JOINT EVOLUTION OF TWO DOMANY-KINZEL CELLULAR AUTOMATA

EMÍLIO P. GUEUVOLIAN and TÂNIA TOMÉ
Instituto de Física, Universidade de São Paulo,
Caixa Postal 63618, 05389-970 São Paulo, SP, Brazil

Received 6 May 1996

We analyze the joint dynamics of two systems each one evolving in time according to the Domany–Kinzel rules. Two prescriptions for the joint evolution are studied. We make analytical approaches, based on dynamical mean-field approximations at the level of three-site correlations, to obtain the phase diagram. Also, the susceptibilities associated with the order parameters are calculated by using a pair approximation.

1. Introduction

An important approach in the study of nonequilibrium phase transitions is the one related to the construction of lattice models that evolve in time according to irreversible stochastic rules.1–3 One of the main purposes of this approach is the study of models that are simple from the mathematical point of view, but that can give relevant contributions to the understanding of the intrinsic aspects of the irreversible phenomena. On the other hand, it has been verified that such formalism can be very useful in the description of biological, chemical and physical systems. In this case, lattice models are constructed in order to mimic the microscopic local interactions related to a specific macroscopic phenomenon. In the context of such approach there are the cellular automata,4 which are systems that evolve in discrete time steps according to a synchronous update of the sites in the lattice. The updating of each site is performed according to a set of local rules. Among the variety of lattice models that have been devised to study nonequilibrium phenomena the Domany–Kinzel cellular automaton5,6 appears to be one of the simplest irreversible models that displays a phase transition in one dimension. Moreover the model and its time evolution are themselves the realization of the directed percolation problem.5 As it is known, the directed percolation is closely related to the propagation of epidemics.2,7 Therefore the Domany–Kinzel cellular automaton is inserted in the class of lattice models which intend to explain some of the aspects relevant to the study of simple epidemics8: a problem coming from the epidemiology and that has been also studied from the point of view of stochastic lattice models which possesses absorbing states.
The recent developments on the study of the Domany–Kinzel cellular automaton related to the spreading of damage\(^9\) evidenced new important features in this model, as the detection of a chaotic phase. The spreading of damage is, here, studied in an analytical way by considering the joint evolution of two automata subjected to the same noise. The dynamics associated with the joint evolution of two automata evolving in time subjected to the same noise has irreversible aspects. The phase transition due to the damage spreading in this model raised another problem related to the study of universality in nonequilibrium critical phenomena.\(^2\) The active-chaotic transition is in fact related to an absorbing subspace of the configurational space associated to the joint dynamics. According to Grassberger\(^2\) this damage spreading transition belongs in the directed percolation class.

Here we perform analytical studies of the automaton itself and the spreading of damage in the automaton (that is the joint evolution of the set of two automata) by using dynamical mean-field approximations.\(^10\) The paper is organized as follows. In Sec. 2, it is shown the analytical definition of the Domany–Kinzel cellular automaton. In Sec. 3, we set up the analytical formulation for the study of the spreading of damage. We devise the evolution equations for the joint evolution of two automata and study them by using two different prescriptions. In Sec. 4, a three-site mean field approximation is used to get the phase diagrams. An extrapolation of the results obtained from the one, two and three-site approximations is made to compare with the results from numerical simulations. The susceptibilities associated with the order parameters\(^11–13\) of this model are calculated in Sec. 5, by using a pair approximation. Conclusions and discussions are presented in Sec. 6.

2. The Automaton

The Domany–Kinzel cellular automaton\(^5,6\) is represented by a one-dimensional lattice with \(N\) sites. The configurations of the system are given by a set of occupation variables \(\sigma = (\sigma_1, \sigma_2, \ldots, \sigma_N)\), with \(\sigma_i = 0\) or \(1\). The system evolves at discrete time steps and at each step all the sites are updated simultaneously according to the following rule: the transition probability in which the site \(i\) acquires, at time \(\ell + 1\), the value \(\sigma_i = 0\) or \(1\) is conditioned to the \(\sigma_{i-1}\) and \(\sigma_i\) values at time \(\ell\):

\[
w(\sigma_{i-1}', \sigma_i' \to \sigma_i).
\] (1)

The transition probabilities that define the model are

\[
w(0, 0 \to 1) = p_0, \tag{2}
\]

\[
w(0, 1 \to 1) = p_1, \tag{3}
\]

\[
w(1, 0 \to 1) = p'_1, \tag{4}
\]

and

\[
w(1, 1 \to 1) = p_2. \tag{5}
\]
The other four remaining probabilities are obtained by taking into account that
\[ w(\sigma'_{i-1}, \sigma_i \to 0) + w(\sigma'_{i-1}, \sigma_i \to 1) = 1 \] (6)
for any values of \( \sigma'_{i-1} \) and \( \sigma'_i \).

