Ordering phase transition in the one-dimensional Axelrod model

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Abstract. We study the one-dimensional behavior of a cellular automaton aimed at the description of the formation and evolution of cultural domains. The model exhibits a non-equilibrium transition between a phase with all the system sharing the same culture and a disordered phase of coexisting regions with different cultural features. Depending on the initial distribution of the disorder the transition occurs at different values of the model parameters. This phenomenology is qualitatively captured by a mean-field approach, which maps the dynamics into a multi-species reaction-diffusion problem.

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1 Introduction

In recent years cellular automata and lattice models have been introduced in many fields in order to investigate the emergence of nontrivial collective phenomena out of simple microscopic interactions between a large number of elementary objects [1–3]. In the context of social phenomena, numerical simulations of simple automata have been used to study the formation and spreading of cultural domains [4–7]. Culture is intended here as the set of behaviors, beliefs, technical standards or values that individuals may mutually exchange. The cultural features are modeled as a set of F variables, which can assume integer values between 1 and Q, specifying the various traits that each feature can assume [4]. In general, the environment where exchanges take place is a two-dimensional square grid, where each site represents an individual or a group of individuals, whose culture is defined by the specific values of the F variables. Starting from an initial random configuration, interactions take place between nearest neighbors, leading to the formation and evolution of regions of homogeneous culture. It is obvious that the assessment of how realistic the model is or to which extent its results can be useful in the interpretation of empirical data in the social science context is a task left to sociologists. From the point of view of statistical physics this model (Axelrod model) is appealing, because it has a non-trivial out of equilibrium dynamics, similar but not equivalent to other well studied models [8,9].

In previous works [4–7], it has been investigated how the model behavior changes with respect to the values of the parameters F and Q. In particular it has been shown by large-scale simulations that, on a two-dimensional lattice, the model exhibits a non-equilibrium transition between a phase with all the system sharing a common culture and a disordered phase of coexisting regions with different cultures. This is a very interesting example of ordering phase transition in the context of far from equilibrium statistical physics. In this paper we perform a thorough analysis of the model defined in reference [4] on a one-dimensional lattice. This geometry acquires a special role in the description of social systems, since it can be used as starting point for complex topologies such as small-world networks [10,11]. Noticeably, in dimension $d = 1$ it is possible to provide an analytical treatment of the model by mapping the evolution dynamics into a multi-species reaction-diffusion system, that we study within a mean-field approximation. We recover also in one dimension the existence of an ordering phase transition, occurring at a critical value of the parameter Q. When the initial value of the cultural variables on each site is chosen randomly with uniform distribution between 1 and Q, we find that the system undergoes a transition between a fully ordered state for $Q < Q_c$ and a disordered one for $Q > Q_c$. When the distribution of initial variables is instead Poissonian of parameter q, the system exhibits a phase transition between order and disorder, but only for $F > 2$. For $F = 2$ any finite value of q leads, in the thermodynamic limit, to an asymptotic disordered state. In order to test the analytical predictions we perform numerical simulations of the original dynamics, finding a good agreement with the theoretical results.

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The paper is organized as follows. In Section 2 the model is introduced, the dynamics qualitatively described and the results of the two-dimensional case briefly summarized. In Section 3 we present the mapping to the reaction-diffusion system and the mean-field approach to it. In Section 4 we report the results of numerical simulations of the model in one dimension, both for the case of uniform and Poisson initial distributions, and compare them with the analytical predictions. Finally in Section 5 we draw some conclusions.

2 The model

We consider a one-dimensional lattice of linear size L. On each site i there are F integer variables $\sigma_{i,f}$ which define the cultural features of the individuals living on that site. In the original model [4], each feature $f = 1, \ldots, F$ on each site i is initially drawn randomly from a uniform distribution on the integers between 1 and Q. The parameter Q is a measure of the initial cultural variability (i.e. disorder) in the system. In reference [6] instead, the initial values were chosen according to a discrete Poisson distribution of parameter q $\text{Prob}(\sigma_{i,f} = k) = q^k e^{-q}/k!$, so that the positive real q was the average of the values extracted. Results were found to be qualitatively similar independently from the initial distribution, and only the Poissonian case was studied in detail. Here we will consider also the case with uniform distribution and we will discuss analogies and difference between the two cases.

The dynamics is defined as follows. At each time step, a pair of nearest neighbor sites i and j is randomly chosen. A feature f is selected and if $\sigma_{i,f} \neq \sigma_{j,f}$ nothing happens. If instead $\sigma_{i,f} = \sigma_{j,f}$ then an additional feature f' is randomly chosen among those taking different values across the bond, $\sigma_{i,f'} \neq \sigma_{j,f'}$. Such a feature is then set equal in the two sites: $\sigma_{i,f'} \to \sigma'_{i,f'} = \sigma_{j,f'}$. Time is measured as the total number of attempts divided by the number of sites L. Axelrod model can be seen as F coupled voter models [8]. The evolution of the system is basically a coarsening dynamics of ordered regions. The initial state is totally disordered since the choice of variables in each site is uncorrelated to any other one. As the dynamics starts, the interaction between sites tends to make neighbors similar, introducing correlations in the system. Ordered regions start to form with all sites sharing exactly the same value of all variables. Clearly there are many different possible types of ordered regions. As time proceeds boundaries between regions move, and the average domain size increases. On a finite lattice the ordering process continues until the system reaches an absorbing state such that no further dynamics is possible. Absorbing states can be of two types. A perfectly ordered absorbing state is made by a single region covering the whole system: all sites have the same set of variables $\sigma_{i,f}$. Otherwise an absorbing state can also be made by different ordered regions such that adjacent regions have all variables different. In that case all sites are either totally equal or totally different from their neighbors and no interaction may take place.

