Application of a renormalization group algorithm to nonequilibrium cellular automata with one absorbing state

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We improve a recently proposed dynamically driven renormalization group algorithm for cellular automata systems with one absorbing state, introducing spatial correlations in the expression for the transition probabilities. We implement the renormalization group scheme considering three different approximations which take into account correlations in the stationary probability distribution. The improved scheme is applied to a probabilistic cellular automaton already introduced in the literature.

I. INTRODUCTION

In order to study cellular automata systems displaying a second order irreversible phase transition to an absorbing state characterized by a scalar order parameter, a dynamical renormalization group (RG) algorithm has been recently proposed. These cellular automata models are in the directed percolation (DP) universality class. The method is based on a Dynamically Driven Renormalization Group (DDRG) scheme (for a recent review about DDRG see [2]), which has been successfully applied to self-organized critical phenomena, as sandpile models [3] and forest fire models [4].

The basic idea introduced in [1] is to couple a real space RG scheme to a stationary condition that drives the RG group equations through the parameter space. The stationary equations, involving the stationary distribution, have to be approximated, since the form of the stationary probability distribution is not known a priori, as in the case of systems in equilibrium. Oliveira and Satulovsky [1] showed, as proposed in [4], that results can be improved using more refined approximations for the stationary probability distribution. The expression for the transition probability used in [1] consists in a product of independent one-site transition probabilities at every step of the RG transformation.

In this work we exploit another aspect of the scheme, not considered before in order to include additional correlations. In fact, correlations can be also introduced in the renormalization scheme if we allow the transition probability to depend upon more neighbors. In the case of non-equilibrium models, the space in which the RG flows is the space spanned by the transition probabilities. As we will see later, our approach broadens this space providing more degrees of freedom to the RG trajectories that flow towards the fixed points.

We apply the modified RG scheme to a probabilistic cellular automaton (PCA) with one absorbing state already introduced in the literature [5]. Using a block renormalization that properly treats the nature of the absorbing state, we figure the value of the critical exponent of the divergence of the spatial correlation length, $\nu_\perp$, using three different approximations involving correlations among clusters of 1, 2, and 4 neighboring sites in the lattice. Our calculations for $\nu_\perp$ at small orders of approximation in the mean field scheme for the stationary distribution, give better values than the ones reported in reference [1].

The paper is organized as follows. We begin with a brief description of the model proposed in [5] and the general renormalization scheme. After this, we define the algorithm used in this work and present the values obtained for $\nu_\perp$. Finally, after mentioning the ideas involved in the simulation technique used to study the model, we present the values of the whole set of critical exponents for the PCA obtained by means of dynamical numerical simulations and stationary simulations. Our results are in well agreement with the values corresponding to (1+1) DP, and differ considerably from the ones reported in reference [1].

II. THE MODEL

The model studied in [5] is a one-dimensional cellular automaton in which each site can be either vacant, $\sigma_i = 0$, or occupied by a particle, $\sigma_i = 1$. At each time step, the state of a given site will depend only on its previous state and the previous state of its nearest neighbors. The transition probability $T(\sigma|\sigma')$ from state $\sigma' = (\sigma'_1, \sigma'_2, \ldots, \sigma'_L)$ to state $\sigma = (\sigma_1, \sigma_2, \ldots, \sigma_L)$ will be given by the product

$$T(\sigma|\sigma') = \prod_{i=1}^{L} \tau(\sigma_i|\sigma'_{i-1}, \sigma'_i, \sigma'_{i+1}), \quad (1)$$

where $L$ is the number of sites and $\tau(\sigma_i|\sigma'_{i-1}, \sigma'_i, \sigma'_{i+1})$ is the one-site transition probability given by the following...
for any value of \( n \). The critical point at \( p_1 = 0 \) is trivial, in contrast to the result obtained in reference [6]. The system has two critical points, one of them at \( p_1 \approx 0.75 \). The critical point at \( p_1 = 0 \) will be shown to be trivial, in contrast to the result obtained in reference [3]. Consequently, we will apply the RG to study the non-trivial transition point. Rule \( \tau(000) = 1 \) implies that the vacuum state is indeed an absorbing state.