Here, we will consider only the case \( p'_1 = p_1 \) and \( p_0 = 0 \), except in Sec. 5 where we allow \( p_0 \neq 0 \). At stationary states, the system can find itself in two different situations:

(a) All sites in state 0, that is, \( \sigma = (0, 0, \ldots, 0) \).

(b) A fraction \( \rho \) of the sites are in state 1, with \( \rho \neq 0 \).

The first situation corresponds to an absorbing state. Once the system enters that state, it cannot leave it, since \( p_0 = 0 \). The points \((p_1, p_2)\) of the phase diagram for which the system always reaches the absorbing state define the frozen phase.\(^5,6\) The points \((p_1, p_2)\) of the phase diagram for which the system can have a nonzero fraction of sites in the state 1 define the active phase.

The time evolution of the automaton is given by
\[ P_{\ell+1}(\sigma) = \sum_{\sigma'} P_{\ell}(\sigma')W(\sigma' \to \sigma), \] (7)
where \( \sigma \) is given by the vector \( \sigma = (\sigma_1, \sigma_2, \ldots, \sigma_N) \), \( P_{\ell}(\sigma) \) is the probability of finding the system in the state \( \sigma \) at time \( \ell \), and \( W(\sigma' \to \sigma) \) is the probability associated to a transition at which the system passes from state \( \sigma' \) to state \( \sigma \), given that at the previous time the system was in state \( \sigma' \). The transition probability \( W(\sigma' \to \sigma) \) is given by
\[ W(\sigma' \to \sigma) = \prod_{i=1}^{N} w(\sigma'_{i-1}, \sigma'_i \to \sigma_i) \] (8)
obeying the normalization condition
\[ \sum_{\sigma} W(\sigma' \to \sigma) = 1. \] (9)
which follows from Eq. (6).

The active phase order parameter is identified as \( P_{\ell}(\sigma_i = 1) = P_{\ell}(1) \), which is the probability that a given site is occupied at time \( \ell \). Using Eqs. (7) and (8) one obtains the evolution equation for this quantity,
\[ P_{\ell+1}(\sigma_i) = \sum_{\sigma'_{i-1}, \sigma'_i} w(\sigma'_{i-1}, \sigma'_i \to \sigma_i)P_{\ell}(\sigma'_{i-1}, \sigma'_i). \] (10)
The Eq. (10) relates \( P(\sigma_i) \) to the probabilities involving two neighbor sites. These last quantities obey a time evolution equation given by
\[ P_{\ell+1}(\sigma_{i-1}, \sigma_i) = \sum_{\sigma'_{i-2}, \sigma'_{i-1}, \sigma'_i} w(\sigma'_{i-2}, \sigma'_{i-1} \to \sigma_{i-1})w(\sigma'_{i-1}, \sigma'_i \to \sigma_i) \]
\[ \times P_{\ell}(\sigma'_{i-2}, \sigma'_{i-1}, \sigma'_i). \] (11)
In general, the probabilities \( P_{t+1}(\sigma_{i+1}, \sigma_{i+2}, \ldots, \sigma_{i+M}) \) are related to the probabilities \( P_t(\sigma_i, \ldots, \sigma_{i+M+1}) \). Thus, if one wishes to know the value of \( P(\sigma_i) \), one needs to work with an infinite number of equations which constitutes a hierarchy of equations. One way of dealing with this problem is to use truncation schemes as will be done in Sec. 4.

3. Prescriptions for the Joint Evolution

The active state of the Domany–Kinzel automaton can behave in two different ways when one looks to the spreading of damage.\(^5,13–15\) The meaning of spreading of damage can be understood by considering the simulation of the automaton using pseudorandom numbers. When a stationary state is reached, a replica of the original system is created, with a fraction of the sites having their occupation variables changed. The two systems, original and replica, are allowed to evolve under the same noise. The Hamming distance is measured. This quantity is defined as the fraction of sites in the replica that have different occupation variable values than the corresponding sites in the original system. If the Hamming distance is different from zero, one says the damage spreads throughout the system and the system is sensitive to the initial damage. In this case the system is in a chaotic phase. Otherwise, it is in a non-chaotic phase and there is no spreading of damage.