The nature of the final absorbing state depends on the full evolution of the system, i.e. it is the result of the competition between the disorder of the initial configuration and the drive toward order due to local interactions. Intuitively one expects that for small initial disorder (small Q or q) local interactions will prevail and the final state will be perfectly uniform, while in the opposite limit the ordering process will not last long enough to fully overcome the disorder of the initial condition. This picture turns out to be correct in two dimensions [6]. In that case extensive numerical simulations have shown that for small values of q, i.e. small initial disorder, the model converges toward an ordered state where a single culture occupies a macroscopically large fraction of the system. On the contrary for large values of q many different cultures coexist in the final absorbing state. In the thermodynamic limit of an infinitely large system one sees a well defined nonequilibrium phase transition for a precise value q_c, separating an ordered phase (for $q < q_c$) from a disordered one (for $q > q_c$). Interestingly, the nature of the transition is different depending on the number F of variables used to define the culture of a site. If $F = 2$ the transition is continuous, with the order parameter (defined below) vanishing for $q \to q_c$. For $F > 2$ instead the order parameter exhibits a jump at the transition. The different behavior is reflected also in the distribution of region sizes at the transition. For $F = 2$ it is a power law with an exponent $\tau < 2$, while for $F > 2$ the exponent is universal and larger than 2, so that the transition does not involve the divergence of a correlation length [6]. It is important to stress that the kind of nonequilibrium phase transition discussed here is not an absorbing phase transition [1]. Here the system always reaches a frozen absorbing state. The transition occurs in the properties of such absorbing state and hence is static in nature, although it is clearly determined by the dynamical evolution of the problem.

In this paper we shall investigate whether the same kind of transition occurs also in a one-dimensional geometry. To monitor the evolution of the model we mainly focus on the density (i.e. the number divided by the system size L) of active bonds $n_A(t)$ and of *fixed* bonds $n_F(t)$. We define as *active* a bond between two adjacent sites such that they have more than 0 and less than F equal features. We define as *fixed* a bond between two adjacent sites such that they have no equal variables. Clearly, active bonds are where the dynamics take place and form the boundary between regions that may interact, leading to further ordering. Boundaries formed by fixed bonds are instead frozen. All bonds connecting sites belonging to the same region are neither active nor fixed. We denote their density as n_0. Clearly, for all times $n_0 + n_A + n_F = 1$. Both the density n_A of active bonds and the density n_F of fixed bonds measure correlations in the system: $1/n_F$ and $1/n_A$ are correlation lengths growing in time. Since for any finite lattice an absorbing state is always reached by the dynamics, $n_A(t)$ goes asymptotically to zero in all cases. The value of $n_F(t = \infty)$ measures the order in the system. If $n_F(\infty)$ keeps finite as L diverges, the system remains

disordered in the thermodynamic limit, while $n_F(\infty) \to 0$ indicates full order.

Another useful quantity that will be considered below, is $\langle S_{max} \rangle / L$, where $\langle S_{max} \rangle$ is the average over different realizations of the size of the largest region existing in the final frozen state [6]. $\langle S_{max} \rangle / L$ is the fraction of the whole lattice occupied by the largest region and is an alternative order parameter, being zero for a disordered state and finite when a macroscopically large region exists in the system.

In the next section we describe an analytical treatment of the problem based on the mapping of the dynamics into a multi-species reaction-diffusion system, which is then analyzed in terms of mean-field equations. This approach turns out to capture remarkably well the qualitative behavior of the system. In some cases it gives predictions that are quantitatively accurate.

3 Theoretical approach

3.1 Mapping to a reaction-diffusion system

The Axelrod model considers the sites as elementary objects, which interact according to the rules described above. This dynamics can also be thought in terms of bonds between sites whose dynamics is induced by the updating of sites. More precisely, let us define as bond of type k a bond connecting two sites with k different features. Clearly k can be any number between 0 and F. Bonds of type 0 connect sites with all variables equal, *i.e.* belonging to the same region. Bonds of type F instead connect sites completely different and are therefore the fixed bonds introduced above. Bonds of type $1, \dots, F-1$ are what we called active bonds in the previous section.

