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FINITE SIZE SCALING BEHAVIOR OF A BIASED MAJORITY RULE CELLULAR AUTOMATON

by

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Palavras Chaves: Cellular automata, biased majority rule, finite (Key words) size scaling, bootstrap percolation, criticality

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(AMS Classification)

Finite size scaling behavior of a biased majority rule cellular automaton

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This paper is dedicated to Joel Lebowitz on the occasion of his 60th birthday.

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Short title: biased majority rule.

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Abstract

We consider the biased majority rule cellular automaton, in which the sites take the majority of the states (0 or 1) of their neighbors to update their states, with a bias towards 1 in case of ties. We observe that in any dimension for any initial density of 1's the probability of final complete occupancy by 1's converges to 1 as the lattice grows. In two dimensions the value $p(L,\alpha)$ of the initial density for which the probability of eventual complete occupancy of a lattice $L \times L$ is $\alpha \in (0,1)$, is shown to satisfy for fixed α the bounds $A/\sqrt{\log L} < p(L,\alpha) < B/\sqrt{\log L}$ for large L, where A and B are positive and finite constants.

1 Introduction

Here we consider the following (deterministic) cellular automaton. The system is defined on the d-dimensional hypercubic lattice of linear size L.

$$\Lambda_L = \{1, \ldots, L\}^d.$$

Two sites $x,y\in\Lambda_L$ are considered to be neighbors in case they have d-1 coordinates in common and the remaining one differing by 1 unit. This means that we are considering open boundary conditions and in particular sites at the boundary of Λ_L have less neighbors than sites in the middle of Λ_L . The system evolves in discrete time. Each site $x\in\Lambda_L$ at each unit of time $t\in\{0,1,2,\ldots\}$ may be in state 0 or 1. This state is denoted by $\eta_t(x)$. The evolution is given by the rule

$$\eta_{t+1}(x) = \left\{ \begin{array}{ll} 0 & \text{if } \sum_{y \in \mathcal{N}_x} \eta_t(y) < 2, \\ 1 & \text{if } \sum_{y \in \mathcal{N}_x} \eta_t(y) \geq 2, \end{array} \right.$$

where \mathcal{N}_x is the set of neighbors of x. At t = 0 we suppose that each site is independently set in state 1 with probability p or in state 0 with the complementary probability.

Remark: The choice of open boundary conditions for Λ_L was made to simplify the comparison between this and other related models that will appear below, and be used as tools in the proofs. The results in this paper hold also in case periodic boundary conditions are used (meaning that two sites are considered to be neighbors if they have all coordinates in common and the remaining one differing by 1 or N-1 units), with minor modifications in the proofs.

This model has been studied numerically under various different names (see Section 4 in [Vic] and Section 3.2, rule A, in [Sta], but interchange 0's and 1's). We call it biased majority rule model, since the state at x at time t+1 is the majority of the states in \mathcal{N}_x at time t with a bias towards 1 in case of a tie. (Since we are considering open boundary conditions this is only true at the boundary sites if we think that they have extra neighbors outside of Λ_L permanently in state 0.)

Let R(L, p) be the probability that the system will reach the configuration with all sites in state 1. It is natural to ask whether for fixed p, R(L, p) converges to 1 as L goes to infinity. Due to simple monotonicity considerations one can in fact define the critical point

$$p_c = \inf\{p: \lim_{L\to\infty} R(L,p) = 1\}.$$

The proposition below states that $p_c = 0$.

Proposition 1 For all dimension d, and all p > 0,

$$\lim_{L\to\infty}R(L,p)=1.$$

Proof: Consider first that L is even, L = 2M. Divide Λ_L into hypercubes of side 2 indexed by points in Λ_M :

$$Q((y_1,\ldots,y_d)) = \{x \in \Lambda_L : x_i \in \{2y_i-1,2y_i\}, i=1,\ldots,d\}$$

= \{2y_1-1,2y_1\} \times \{2y_2-1,2y_2\} \times \ldots \{2y_d-1,2y_d\}.