The complete analysis of the phase diagram requires the obtention of equations to evaluate the spreading of damage, which is done by considering the problem of the joint evolution of two systems.\(^13,15\) Consider a system and its replica given by \( \sigma = (\sigma_1, \ldots, \sigma_N) \) and \( \tau = (\tau_1, \ldots, \tau_N) \). The time evolution of the joint probability \( P_t(\sigma; \tau) \) is given by

\[
P_{t+1}(\sigma; \tau) = \sum_{\sigma', \tau'} P_t(\sigma', \tau') W(\sigma', \tau' \rightarrow \sigma, \tau)
\]

where

\[
W(\sigma', \tau' \rightarrow \sigma, \tau) = \prod_{i=1}^{N} w(\sigma'_{i-1}, \sigma'_i, \tau'_{i-1}, \tau'_i \rightarrow \sigma_i, \tau_i),
\]

which obeys the normalization condition

\[
\sum_{\sigma, \tau} W(\sigma', \tau' \rightarrow \sigma, \tau) = 1,
\]

by requiring that

\[
\sum_{\sigma_i, \tau_i} w(\sigma'_{i-1}, \sigma'_i, \tau'_{i-1}, \tau'_i \rightarrow \sigma_i, \tau_i) = 1.
\]

A relation between \( w(\sigma'_{i-1}, \sigma'_i, \tau'_{i-1}, \tau'_i \rightarrow \sigma_i, \tau_i) \) and \( w(\sigma'_{i-1}, \sigma'_i \rightarrow \sigma_i) \) is determined by requiring that each system evolves in time independently of the other, which implies that the following equations are satisfied:
Joint Evolution of Two Domany-Kinzel Cellular Automata

\[
\sum_{\sigma_i} w(\sigma_{i-1}, \sigma_i, \tau_{i-1}, \tau_i \rightarrow \sigma_i, \tau_i) = w(\tau_{i-1}', \tau_i' \rightarrow \tau_i),
\]
(16)

\[
\sum_{\tau_i} w(\sigma_{i-1}', \sigma_i', \tau_{i-1}', \tau_i' \rightarrow \sigma_i, \tau_i) = w(\sigma_{i-1}', \sigma_i \rightarrow \sigma_i).
\]
(17)

In addition, we should impose the condition that the two systems evolve in time under the same noise. The following table gives the transition probabilities \( w(\sigma_{i-1}', \sigma_i', \tau_{i-1}', \tau_i' \rightarrow \sigma_i, \tau_i) \) obtained in this way:

<table>
<thead>
<tr>
<th>(w)</th>
<th>(11,11)</th>
<th>(10,10)</th>
<th>(00,00)</th>
<th>(11,00)</th>
<th>(10,00)</th>
<th>(11,10)</th>
</tr>
</thead>
<tbody>
<tr>
<td>(1,1)</td>
<td>(p_2)</td>
<td>(p_1)</td>
<td>0</td>
<td>0</td>
<td>0</td>
<td>(a)</td>
</tr>
<tr>
<td>(1,0)</td>
<td>0</td>
<td>0</td>
<td>0</td>
<td>(p_2)</td>
<td>(p_1)</td>
<td>(b)</td>
</tr>
<tr>
<td>(0,1)</td>
<td>0</td>
<td>0</td>
<td>0</td>
<td>0</td>
<td>0</td>
<td>(c)</td>
</tr>
<tr>
<td>(0,0)</td>
<td>(1-p_2)</td>
<td>(1-p_1)</td>
<td>1</td>
<td>(1-p_2)</td>
<td>(1-p_1)</td>
<td>(d)</td>
</tr>
</tbody>
</table>

The other transition probabilities are obtained using the symmetries inherent to this model. For example:

\[
w(00,11 \rightarrow 0,1) = w(11,00 \rightarrow 1,0).
\]
(19)

In the table given above there are four quantities, \(a, b, c\) and \(d\), not yet specified. Two different prescriptions for these quantities have been suggested. They are:

1. Prescription A, introduced in Ref. 13 and given by
   \[
   a = p_1, \quad b = p_2 + p_1, \quad c = 0, \quad d = 1 - p_2, \quad \text{if} \quad p_1 \leq p_2,
   \]
   (20)
   \[
   a = p_2, \quad b = 0, \quad c = p_1 - p_2, \quad d = 1 - p_1, \quad \text{if} \quad p_2 \leq p_1,
   \]
   (21)

2. Prescription B, introduced in Ref. 15, given by
   \[
   a = p_1 p_2, \quad b = p_2 (1 - p_1), \quad c = p_1 (1 - p_2) \quad \text{and} \quad d = (1 - p_1) (1 - p_2).
   \]
(22)

Prescription B implies that one must use, in certain cases, two different random numbers to update the original and the replica.