To understand how the update of sites induces a dynamics for bonds, let us consider three neighbor sites (A), (B), (C). Site (B) is updated depending on the configuration of its neighbor (A). If the bond between sites (A) and (B) is of type 0 or F nothing occurs. Otherwise, if the bond is of type n one variable on site (B) is set equal to the corresponding variable on site (A). Hence the bond (A)-(B) becomes of type $n-1$. The update of site (B) modifies in general also the state of bond (B)-(C), which initially was of type m. Notice that for this bond the number of features which are different may increase, decrease or even remain unchanged, so that after the update the bond may be of type $m-1$, m or $m+1$. In summary, if we denote a bond of type k as A_k, the update of a site is then equivalent to a two-particle reaction

$$A_n + A_m \to A_{n-1} + A_{m+j} \qquad (j = 0, \pm 1). \qquad (1)$$
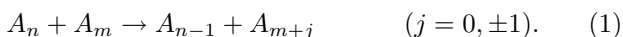
A specific example is presented in Figure 1. Bonds of type 0 can be considered as a sort of vacuum state where other types of bonds move. Reactions of the type $A_1 + A_0 \to A_0 + A_1$ are then diffusion processes for bonds of type 1. These are the only diffusion processes allowed.

In order to fully specify the dynamics we must provide the transition rates for the reactions (1). Let us consider
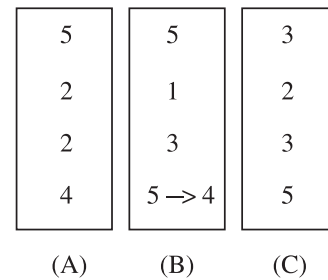

Fig. 1. Example of the evolution of three neighboring sites for $F = 4$. Site (B) and its neighbor (A) are selected and their feature $f = 1$ is compared. Since $\sigma_{A,1} = \sigma_{B,1} = 5$, the two sites interact and feature $f' = 4$ of site (B) is set equal to $\sigma_{A,4} = 4$. Bond (A)-(B), which was of type 3 becomes of type 2. Bond (B)-(C), initially of type 2 becomes of type 3.

the three sites of Figure 1. One of the features of site (B) is selected and compared with the corresponding one of site (A). In order for a reaction to occur the two variables must be the same. This occurs with a probability $R_n^{(1)} = (1 - n/F)(1 - \delta_{n,0})$ where we have taken into account that nothing happens if the bond is of type 0.

Hence with probability $R_n^{(1)}$, another variable $\sigma_{B,f'}$ is set equal to $\sigma_{A,f'}$. What is the effect of this change on the bond (B)-(C)? If $\sigma_{C,f'}$ was equal to $\sigma_{B,f'}$, then the update increases by one the number of features different in the bond (B)-(C). The probability that $\sigma_{C,f'} = \sigma_{B,f'}$ is the probability that we randomly select one of the $F - m$ equal variables out of the F total variables

$$R_{m,+1}^{(2)} = \frac{F - m}{F} = 1 - \frac{m}{F} \cdot \qquad (2)$$

With probability $1 - R_{m,-1}^{(2)}$ instead, the variable selected will be different in site (B) and (C), $\sigma_{C,f'} \neq \sigma_{B,f'}$. In this case, since $\sigma_{B,f'}$ is set equal to $\sigma_{A,f'}$ the final state of bond (B)-(C) depends on whether $\sigma_{A,f'}$ and $\sigma_{C,f'}$ are equal or not. Let us denote as λ the probability that $\sigma_{A,f'} = \sigma_{C,f'}$. Then the probability that bond (B)-(C) goes from type m to type $m - 1$ is

$$R_{m,-1}^{(2)} = \frac{m\lambda}{F} \cdot \qquad (3)$$

The probability $R_{m,0}^{(2)}$ is obtained *via* the normalization condition

$$R_{m,0}^{(2)} = \frac{m(1 - \lambda)}{F} \cdot \qquad (4)$$

In summary the reaction $A_n + A_m \to A_{n-1} + A_{m+j}$ occurs with rate

$$R_n^{(1)} R_{m,j}^{(2)}. \qquad (5)$$

The reactions (1) and the rates (5) fully specify the dynamics of the model. Provided one is able to write down the appropriate form of λ the mapping from the original Axelrod model is exact and equations (1) and (5) are an alternative formulation of the same dynamics.
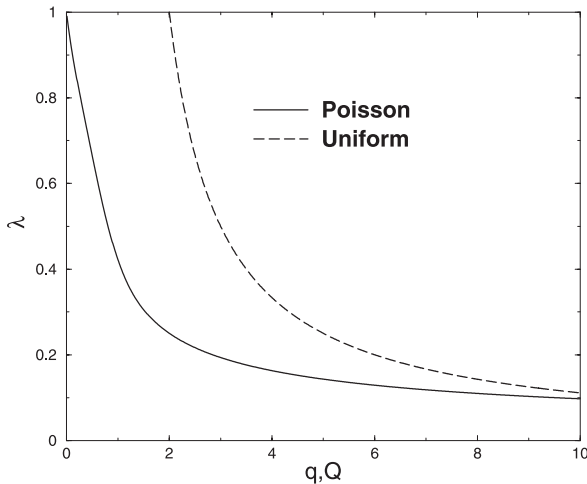
Fig. 2. Plot of λ as a function of Q (uniform case) or q (Poisson case).

