results on RM and LH1D automata in one figure, we have to put for both cases the same function f of the number of states on the horizontal axis. The calculations for LH1D case are performed with an assumption of two states per cell; so, the number of states in this case is equal to $2N$. For reasons which will be given below we choice $f = \log 2w$ for the case of RM. Then, we compare $\langle t \rangle$ as dependent on $\log 2w$ for the case of RM with $\langle t \rangle$ as dependent on N for the case of LH1D. The former curve is obtained just from the analytical formula [21]

$$\langle t \rangle = \frac{w!}{w^{w+1}} \sum_{k=0}^{w} k \sum_{i=0}^{w-k-1} \frac{w^k}{k!} \tag{1}$$

and the latter one from direct verification of 256 automata and 2^N initial states. The result is given in the Fig. 1. We see that for the random map model, average relaxation time dependence on w can be satisfactorily approximated by its asymptote [15]

$$\langle t \rangle \approx \sqrt{\frac{\pi w}{8}}, \tag{2}$$

even for small values of w. (The coefficient $(\pi/8)^{1/2}$ is erroneously written as $1/2$ in [16, 17].) We checked also some moments of the distribution $P(t)$; n-th moment seems to be proportional to $w^{n/2}$ for $n = 1, 2, 3, 4$. The results obtained for LH1D automata seem to be linear with N. The logarithmic scale is chosen just to demonstrate this proportionality. The proportionality coefficient slightly depends on whether N is even or odd; for upper parts of the curves its values are 0.255 and 0.248, respectively.

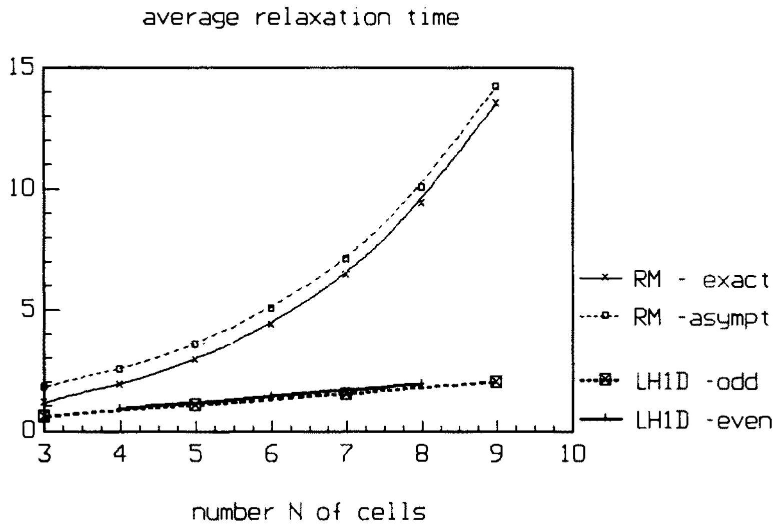

Fig. 1. Average relaxation time of LH1D automata (N even and odd), compared with the results of the RM model.

In paper [21], the distribution $P(t,c)$ for random mapping model was obtained analytically. The formula is

$$P(t,c) = P(t+c) = \frac{w!}{(w-t-c)!w^{t+c+1}} \,. \tag{3}$$

Obviously we have w^w automatons and w initial states; then we can get the number of cases $N(t,c)$, just by multiplying the distribution $P(t,c)$ by w^{w+1}. We are interested in the number N_a of attractors per an automaton; it is easy to obtain it from the following formula:

$$N_a = \frac{1}{w^w} \sum_{c=1}^{w} \frac{N(t=0,c)}{c} \,, \tag{4}$$

because $N(t=0,c)$ is the number of cases, when an initial state belongs to an attractor of length c. Dividing it by the attractor length, we get 1 for each attractor. Eq. 4 is useful for any set of CA, and not only for the random mapping model, if w^w is substituted by the number of automata in a given class.

To compare the RM and LH1D classes, we calculated the $N(t,c)$ function for LH1D automata. The results on $N(t,c)$ are presented in Fig. 2, both for LH1D (Fig. 2a) and RM (Fig. 2b). Next we used the Eq. 4 to calculate N_a as dependent on the number of cells N. The results are presented in Fig. 3. For the RM model it is known [20] that the asymptotic curve for

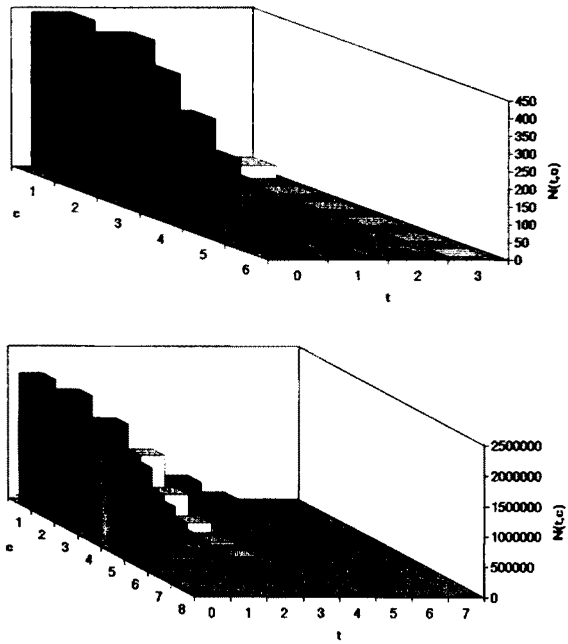

Fig. 2. The function $N(t,c)$ calculated for (a) LH1D automata, (b) RM model.

