

Model of biological evolution with threshold dynamics and infinitely many absorbing states

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We study a model of biological evolution where the survival of a given species depends on its interactions with neighboring species. In the steady state the model has an active phase and an absorbing phase, which are separated by the critical point of the directed percolation universality class. The absorbing phase is infinitely degenerate and the dynamical behavior of our model is found to be nonuniversal. [S1063-651X(99)12908-8]

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Biological systems, which consist of many interacting entities like cells, individuals, or species, are certainly within the scope of statistical mechanics. One of the modern topics in this field is the modeling of biological evolution. To a large extent this interest is inspired by the so-called Bak-Sneppen (BS) model, which relates the apparent scale invariance of the extinction of species with the widely applicable concept of the self-organized criticality [1]. The BS model provides a coarse-grained description of an ecosystem. In this lattice model each species i is described by its fitness f_i , which is a real number ($0 < f_i < 1$). In each time step the species with the smallest f_i becomes extinct and is replaced by a new species with the fitness chosen randomly. Moreover, as inspired by biological observation, the nearest species are also affected and their fitness is also chosen anew randomly. A remarkable prediction of the BS model is that without tuning any parameters the model spontaneously evolves toward the critical state, where arbitrary-size avalanches of extinctions are observed, which is in agreement with some fossil records [2]. The BS model inspired an intensive research and a number of variants of this model were proposed, which cure some of its deficiencies [3]. For example, the BS model as defined above is driven by the so-called extremal dynamics, i.e., at a given time it is only a species with the smallest f_i , which mutates and all the others (except its neighbors) remain unchanged. This assumption, which is crucial for the scale-invariant properties of the model, seems to be rather unrealistic. One can mention, however, that an interesting model of biological evolution, which is not driven by such a dynamics and still exhibits a robust critical behavior, was proposed by Choi *et al.* [4]. An interesting aspect of the BS model concerns a possible universality class of its critical behavior. Although earlier simulations suggested that the one-dimensional version of this model might belong to the directed-percolation (DP) universality class [5], more extensive calculations seem to exclude this possibility [6]. Nevertheless, the relation with the directed percolation is still intriguing, since one can construct certain variants of the BS model, which are exactly equivalent to the directed percolation [7].

In the present paper we propose a certain model of biological evolution in which fitness of a given species is determined by its interactions with surrounding species. In our opinion, this is not an unrealistic assumption: putting into or removing from a certain niche another species is likely to

affect, at least some, species that already existed in that niche. Our model is not driven by the external dynamics: active species are those with fitnesses below certain threshold parameter r , which might be regarded as some kind of ecological pressure. It turns out that depending on the value of r the model is either in the active phase with constant extinction and replacement of species taking place or in the absorbing phase where the evolutionary struggle comes to rest and species no longer extinct. Although our model cannot describe a long-time aspect of evolution in real ecosystems, we hope that it might describe them at least in a restricted sense. The model shows that a small change of external parameters (r) might induce a transition in an ecosystem between the stasis and the active phase.

Our model has also an interesting critical behavior. Monte Carlo simulations for this model show that as far as the steady-state properties are concerned, the model undergoes a phase transition of the DP universality class. However, certain exponents, namely, η and δ (defined below) describing dynamics of our model, are different from those of the DP and are clearly nonuniversal. This nonuniversality is most likely related to the fact that our model has infinitely many absorbing states, since similar behavior was observed for some other models with this property [9,10]. Moreover, numerical evidence for up to now examined models with infinitely many absorbing states suggests that although these exponents are indeed nonuniversal (and depend on the choice of the absorbing state), their sum is universal (and independent on the absorbing state) [9]. We will show that our model provides additional support to this observation.

Models with absorbing states and nonequilibrium phase transitions are currently intensively studied. It is believed that models, which have a single absorbing state, belong to the DP universality class [12] and this conjecture is supported by a number of examples ranging from the Reggeon field theory [13] to contact processes [14] or to Schlögl's models [15]. There is also convincing numerical evidence that a group of models with double absorbing state constitutes another universality class, characterized by a different set of critical exponents [8]. Although little is known about further classification of models with finitely many absorbing states, some knowledge is already accumulated about models with infinitely many absorbing states [9,10,16]. Such models are mainly used to describe some oxidation processes. As far as steady-state properties are concerned, it is conjectured that