3.2 Mean-field approximation

As discussed above, λ is the probability that two independent random variables (A and C), different from a third one (B), are equal. Here we will determine it by introducing a mean-field approximation, *i.e.* assuming spatial uniformity.

Let us call k the value of variable (B) and $p_B(k)$ its distribution. The λ can be written as $\sum_k p_B(k)\lambda_k$ where λ_k is the probability that A and C assume the same value, different from k. Clearly

$$\lambda_k = \sum_{i\neq k, j\neq k} \tilde{p}_A(i)\tilde{p}_C(j)\delta_{i,j} \qquad (6)$$

where $\tilde{p}_A(i) = p_A(i)/\sum_{i\neq k} p(i)$ is the probability distribution of the variable A constrained to be different from k. We assume that the distributions of all variables A, B and C remain equal to the initial ones at all times. For uniform initial distribution $p(i) = 1/Q$, we recover the expected value

$$\lambda = \frac{1}{Q-1} \cdot \qquad (7)$$

For variables distributed according to a Poissonian, the plot of λ as a function of q, is presented in Figure 2. The two behaviors are qualitatively similar. However, one has to remark that in the Poissonian case $\lambda = 1$ for $q = 0$, in the trivial situation when all variables are the same. For uniform initial condition instead $\lambda = 1$ for $Q = 2$, *i.e.* when the variables may assume *two* values.

From the knowledge of the possible reactions and their associated transition rates it is straightforward to write down the mean-field equations for the densities n_k of bonds of type k.

We obtain the set of equations ($k = 0, \ldots, F$)

$$\dot{n}_k = -R_k^{(1)}n_k + R_{k+1}^{(1)}n_{k+1}$$
$$+ \sum_{N=1}^{F-1} R_N^{(1)}n_N \left[-n_k\left(1 - R_{k,0}^{(2)}\right)\right.$$
$$\left. + n_{k-1}R_{k-1,1}^{(2)} + n_{k+1}R_{k+1,-1}^{(2)}\right] \qquad (8)$$

where clearly $n_{-1} \equiv 0 \equiv n_{F+1}$. More explicitly

$$\dot{n}_k = -\left(1 - \frac{k}{F}\right)(1 - \delta_{k,0})n_k + \left(1 - \frac{k+1}{F}\right)n_{k+1}$$
$$+ \sum_{N=1}^{F-1}\left(1 - \frac{N}{F}\right)n_N\left[-n_k\left(1 - \frac{k}{F}(1-\lambda)\right)\right.$$
$$\left. + n_{k-1}\left(1 - \frac{k-1}{F}\right) + n_{k+1}\frac{k+1}{F}\lambda\right]. \qquad (9)$$

It is easily verified that $\sum_{k=0}^{F} \dot{n}_k = 0$. Equations (8) are mean-field equations, since they neglect spatial fluctuations and noise in the system. They are complemented by the initial conditions, which are

$$n_k(t = 0) = P_{eq}^{F-k}(1 - P_{eq})^k \binom{F}{k} \qquad (10)$$

where P_{eq} is the probability that a feature takes the same value in two adjacent sites. Clearly $P_{eq} = 1/Q$ in the uniform case, while

$$P_{eq} = \sum_{h=0}^{\infty} \frac{q^{2h}e^{-2q}}{(h!)^2} \qquad (11)$$

for a Poisson initial distribution.

The mean-field system of equations of motion (9) consists of F coupled nonlinear equations. A detailed study of the temporal evolution is necessarily performed by integrating them numerically. However some important conclusions on the asymptotic state of the system can be drawn analytically by considering the fixed points of equations (9). A first crucial observation is that, for any F, a state with all $n_k = 0$ ($k = 1, \ldots, F-1$) is a fixed point of the equations. Therefore the system always admits a family of frozen asymptotic states, parametrized by the density of fixed bonds n_F ($n_0 = 1 - n_F$ because of normalization). To understand which of these fixed points is selected by the dynamics we perform a stability analysis, by linearizing the dynamical system (9) around the generic fixed point $n_k = 0$.

The stability matrix has F eigenvalues. One eigenvalue is always zero, corresponding to the direction parametrized by n_F and all made of fixed points. $F - 2$ other eigenvalues are real negative numbers or complex ones with negative real part, corresponding to stable directions. The last one, that we denote as μ, is always real and it crucially depends on the value of λ [12]. Its value as a function of λ, computed analytically for $F = 2$ and $F = 3$, is plotted in Figure 3 for two different values of n_F. Clearly
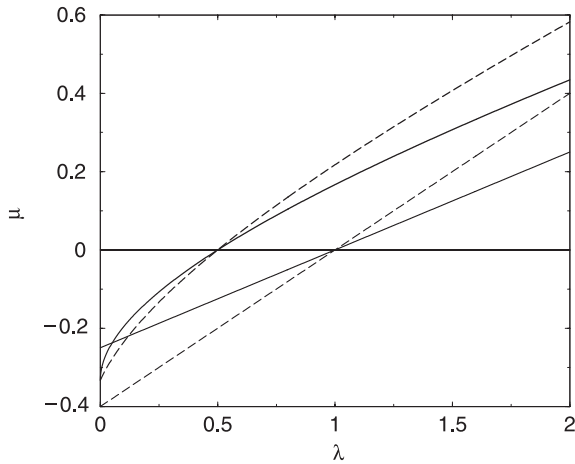
Fig. 3. Plot of the eigenvalue μ *versus* λ for $F = 2$ (thin lines) and $F = 3$ (thick lines), and $n_F = 0.5$ (solid) and $n_F = 0.8$ (dashed).

