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Damage Spreading in a Gradient

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We propose a new method of analyzing the frozen–chaotic transition in a cellular automaton by propagating damage in a gradient. We obtain estimations for p_c and for the critical exponents for the Kauffman model and the mixture of OR and XOR rules.

KEY WORDS: Cellular automata; phase transition; interface; multispin coding.

The dynamic phase transition in cellular automata between a frozen and a chaotic phase is of interest because of its various applications in biology and statistical physics and has been intensively studied in the last 2 years. It was first described in the Kauffman model,[1-5] a random mixture of all possible Boolean rules, but is also found in various other mixtures of rules[6,7] and even at usual thermodynamic transitions.[8]

The dynamic phases of automata are characterized by the behavior of the trajectories in phase space. If one considers binary variables $\sigma_i = 0, 1$, the distance D between two configurations $\{\sigma_i\}$ and $\{\rho_i\}$ can be defined through

$$D(t) = \frac{1}{N} \sum_{i=1}^{N} [\sigma_i(t) - \rho_i(t)]^2 \tag{1}$$

where N is the number of sites and t the time. If one considers two configurations that were initially close, i.e., small distance of order $1/N$ at $t = 0$, the phase is called frozen if after a long time the average distance is zero (for $N \to \infty$) and is called chaotic if it is nonzero.

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In the (finite-dimensional, quenched) Kauffman model one considers a regular lattice and for each sites one chooses a Boolean function of the variables on the κ nearest neighbors of this site. This Boolean function is picked such that the 2^κ binary numbers that characterize its output values are 1 with probability p and 0 otherwise. Once the functions are determined they are kept for all times the same. p is a parameter of the model and one knows[1,2] that for $0 \leqslant p \leqslant p_c$ one has a frozen phase and for $p_c < p \leqslant 0.5$ a chaotic phase. One has $p_c \approx 0.3$ for the square lattice.[5]

If one chooses the functions for the sites not among all the 2^{2^κ} possible ones, but within a restricted, properly chosen subset of functions, one can obtain a similar phenomenon. So, for the XOR–OR mixture one lets the function on a site be OR with probability p and XOR otherwise. The OR function of κ variables is zero iff all κ entries are zero and the XOR of κ variables is one iff the sum of all κ entries is odd. For $0 < p < p_c$ one finds a chaotic phase and for $p_c < p \leqslant 1$ a frozen phase in $2d$.[7] On the square lattice p_c is about 0.4.

The usual numerical method of determining p_c has been: fixing a value of p, start with two configurations that differ only at a few sites and watch how they both develop in time under the application of the same set of rules. This method, however, has to cope with large statistical fluctuations and slow relaxation toward the final state close to p_c, which makes it very time-consuming on a computer. In this paper we present an alternative method, which also yields some critical exponents, and show its performance for two examples: the Kauffman model and the XOR–OR mixture on the square lattice of size $L \times L$.

Instead of having the same value of p in the whole system, we impose a gradient in the vertical direction.[10] So, at the top line we choose our functions according to a probability $p(1)$, at the bottom line according to $p(L)$, and for the intermediate lines j according to the interpolated value

$$p(j) = p(1) + [p(L) - p(1)](j-1)/(L-1) \tag{2}$$

In the horizontal direction the value of p is kept constant and we impose periodic boundary conditions.

We choose $p(1)$ such that it lies in the chaotic phase and $p(L)$ such that it lies in the frozen phase; how far inside the frozen phase will become clear soon. We consider two configurations, the first chosen randomly and the second equal to the first on all sites except on line one, where its values are exactly flipped with respect to the first configuration (maximum damage at the first line). We then apply our (quenched) set of rules many times. The "damage," i.e., the sites where the two configurations differ, evolves from line one toward the bottom. But since after a certain line j it

will encounter values of $p(j)$ that belong to the frozen phase, the propagation of the damage will be suppressed. $p(L)$ is chosen such that even after very long times the two configurations stay identical on line L, i.e., the damage never reaches the bottom. In the thermodynamic limit $L \to \infty$ this would occur for $p(L) = p_c$, but in a finite system one has a finite instead of an infinitesimal gradient and the damage penetrates somewhat into the frozen phase.