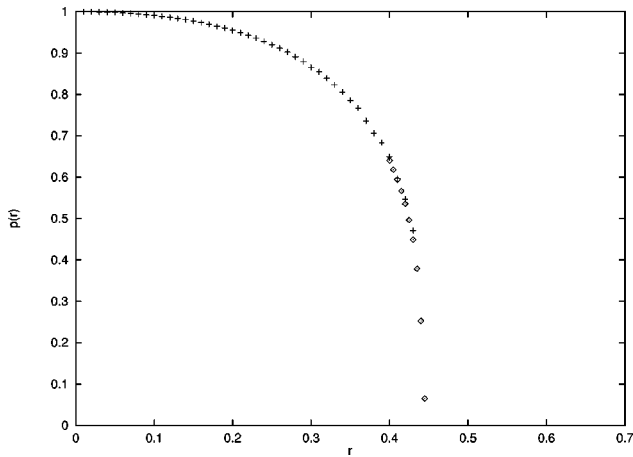


FIG. 1. The density of active sites p as a function of r for $L = 10^4$ (crosses) and $L = 10^5$ (diamonds). Simulation time in the vicinity of the transition was typically 10^4 of Monte Carlo steps (single update/site).

these models belong to directed percolation universality class [17] but, as we have already mentioned, some of their dynamical properties are universal only in a weaker sense.

Our model is defined on a d -dimensional Cartesian lattice. Each site of the lattice represents a certain species. Moreover, between each pair of neighboring species i and j we introduce an “interaction” $w_{i,j}$ ($0 < w_{i,j} < 1$), which describes an amount of frustration which the species i and j experience due to their close coexistence. Usually, initial interactions $\omega_{i,j}$ are chosen randomly. Introducing certain threshold parameter r ($0 < r < 2d$), we define dynamics of our model as follows: (i) Choose a site i at random. (ii) Calculate $\omega = \sum_j w_{i,j}$, where summation is over all nearest neighbors j . (iii) If $\omega > r$, then the chosen species, due to too much frustration, becomes extinct and the site becomes occupied by a new species with the interactions $w_{i,j}$ chosen anew. If $\omega < r$, the species at the site i survives.

Before describing our numerical results, let us notice that it is possible to have $w_{i,j}$ set in such a way that at each site $\omega < r$, which means that the model comes to rest. Such a state is called an absorbing state and in our model this state has obviously infinite (continuous) degeneracy. Let us also notice that models with infinitely many absorbing states,

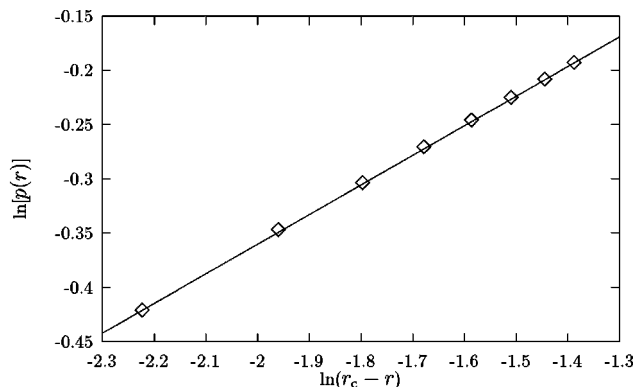


FIG. 2. The log-log plot of $p(r)$ as a function of $r_c - r$. The data are obtained for the system size $L = 10^5$. The straight line has a slope $\beta = 0.273$.

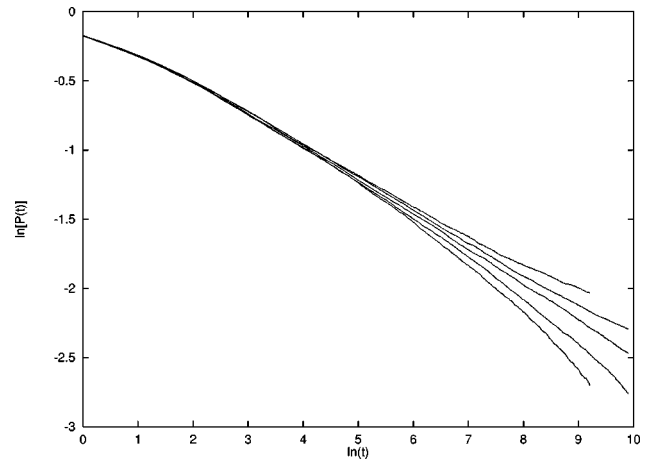


FIG. 3. The log-log plot of $P(t)$ as a function of t for $r_0 = 0$ and $r = 0.44, 0.4405, 0.441, 0.4415, \text{ and } 0.442$ (from top to the bottom).

