A Model of Evolution with Interaction Strength

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Interaction strength, denoted by $\alpha_I$, is introduced in a model of evolution in $d$-dimension space. It is realized by imposing a constraint concerning $2d$ differences of fitnesses between that of any extremal site and those of its $2d$ nearest neighbours at each time step in the evolution of the model. For any given $\alpha_I(0 < \alpha_I \leq 1)$ the model can self-organize to a critical state. Two exact equations found in Bak-Sneppen model still hold in our model for different $\alpha_I$. Simulations of one- and two-dimensional models for ten different values of $\alpha_I$ are given. It is found that self-organized threshold, $f_c$, decreases with $\alpha_I$ increasing. It is also shown that the critical exponent, $\gamma$, and two basic exponents, $\tau$, avalanche distribution, and $D$, avalanche dimension, are $\alpha_I$ dependent.

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The concept of self-organized criticality (SOC) concerns the spatiotemporal complexity in the systems that contain information over a wide range of length and time scales. It implies that through a dynamical process a system can start in a state with uncorrelated behavior and end up in a complex critical state with a high degree of correlation. This concept and the prototype model, sandpile model, are proposed by Bak, Tang and Wiesenfeld in 1987. Self-organized criticality is so far the only known general mechanism to generate complexity, and hence the one trying to understand why nature is complex, not simple.

Systems which can exhibit SOC are common in physics, biology, and even social sciences such as economy. Such kinds of complex phenomena are ubiquitous in macroscopic world. Recently, it has been proposed by Meng et al. that SOC may exist in microscopic systems—at the level of quarks and gluons, as well as in macroscopic world.

Evidence from the biology has suggested that the ecology of interacting species had self-organized to a critical state. In 1990, Bak, Chen, and Crutz created a cellular automaton simulating a society of living organisms operates at, or very close to, the critical state when driven by random mutations. However, the model is very sensitive in the sense that small modifications of the details may drive it away from the critical state. NKC model proposed by Kauffman and Johnsen can exhibit a transition from order to disorder, but the criticality emerged in the system is obtained through parameter tuning, not self-organizing. In 1993, a simple model of evolution, Bak-Sneppen model, was introduced by Bak and Sneppen. Instead of considering the evolution on the individual level they present the co-evolution of species on a coarsed-grained scale. In their model the whole species is represented by a single fitness, i.e., a random number chosen arbitrarily from a distribution between zero and 1. And mutations correspond to updating the fitness, i.e., a random number chosen arbitrarily from a flat distribution between zero and 1.

Our model of evolution is based on B-S model, but differs decisively in driving mechanism of interaction between neighboring species. We also consider co-evolution of an interacting species system and each species is represented by a single fitness, i.e., a random number chosen arbitrarily from a flat distribution between zero and 1. But when considering the interaction between neighboring species we impose a constraint concerning the differences of fitnesses between that of the extremal species and those of its nearest neighbors at each time step. Before knowing how the constraint is imposed let us take a first look at another case of evolution, a non-interactive biology. In a non-interactive biology each species would tend to evolve towards a stable state where the fitness of each species approaches 1, but the evolution process is extremely slow. If we use $\alpha_I$ to denote interaction strength, which represents the degree of interaction between the extremal site and its nearest neighboring species, it is natural to let $\alpha_I$ be 1 in B-S model and $\alpha_I$ be zero in the non-interactive biology. If so, it seems that these two cases of $\alpha_I$ correspond to two extreme cases of interaction strength. Then, if $\alpha_I$ is allowed to take any value between zero and 1, what can we do with our model? Thus, several questions arise there:

1) What does interaction strength mean for an evolution model?

2) How to present the definition of interaction strength $\alpha_I$ and impose it into a model of evolution?

3) If the two questions are solved, then are the model of evolution and some features of it affected by the values of interaction strength?

It will be shown that these questions could be solved successfully in the following text.
biology, in order to live better and/or longer in nature. Only through mutations the species with a bad fitness can have the chances of choosing a better fitness in order to avoid extinction. Furthermore, the fitness of each species is affected by other species which are also parts of the ecosystem. Any adaptive change of any species may change the fitness and the fitness landscape of its coevolutionary parts coupled in the same ecosystem. So the species may interact with each other through, say, a food chain. Hence, the species with a high fitness may live well and comfortably unless its bad neighbours are going to mutate.