Suppose we have fixed L, $p(1)$, and $p(L)$. We then calculate the density $\rho(j)$ of the total damage per line, i.e., the number of sites in line j on which the two configurations have been different at least once, divided by L. The total damage, i.e., the sites that have been damaged at least once, forms a cluster that is connected to the top and does not touch the bottom. Its total mass is equal to $L \sum_j \rho(j)$ and we call p_m the average position of its outer boundary. For a concrete calculation of p_m it is, however, easier to consider the sites that lie on the other side of this boundary. We use

$$p_m = p(L) + [p(1) - p(L)] \mathcal{N}/L^2 \tag{3}$$

where $\mathcal{N}$ is the number of all sites that have never been damaged and that are connected to the bottom line via nearest neighbor relations through other sites that have never been damaged. $\rho(j)$ and p_m are obtained after so many iterations that the total damage no longer changes. More precisely, we iterate t_0 time steps such that for no line j the $\rho(j)$ is more than 0.1% different from the value it had at time step $t_0/2$. For $L = 192$ we needed about 500 time steps, and for $L = 768$ about 15,000 time steps. We repeat our simulation m times, choosing each time a different set of functions and a different initial configuration. $\rho(j)$ and p_m are averages over these samples.

We implemented multispin coding (64 sites/word updated simultaneously) in our program, which was vectorized on a Cray XMP yielding a speed of about 66 million updates/sec (MHz) for the Kauffman model and of about 75 MHz for the XOR-OR mixture. Our updating uses only logical bit-by-bit operations. For instance, for the Kauffman model on the square lattice we construct for each of the 16 different possible configurations of the nearest neighbors a mask (of 64 bits = sites) that is one if the site has this configuration and zero otherwise. The new state of the sites is obtained via an AND with the word that contains the (quenched) outputs of the functions for this configuration followed by an OR of the results for all the 16 configurations. If one calls NR(i, j, k), $k = 1,..., 16$, the 16 possible outputs of the rule at the sites in word (i, j) and N1,..., N4 the four words that contain the nearest neighbor sites to the sites contained in word N(i, j), then in the program the 16 masks are constructed via

$$\begin{aligned} \mathrm{M1} &= \mathrm{AND(N1, N2, N3, N4)} \\ \mathrm{M2} &= \mathrm{AND(N1, N2, N3, NOT(4))} \\ &\vdots \\ \mathrm{M16} &= \mathrm{AND(NOT(N1), NOT(N2), NOT(N3), NOT(N4))} \end{aligned}$$

and the new values at the sites are given by

$$\mathrm{N}(i, j) = \mathrm{OR[AND(NR}(i, j, 1), \mathrm{M1}), \ldots, \mathrm{AND(NR}(i, j, 16), \mathrm{M16})]$$

Due to the nature of multispin coding, we are limited to sizes $L = l \times 64$, $l \in \{1, 2, \ldots\}$. To calculate $\mathcal{N}$ in Eq. (3), we use the burning method[9] also in multispin coding.

The relevant quantity controlling the finite-size effects is the gradient $\nabla p = |p(1) - p(L)|/L$. In order to separate its influence from other finite-size effects, we tried to keep $p(1)$ and $p(L)$ fixed and to vary only L. Figure 1 shows $\rho(p)$ for both models for different values of ∇p. We see that for smaller ∇p the profile becomes sharper on the p axis and expect that it might fall to zero at p_c for $\nabla p \to 0$. In the chaotic phase we see some transient due to the fact that we force the line at $p(1)$ to have all sites damaged.