Fig. 4. Mean-field phase diagram of the model. The two critical lines are for uniform initial distribution (circles) and for Poisson initial distribution (diamonds).

μ depends from the value of n_F, but for any $n_F > 0$ it is negative for $\lambda < 1/(F-1)$ and positive for $\lambda > 1/(F-1)$. For $n_F = 0$ (homogeneous absorbing state) $\mu = 0$ for any value of λ, so that the stability of this fixed point cannot be assessed *directly* within a linear analysis. However its stability can be inferred indirectly from the stability of other fixed points: if all other fixed points are unstable the fixed point with $n_F = 0$ must be stable; if all others are stable, the dynamical system will not go to $n_F = 0$. This allows us to conclude that for values of the parameter Q or q of the model such that $\lambda < 1/(F-1)$ the equations will converge exponentially fast to a finite value $n_F > 0$ implying that the system remains disordered. If instead $\lambda > 1/(F-1)$ the only possible attractive fixed point is $n_F = 0$, which will attract the solution more slowly than exponentially. In this case the system exhibits a power-law convergence to an ordered state. Whether this transition actually takes place and for which value of the parameter of the initial distribution, it depends on the precise value of λ, that is plotted in Figure 2.

For uniform initial distribution, since $\lambda = 1/(Q-1)$ it is immediate to see that a phase transition occurs for

$$Q_c = F \tag{12}$$

so that for $Q < Q_c$ the system is ordered, while the system remains asymptotically disordered for $Q > Q_c$.

For Poisson initial distribution and $F > 2$, the scenario is the same, with an ordered phase for small q separated by a sharp transition from an ordered phase for large q. For $F = 2$ all finite values of q imply a positive eigenvalue μ and hence a disordered state. Only for $q = 0$ order is recovered, but of a very trivial type, since $q = 0$ means that all variables are the same *already in the initial state*. Notice that, since λ decays as $q^{-1/2}$ for large q, the transition point diverges for large F as $q_c \sim F^2$, differently from the uniform case.

For easier insight into the behavior of the model we plot in Figure 4 the mean-field phase diagram.
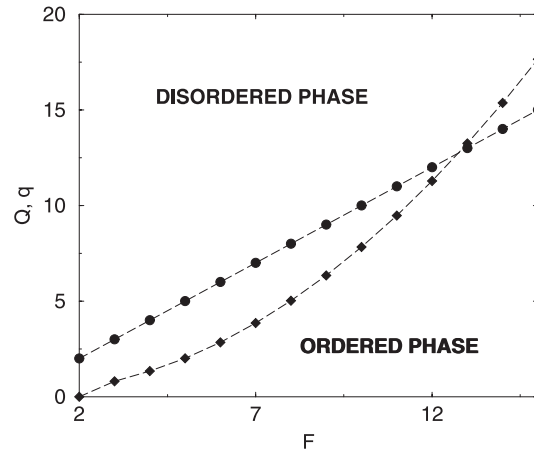
3.3 Uniform initial distribution with F = 2

Let us now give a closer look at the case of uniform initial distribution with $F = 2$. In this case the set of mean-field equations (9) is reduced to two coupled equations

$$\dot{n}_1 = -\left[\frac{3}{4} + \frac{1}{4(Q-1)}\right]n_1^2 + \frac{2-Q}{2(Q-1)}n_1 n_F \tag{13}$$

$$\dot{n}_F = \frac{1}{4}n_1^2 - \frac{1}{2(Q-1)}n_1 n_F \tag{14}$$

where n_0 has been eliminated using normalization. In the case $Q = 2$ it is easy to solve (14) explicitly, since the equation for n_1 does not depend on n_F. One obtains

$$n_1(t) = \frac{1}{2+t} \tag{15}$$

$$n_F(t) = \frac{1}{(2+t)^{1/2}} - \frac{1}{2(2+t)}. \tag{16}$$

Hence we find, as expected, that both the density of active bonds and of fixed bonds vanish asymptotically as power-laws.

For $Q > 2$ the two equations (14) become fully coupled. The asymptotic value of n_F is found to be

$$n_F(t = \infty) = \frac{Q-2}{Q} \tag{17}$$

for all values of Q, which will be shown below to agree very well with numerical results.