### III. Renormalization Scheme

The RG scheme proposed in [4] is a real space RG scheme in which one renormalizes the transition probability, \( T \). The RG flow takes place in the space of parameters defining \( T \). A blocking procedure transforms cells of \( b \) sites into one site at the new scale. In order to account for the fact that the vacuum state is absorbing, a cell devoided of particles will always renormalize into an empty site. Cells with at least one particle have been chosen to renormalize into an occupied site. Other options have been tried, but they do not preserve the existence of the absorbing state.

Let \( \sigma = (\sigma_1, \sigma_2, \cdots, \sigma_L) \) be the state of a system with \( L \) degrees of freedom, and the vector \( S = (S_1, S_2, \cdots, S_L) \) be the state of the renormalized system with \( L' = L/b \) degrees of freedom, where \( b \) is the size of the renormalization block.

The conditional probability of state \( S \) given state \( \sigma \), \( \mathcal{R}(S|\sigma) \), must satisfy

\[
\mathcal{R}(S|\sigma) \geq 0, \quad \sum_S \mathcal{R}(S|\sigma) = 1. \tag{3}
\]

Given \( T \) and the probability of a state \( \sigma' \) at time \( t \), \( W(\sigma') \), one can write the joint probability of state \( \sigma' \) at time \( t \) and state \( \sigma \) at \( n \) time steps later, \( W_n(\sigma, \sigma') \), by simply applying \( T \) to \( W(\sigma') \) \( n \) successive times

\[
W_n(\sigma, \sigma') = T^n(\sigma|\sigma')W(\sigma'). \tag{4}
\]

In addition, in the stationary regime, the probability distribution \( W(\sigma) \) must satisfy

\[
W(\sigma) = \sum_{\sigma'} T^n(\sigma|\sigma')W(\sigma'), \tag{5}
\]

for any value of \( n \).

In the same way one can write these expressions at the coarse grained level. Denoting by \( \tilde{T}(S', S) \) the probability of occurrence of state \( S' \) at a given time and state \( S \) one time step later, the RG transformation is obtained

\[
\tilde{W}(S, S') = \sum_{\sigma} \sum_{\sigma'} \mathcal{R}(S|\sigma)\mathcal{R}(S'|\sigma')W_n(\sigma, \sigma'). \tag{6}
\]

from which follows

\[
\tilde{W}(S') = \sum_S \tilde{W}(S, S') = \sum_{\sigma'} \mathcal{R}(S'|\sigma')W(\sigma'). \tag{7}
\]

Once knowing the transition probabilities at the coarse grained scale, one can easily build the rescaled transition matrix, \( \tilde{T}(S|S') \), as

\[
\tilde{T}(S|S') = \frac{\tilde{W}(S, S')}{\tilde{W}(S')}. \tag{8}
\]

Using now equations (4), (6), and (7), we obtain the final expression for the renormalization equations

\[
\tilde{T}(S|S') = \frac{\sum_{\sigma} \sum_{\sigma'} \mathcal{R}(S|\sigma)\mathcal{R}(S'|\sigma')T^n(\sigma|\sigma')W(\sigma')}{\sum_{\sigma} \mathcal{R}(S'|\sigma')W(\sigma')}. \tag{9}
\]

Let us note that, while this expression expresses rescaled transition probabilities, \( \tilde{T} \), in terms of transition probabilities at a lower scale, \( T \), the stationary weight of each state present in equation (8), \( W(\sigma') \), is yet unknown. Contrary to the case of closed systems in thermal equilibrium, we do not know a priori the expression for the stationary probability distribution. However, including equation (6), one can get a closed set of equations to solve at each renormalization step. The stationarity condition (8) is actually essential in driving the RG equations (9) through parameter space. Equation (9), together with a given approximation for the stationary probability, provide then a well defined RG transformation \( T \to \tilde{T} \).