To better control the finite-size effects, we propose the scaling law for $p \to p_c$ and $\nabla p \to 0$

$$\rho(p) = (\nabla p)^x f((p - p_c)(\nabla p)^{-y}) \tag{4}$$

where f is a scaling function. In the thermodynamic limit $\nabla p \to 0$ we expect ρ to behave like the order parameter, i.e., $\rho \propto (p - p_c)^\beta$, so that $\beta = x/y$. Figure 2 shows the scaling according to Eq. (4) with the parameters p_c, x, and y adjusted such that one gets data collapse for different ∇p. We find for the Kauffman model $p_c = 0.299 \pm 0.005$, $x = 0.06 \pm 0.05$, and $y = 0.45 \pm 0.10$ and for the XOR–OR mixture $p_c = 0.395 \pm 0.004$, $x = 0.20 \pm 0.03$, and $y = 0.6 \pm 0.2$, i.e., for all these values the collapse is more or less reasonable. We see that this method is quite sensitive to p_c and quite insensitive to y.

The $p_m(\nabla p)$ defined in Eq. (3) turns out to have quite small statistical error bars (about 0.5%) even for few statistics. We extrapolate in Fig. 3 the value of $p_m(\nabla p)$ to the limit $\nabla p \to 0$, supposing a convergence of the type

$$p_m(\nabla p) - p_m(0) \propto (\nabla p)^x \tag{5}$$

where we took for the XOR–OR mixture the value of x that we found from the data collapse of Fig. 2. We find for the extrapolated values $p_m = 0.2986 \pm 0.0010$ for the Kauffman model and $p_m = 0.392 \pm 0.002$ for the