Define

$$\xi_t(y) = \left\{ \begin{array}{ll} 0 & \text{if } \eta_{(d+1)t}(x) = 0 \text{ for some } x \in Q(y), \\ 1 & \text{if } \eta_{(d+1)t}(x) = 1 \text{ for all } x \in Q(y). \end{array} \right.$$

Now we observe that the process (ξ_i) evolves in a fashion that dominates the model called *modified basic model* in [Sch1]. To define this model, which will be denoted by (ζ_i) here, we use the notation $\mathcal{N}_y^i, i = 1, \ldots, d$ for the set of neighbors to the site y which differ from y only in the i-th coordinate. Now

$$\zeta_{i+1}(y) = \begin{cases} 0 & \text{if } \zeta_i(y) = 0 \text{ and for some } i \in \{1, \dots, d\} \\ & \zeta_i(z) = 0 \text{ for all } z \in \mathcal{N}_y^i, \\ 1 & \text{otherwise.} \end{cases}$$

This means that 1's never change to 0 and a 0 flips to 1 if and only if it has at least one neighboring 1 in each coordinate direction. The domination mentioned before is contained in the statement that if $\xi_0(y) \ge \zeta_0(y)$ for all $y \in \Lambda_M$, then $\xi_t(y) \ge \zeta_t(y)$ for all $y \in \Lambda_M$, $t \ge 0$. This can be easily seen (first observe that if $\xi_t(y) = 1$ then $\xi_s(y) = 1$ for all $s \ge t$), for a formal argument see Lemma V.1 in [Sch1].

Let $R^{MBM}(M,q)$ be the probability that Λ_M becomes eventually completely full of 1's for the modified basic model (ζ_t) started from density q

(i.e., at t=0 the sites are independently in state 1 with probability q). Clearly at t=0 the variables $\{\xi_0(y), y \in \Lambda_M\}$ are independently equal to 1 with probability $p^4 > 0$. From the remarks above we obtain

$$R(L,p) \geq R^{MBM}(M,p^4).$$

The proposition follows now, when L is even, from the fact that for all dimension d and q > 0

$$\lim_{M\to\infty}R^{MBM}(M,q)=1,$$

proved in Section III of [Sch1] (Theorem III.1 plus Lemma III.2).

In case L is odd, consider the four lattices $\{1,\ldots,L-1\}\times\{1,\ldots,L-1\}$, $\{1,\ldots,L-1\}\times\{2,\ldots,L\}$, $\{2,\ldots,L\}\times\{1,\ldots,L-1\}$ and $\{2,\ldots,L\}\times\{2,\ldots,L\}$. A simple comparison shows that

$$1 - R(L, p) \le 4(1 - R(L - 1, p)).$$

Hence the result follows in this case from the previous case.

In numerical analysis of this and other related models one usually consideres the values of the initial density $p(L,\alpha)$ defined by

$$R(L, p(L, \alpha)) = \alpha,$$

where $0 < \alpha < 1$ is fixed as L varies (commonly $\alpha = 0, 5$). $p(L, \alpha)$ is well defined by the expression above since for each fixed value of L R(L,p) is easily seen to be a strictly increasing polynomial in p. In order to extrapolate from the values of $p(L,\alpha)$ for various values of L to p_c one assumes a finite size scaling hypothesis. In several papers (see for instante [AA], [ASA], [Fro], [Dua], [Sta], [MSH]) $p(l,\alpha)$ is plotted against $1/\log L$ and a straight line is traced through the observed points; its crossing with the $L=\infty$ axis is taken as the estimate of p_c . This corresponds to the hypothesis that asymptotically as $L\to\infty$

$$p(L, \alpha) \cong p_c + \frac{C}{\log L}$$

for some constant C. A weak form of this assumption was rigorously proven by Aizenman and Lebowitz [AL] for the modified basic model in d=2 and for the related bootstrap percolation model also in d=2, defined by the rules

$$\sigma_{t+1}(x) = \begin{cases} 0 & \text{if } \sigma_t(x) = 0 \text{ and } \sum_{y \in \mathcal{N}_s} \sigma_t(y) < 2, \\ 1 & \text{otherwise.} \end{cases}$$

(1's do not change and 0's flip to 1 when they have 2 or more neighboring 1's.) Let $R^{BP}(L,p)$ be the probability that Λ_L becomes fully occupied by 1's for this evolution starting from density p. In [AL] it was proven that there are two constants $0 < C_1 \le C_2 < \infty$ such that if one lets $p \to 0$ and $L \to \infty$, then

$$R^*(L,p) \longrightarrow \begin{cases} 0 & \text{if } L < e^{C_1/p}, \\ 1 & \text{if } L > e^{C_2/p}, \end{cases}$$
 (1)

where * stands for MBM or BP. It follows (with a self explanatory notation) that for these two models $p_c^* = 0$ (as had been proven before in [vE]) and for each fixed $\alpha \in (0,1)$

$$\frac{C_1}{\log L} \le p^*(L,\alpha) \le \frac{C_2}{\log L},$$

for large L.