In practice, equation (9) can hardly be solved and one must resort to approximations. The values of critical exponents obtained using the present RG approach are expected to improve as these approximations improve. We have used three different levels of approximations, in which correlations among clusters of 1, 2, and 4 sites are considered respectively.

In this work we will be concerned with another way to improve the RG scheme. An important point is that, in order to solve equations (9), an assumption needs to be made on how the transition probability between states \( S' \) and \( S \), \( \tilde{T}(S|S') \), depends on local transition probabilities at the coarse grained level. This choice will determine the degree of proliferation that the RG will have, since the form of the renormalized transition probability will be preserved along the RG trajectories.

In the former approach (9), the authors carried out the most general RG transformation considering one-site transition probabilities. By preserving the form of the renormalized transition probabilities, the RG trajectories are found to flow to the attractive fixed points in a five-dimensional space spanned by the dynamical parameters. In contrast to usual RG methods in which new
couplings arise at each step of the transformation, this RG procedure is not able to proliferate the dynamical parameters since the form of the transition probabilities are kept fixed at the coarse grained level. However, new dynamical parameters can be considered from the very beginning if we allow the transition probabilities to depend upon more neighbors, i.e., introducing more correlations in them. This feature of the method should be compared with other dynamical RG procedures [12] where the introduction of new couplings since the very beginning is an alternative way to carry out the RG transformation.

We propose, then, a form for the coarse grained transition probability consisting of a product of independent two-site transition probabilities instead of one-site transition probabilities. Denoting the position of each lattice site with $i$, the new transition probability is defined at even time steps as

$$T(S_{i}|S_{i}') = \prod_{k=1, (i=2k)}^{L/2} \tilde{T}(S_{i}, S_{i+1}|S_{i}', S_{i+1}', S_{i+2}, S_{i+2}'),$$  \hspace{1cm} (10)$$

and at odd time steps as

$$T(S_{i}|S_{i}') = \prod_{k=1, (i=2k+1)}^{L/2} \tilde{T}(S_{i}, S_{i+1}|S_{i}', S_{i+1}', S_{i+2}, S_{i+2}').$$  \hspace{1cm} (11)$$

Here we have used the same symbol, $\tilde{T}$, to indicate a different type of transition probability than the ones appearing in (1). In formulas (10) and (11) periodic boundary conditions are assumed.

One can retrieve at any time one-site transition probabilities knowing both two-site probabilities and the stationary distribution. It is straightforward to show that

$$\tilde{T}(S_{i}|S_{i}', S_{i}', S_{i+1}) = \sum_{S_{i+1}, S_{i+2}} \tilde{T}(S_{i}, S_{i+1}|S_{i}', S_{i}', S_{i+1}, S_{i+2}) \frac{W(S_{i}', S_{i}', S_{i+1}, S_{i+2})}{W(S_{i}', S_{i}', S_{i+1}, S_{i+1})}. $$  \hspace{1cm} (12)$$

Using expressions (10) and (11) in equation (8) one can implement the RG transformation. The algorithm we used is explained in more detail in the next section.

IV. RENORMALIZATION ALGORITHM

We have used a temporal coarse graining of two time steps ($n = 2$). The blocking operator, $R$, was chosen in the same way as in (1), renormalizing cells of size $b = 2$ into one site

$$R(S_{k}|\sigma_{2k-1}, \sigma_{2k}) \geq 0, \hspace{1cm} (14)$$

and

$$\sum_{S_{k}} R(S_{k}|\sigma_{2k-1}, \sigma_{2k}) = 1. \hspace{1cm} (15)$$

In order to preserve the nature of the absorbing state, we have also required $R$ to satisfy

$$R(0,0,0) = 1, \hspace{1cm} (16)$$

and

$$R(0|\sigma_{2k-1}, \sigma_{2k}) = 0. \hspace{1cm} (17)$$

whenever $\sigma_{2k-1} \neq 0$, or $\sigma_{2k} \neq 0$.