4 Numerical results

In order to validate the results of the theoretical approach we compare them with extensive numerical simulations of the model. For each value of the parameters, we average over 10 000 or more realizations. For both types of initial
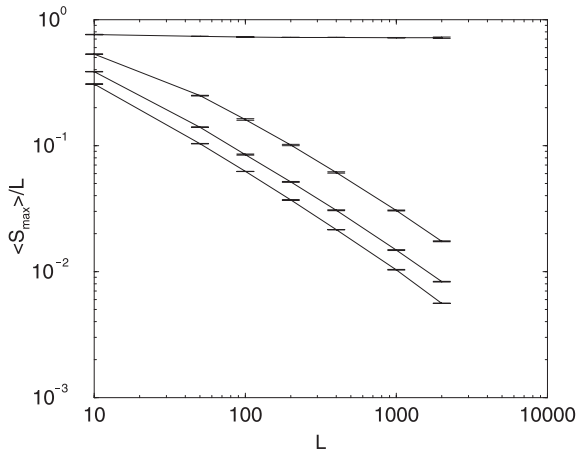
Fig. 5. The order parameter $\langle S_{max}\rangle/L$ as a function of the system size L for $F = 2$. From top to bottom the curves are for $Q = 2$, $Q = 3$, $Q = 4$ and $Q = 5$.

distributions, all values of F and of q or Q, we find that the system reaches for long times an absorbing state with no active bonds ($n_A = 0$). Extrapolation to the limit $L \to \infty$ indicates that also in the thermodynamic limit the system freezes asymptotically. This is the first prediction of the mean-field approach that is verified numerically. We now turn to a more detailed analysis of the asymptotic state as parameters are changed.

4.1 Uniform initial distribution

Let us consider first the case with $F = 2$ variables on each site, which in two dimensions gives a continuous transition. The mean-field approach predicts the existence of a transition between an ordered and a disordered phase for $Q_c = 2$. Such a prediction is confirmed by the behavior of the order parameter $\langle S_{max}\rangle/L$. As Figure 5 illustrates, $\langle S_{max}\rangle/L$ keeps for $Q = 2$ a finite value close to 0.71 in the thermodynamic limit, while it goes to zero for $Q > 2$. Hence one macroscopic region occupies a finite fraction of the system for $Q = 2$, while for larger values of Q, no macroscopic domain is formed.

We remark that in the ordered case the asymptotic value of $\langle S_{max}\rangle/L$ is not 1. This should not be taken as evidence that the system reaches a partially ordered state with the largest region spanning only a finite part of the whole lattice. In fact the situation is more complex. $\langle S_{max}\rangle$ is the average over a large number of realizations. In many of them the system becomes fully ordered and $S_{max}/L = 1$. However in a finite fraction of the realizations the system remains partially disordered so that the order parameter has a value smaller than 1. In practice the distribution of the values of S_{max}/L for $L \to \infty$ is a δ-function for $S_{max}/L = 1$ plus a finite nontrivial contribution for $S_{max}/L < 1$ This leads to $\langle S_{max}\rangle/L \simeq 0.71$.

For $Q > 2$ the system remains disordered and a finite fraction n_F of the bonds is fixed. In the previous section, equation (17) is the mean-field result for n_F in the asymptotic state as a function of Q. Such a formula is
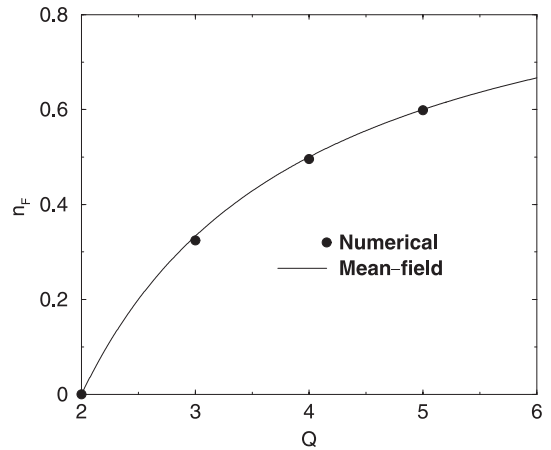

Fig. 6. Comparison of the numerical results with the mean-field formula $(Q - 2)/Q$ for the final density of fixed bonds in the case $F = 2$.
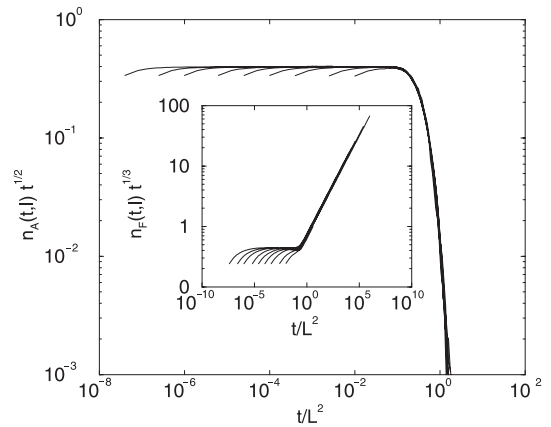

Fig. 7. Main: Scaling plot of the density of active bonds n_A versus time for $F = 2$, $Q = 2$ and system size (left to right) $L = 10, 20, 50, 100, 200, 400, 1000, 2000, 5000$. Inset: Scaling plot of the density of fixed bonds n_F versus time for the same set of parameters.

compared with numerical results in Figure 6. The agreement is excellent, indicating that the mean-field approach is *quantitatively* correct in this case.