Now turning back to the question of the spreading of damage, we need an expression for the chaotic phase order parameter. This is given by the Hamming distance

\[
D_\ell = \langle (\sigma_i - \tau_i)^2 \rangle_\ell = P_\ell (\sigma_i = 1, \tau_i = 0) + P_\ell (\sigma_i = 0, \tau_i = 1).
\]
(23)

Since the two quantities in the right hand side are equal, the Hamming distance is just \(2P(1,0)\). Using Eqs. (12) and (13) we obtain the time evolution equation for this quantity

\[
P_{\ell+1}(1,0) = \sum_{\sigma_{i-1}', \sigma_i', \tau_{i-1}', \tau_i'} w(\sigma_{i-1}', \sigma_i', \tau_{i-1}', \tau_i' \rightarrow \sigma_i, \tau_i) P_\ell(\sigma_{i-1}', \sigma_i', \tau_{i-1}', \tau_i').
\]
(24)
It can be verified that the probabilities $P(\sigma_i, \ldots, \sigma_{i+M}; \tau_i, \ldots, \tau_{i+M})$ are related to the probabilities $P(\sigma_i, \ldots, \sigma_{i+M+1}; \tau_i, \ldots, \tau_{i+M+1})$ which means that we need an infinite number of equations to evaluate the Hamming distance.

4. Three-Site Approximation

Our aim, in this section, is to obtain the phase diagram of this automaton in the stationary regime using a three-site dynamical mean-field approximation. One-site and pair mean-field approximations have already been used to obtain the phase diagram of this model. Here, we will use a three-site approximation, in which the probabilities of clusters of four or more sites are written in terms of probabilities of three or less sites, that is,

$$P(\sigma_i, \sigma_{i+1}, \sigma_{i+2}, \sigma_{i+3}) = \frac{P(\sigma_i, \sigma_{i+1}, \sigma_{i+2})P(\sigma_{i+1}, \sigma_{i+2}, \sigma_{i+3})}{P(\sigma_{i+1}, \sigma_{i+2})} \quad (25)$$

and

$$P(\sigma_i, \sigma_{i+1}, \sigma_{i+2}, \sigma_{i+3}, \tau_i, \tau_{i+1}, \tau_{i+2}, \tau_{i+3}) = \frac{P(\sigma_i, \sigma_{i+1}, \sigma_{i+2}, \tau_i, \tau_{i+1}, \tau_{i+2})P(\sigma_{i+1}, \sigma_{i+2}, \sigma_{i+3}, \tau_{i+1}, \tau_{i+2}, \tau_{i+3})}{P(\sigma_{i+1}, \sigma_{i+2}, \tau_{i+1}, \tau_{i+2})} \quad (26)$$

Moreover, we have used many relations that come from considerations of the symmetry between the original system and its replica, from the homogeneity of the individual systems and from the occurrence of complementary events.

Using the analytical formulation presented in this section, we obtained in the three-site approximation a nonlinear system with twenty equations and twenty variables, namely:

$$P(1), P(11), P(101), P(111),$$
$$P(1, 0), P(10, 01), P(11, 00), P(11, 10),$$
$$P(000, 001), P(000, 011), P(001, 011), P(001, 101), P(001, 111), P(010, 001),$$
$$P(010, 011), P(011, 111), P(100, 001), P(100, 011), P(101, 011), P(110, 011).$$

We will not write down the equations here because they are too cumbersome. Numerically, we verified that the solutions of these equations are of three types:

(a) $P(1) = P(1, 0) = 0$, characterizing the frozen phase.
(b) $P(1) \neq 0$, $P(1, 0) = 0$, corresponding to the active phase.
(c) $P(1) \neq 0$, $P(1, 0) \neq 0$ which characterizes the chaotic phase.

Figures 1 and 2 show the phase diagrams obtained, in the three-site approximation, for the prescriptions $A$ and $B$, respectively. It is convenient to give the values of some special points. When $p_1 = 1$ the transition active-chaotic occurs at
Fig. 1. Phase diagram of the Domany–Kinzel cellular automaton according to prescription $A$ obtained by using three-site dynamical mean-field approximation.

