Generic criticality in a model of evolution

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Using Monte Carlo simulations, we show that for a certain model of biological evolution, which is driven by non-extremal dynamics, active and absorbing phases are separated by a critical phase. In this phase both the density of active sites $\rho(t)$ and the survival probability of spreading $P(t)$ decay as $t^{-\delta}$, where $\delta \sim 0.5$. At the critical point, which separates the active and critical phases, $\delta \sim 0.29$, which suggests that this point belongs to the so-called parity-conserving universality class.

The model has infinitely many absorbing states and, except for a single point, has no conservation law.

Recently statistical mechanics of complex systems attracts a lot of attention. The main motivation of studying these systems is the belief that their qualitative understanding can be obtained by studying relatively simple mathematical models. Indeed, there is a number of examples where (spin-)glasses, proteins, biological evolution, societies or economies were described in terms of very simple models. In quantitative terms, complexity is very often related with the absence of a characteristic length- or time scale (i.e., scale invariance). For example, paleontological data suggest that outbreaks of evolutionary activity substantially varied in sizes and in addition were correlated over large periods of time. Similar features seem to characterize other, at first sight unrelated, processes like earthquakes, stock-exchange fluctuations or flow of sand.

The absence of characteristic scales is a well-known property of critical systems in the field of equilibrium statistical mechanics. However, in the equilibrium statistical mechanics, criticality is an exception rather than a rule and it requires fine-tuning of control parameter(s). On the other hand, the apparent abundance of scale-invariance among complex systems suggests that this property should be in some sense generic and should not require such a fine tuning.

An interesting idea, which tries to explain the scale invariance in various systems, was proposed by Bak, Tang and Wiesenfeld under the name of self-organized criticality (SOC). They have shown that dynamics of some simple systems might naturally lead these systems to the critical state. Such a behaviour was subsequently observed in a number of other models.

However, models exhibiting SOC are usually driven by very special dynamics. This is either the so-called extremal dynamics (which drives some evolutionary models) or conservative dynamics (which drives sandpile-like models). When these dynamical rules are even slightly violated, the criticality is usually destroyed. For example, in the Bak-Sneppen model describing the evolution of an ecosystem, the criticality is lost when we modify the rule that only the least-fitted species dies out and is replaced by a new one. However, on biological grounds, one expects that extinction might happen to a better-fitted species as well. It would be desirable to construct a model which would not be driven by such a special dynamics but whose criticality would be in some sense generic.

In search of the generic criticality, we might recall that such models exist in equilibrium statistical mechanics, and the prime example is the XY model. In this model the low-temperature phase is critical and correlation functions decay in a power-law way. Above certain temperature the criticality of the model is destroyed and the system is in a disordered phase, where correlation functions decay exponentially.

Despite the wealth of models with critical behaviour, the existence of generic criticality in the nonequilibrium statistical mechanics is still an open problem. In some cases, certain symmetries, conservation laws or separation of time scales are responsible for the criticality of the system. These factors play also an important role in SOC models. Recently, some SOC models were related with more general models. It turns out that in some cases the SOC corresponds to the critical points of these more general models. However, the criticality of the latter models most likely resembles an ordinary criticality (i.e., the criticality exists only at some isolated points).

In the present paper we study a model of biological evolution. The model describes an ecosystem at the coarse-grained level similarly to the Bak-Sneppen model, but it is driven by non-extremal dynamics. We show that in a certain range of a control parameter certain quantities exhibit power-law behaviour and thus the model might be said to be generically critical. The behaviour of our model is a consequence of a certain symmetry, which places the model in the so-called parity-conserving (PC) universality class.

Our model is a variant of other recently introduced models. It is defined on a one-dimensional lattice, where for each bond between the nearest-neighbouring sites $i$ and $i+1$, we introduce bond variables $w_{i,i+1} \in (-0.5, 0.5)$. Introducing the parameter $r$, we call the site $i$ active when...
\[ w_{i,i+1}w_{i-1,i} < r. \]  

Otherwise, the site is called nonactive. The model is driven by random sequential dynamics and when the active site \( i \) is selected, we assign anew, with uniform probability, two bond variables \( w_{i,j+1} \) and \( w_{i-1,j} \). Nonactive sites are not updated, but updating a certain (active) site might change the status of its neighbours. The above rules immediately imply the existence of an absorbing state, i.e., the one without active sites.