The diagram in figure (3) indicates how two-site transition probabilities are renormalized. Indexes appearing in equation (8)–(20) refer to this diagram.

![Diagram showing the blocking scheme procedure. Numbers correspond to the indexes used in equation (8)–(20).](image)

Using equations (9), (10), and (11), we can write down the expression relating $\tau$ to $\tilde{T}$, which is given by

$$\tilde{T}(S_{1}, S_{2}|S_{3}, S_{4}, S_{5}, S_{6}) = [N(S_{3}, S_{4}, S_{5}, S_{6})]^{-1} \sum_{\sigma_{1}, \sigma_{2}, \sigma_{3}, \sigma_{4}, \sigma_{11}, \cdots, \sigma_{18}} R(S_{1}|\sigma_{1}, \sigma_{2})R(S_{2}|\sigma_{3}, \sigma_{4})R(S_{3}|\sigma_{11}, \sigma_{12}) \nonumber \quad R(S_{4}|\sigma_{13}, \sigma_{14})R(S_{5}|\sigma_{15}, \sigma_{16})R(S_{6}|\sigma_{17}, \sigma_{18}) \quad D(\sigma_{1}, \sigma_{2}, \sigma_{3}, \sigma_{4}|\sigma_{11}, \cdots, \sigma_{18})W(\sigma_{11}, \cdots, \sigma_{18}), \hspace{1cm} (18)$$

where

$$D(\sigma_{1}, \sigma_{2}, \sigma_{3}, \sigma_{4}|\sigma_{11}, \cdots, \sigma_{18}) = \sum_{\sigma_{9}, \cdots, \sigma_{10}} \tilde{T}(\sigma_{1}, \sigma_{2}|\sigma_{9}, \sigma_{10}) \tilde{T}(\sigma_{3}, \sigma_{4}|\sigma_{17}, \sigma_{18}) \tilde{T}(\sigma_{5}, \sigma_{6}|\sigma_{11}, \sigma_{12}) \tilde{T}(\sigma_{7}, \sigma_{8}|\sigma_{13}, \sigma_{14}) \tilde{T}(\sigma_{9}, \sigma_{10}|\sigma_{15}, \sigma_{16}, \sigma_{17}, \sigma_{18}), \hspace{1cm} (19)$$

and

$$\tilde{T}(\sigma_{1}, \sigma_{2}|\sigma_{9}, \sigma_{10}) \tilde{T}(\sigma_{3}, \sigma_{4}|\sigma_{17}, \sigma_{18}) \tilde{T}(\sigma_{5}, \sigma_{6}|\sigma_{11}, \sigma_{12}) \tilde{T}(\sigma_{7}, \sigma_{8}|\sigma_{13}, \sigma_{14}) \tilde{T}(\sigma_{9}, \sigma_{10}|\sigma_{15}, \sigma_{16}, \sigma_{17}, \sigma_{18}) \hspace{1cm} (20)$$
\[ N(S_3, S_4, S_5, S_6) = \sum_{\sigma_{11}, \ldots, \sigma_{18}} R(S_3|\sigma_{11}, \sigma_{12}) R(S_4|\sigma_{13}, \sigma_{14}) R(S_5|\sigma_{15}, \sigma_{16}) R(S_6|\sigma_{17}, \sigma_{18}) W(\sigma_{11}, \ldots, \sigma_{18}). \]  

(20)

Since we do not know a priori the stationary weights, \( W(\sigma_{11}, \ldots, \sigma_{18}) \), we need an approximate method to estimate them. The simplest approximation, known as simple mean field approximation, consists in neglecting correlations among different sites. That is

\[ W(\sigma_{11}, \ldots, \sigma_{18}) = \prod_{i=11}^{18} W(\sigma_i), \]  