Our model is defined and simulated through the following items:

(1) A number of, say, $L^d$ species are located on a $d$-dimensional lattice of linear size $L$. Initially, random numbers chosen arbitrarily from a uniform distribution between zero and 1, $p(f)$, are assigned independently to each species. At each time step,

(2) choose the extremal site, that is, the species with the lowest fitness, $f_{\text{min}}$, among all the species and update it by assigning a new random number also chosen from $p(f)$ to it and

(3) mutate those of its $2d$ neighbours whose fitnesses satisfy the constraint $f_{i} - f_{\text{min}} < \alpha$ by assigning new random numbers between zero and 1, $f_{i}$ (denotes the fitness of the $i$th nearest neighbours.), $\alpha$ is a parameter between zero and 1 and is fixed for a given model.

It should be pointed out that different values of $\alpha$ correspond to different versions of the model, even to say, different models. Consider two special values of $\alpha$, 0 and 1. For $\alpha = 0$ the model returns to the non-interactive biology since difference of fitness between those of any two neighbours is always greater than zero, so in the model in which $\alpha = 0$ none of the neighbours of any extremal species will be chosen for updating at each time step. This is the case where there is no interaction between neighbours. For $\alpha = 1$ the model returns to a $d$-dimensional B-S model. It is because that difference of fitness between those of any two neighbours is less than 1 so at each time step all the $2d$ nearest neighbours of the extremal site will be chosen for updating.

For a given $\alpha$ let the model evolve from the beginning when the first extremal species is chosen and we determine how many of its $2d$ neighbours will be chosen, according to the constraint on difference of fitness, for updating at the same time step. The updating process, i.e., the evolution of the model, continues indefinitely. For a given $\alpha$ satisfying $0 < \alpha < 1$ the updating of the $2d$ nearest neighbours of the extremal site at each time step will have many kinds of probabilities. For instance, maybe none of the $2d$ neighbours will be updated, maybe half of the $2d$ neighbours will be chosen for updating, etc. If we do not distinguish the neighbours when we only care the number of the updated neighbours at each time step it is straightforward that the updating of the neighbours will have $2d + 1$ probabilities. Say, at some time step, an extremal site and $m$ of its $2d$ nearest neighbours are chosen for updating according to the constraint. Such an updating is called by us a $m$-event. As the evolution goes on we can observe many kinds of such events, during which $m$ can be different. If the evolution time is large enough we can observe $2d + 1$ kinds of events during which $m$ spans through 0 and $2d$. If we define $P_d(m)$ the probability of $m$-event among all events during time period $T$, i.e.,

$$P_d(m) = \frac{N(m)}{N_T},$$

where $N(m)$ is the number of $m$-event during the time period $T$ and $N_T$, the total number of all events, and $d$ denotes dimension. In the $T \gg L^d$ limit we will obtain the distribution of $m$-event, that is,

$$P_d(m) = \lim_{T \to \infty} \frac{N(m)}{N_T}.$$  

And $P_d(m)$ should satisfy the normalization,

$$\sum_{m=0}^{2d} P_d(m) = 1.$$  

Next we will present the definition of interaction strength $\alpha_I$ related to $P_d(m)$,