For some models related to those discussed above the numerical analysis based on the scaling above gave indications of non-trivial critical points, latter proved to be in fact zero (see [AA], [Dua], [MSH], [Sch1] and [Sch2]). For the biased majority rule model this sort of analysis with the data from [Sta] (see fig.4 there) would predict for p_c a value close to 0,05. These discrepancies pointed out the relevance of discussing the validity of the scaling used. In [EAD] the authors suggest that in fact different scaling behaviors hold for some models considered in the papers quoted above.

For the biased majority rule model in d=2 we will prove that indeed the scaling is different, by showing a result similar to that of Aizenman and Lebowitz but with p replaced by p^2 .

Theorem 1 For the two-dimensional biased majority rule model there are two constants $0 < C_3 \le C_4 < \infty$ such that if we let $p \to 0$ and $L \to \infty$, then

$$R(L,p) \longrightarrow \left\{ \begin{array}{ll} 0 & \text{if } L < e^{C_3/p^2}, \\ 1 & \text{if } L > e^{C_4/p^2}. \end{array} \right.$$

Proof: First we observe that 1's that are far from other 1's at t=0 disappear before they can cause any effect. To be more precise define the extended neighborhood of z

$$\bar{\mathcal{N}}_x = \mathcal{N}_x \bigcup (\bigcup_{y \in \mathcal{N}_x} \mathcal{N}_y) \setminus \{x\}.$$

Given a configuration $\alpha \in \{0,1\}^{A_L}$ define the configuration $\tilde{\alpha}$ by

$$\tilde{\alpha}(x) = \left\{ \begin{array}{ll} 0 & \text{if } \alpha(x) = 0 \text{ or } \alpha(y) = 0 \text{ for all } y \in \bar{\mathcal{N}}_x, \\ 1 & \text{otherwise.} \end{array} \right.$$

We addopt the notation (η_t^{α}) for the biased majority model started at t=0 from the configuration α . One can easily see that

$$\eta_t^{\alpha} = \eta_t^{\dot{\alpha}} \text{ for } t \ge 1. \tag{2}$$

But the biased majority model is clearly dominated by the boostrap percolation model in the sense that for any configuration β ,

$$\eta_t^{\beta}(x) \le \sigma_t^{\beta}(x) \text{ for all } t \ge 0, \text{ all } x \in \Lambda_L,$$
(3)

where (σ_t^{β}) is the boostrap percolation model started from the configuration β .

The first statement of the theorem follows from (2), (3) and techniques from [AL]. Lemma 1 in that paper states that if for some t, $\sigma_i^{\rho}(x) = 1$ for all $x \in \Lambda_L$ then for all integer $k \leq (L/2) - 1$ there must be a rectangle $R \subset \Lambda_L$ whose largest side is in the range $k, \ldots, 2k + 2$ and such that if γ is defined by

$$\gamma(x) = \begin{cases} 0 & \text{if } x \notin R \text{ or } \beta(x) = 0, \\ 1 & \text{if } x \in R \text{ and } \beta(x) = 1. \end{cases}$$

then for some t, $\sigma_t^{\gamma}(x) = 1$ for all $x \in R$ (R is said to be internally spanned by β .)

Suppose that $P(\alpha(x) = 1) = p$, independently from site to site. From the observations above it follows that for any $k \le (L/2) - 1$

$$R(L,p) \leq P(\sigma_t^{\tilde{\alpha}}(x) = 1 \text{ for all } x \in \Lambda_L, \text{ for some } t)$$

$$\leq P(\bigcup_{R \in S(k)} \{R \text{ is internally spanned by } \tilde{\alpha}\})$$

$$\leq |S(k)| \max_{R \in S(k)} P(R \text{ is internally spanned by } \tilde{\alpha}), \qquad (4)$$

where S(k) is the set of rectangles contained in Λ_L with largest side in the range $k, \ldots, 2k+2$, and $|\cdot|$ stands for the cardinality of a set. Suppose that $R \in S(k)$ is a rectangle with sides $m \leq n, n \in \{k, \ldots, 2k+2\}$. In order for R to be internally spanned by $\tilde{\alpha}$, it is clear that every pair of neighboring lines or rows in R must contain at least one site x such that $\tilde{\alpha}(x) = 1$. Suppose, with no loss of generality, that n is the number of rows of R. Choose now as many as possible pairs of neighboring rows of R separated from each other by four consecutive rows. (This separation garanties that what happens with $\tilde{\alpha}$ inside the various pairs of rows are independent events.) One concludes that for small p