Let us now analyze the whole dynamical evolution. In the main part of Figure 7 we plot the temporal behavior of the density of active bonds n_A in the case $Q = 2$, for different system sizes. All curves collapse on the same one when time is rescaled by L^2, *i.e.* n_A obeys the scaling form

$$n_A(t, L) = t^{-1/2}g_A(t/L^2). \qquad (18)$$

The scaling function $g_A(x)$ goes to a constant as $x \ll 1$ and goes to zero exponentially for $x \gg 1$. In the inset of the same figure it is shown that also the density of fixed bonds obeys a scaling form

$$n_F(t, L) = t^{-1/3}g_F(t/L^2) \qquad (19)$$

where $g_F(x) = $ const for $x \ll 1$ and $g_F(x) \sim x^{1/3}$ for $x \gg 1$.

The physics behind Figure 7 is clear. In the initial state a finite number of active bonds is present. Notice that for $F = 2$ and $Q = 2$ a single type of active bond exists, connecting sites with one equal and one different feature. Interaction between sites implies diffusion of active bonds and annihilation whenever two active bonds meet. Fixed bonds are affected by active bonds but the converse is not true: As far as active bonds are concerned, the system is equivalent to the reaction-diffusion system $A + A \rightarrow 0$. The decay as $t^{-1/2}$ of the density of active bonds is easily related to the combination of diffusive wandering and mutual annihilation [13]. The inverse of n_A is a correlation length that grows in time. In an infinite system such length grows indefinitely. In a finite lattice, growth stops when $1/n_A$ reaches the system size L, and this yields a cutoff time scaling as L^2. The evolution of fixed bonds is enslaved by the dynamics active bonds but it is slower. $1/n_F \sim t^{1/3}$ is a correlation length non equivalent to $1/n_A \sim t^{1/2}$. It grows with time but remains finite when the cutoff time is reached, so that the in the frozen state n_F reaches a finite value decreasing as $L^{-2/3}$, which vanishes in the thermodynamic limit.

A comparison of the exponents found numerically with the mean-field values (Eq. (16)) indicates that the mean-field approximation correctly reproduces that n_F decays more slowly than n_A, but it does not predict the correct exponents. This is not a surprising result: we have computed the mean-field rates assuming the system to be homogeneous, while instead ordered regions grow indefinitely. The problem is here the same of the mean-field treatment for the reaction-diffusion system $A+A \rightarrow 0$ [13]. For higher values of Q the disagreement between the mean-field and numerical results is similar. It is somewhat striking that despite the dynamics is not captured quantitatively by the mean-field approximation, the asymptotic value for n_F is remarkably accurate (Fig. 6).

Let us now discuss the case $F > 2$ corresponding to a discontinuous transition in $d = 2$. For illustrating the behavior common to all values $F > 2$ let us focus on the case $F = 10$. As in the two-dimensional case [6], the system exhibits a discontinuous transition between a fully ordered phase for small Q and a disordered phase for $Q > Q_c$. This can be inferred from Figure 8, where $1 - \langle S_{max} \rangle / L$ is plotted *versus* Q. By observing that the convergence of $\langle S_{max} \rangle / L$ to 1 is exponential for $Q \leq 6$, while curves are bent upward for $Q > 7$ one is led to conclude that the transition occurs for $Q_c \simeq 7$.

4.2 Poissonian initial distribution

Let us consider now a system such that the initial values of the variables are chosen according to a discrete Poisson distribution of parameter q. q plays here a role similar to the parameter Q for the uniform initial distribution, since it fixes the average value of the variables in the initial state. However, no matter how small is q, arbitrarily large values can be extracted with a Poisson distribution.

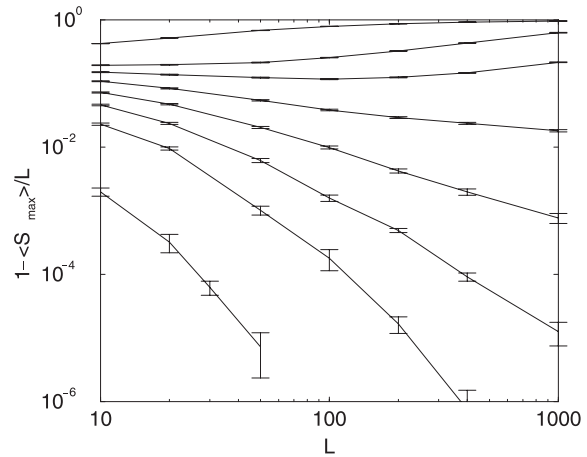Let us consider first the case $F = 2$ (Fig. 9).