$$\alpha_I = \lim_{T \to \infty} \frac{1}{2d} \sum_{m=0}^{2d} m P_d(m).$$  

One can see that $\alpha_I$ is actually the statistical ratio of number of updated neighbours among $2d$ ones during the evolution. This can be easily seen from two extremal cases when $\alpha = 0$ and $\alpha = 1$. For $\alpha = 0$, $\alpha_I = 0$, this is because $P_d(0) = 1$ and $P_d(m) = 0$ for $0 < m \leq 2d$; for $\alpha = 1$, $\alpha_I = 1$, this is because $P_d(2d) = 1$ and $P_d(m) = 0$ for $0 \leq m < 2d$. That is, in the noninteractive biology interaction strength $\alpha_I$ is zero while in the B-S model $\alpha_I$ is 1. Hence, it is natural to expect that the definition of $\alpha_I$ can give a good description of the change of strength of interaction between neighboring sites when $\alpha$ changes.
So, it is also natural to expect that $0 < \alpha_I < 1$ for $0 < \alpha < 1$, and that $\alpha_I$ increases as $\alpha$ increases. There should also exist one-to-one correspondence between $\alpha_I$ and $\alpha$. Having these in mind we measure the distribution $P_d(m)$ and $\alpha_I$ for ten different values of $\alpha$ for one- and two-dimensional models on the computer. Simulation results are given in Fig. 1 and Fig. 2 respectively. Figures (a) and (b) in Fig. 1 show the distribution of an event ($0 \leq m \leq 2d$) for ten different values of $\alpha$ in one- and two-dimensional models respectively. It is clearly shown in the above figures that $P_d(0)$ decreases with increase of $\alpha$ and $P_d(2d)$, i.e., $P_{d=1}(2)$ for $d = 1$ and $P_{d=2}(4)$ for $d = 2$, increases as $\alpha$ increases. Note in the figures change of $P_d(m)$ ($0 < m < 2d$) with increase of $\alpha$. Their exists a peak in the curve of $\alpha$ dependence of $P_d(m)$ ($0 < m < 2d$). This can ensure the normalization of $P_d(m)$. Two plots in Fig. 2 show the dependence of $\alpha_I$ on $\alpha$ in one- and two-dimensional models respectively. As shown in Fig. 2 $\alpha_I$ almost increases linearly as $\alpha$ increases, and most important of all is that one $\alpha_I$ corresponds to one and only one $\alpha$. From here one can clearly see that our definition of $\alpha_I$ can be explicitly related to $\alpha$ and hence can be put into our model naturally. Relating Fig. 1 and Fig. 2 one can see that increase of interaction strength increases $P_d(2d)$. That is, when $\alpha_I$ increases any extremal site will possibly affect its nearest neighbours more strongly. Furthermore, different values of $\alpha_I$ correspond to different interaction strength. Generally speaking, larger $\alpha_I$ represents stronger interaction, and vice versa. Hence, the definition of $\alpha_I$ can provide a good description for the strength of interaction between neighboring sites. It is a good quantity in describing the interaction. In the following text dependence of self-organized threshold and some critical exponents on $\alpha_I$ will be given. Since $\alpha_I$ has one-to-one correspondence with $\alpha$ and increases as $\alpha$ increases, it is hence convenient and equivalent to present the dependence of these quantities on $\alpha$.

The model is already defined, it is natural to investigate whether the model can self-organize to a critical state. That is, we should observe the “fingerprint” of SOC [4]. If so, it is also worthwhile to know whether the criticality is sensitive to the value of $\alpha$. In addition, the self-organization, referred to a dynamical process whereby a system starts in a state with uncorrelated behavior and ends up in a complex state with a high degree of correlation, of the system and punctuated equilibrium, the most important feature of evolution, should also be observed.

Fig. 3 shows the space-time fractal activity pattern for a one-dimensional model of size $L = 100$ with $\alpha = 0.8$. We track the updated sites at each time step. $S$ and $R$ in the figure denote number of updated time steps and location of updated sites respectively. Simulations of one- and two-dimensional models for different values of $\alpha$ are also done and exhibit the similar space-time fractal activity. Indeed, spatiotemporal complexity emerges in our model and its appearance is independent of the value of $\alpha$ choosen.

We now present some explanations of the quantities which will appear in the following equations for those readers who are not so familiar with SOC. $f_{\text{min}}$ denotes the extremal fitness at each time step in the evolution. $G(s)$, the gap appeared in punctuated equilibrium, is an envelope function that tracks the increasing peaks in $f_{\text{min}}$. Its definition is : at time step $s$ the gap $G(s)$ is the maximum of all the minimum random numbers chosen, $f_{\text{min}}(s')$, for all $0 \leq s' \leq s$. $f_c$ is the value of $G(s)$ at critical state, i.e.,