large N is N/e. This asymptote is included to the plot. The vertical axis is in logarithmic scale. As before, the results on LH1D are different for N even and odd, but now this difference is much more distinct. We observe also a small deviation of both curves from an exponential one (linear in the applied scale). We should add, however, that the number of points is much too small to conclude any asymptotic behaviour.

In Fig. 4 we show the average length of a limit cycle for LH1D automata. This should be compared with the same quantity obtained within the RM model. As the latter distribution is the same as for the relaxation time (Fig. 1), only the asymptotic curve is given in the plot.

We have also found the distribution of the size of bassins of attractor for LH1D automata for $N = 3, \ldots, 9$. This distribution can be partially described [15] by the parameter

$$\langle Y_2 \rangle = \left\langle \sum_s W_s^2 \right\rangle , \tag{5}$$

where S counts bassins of attraction, W_S is the ratio of a size of a S-th bassin to the number of all possible states, and the average $\langle \ldots \rangle$ is taken over all LH1D automata. The value of $\langle Y_2 \rangle$ describes a multivalley structure of attractors; it tends to zero if there is no "dominating" bassins of attraction

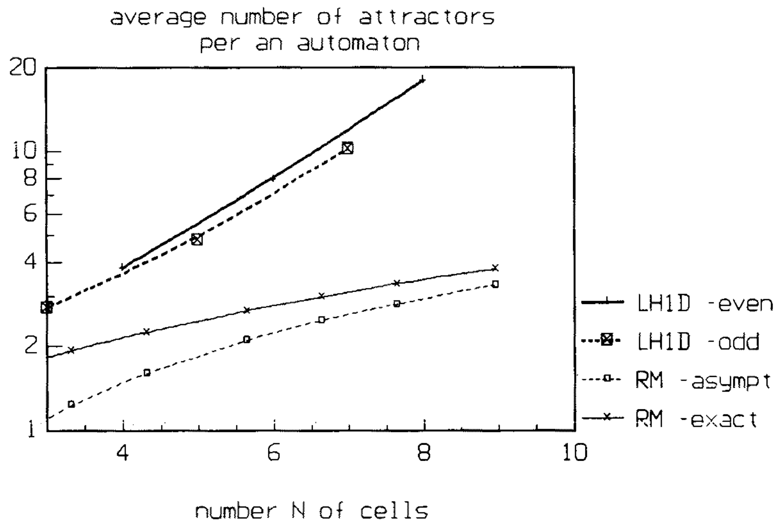

Fig. 3. Average number of attractors per an automaton, calculated for LH1D automata (N even and odd) and compared with the results of the RM model.

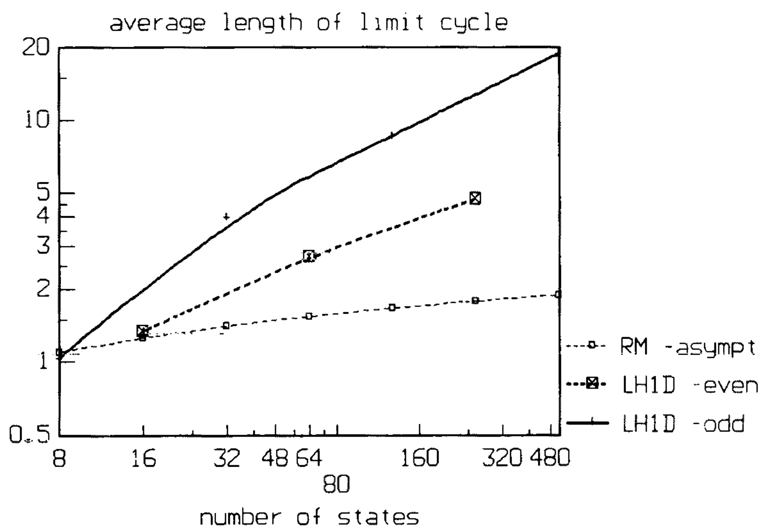

Fig. 4. Average length of limit cycles for LH1D automata (N even and odd), compared with asymptotic curve for the RM model.