Fig. 8. Plot of $1 - \langle S_{max} \rangle / L$ as a function of the system size L for $F = 10$. From bottom to top the curves are for $Q = 3$, $Q = 5$, $Q = 6$, $Q = 7$, $Q = 8$, $Q = 9$, $Q = 10$ and $Q = 15$.
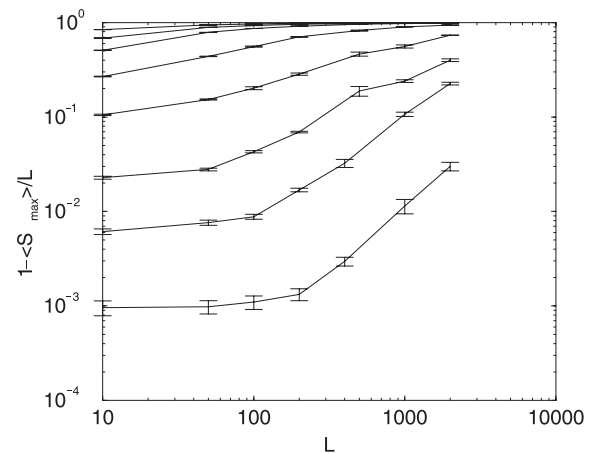

Fig. 9. Plot of $1 - \langle S_{max} \rangle / L$ as a function of the system size L for $F = 2$ for Poisson initial distribution. From bottom to top the curves are for $q = 0.02$, $q = 0.05$, $q = 0.1$, $q = 0.25$, $q = 0.5$, $q = 1$, $q = 2$ and $q = 10$.

The behavior differs qualitatively from the uniform case. For any value $q > 0$ it is clear that the order parameter goes asymptotically to zero, even if for small q, $\langle S_{max} \rangle / L$ remains close to 1 for relatively large L. We conclude that there is strong evidence that for $F = 2$ an initial distribution of Poisson type destroys long range order for any value of $q > 0$, as predicted by the mean-field approach.

We finally turn to the case $F = 10$, as an example of what happens in general for $F > 2$. The value of $1 - \langle S_{max} \rangle / L$ is plotted in Figure 10. For small q it is clear that the system becomes ordered as L grows while for large q, the curves tend to go toward 1, indicating the existence of a discontinuous phase transition for intermediate q. A rough estimate of the transition point is between $q = 4$ and $q = 5$.

These numerical data corroborate the picture emerging from the mean-field approach. For $F = 2$ we actually find no evidence of long range order in the system, no matter
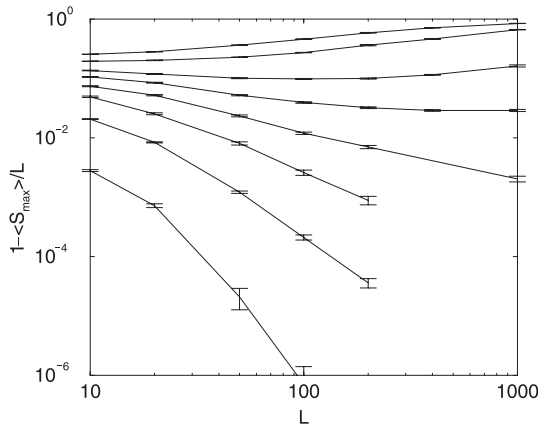
Fig. 10. Plot of $1 - \langle S_{max} \rangle / L$ as a function of the system size L for $F = 10$ for Poisson initial distribution. From bottom to top the curves are for $q = 1$, $q = 2$, $q = 3$, $q = 4$, $q = 5$, $q = 6$, $q = 8$, and $q = 10$.

how small q is taken. For $F = 10$ we observe instead the pattern already found with uniform initial distribution: a transition between a disordered phase for large q and an ordered one for smaller values of the parameter q. Also the location of the transition seems to be captured with good accuracy.

5 Conclusions

In this paper we have analyzed in detail the behavior in one dimension of the Axelrod model, a cellular automaton introduced in reference [4] for the description of social influence. Interestingly, the one-dimensional version of the model displays a phenomenology as rich as the two-dimensional case. More precisely, we find by numerical simulations a non-equilibrium phase transition between a disordered and an ordered phase. This phenomenology is recovered accurately by a simple mean-field treatment of the problem, which exploits a mapping onto a reaction-diffusion problem involving F different species. The mean-field approach is successful in several aspects. First, it correctly predicts that the system always reaches an asymptotically absorbing state. Secondly, it captures the existence of a transition in the final absorbing state or the absence of it (for Poissonian initial conditions and $F = 2$). Finally, it provides reasonably accurate estimates of the

critical value of the control parameter Q or q. Mean-field fails instead in the prediction of the exponents of the temporal behaviors close to the transition. This is a typical scenario for mean-field treatments: transition points can be computed with good accuracy while exponents are not captured correctly. The theoretical approach presented in this paper is the simplest suitable for this kind of problem. For more precise values of the exponents one should go beyond mean-field, by including diffusion terms and noise in equation (9) and applying dynamic renormalization group techniques [14,15].

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