(21)

where \( W(\sigma_i) \) is the solution of

\[ W(\sigma_1) = \sum_{\sigma_2, \sigma_3, \sigma_5, \sigma_6} \tilde{\tau}(\sigma_1 \sigma_2 | \sigma_3 \sigma_4 \sigma_5 \sigma_6) W(\sigma_2) W(\sigma_3) W(\sigma_4) W(\sigma_5) W(\sigma_6). \]  

(22)

Correlations, however, are actually taken into account in the geometrical aspects of the blocking procedure, leading to non classical exponents. Better approximations can be also implemented (as a reference see [13]).

Equations (18)-(23) involve each transition probability. Since we do not know a priori the stationary weights, \( W(\sigma_{11}, \ldots, \sigma_{18}) \), we need an approximate method to estimate them. The simplest approximation, known as simple mean field approximation, consists in neglecting correlations among different sites. That is

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We have found one relevant parameter. Since we are only dealing with stationary properties of the model, it is reasonable to assume that this parameter is associated to the divergence of the spatial correlation length and not to the temporal correlation length \( \theta \). In order to calculate the eigenvalue, \( \Lambda \), associated to that parameter, we have to find the linear region of the RG transformation.

Let us take a trajectory passing close enough to the unstable point, and construct a sequence of numbers consisting in the distance between two successive points along that trajectory. Now, let us call \( r \) to the ratio between two consecutive numbers in that sequence. In the portion of the trajectory corresponding to the linear region of the RG transformation (around the unstable fixed point), one expects to see two plateaus in the values of \( r \).

V. RG RESULTS

The behavior of the RG equations can be described as follows. For values of \( p \) which are small enough, the set of transition probabilities flows towards an attractive fixed point characterized by a lattice devoid of particles. Increasing \( p \) above a critical value, \( p_{cr} \), the flow is driven to another attractive fixed point, consisting of a lattice full of particles. The value of \( p_{cr} \), for each level of approximation used, can be found in table (23). Starting around the critical values, the representative point of the parameter set spends a long time near an unstable fixed point before leaving towards one of the two attractive fixed points. A projection of the RG flow along two specific transition probabilities is shown in figure (2).
The first plateau corresponds to a trivial parameter, while the value of \( r \) at the second plateau corresponds to the eigenvalue \( \Lambda \) of the RG transformation. Figure \( 6 \) shows an example of one of such curves for the simple mean field approximation. So, figuring the eigenvalue \( \Lambda \) associated to the relevant parameter, we get \( \nu_\perp = \ln 2 / \ln \Lambda \). The value measured numerically for the plot in figure \( 6 \) (simple mean field approximation) is \( \nu_\perp = 0.965 \pm 0.001 \).

To the best of our knowledge, the best value of \( \nu_\perp \) is \( \nu_\perp = 1.0972 \pm 0.0005 \) [6], and the most accurate value for the critical point \( p_2 \), obtained by dynamical numerical simulations (see following sections), is \( p_2 \approx 0.7513 \). Although our value of the critical exponent \( \nu_\perp \) is still inaccurate, it is worth at this point comparing it with the one obtained using the same approximation (simple mean-field) in [6]. In that work the authors obtained \( \nu_\perp = 0.931 \pm 0.005 \), so that our result is a better approximation for the actual \( \nu_\perp \). Our scheme is able to take into account correlations in a more accurate way than the original one.