$$f_c = \lim_{s \to \infty} G(s). \quad (5)$$

$S_G(s)$ is the size of avalanches correspond to plateaus in $G(s)$ during which $f_{\text{min}}(s) < G(s)$ and $\langle S_G(s) \rangle$ is the average value of $S_G(s)$. An avalanche is defined as subsequent mutations below a certain threshold. Hence with this definition there is a hierarchy of avalanches each defined by their respective thresholds. So we can have $f_0$-avalanche where $f_0$ is only an auxiliary parameter between zero and 1 to define avalanches. More detailed definition of $f_0$-avalanche is given in Ref. [5]. The size of an avalanche, $S$, is the number of subsequent mutations below the threshold. And $\gamma$ is a critical exponent which governs the divergence of $S_G(s)$ when $s$ approaches infinity. And $n_{\text{cov}}$ is the number of sites covered by an avalanche. Apparently $n_{\text{cov}} \leq (2d + 1)S$ ($S$ is the avalanche size) in d-dimensional space. $\langle n_{\text{cov}} \rangle$ denotes the average value of $n_{\text{cov}}$. The above defined quantities will have their counterparts in our model. So we will use the same definitions of these quantities while make some minor corrections on the symbols of them.

Following the method used in Ref. [2] we monitor the extremal signal $f_{\text{min}}$ as a function of $s$ during the transient in the one- and two-dimensional models for different values of $\alpha$. Again, we observe Devil’s staircase [4] in all these cases. Fig. 4 shows punctuated equilibrium behavior in one-dimensional model of size $L = 100$ with $\alpha = 0.5$. Hence, we can see punctuated equilibrium does...
emerge in our model of evolution and its emergence is $\alpha$ independent.

Observations through above simulations suggest that our model can self-organize to a critical state. But how to determine the self-organized threshold $f_c$ is still a hard bone to us. Fortunately Ref. [2] provides us a method. In Ref. [2] the author presents two exact equations for Bak-Sneppen model. With a reasonable scaling ansatz of average size of avalanches they can determine $f_c$ very accurately. It is straightforward to expect that the two exact equations found in Bak-Sneppen model have the corresponding ones in our model. According to the derivation of these two equations [2] we can directly write down two similar exact equations in our model except for some dependent, which can be seen from our simulations: as $\alpha$ increases $f_c$ has a tendency to decrease. Having this in mind we make replacements of symbols of some quantities:

- $G(s) \rightarrow G(s, \alpha)$,
- $f_c \rightarrow f_c(\alpha)$,
- $\gamma \rightarrow \gamma(\alpha)$,
- $\tau \rightarrow \tau(\alpha)$,
- $D \rightarrow D(\alpha)$.

Two exact equations are given as below,

$$\frac{dG(s, \alpha)}{ds} = \frac{1 - G(s, \alpha)}{S^{d}(S)G(s, \alpha)} \tag{6}$$

$$\frac{dh(S)f_0}{df_0} = \frac{(n_{\text{cor}})f_0}{1 - f_0} \tag{7}$$

In order to solve the two equations a scaling ansatz of $\langle S \rangle_{G(s, \alpha)}$ should be given,

$$\langle S \rangle_{G(s, \alpha)} \sim [f_c(\alpha) - G(s, \alpha)]^{-\gamma(\alpha)}. \tag{8}$$

Inserting Eq. (8) into Eq. (7) one obtains

$$\gamma(\alpha) = \lim_{f_0 \rightarrow f_c(\alpha)} \frac{(n_{\text{cor}})f_0[f_c(\alpha) - G(s, \alpha)]}{1 - f_0}. \tag{9}$$

Using Eq. (9) we can determine $f_c(\alpha)$ and $\gamma(\alpha)$ very accurately. We measure $f_c(\alpha)$ and $\gamma(\alpha)$ in the one- and two-dimensional models for different values of $\alpha$. It is to our expectation that these two quantities are $\alpha$ dependent. Fig. 6 shows the dependence of $f_c(\alpha)$ on $\alpha$ and figure (a) in Fig. 7 shows that of $\gamma(\alpha)$ on $\alpha$. In addition, we measure two basic exponents of the model, $\tau(\alpha)$, avalanche size distribution, and $D(\alpha)$, avalanche dimension. We find they are also $\alpha$ dependent. Figures (b) and (c) in Fig. 7 show their dependence on $\alpha$ respectively.