Fig. 2. Phase diagram of the Domany–Kinzel cellular automaton according to prescription $B$ obtained by using three-site dynamical mean-field approximation.
For $P_2 = 0$ the transition frozen-chaotic is given by $P_1 = 0.709$. The two prescriptions give the same results for these points because the prescriptions become identical when $P_1 = 1$, or when $P_2 = 0$. The point where the three phases meet each other is the point $p_1^* = 0.696$ and $p_2^* = 0.251$, for the case of prescription $A$ and given by $p_1^* = 0.678$ and $p_2^* = 0.466$ for the case of prescription $B$.

Below we write down the values of $p_1^*$, $p_2^*$, $p_1^*(A)$, and $p_1^*(B)$ for both prescriptions obtained by various mean-field approximations together with an extrapolation and Monte Carlo results.

<table>
<thead>
<tr>
<th>approximation</th>
<th>$p_1^*$</th>
<th>$p_2^*$</th>
<th>$p_1^*(A)$</th>
<th>$p_2^*(A)$</th>
<th>$p_1^*(B)$</th>
<th>$p_2^*(B)$</th>
</tr>
</thead>
<tbody>
<tr>
<td>one-site</td>
<td>0.5</td>
<td>0.667</td>
<td>0.5</td>
<td>0.333</td>
<td>0.5</td>
<td>1</td>
</tr>
<tr>
<td>two-site</td>
<td>0.667</td>
<td>0.482</td>
<td>0.650</td>
<td>0.287</td>
<td>0.619</td>
<td>0.617</td>
</tr>
<tr>
<td>three-site</td>
<td>0.709</td>
<td>0.427</td>
<td>0.696</td>
<td>0.251</td>
<td>0.678</td>
<td>0.466</td>
</tr>
<tr>
<td>extrapolation</td>
<td>0.80</td>
<td>0.33</td>
<td>0.80</td>
<td>0.80</td>
<td></td>
<td></td>
</tr>
<tr>
<td>Monte Carlo</td>
<td>0.810</td>
<td>0.312</td>
<td>0.810</td>
<td>0.810</td>
<td>0</td>
<td>0</td>
</tr>
</tbody>
</table>

The extrapolated values for $p_1^*$, $p_2^*$, $p_1^*(A)$, and $p_1^*(B)$ where obtained by a linear fitting of these values versus $1/n$ where $n$ is the degree of mean-field approximation. The points are fairly aligned so that the extrapolation values are sensible. For the case of $p_2^*(A)$ and $p_2^*(B)$ it is not possible to use the same procedure since the points are not aligned. However, if one plots $p_2^*(A)$ against $n^{-1/4}$ the points are fairly aligned, yielding the extrapolated value $p_2^* = 0$.

5. Conjugate Fields

The models studied in the scope of the equilibrium statistical mechanics, a conjugate field $H$ associated with a quantity $M$ is introduced by adding, in the Hamiltonian that defines the system, a term linear in $H$. In this cellular automaton this procedure must be modified, since the system is defined by a set of irreversible dynamic rules. In fact, it has been suggested that one can consider conjugate fields related to the dynamic rules. Following the analytical formulation given in Ref. 13, we study conjugate fields to the transition probabilities and the associated susceptibilities. Here we calculate these susceptibilities by using the pair approximation.

The order parameter associated with the active phase is given by the occupied sites density, $P(1)$. One can consider the conjugate field as the transition probability $w(0,0 \rightarrow 1) = p_0$, given by Eq. (2), because if $p_0 \neq 0$, then $P(1)$ must have stationary values different from zero. The associated susceptibility is given by $\chi_1 = \partial P(1)/\partial p_0$.

Using Eq. (10) and considering $p_0 \neq 0$ we obtain the following expression

$$
P_{\ell+1}(1) = p_2 P_{\ell}(11) + 2p_1 P_{\ell}(10) + p_0 P_{\ell}(00). \tag{27}
$$
We derive the evolution equation for $P_t(11)$ and evaluate this equation by using the approximation $P(\sigma, \sigma_{i+1}, \sigma_{i+2}) = P(\sigma, \sigma_{i+1})P(\sigma_{i+1}, \sigma_{i+2})/P(\sigma_{i+1})$. As the other pair correlation functions in Eq. (27) are defined as functions of $P(11)$ and $P(1)$, this Eq. (27) with the evolution equation for $P(11)$ form a closed set of equations, which we use to derive the susceptibility at the level of pair approximation.