which are already described in the literature [9,10,16], have discrete site variables and thus for finite lattices the degeneracy of the absorbing state is also finite (albeit rapidly increasing with system size). Since our model has continuous site variables, the degeneracy of the absorbing state is infinite even for finite lattices. It is well known, especially in equilibrium statistical mechanics, that models with continuous variables often have very different behavior than their discrete counterparts and it would be desirable to examine whether this feature is of any relevance in our model.

To examine the properties of the one-dimensional version of this model, we used Monte Carlo simulations. First, we studied the density p of active sites (i.e., those with $\omega > r$) in the steady state for the system size $L = 10^4$ and $L = 10^5$ and with initial interactions chosen randomly. The results, shown in Fig. 1, clearly indicate the existence of the phase transition in the present model around $r \sim 0.44$, which separates the active ($p > 0$) and the absorbing ($p = 0$) phases. Assuming that in the vicinity of the transition p has a power-law singularity $p \sim (r_c - r)^\beta$ and using the least-squares method, we estimated $r_c = 0.4409$ and $\beta = 0.273$. These estimates are based on results for $L = 10^5$ which, in our opinion, is sufficiently large to overcome the finite-size effects. The log-log plot of our data around the critical point is shown in Fig. 2.

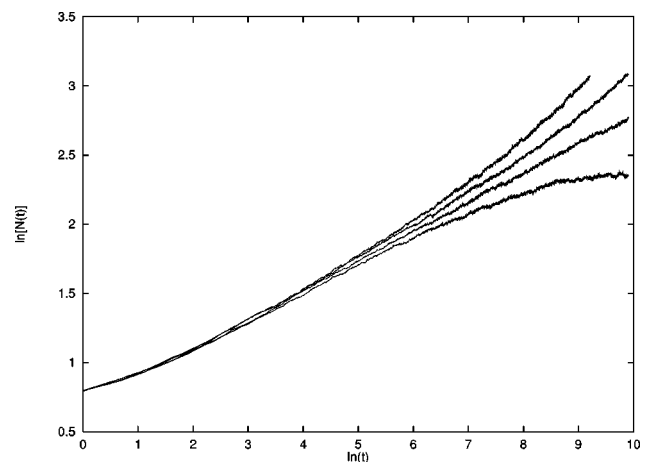


FIG. 4. The log-log plot of $N(t)$ as a function of t for $r_0 = 0$ and $r = 0.44, 0.4405, 0.441, \text{ and } 0.4415$ (from top to the bottom).

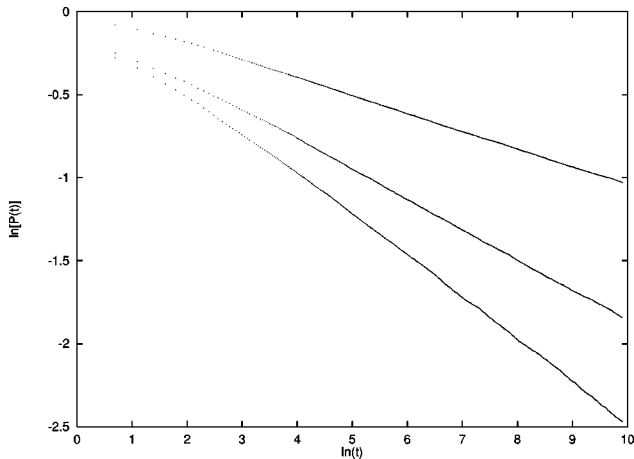


FIG. 5. The log-log plot of $P(t)$ as a function of t for $r = 0.441$ and $r_0 = 0.2, 0.1,$ and 0.0 (from top to the bottom).

The value of the exponent β is close to the value in the directed percolation $\beta_{DP} = 0.2765$ [11]. Since the transition in our model is between the active and absorbing phases, we believe that as far as the steady-state properties are concerned our model belongs to the DP universality class.