By increasing the order of the approximation, results improve, as shown in table (23). The value we found using the two-site approximation was \( \nu_\perp = 1.013 \pm 0.001 \), while the value found in the four-site approximation was \( \nu_\perp = 1.015 \pm 0.001 \), which is closer to the actual one. Below we show the critical value, \( \nu_{\text{cr}} \), for the three approximations, as well as the corresponding value of \( \Lambda \) and \( \nu_\perp \).

| appr. | \( p_{\text{cr}} \) | \( \Lambda \) | \( \nu_\perp \) |
|-------|-----------------|----------|--------|
| 1     | 0.639829        | 2.050    | 0.963 ± 0.001 |
| 2     | 0.681490        | 1.982    | 1.013 ± 0.001 |
| 4     | 0.695017        | 1.979    | 1.015 ± 0.001 |

It should be noted that the present RG scheme leads to fairly good values for the exponent \( \nu_\perp \) already within lower order mean-field approximations. This fact indicates that the introduction of new correlations in the transition probabilities plays a relevant role within the lower order mean-field approaches. For mean-field approximations of order higher than two, the convergence of the scheme becomes slower.

Reconsidering the ideas which led us to Eqs. (10) and (11) for the transition probabilities, one may think of obtaining better approximations for \( \nu_\perp \) by allowing the transition probabilities to depend upon even more neighboring lattice sites. While this idea is clearly right, one can presently not overcome, in practice, the huge amount of computer time needed to obtain values that are accurate enough.

### A. Spreading analysis

The basic rules governing the dynamical evolution of the system have been formulated in section II. As in ordinary cellular automata, all lattice sites are updated simultaneously. Simulations were performed on lattices of size \( L = 10000 \), taking periodic boundary conditions. We briefly discuss here the scaling theory for directed percolation which supports the spreading analysis. A detailed treatment can be found elsewhere [10].

It should be stressed that for \( L \) finite, the steady state of the system is meta-stable since, due to fluctuations of the stochastic process, there is always a finite probability for the system to become empty. This probability increases when approaching the critical point. Consequently, it is very difficult to calculate critical points and critical exponents by means of numerical simulations. Furthermore, since the transition between the stationary regime and the absorbing state is second order, a mean field treatment is not adequate. These shortcomings can be avoided by evaluating critical exponents related to the dynamic critical behavior of the system. For this purpose one starts, at \( t = 0 \), with a particle at the center of the lattice otherwise empty, i.e. a configuration very close to the absorbing state. Then, the following quantities are computed: (i) the survival probability, \( P(t) \), that is, the probability that at least a particle is still in the system at time \( t \); (ii) the average number of particles, \( N(t) \), and; (iii) the average mean distance, \( R(t) \), over which particles have spread. Averages are taken over \( 5 \times 10^4 \) samples, and runs are performed up to \( t = 10^4 \). Finite size effects are avoided, since the epidemic disk never reaches the edge of the lattice during the simulation. Close to the critical point, and for long enough times, the following scaling laws should hold [10]:

\[
P(t) \propto t^{-\delta} \phi(\Delta t^{\nu_\parallel/\nu}),
\]

\[
N(t) \propto t^{\eta} \phi(\Delta t^{\nu_\parallel/\nu}),
\]

\[
R(t) \propto t^{z/2} \Xi(\Delta t^{\nu_\parallel/\nu}),
\]

where \( \Delta = |p - p_c| \), \( \xi_t = \Delta^{-\nu_\parallel} \) gives the temporal correlation length close to \( p_c \), \( \nu_\parallel \) is the correlation length exponent (time direction), \( \Phi, \phi, \) and \( \Xi \) are suitable scaling functions, and \( \delta, \eta, \) and \( z \) are critical exponents. In the absorbing state, \( P(t) \) and \( N(t) \) are expected to decay exponentially, since correlations are short-ranged. This can only happen if \( \phi(\Delta, t) \propto \Delta^{\nu_\parallel} \exp(-\Delta^{\nu_\parallel} t) \)

for \( t \to \infty \). Therefore, one has from Eq. (4):

\[
N(t) \propto \Delta^{-\nu_\parallel} \exp(-\Delta^{\nu_\parallel} t), \quad t \to \infty.
\]

At criticality, one expects that log-log plots of \( P(t) \), \( N(t) \), and \( R(t) \) would give straight lines, while upward and downward deviations would occur even slightly off-criticality. This behavior would allow a precise determination of the critical point and the critical exponents \( \delta, \eta, \) and \( z \).
η, and z. It should be noted that by means of Eq. (27) it would be also possible to calculate $\nu_\parallel$.