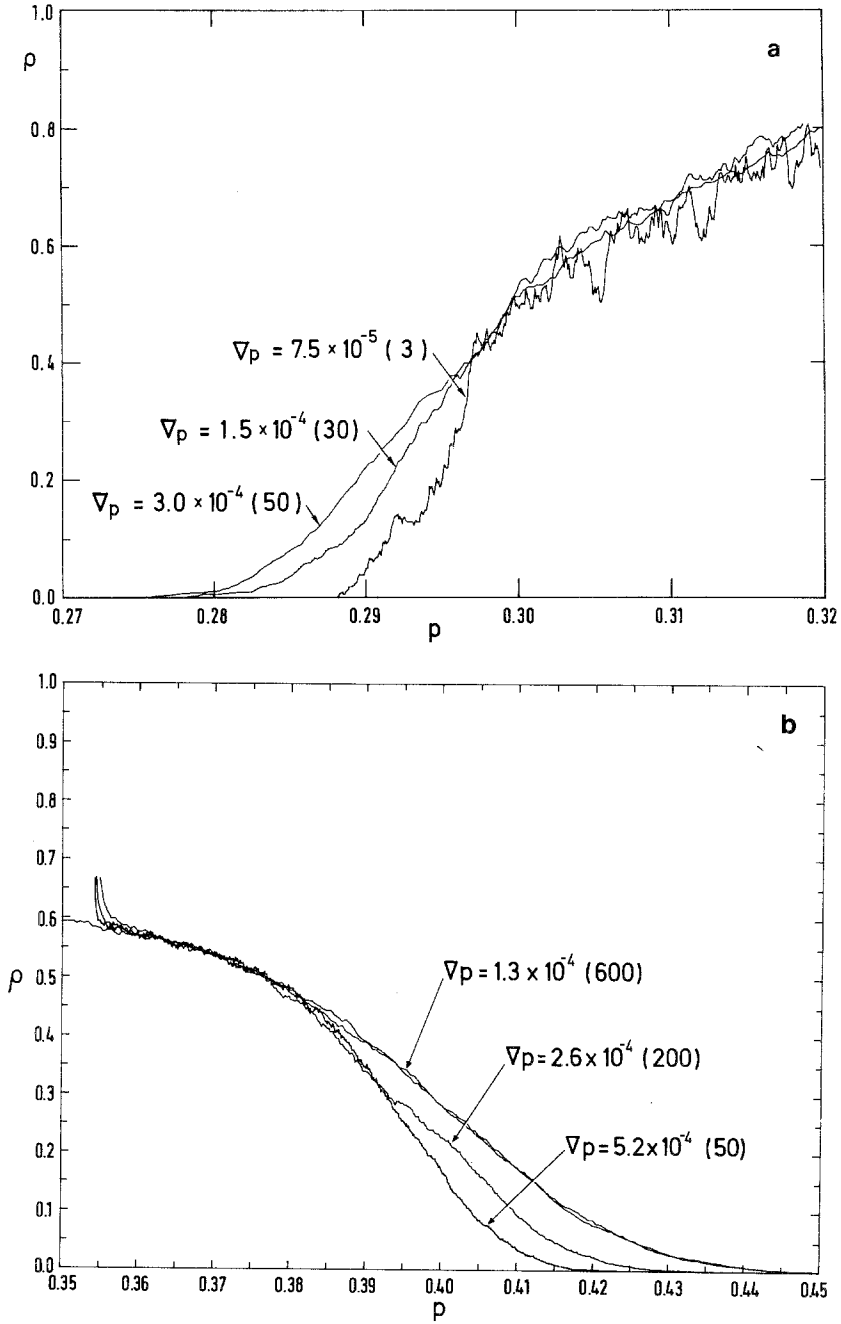

Fig. 1. Plot of $\rho(j)$ as a function of $p(j)$ for different gradients ∇p for (a) the Kauffman model and (b) the XOR–OR mixture. Parentheses following the values of ∇p show the number of samples m over which we made the statistics.