$$P(R \text{ is internally spanned by} \tilde{\alpha}) \leq [2m(12p^2 + 0(p^3))]^{\frac{n}{6}-1} \leq [25(2k+2)p^2]^{\frac{1}{6}-1},$$
 (5)

where we used the facts that

$$P(\tilde{\alpha}(x) = 1) = |\vec{N}_x| p^2 + 0(p^3),$$

and that we are looking to at least (n/6) - 1 pairs of rows in R. In case $L > 1/(100p^2)$, (4) and (5) imply, with $k = \lfloor 1/(200p^2) \rfloor - 1$ (where $\lfloor \cdot \rfloor$ stands for integer part of)

$$R(L,p) \leq [L^2 \cdot (1/(100p^2))^2][1/4]^{1/(1200p^2)-2},$$

which goes to 0 as $p \to 0$ in case $L < e^{C_3/p^2}$, where $C_3 = (\log 4)/2500$. The case $L \le 1/(100p^2)$ is in fact easier to handle, since then for small p

$$R(L, p) \leq P(\Lambda_L \text{ is internally spanned by } \tilde{\alpha})$$

$$\leq [2L(12p^2 + 0(p^3))]^{(L/6)-1}$$

$$\leq 4 \cdot [1/4]^{L/6},$$

which goes to zero as $L \to \infty$. This finishes the proof of the first statement of the theorem.

To prove the other statement we suppose first that L is even (L=2M) and use again the squares Q(y) introduced in the proof of Proposition 1. If $y=(y_1,y_2)$, the set $\{(2y_1-1,2y_2),(2y_1,2y_2-1)\}$ will be called the first diagonal of Q(y), while $\{(2y_1-1,2y_2-1),(2y_1,2y_2)\}$ will be called the second diagonal of Q(y). We say that the square Q(y) suffers from the illness A at time t in case

- i) t is even and $\eta_t(x) = 1$ for both x in the first diagonal of Q(y), or
- ii) t is odd and $\eta_t(x) = 1$ for both x in the second diagonal of Q(y). We say that Q(y) suffers from the illness B at time t under similar conditions, with the words "even" and "odd" interchanged.

Observe that once a square Q(y) becomes infected by A or by B it will never recover from this illness. Moreover if we look only at times that are multiples of 4, these diseases are spread in a fashion that dominates the evolution of the modified basic model (the verification is easy and is left to the reader). The precise statement is as follows. Define

$$c_t(y) = \begin{cases} 0 & \text{if } Q(y) \text{ does not have the illness } A \text{ at time 4t,} \\ 1 & \text{otherwise.} \end{cases}$$

Then for all $y \in \Lambda_M$ and $t \ge 0$

$$\zeta_t(y) \geq \zeta_t(y),$$

where (ζ_t) is the modified basic model started at t = 0 from density p^2 (which is the probability that each square Q(y) suffers from A at time 0). A similar statement holds with A replaced by B.

Using now (1) for the modified basic model and taking $C_4 = C_2$ we obtain in case $p \to 0$, $L \to \infty$, with $L > e^{C_4/p^2}$

 $\lim R(L,p)$

 $\geq \lim P(\text{all squares } Q(y), y \in \Lambda_M \text{ eventually get both illnesses } A \text{ and } B)$ = 1.

The case in which L is odd can be handled in the same way it was done in the proof of Proposition 1, finishing the proof.

It follows from the theorem that for any fixed α , for large enough L

$$\frac{\sqrt{C_3}}{\sqrt{\log L}} \le p(L,\alpha) \le \frac{\sqrt{C_4}}{\sqrt{\log L}}.$$

This indicates that $p(L, \alpha)$ should be plotted against $1/\sqrt{\log L}$ in numerical analysis. Doing it with the data from [Sta] and extrapolating linearly gives already a value of p_c closer to 0 than that obtained with the $1/\log L$ scaling. At the moment that this note is being written up, D. Stauffer (private communication) is extending the numerical work on this model.

We have to point out nevertheless that since the theorems that indicate the correct scaling behavior are only statements about the asymptotic behavior as $p \to 0$ and $L \to \infty$, the numerical extrapolations can give erroneous results even when the correct form of scaling is used. This is the case observed in [Fro]. for a model for which the $1/\log L$ scaling is known to be the right one the prediction based on simulations with L up to more than 20,000 with this scaling provided an extrapolation for the critical point incompatible with the rigorous results. Good methods are lacking at this stage to estimate how large the systems must be for the asymptotic behavior to be a good approximation.

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