One can interpret the sites as species with the fitness being a product of the attached bond variables. When the fitness of a certain species is lower than a threshold value \( r \), the species becomes extinct and is replaced by another species.

To examine the properties of our model, we used Monte Carlo simulations. Since the implementation of the above dynamical rules on a computer is straightforward, below we present only the results of these simulations. An important quantity characterizing this model is the steady-state density of active sites \( \rho \). Fig. 2 shows the density \( \rho \) as a function of \( r \). The simulations were performed for the linear system size \( L = 10^5 \) and we checked that the presented results are, within a small statistical error, size-independent. For each \( r \), after relaxing the random initial configuration for \( t_{\text{rel}} = 10^4 \), we made measurements during runs of \( t = 10^5 \) (the unit of time is defined as a single on average update/lattice site). This figure suggests that the model undergoes a continuous transition at \( r = r_c \sim 0.027 \) and for \( r < r_c \) the model should be in the absorbing phase with \( \rho = 0 \). The simulations close to the critical point \( (r < 0.03) \) were more extensive and we used \( L = 5 \cdot 10^5 \), \( t_{\text{rel}} = 5 \cdot 10^4 \) and \( t = 10^6 \). Let us also notice that since bond variables are continuous, there is a continuous degeneracy of the absorbing state.

We also observed that for \( r < r_c \) the system is rather reluctant in reaching an absorbing state. Only for \( r < 0 \), the system reaches such a state quite quickly. Results of our simulations presented below show that for \( 0 < r < r_c \) the model remains in the critical phase.

First, we examined the time evolution of the density of active sites \( \rho(t) \). After the system starts from an arbitrary initial configuration, containing a finite fraction of active site, \( \rho(t) \) should decay to zero in the absorbing phase and this decay should be faster than the power law. At the critical point one expects a power-law decay \( \rho(t) \sim t^{-\delta} \). In the active phase \( \rho(t) \) asymptotically remains positive.

In Fig. 3 we show \( \rho(t) \) as a function of \( t \) plotted in the logarithmic scale. For \( r = 0.03 \) the density \( \rho(t) \) clearly approaches a positive value, which confirms that in this case the model is in the active phase. Moreover, a faster than power-law decay is observed for \( r = -10^{-4} \) and \( -10^{-6} \). However, for \( r = 0 \) and \( 0.02 \) our simulations show a power-law decay with the exponent \( \delta = 0.50(1) \). For \( r = 0.027 \), which is very close to the critical point (see Fig. 4), the exponent \( \delta = 0.29(1) \).

Critical properties of models with absorbing states can be also studied using the so-called dynamic (or epidemic) method \[15\]. In this method, we prepare the system in one of the absorbing states except a localized (usually at a single site) activity. Subsequently, the system evolves according to its dynamical rules and and we monitor statistical properties of such runs. One of the important quantities in this technique is a probability \( P(t) \) that a given activity survives until time \( t \). On general grounds, one expects that \( P(t) \) behaves similarly to \( \rho(t) \). Namely, in the active phase \( P(t) \) tends to a finite value, in the absorbing phase it rapidly (faster than a power law) decreases to zero and in the critical phase it decays as \( t^{-\delta'} \), where \( \delta' \) is an exponent, which in general might be different than \( \delta \) \[16,17\].

Fig. 5 shows the results of our dynamical simulations. Simulations were performed for sizes which ensured that the spreading activity did not reach the boundaries of the lattice (typically \( L = 2 \cdot 10^4 \) is sufficient). The number of runs varied from \( 10^6 \) for \( r = -10^{-4}, -10^{-6} \) and 0 to \( 2 \cdot 10^4 \) for \( r = 0.03 \). The results shown in Fig. 5 lead to the same conclusions as those in Fig. 3 for \( 0 \leq r < r_c \); the model remains in the critical phase with \( \delta' = 0.50(1) \). For \( r < 0 \) the survival probability decays most likely faster than an inverse power of \( t \).