To examine time-dependent properties of our model, we used the so-called dynamic Monte Carlo method [18,19], which is a frequently used technique for studying models with absorbing states. Following the general prescription of this method, we prepared the initial configuration, which consists of a single active site and $L-1$ inactive sites. Thus we assign $w_{1,2} = w_{2,3} = 0.23$ and $w_{i,i+1} = r_0$ for $i = 3, 4, \dots, L$ and $2r_0 < r_c$. With such an assignment and for r close to r_c only the site with $i=2$ is active. Since the periodic boundary conditions are imposed in our simulations, the system is translationally invariant and the initial location of the active site is obviously irrelevant. The model subsequently evolves according to its dynamical rules. We measured the probability of survival $P(t)$ until time t and the average number of active sites $N(t)$ at time t . One expects [18] that asymptotic behavior of these quantities strongly depends on whether the system is at or off its critical point. In particular, at the critical point, one should have $P(t) \sim t^{-\delta}$ and $N(t) \sim t^\eta$. Off-critical asymptotic behavior of $P(t)$ and $N(t)$ deviates from the above power laws and thus enables precise location of the critical point.

The time dependence of $P(t)$ and $N(t)$ in the log-log scale is shown in Figs. 3–6. Our statistics is based on runs up to $t = 2 \times 10^4$ [Monte Carlo steps per site] and we usually made 2×10^4 independent runs. As usual in this type of calculation, it is more efficient to keep records of active sites since only they are updated in the course of simulations. Moreover, one has to choose the size of the system L suffi-

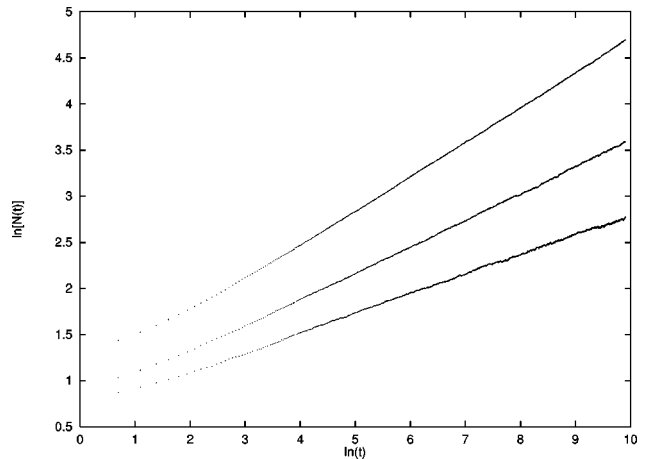


FIG. 6. The log-log plot of $N(t)$ as a function of t for $r = 0.441$ and $r_0 = 0.2, 0.1,$ and 0.0 (from top to the bottom).

ciently large to ensure that during the run the “growing” cluster of active sites never wraps around the lattice. In Figs. 3 and 4 we present the results for $r_0 = 0$. One can see that the best linearity is obtained for $r = 0.441$, which is in agreement with the steady-state estimation of r_c . Estimating the slope of the data for $r = 0.441$, we obtain $\delta = 0.259$ and $\eta = 0.215$. These values are clearly different from the DP values [20], $\delta_{DP} = 0.159$ and $\eta_{DP} = 0.313$. However, the sum $\delta + \eta$ is remarkably close to the corresponding DP value $\delta_{DP} + \eta_{DP}$.

We performed similar calculations for other values of r_0 and the results are basically the same: at $r = 0.441$ the power-law fit seems to be the best and the exponents δ and η change continuously with r_0 but their sum remains nearly constant and is equal to $\delta_{DP} + \eta_{DP} = 0.473$. The results for $r = 0.441$ and $r_0 = 0, 0.1, 0.2$ are shown in Figs. 5 and 6. For $r_0 = 0.1$ and 0.2 we obtained that the sum $\delta + \eta$ equals 0.474 and 0.482 , respectively. These results confirm the earlier observations that for models with infinitely many absorbing states exponents δ and η are nonuniversal with respect to the choice of the absorbing state, but their sum is universal.

Although dynamical variables in our model are continuous, in some respects the model seems to be simpler. Let us notice that one can easily generate any of the absorbing states with the macroscopically preassigned characteristics. In the present paper we investigated homogeneous absorbing states with a constant value of r_0 . Obviously, one can easily generate nonhomogeneous absorbing states and thus examine the role of such nonhomogeneities. Let us notice that the generation of absorbing states for some other models is a highly nontrivial and computationally demanding task [10].

We hope that the present model being biologically motivated, at the same time will provide additional insights into the physics of models with nonequilibrium phase transitions.

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