[15]. This parameter has a definite meaning in the spin-glass theory. The obtained values of $\langle Y_2 \rangle$ are given in Table I. They should be compared with the same value obtained for the RM model, which can be expressed by the Euler integral; it is equal to $B(2, 1/2)/2$. There, the asymptotic value of

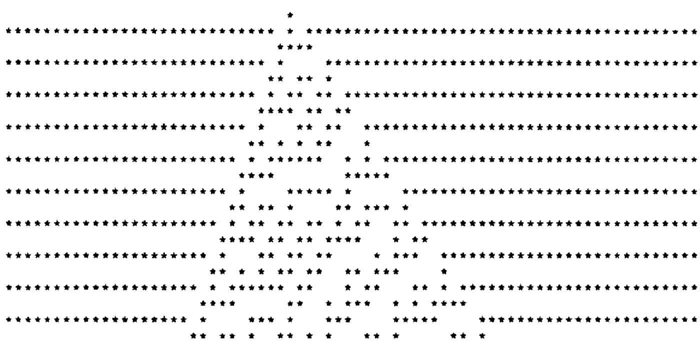

Fig. 5. Action of a "chaotic" automaton (00101101) from a single seed in a homogeneous, initially empty state.

$\langle Y_2 \rangle$ for N infinite is equal to 2/3 [15].

TABLE I

The values of $\langle Y_2 \rangle$ for LH1D automata, as dependent on the number N of cells in a ring.

N	$\langle$Y2$\rangle$
3	0.568
4	0.487
5	0.518
6	0.389
7	0.416
8	0.302
9	0.297

3. Discussion

Direct comparison of the properties of LH1D automata with the properties of all possible automata (RM) shows that the conditions of locality and homogeneity strongly influence the properties of CA. LH1D automata have shorter relaxation time, more attractors and relatively long limit cycles, if compared with "average" automaton, represented by random mapping. The data on the parameter $\langle Y_2 \rangle$ (Table I) confirm the result on the large number of attractors for the LH1D CA; the values of $\langle Y_2 \rangle$ are smaller than 2/3 and decrease with N. The difference between LH1D automata for even and odd numbers of sites can be interpreted as a finite size effect; the step value is equal to 2 because we have assumed that there are two states of a cell. The existence of such a step value was found also for other automata, *e.g.* "Life" [23] or Ising CA [24]. On the contrary, there is no characteristic scale for the random mapping model, as seen in Fig. 2b.

In Fig. 2a we observe a structure of maxima of the number of automata against the length c of limit cycles. The period of this structure is just the number N of cells in a ring. We have checked that this structure is partially due to a subclass of automata whose action is mainly to shift the whole configuration of cells, one step right or left. While shifting, the structure can be reversibly modified, what doubles the value limit cycle length. However, the largest values of c are produced by another class of automata, which could be termed as "chaotic" [11]. Their action can hardly be described in a general way; for small initial disturbance of a homogeneous state (all "0" or all "1") they form asymmetric and irregular fractals, expanding along a ring (Fig. 5). To separate out these automata, we just check which CA produce the longest limit cycles. For $N = 5, 6, 7$ and 9 these automata are found to be the same: 45 (00101101), 75 (01001011), 89 (01011001) and 101 (01100101), in the notation of [11] and [8], respectively. As we see, "hot bits" [11] are set reversely in all of them: 000 gives 1, and 111 gives 0. We have checked that both "chaotic" and "shifting" CA have very short relaxation times.

We have demonstrated that the RM model can be treated as a reference automaton to be compared with more limited families of cellular automata. We believe that such a comparison can give valuable and simple information on a given family of CA. In particular, the introduction of relaxation time of an automaton is found to be helpful. There is also some interesting, although far, analogy between the RM model and diffusion: let us consider relaxation time as a time which is necessary to fulfill the subset of state space, available for a given automaton. Then we can see the RM model as a model of diffusion in the space of states. Average length of a trajectory in such space is found to be proportional to square root of w, *i.e.* square root of the number of steps to be made to reach limits of the available space. On the other hand, average length of a trajectory of a random walker is known to be proportional to square root of the number of steps.

Let us also remark some applications of the RM model; as was mentioned above, this model is equivalent to the Kauffman model for the case of maximal connectivity. The Kauffman model can be used to the evaluation of the size of sets of genes, which take part in human reaction. Time of reaction of a human genetic system was evaluated [25] to be about 10 minutes. People have 10^5 genes. Each gene can be on or off. If the trajectory of a genome contains all possible states, the reaction time would be much longer than the age of Universe. Therefore, only some islands of genes are expected to be active [16]. Their size N can be evaluated from the Eq. 2: $\langle t\rangle \alpha w^{1/2} = 2^{N/2} \approx 10\text{min} / \mu\text{s} = 6 * 10^8$, where 1 μs is a lower limit for one step [25]. This gives N to be about 58 genes per an island. Another possibility is that only a limited set of automata should be active during the reaction; to look for the appropriate constraint of CA [26] is an attractive task. The Kauffman model has also some relations to the spin glass theory [27] and to the Ising CA [28], but a discussion of these relations exceeds the frames of this paper.

Concluding, we postulate the random map model to be a standard "average" algorithm to be compared with any deterministic automaton or a family of automata, which could be of interest.

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