The following text will present our analysis of the simulations and our conclusion. Let us first check the “fingerprint” of SOC. Fig. 5 shows avalanche distribution $P_{\text{aval}}(S)$ for one-dimensional model of size $L = 100$ with $\alpha = 0.7$. Such distribution can also be found in one- and two-dimensional models for different $\alpha$. Indeed, power law emerges in our model and its appearance is $\alpha$ dependent. Then let us come to the results of $f_c(\alpha)$. Two plots, (a) and (b), in Fig. 6 show the dependence of $f_c(\alpha)$ on $\alpha$ in the one- and two-dimensional models respectively. It is clearly shown that these two figures display the similar behaviors of $f_c(\alpha)$. Firstly, we can see that in both figures $f_c(\alpha)$ decreases as $\alpha$ increases. It is not difficult to understand this kind of behavior. As $\alpha$ increases, i.e., $\alpha_I$ increases, the chances for the nearest neighbours of a given extremal site to be chosen for updating at each time step will be greater. This can be easily seen from Fig. 1. As shown in Fig. 1 $P_d(2d)$ increases as $\alpha$ increases and reaches 1 for $\alpha = 1$, and $P_d(0)$ decreases as $\alpha$ increases and reaches zero when $\alpha = 1$. So, with the increase of $\alpha$, that is the increase of $\alpha_I$, more possible neighbours will be involved in the evolution, hence, the threshold $f_c(\alpha)$ will be lowered further. This can be explained in another way. Compare the values of $f_c(\alpha)$ for the same $\alpha$ in one- and two-dimensional models. Say, compare $f_c(1)$ in one dimensional model with that in two-dimensional model. It has been shown that $f_c(1)$ in the former case is greater than that in the latter case. In one-dimensional model in which $\alpha = 1$ when an extremal site is chosen, two of its nearest neighbours will also be chosen, for updating at each time step. While in two-dimensional model with $\alpha = 1$, an extremal site, together with its four nearest neighbours, will be chosen for updating at each time step. Why we mention this two cases here is just trying to show that the increase of average number of neighbours involved in the evolution will lower the self-organized threshold. Thus, one can see, the increase of interaction strength will increase the number of neighbouring sites involved in the evolution and hence lowers down the value of $f_c(\alpha)$. Secondly, it is shown in both figures of Fig. 6 that $f_c(\alpha)$ almost decreases linearly as $\alpha$ increases for $0 < \alpha < 0.6$ and decreases asymptotically as $\alpha$ increases for $\alpha$ between 0.6 and 1.0. This implies that effect of the constraint on the
evolution grows implicitly as $\alpha$ increases. When interaction strength is small the effect is very explicit. But as interaction strength increases the effect will be not so explicitly shown. Specifically, we measure $f_c(\alpha)$ when $\alpha = 1$ for one- and two-dimensional models. We find $f_c(1) = 0.668 \pm 0.001$ for $d = 1$ system of size $L = 100$, which is very close to the value in Refs. [2] and [13], who found $f_c(1) = 0.660702 \pm 0.00003$; for $d = 2$ system of size $L = 20$, $f_c(1) = 0.334 \pm 0.00006$ which is close to the corresponding value in Ref. [2], who found $f_c(1) = 0.328855 \pm 0.000004$. In addition, for $d = 1$ we find $f_c(0.1) = 0.96388 \pm 0.000002$ for a system of size $L = 100$ and for $d = 2$, $f_c(0.1) = 0.9179 \pm 0.00001$ for a system of size $L = 20$.

We also measure $\gamma(\alpha)$ for different $\alpha$ in one- and two-dimensional models. It is found that $\gamma$ is also $\alpha$ dependent. Dependence of $\gamma(\alpha)$ on $\alpha$ is given in Fig. 7. In figure (a) in Fig. 7 $\gamma(\alpha)$ first increases and then decreases as $\alpha$ increases. For $d = 1$, $\gamma(1) = 2.6166 \pm 0.0004$, which is close to the value found in Refs. [2,13,14], who found $\gamma(1) = 2.70 \pm 0.01$. For $d = 2$, we find $\gamma(1) = 2.249 \pm 0.0004$, which is not in agreement with Ref. [2], who found $\gamma(1) = 1.70 \pm 0.01$. Maybe this is because of our small size of system. If the size is larger the results will be more precise.