We find that, approaching the critical points in the frozen/active transition from both sides, the susceptibility calculated at $p_0 = 0$ is

$$\chi_1 = G(p_1, p_2)|p_2 - F(p_1)|^{-1},$$

where

$$F(p_1) = \frac{p_1(2 - 3p_1)}{(1 - p_1)^2}$$

and

$$G(p_1, p_2) = \frac{[2p_1(p_2 - p_1) - 1][2p_1 - p_2] + 2(2p_1 - 1)(1 - p_2)^2}{(1 - p_2)(1 - p_1)^2}.$$ (30)

The susceptibility $\chi_1$ diverges at

$$p_2 = \frac{p_1(2 - 3p_1)}{(1 - p_1)^2}$$

which defines the frozen-active transition line (within the pair approximation). Moreover, the susceptibility at $p_0 = 0$ diverges as $\chi_1 \sim |p_2 - F(p_1)|^{-\gamma}$ with a classical critical exponent $\gamma = 1$, characterizing a second-order transition. These results agree with the one-site approximation results.13

The other order parameter of this problem, the Hamming distance, which is related to the spreading of damage is given by $P(1, 0)$. A possible choice to the conjugate field $h$, in this case, is

$$W_M(\sigma', \tau' \rightarrow \sigma, \tau) = (1 - h)W(\sigma', \tau' \rightarrow \sigma, \tau) + hW(\sigma' \rightarrow \sigma)W(\tau' \rightarrow \tau),$$ (31)

where $W(\sigma' \rightarrow \sigma)$ and $W(\sigma', \tau' \rightarrow \sigma, \tau)$ are given, respectively, by Eqs. (8) and (13) and $W_M(\sigma', \tau' \rightarrow \sigma, \tau)$ is a modified joint transition probability. One can verify that, when $h$ gets the value one, the two systems, original and replica, are completely disjoint. Thus, when $h \neq 0$, the Hamming distance attains a non-zero stationary value. The associated susceptibility is defined by $\chi_2 = \partial P(1, 0)/\partial h$.

The joint time evolution equation is now,

$$P_{t+1}(\sigma, \tau) = \sum_{\sigma', \tau'} W_M(\sigma', \tau' \rightarrow \sigma, \tau)P_t(\sigma', \tau').$$ (32)

Using Eq. (32) we obtain:

$$P_{t+1}(1, 0) = 2p_1 P_t(10, 00) + p_2 P_t(11, 00) + 2(b + c)P_t(11, 10) + h\{2p_1(1 - p_1)[P_t(10, 01) + P_t(10, 10)] + p_2(1 - p_2)P_t(11, 11) + 2[p_1 + p_2 - 2p_1p_2 - (b + c)]P_t(11, 10)\}. \quad (33)$$
Evaluating the evolution equations for the correlations in the pair approximation and considering the conditions where we are very close to the active-chaotic transition line we obtained an expression for $\chi_2$ at $h = 0$. Using the expression for the active-chaotic line given in the pair approximation we have obtained, numerically, that $\chi_2$ at $h = 0$ diverges at the critical line active-chaotic with a classical critical exponent equal to 1.

6. Conclusions

In this paper we obtained the phase diagram of the Domany–Kinzel cellular automaton using a three-site approximation. Our extrapolated results are in agreement with simulations. We have calculated the susceptibilities using a pair approximation and confirmed the one-site approximation results obtained previously. Our calculations were done for two prescriptions ($A$) and ($B$). In prescription $A$ the evolution of the system and its replica is subjected to the same noise. In prescription $B$ the system is updated with the same noise in some cases and in others it is necessary to generate two random numbers to update the system and the replica. It is important to observe that the joint dynamics of the two systems must be understood as a third dynamics with more states per site. In this sense, distinct (joint) prescriptions define different dynamics. So, a priori, two different prescriptions can give distinct results for the active-chaotic line. This is what really happens for the case of prescriptions $A$ and $B$ here presented. However if a numerical simulation of the spreading of damage is made with one sequence of random numbers, as performed in the pioneering work by Martins et al., then the analytical prescription to be considered must contain the element of joint evolution subjected to the same noise. A prescription where this fact is taken into account is given in Ref. 13, and it is here stated in Eqs. (20)–(21). It does not mean that the prescription $A$ is the only prescription capable to describe the joint evolution. One can devise other dynamics as long as one includes the element of the joint evolution subjected to the noise.

References