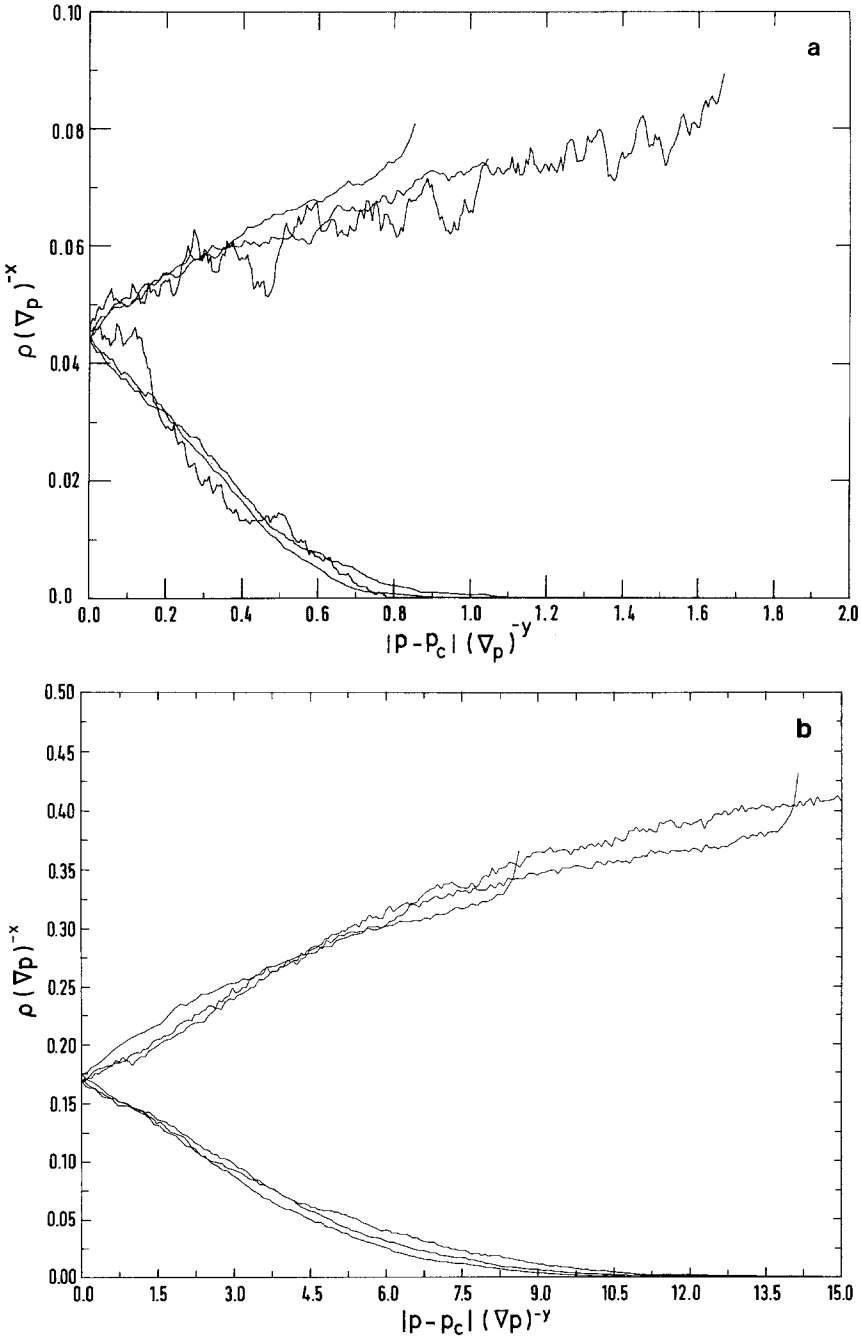

Fig. 2. Scaling plot of $\rho(\nabla p)^{-x}$ against $|p-p_c|(\nabla p)^{-y}$ for (a) the Kauffman model and (b) the XOR–OR mixture. (a) $p_c=0.315$, $x=0.4$, $y=0.85$; (b) $p_c=0.397$, $x=0.23$, $y=0.7$.

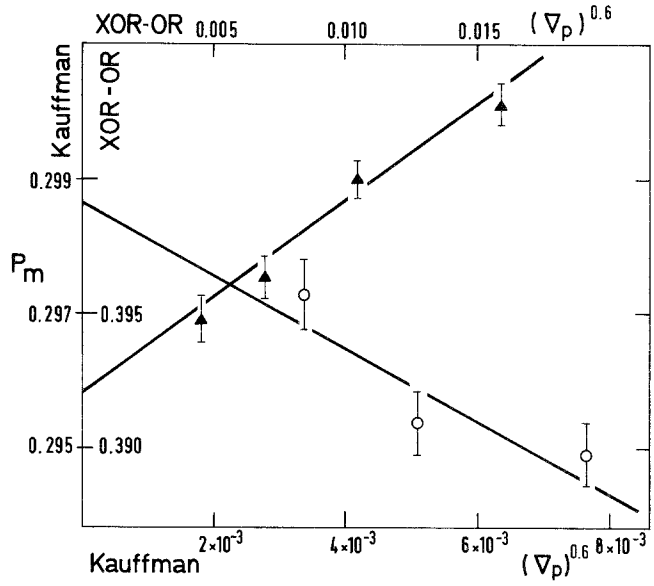

Fig. 3. Plot of p_m as a function of $(\nabla p)^x$ for (○) the Kauffman model with $x = 0.6$ and (▲) the XOR–OR mixture with $x = 0.6$; the statistics are the same as in Fig. 1.

XOR–OR mixture. Although both p_m values lie within the error bars of p_c, we cannot exclude that asymptotically p_m does not coincide with p_c. Since the frontier is quite asymmetric (i.e., holes in the chaotic phase, no holes in the frozen phase), a scenario in which even in the limit $\nabla p \to 0$ the frontier does not converge to a sharp value of p is possible and in three dimensions even quite probable. In this case p_m will not go to p_c for $\nabla p \to 0$. A further investigation of the length, structure, and asymmetry of this frontier would certainly be very interesting.

We have studied the damage frontier into a gradient and looked at the form of its profile $\rho(p)$. Using scaling laws for the profile, it is possible to extract quite precise values for the critical concentration p_c. Still, our p_c for the Kauffman model is a little larger than the value 0.29 obtained in refs. 3–5 and it is not clear which of the two estimates is better. The average concentration p_m of the outer frontier can be determined even more precisely, but it yields numbers that seem to lie marginally in the chaotic phase. It is, however, possible that $p_m \neq p_c$ if the frontier has a finite width in the thermodynamic limit. In ref. 10 a similar type of method had been applied to percolation. There p_m agrees with p_c in 2D and is larger than p_c in 3D. It is not completely clear which of the two situations applies to our case. This point should be further investigated. We looked at two values of

p that characterize the damage frontier; many others can be defined and it would be interesting to study how they behave and if they can yield independent and more precise determinations of p_c.

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