B. Finite size scaling analysis

As in standard second order phase transitions it is assumed that in the supercritical region, and close to the critical point, the system displays spatial correlations characterized by a typical length scale, $\xi_s$, which diverges at criticality according to

$$\xi_s \propto \Delta^{-\nu_\perp}, \quad \Delta \to 0,$$

where $\nu_\perp$ is the correlation length exponent in the spatial direction. The natural order parameter of the model is the density of particles, $\rho$, which at criticality depends on the system size $L$ and $\Delta$ as

$$\rho(p, L) = L^{-\beta/\nu_\perp} f(\Delta L^{1/\nu_\perp}),$$

where $f$ is a suitable scaling function and $\beta$ is the order parameter critical exponent. For small positive $\Delta$, and $L \to \infty$, $f(x)$ should have the following form

$$f(x) \propto x^\beta,$$

in order to recover the well known critical behavior of the order parameter in the thermodynamic limit

$$\rho \propto \Delta^\beta.$$  

VII. SIMULATION RESULTS

Before presenting the simulation results we will briefly discuss the critical point at $p = 0$. If we start at $t = 0$ with a random initial configuration of density $\rho_0 = 0.5$, the stationary density of the system is $\rho \approx 1/8$. It should be noted that at $p = 0$ the system reaches a static stationary state in one time step (see the evolution rules in table 2). Taking into account this observation, the stationary density of the system can be obtained as follows. It is clear from the evolution rules that the probability of having an occupied site at $t = 1$ is equal to the probability of finding an occupied site surrounded by empty sites at $t = 0$. Since there are no correlations in the initial state, the stationary density of the system at $p = 0$ can be determined as

$$\rho = \rho_0(1 - \rho_0)^2$$

Then, since we used $\rho_0 = 0.5$, the expected value of the stationary density is $\rho = 1/8$.

For arbitrary small values of $p$, the stationary state is the vacuum state. We now consider the relaxation process to the vacuum state. We take as starting configuration ($t = 0$) any of the static stationary states at $p = 0$. Then, we follow the evolution of the density for $p$ close to zero. It is clear from the evolution rules that after a particle is created, two particles are removed from the system at the next time step. Then, the system stays in another static state until the next creation process occurs. Suppose that a creation process happens at position $x_i$. If no new particle is created in the neighborhood of $x_i$ at the next time step, correlations can not be generated (see the evolution rules in table 2). The probability of two consecutive creation processes is $p^2 < p$. Then, the system can not develop long range correlations and a mean field analysis should be appropriate. For $p$ close to zero it is possible to consider the creation process as a creation-induced annihilation process. We then have

$$d\rho/dt = -p\rho.$$  

Consequently, $p = 0$ is a trivial critical point since the relaxation time behaves as $\tau = (1/p)^\lambda$. This result is in disagreement with the one reported in reference 3, probably due to a poor statistics of the simulation data.

In the following, the results of the epidemics analysis at $p = p_2$ are presented. We measure the time evolution of $P(t)$, $N(t)$, and $R(t)$ for different values of the parameter $p$. Log-log plots of these quantities as a function of time are straight lines at the phase transition and show curvature away from the transition. It is important to mention that the epidemics analysis is a very sensitive method since it is possible to distinguish among supercritical and sub-critical behavior for $p$ values that differ in the fourth decimal. Our best estimation of the critical point is $p_2 = 0.7513 \pm 0.0002$, and the dynamical critical exponents are $\delta = 0.162 \pm 0.0004$, $\eta = 0.304 \pm 0.0005$, and $z/2 = 0.643 \pm 0.0007$. It should be remarked that the error bars merely indicate the statistical error obtained from regressions. The values of the dynamical exponents are in well agreement with those corresponding to directed percolation in $(1+1)$ dimensions, as it was expected.