The fact that for \( r < 0 \) the model is in the absorbing phase is to some extent understood. Namely, for \( r < 0 \) there exists a finite probability that after updating a pair of sites will become nonactive forever. Indeed, when one of the anew selected bonds (say, \( w_{i,i+1} \)) satisfies the condition

\[ |w_{i,i+1}| < -r/(0.5), \]  

then the sites \( i \) and \( i+1 \) become permanently nonactive. Namely, no matter what are the other bonds (i.e., \( w_{i-1,i} \) and \( w_{i+1,i+2} \)) attached to these sites, they will always remain nonactive. For \( r < 0 \) there is a finite probability of satisfying Eq. 2 and the above mechanism leads to the rapid decrease of active sites and hence the system quickly reaches an absorbing state. The above mechanism is not effective for \( r \geq 0 \) since there is no value which would ensure permanent nonactivity of a certain site. Basically the same mechanism is at work in another model with absorbing states \[14\].

More detailed analysis of \( \rho \) in the vicinity of the critical point suggests that the exponent \( \beta \) is slightly less than unity. Together with the value of \( \delta \sim 0.29 \) at the critical point \( r = r_c \sim 0.027 \) (as estimated from the results in Fig. 5), this strongly suggests that this model behaves similarly to some other models, which are commonly termed as
the parity-conserving universality class \[18,19\]. In this class of models, it is already known that in the critical phase \(\delta = 0.5\). An interesting feature of our model is the fact that the critical phase terminates at a certain point \((r = 0)\) and (most likely) an exponential decay sets in. Let us also notice that for \(r = 0.027\) the slope in Fig. 3 is also close to 0.29. However, this might be a coincidence, since some variability of this exponent in dynamic Monte Carlo method is an anticipated feature \([16,17]\).

Initially, the behaviour of models belonging to the PC universality class was thought to be determined by the local conservation laws \([13]\). Later, however, some models were found which do not possess this property but which exhibit the same critical behaviour \([14]\). Since these models have a symmetric and double-degenerate absorbing state, it seemed that this is another property which leads to the PC criticality. Recently, a model with infinitely many absorbing states was found, which also belongs to the PC universality class but this might be again attributed to some conservation law in its dynamics \([17]\). The present model has an infinitely-degenerate absorbing state and no conservation law. We attribute the PC criticality of this model to a certain global symmetry of this model. Namely, one can easily see that inverting all bond variables \((w_{i,i+1} \rightarrow -w_{i,i+1})\) one does not change (non-)activity of any site. This Ising-like symmetry determines the structure of any absorbing state for \(r \geq 0\): all bond variables must be either positive or negative.

Let us note that although there is no conservation law in this model in general, there is such a law for \(r = 0\). Indeed, for \(r = 0\) the dynamics of the model is special: it is only the sign of \(w_{i,i+1}\) which matters and only those sites are active where negative and positive \(w_{i,i+1}\) meet. As a result, the dynamics of the model is equivalent to a certain branching annihilating random walk (BARW) with an even number of offsprings \([20]\). The power-law characteristics \(t^{-0.5}\) are already known for related BARW models \([21]\).

In summary, we have shown that a certain evolutionary model with non-extremal dynamics exhibits generic criticality. Such a behaviour is most likely related with a special symmetry of this model. One might hope that this criticality is to some extent robust with respect to structural perturbations of this model (other lattices, definitions of fitness function, etc.,). Since for some of these variants the analogy with random walk models might not hold, it is possible that the criticality of such models will exhibit some sort of non-universality. However, analysis of such extensions is left as a future problem.

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FIG. 1. The steady-state density of active sites \( \rho \) as a function of \( r \).

FIG. 2. The density of active sites \( \rho(t) \) as a function of \( t \) plotted in the log-log scale. Simulations were made for \( L = 10^5 \) and for each \( r \) we averaged over about 50 independent runs.

FIG. 3. The survival probability \( P(t) \) as a function of \( t \) plotted in the log-log scale. Initially we set \( w_{i,i+1} = w_0 = 0.2 \) for all bonds except for those surrounding a certain site which was set as active. Different choice of \( w_0 \) might change the asymptotic slope at \( r = r_c \sim 0.027 \), but it should not affect the asymptotic \( t^{-0.5} \) decay for \( 0 \leq r < r_c \).
Fig. 3