It is possible to calculate the exponent $\nu_\parallel$ from the analysis of the sub-critical behavior (see eq. (27)). In fact, the decay constant, $\lambda = \xi_t^{-1}$, governing the long time behavior of $N(t)$, behaves according to

$$\lambda = \xi_t^{-1} = \Delta^\nu_\parallel,$$

so, if $p_2$ is known, we can calculate $\lambda$ for different values of $\Delta$. Then, a log-log plot of $\lambda$ vs $\Delta$ allows us to evaluate the exponent $\nu_\parallel$. This analysis gives an exponent $\nu_\parallel = 1.738 \pm 0.002$ which is quite close to the value $\nu_\parallel = 1.73$ corresponding to $(1+1)$ DP 4. It should be pointed out that our value of $\nu_\parallel$ sharply differs from the one reported in reference 3 ($\nu_\parallel \approx 1.087$). The error in the last value of the exponent $\nu_\parallel$ is due to the fact that it was calculated taking into account not only sub-critical, but also supercritical curves.

We have also calculated the order parameter critical exponent measuring the density, $\rho$, as a function of $\Delta$ in the supercritical regime (see eq. 31)). We obtain
\[ \beta = 0.277 \pm 0.002, \] which is once again very close to \[ \beta = 199/720, \] corresponding to (1 + 1) DP. It should be mentioned that the reported value of the order parameter critical exponent in reference [1] is \( \beta \approx 0.32 \) which differs around 16\% from the theoretical value. This difference may be due again to the poor statistics of the data.

We finally present the finite size scaling analysis. Figure (4) shows a log-log plot of \( \rho L^{\nu_{\perp}} \) vs \( \Delta L^{1/\nu_{\perp}} \) for different values of \( p \), and lattice sizes, \( L \), where we have used \( \beta = 199/720 \) and \( \nu_{\perp} = 1.0972 \) corresponding to (1 + 1) DP. We obtain an excellent collapse of the data on an universal curve, as it is predicted by eq. (29).

Right before submitting this manuscript for publication, the author of reference [5] improved some of his previous results [14]. Although no new results are reported for the trivial critical point \( p_1 \), the conclusions concerning the universality class of the model are in complete agreement with the ones found in this work.

VIII. CONCLUSIONS

We have introduced a new renormalization group algorithm for probabilistic cellular automata with one absorbing state. The new scheme introduces correlations in the RG procedure by allowing the transition probabilities to depend upon two neighboring lattice sites. Three different approximations for the stationary probability distribution have been used, namely the simple mean-field approximation, the pair mean-field approximation, and the four-site mean-field approximation.

The new RG scheme leads to fairly good values for \( \nu_{\perp} \) even within mean-field approximations of low order. This result shows that the introduction of spatial correlations in the transition probabilities is the relevant reason for the improvement of the results.

The critical exponents \( \nu_{\perp} \), especially for low order approximations, are better than the ones obtained with schemes that make use of an independent product of one-site transition probabilities [15, 16].

Using very simple arguments, we have shown that \( p_1 = 0 \) is a trivial critical point, since the time relaxation constant behaves as \( \tau = (1/p)^{1/\nu_{\perp}} \). This behavior differs from the one reported in reference [5] (\( \tau = (1/p)^{0.86} \)).

We have also obtained, by means of numerical simulations, the critical point \( p = p_2 \), and the whole set of critical exponents. The value of the critical point \( p_2 = 0.7513 \pm 0.0002 \) is in agreement with [5]. However, we found very different values for exponents \( \nu_{\parallel} \) and \( \beta \). Our values of the exponents at \( p = p_2 \) are in well agreement with those corresponding to (1 + 1) DP as it was expected, since there is only one absorbing state for the system [5, 16].

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