For different values of $\alpha$ in one- and two-dimensional models we measure two basic exponents, $\tau(\alpha)$, which characterizes the distribution of avalanche sizes, and $D(\alpha)$, the avalanche dimension. The definition of $\tau(\alpha)$ is $P_{\text{aval}}(S) \sim S^{-\tau(\alpha)}$, and that of $D(\alpha)$: $n_{\text{cov}} \sim S^{D(\alpha)/d}$. Results of these two basic exponents are given in Fig. 7(b) and Fig. 7(c) respectively. It is shown in the plots that $\tau(\alpha)$ first decreases as $\alpha$ increases and then changes slowly with variation of $\alpha$. Specifically, for $d = 1$, we find $\tau(1) = 0.858 \pm 0.001$, which is not in agreement with Ref. [2], who measured $\tau = 1.07 \pm 0.001$, but agrees with Ref. [10], who measured $\tau = 0.8 \pm 0.1$. This is because our size $L = 100$ is close to the size $L = 64$ in Ref. [10] but far from the size $L = 10^4$ in Ref. [2]. For $d = 2$, $\tau(1) = 1.131 \pm 0.0005$, which is close to Ref. [2], who measured $\tau = 1.245 \pm 0.01$.

Fig. 7(c) shows the dependence of $D(\alpha)$ on $\alpha$ for one- and two-dimensional models. It can be inferred from the plots that $D(\alpha)$ first decreases rapidly and then slowly as $\alpha$ increases. For $d = 1$, $D(1) = 2.4189 \pm 0.0001$, which is close to Ref. [2], who measured $D = 2.43 \pm 0.01$, and for $d = 2$, $D(1) = 2.94 \pm 0.0001$, which agrees with Refs. [2,9,10], who measured $D = 2.92 \pm 0.02$. It is clearly shown that for all $\alpha$ $D(\alpha)$ is larger than the dimension space $d$.

It should be emphasized that interaction strength, $\alpha_I$, is not a parameter tuning the model to a critical state, since in our model when a model is chosen the corresponding $\alpha_I$ is fixed during the whole evolution process. Thus, criticality emerged in our model is self-organized, not tuned. And appearance of criticality in our model is independent of $\alpha_I$ chosen, which you can test on your own PC. This can strongly support the idea that SOC does not depend on the dynamical details of the system. That is, self-organized criticality should be universal. Furthermore, self-organized fractal growth is basically different from growth processes, say, described by (variants of) the Kardar-Parisi-Zhang (KPZ) equation [15,16]. The KPZ equation is scale invariant by symmetry, thus the criticality is not self-organized. SOC cannot, even in principle, be regarded as sweeping a system through a critical point, which contrasts to the claims in Ref. [17]. SOC should be an attractor of the complex system, but this attractor is vastly different from the one found in chaos—"strange attractor".

As shown in this paper and in others [2,4,10], interaction plays a very important role in the models which exhibit SOC. If there is no interaction between individuals in a system, the system will evolve towards a frozen state and the evolution process will be indefinitely long. This is clearly shown in non-interactive biology in which fitness of each species tends to be 1. Our model and simulations of its different versions corresponding to different degrees of interaction between neighbours imply that only the coevolutionary system can evolve to a self-organized critical state despite the fact that interaction strength may be relatively small. Through our simulations that we have learned it would take longer time for the system to involve to a critical state when the interaction strength $\alpha_I$ is smaller. It is also worthwhile to perform two simulations of the models in which $\alpha_I$ is very close to zero and 1 respectively. We can expect in the former case the model will evolve to a frozen state, while in the latter case we will approach B-S model.

Another important feature of our model is that fitness itself is directly involved in the interaction, which is not realized in the B-S model. As a co-evolutionary system, interaction between any extramal species and its neighbours should and must involve the features of the extremal site and that of the neighbours. Because of model’s simplicity each species has only one feature: fitness, represented by a random number chosen arbitrarily from a flat distribution between zero and 1. Hence, this fea-
ture should enter the evolution model. Through a constraint which can be related to interaction strength the fitness is involved in and injected into the evolution process of the system. It is shown in our model that evolution is indeed an coevolutionary phenomena, which agrees with Darwin’s opinion on evolution of the biology [18].

Thus, in conclusion:

(1) A simple model of evolution with interaction strength defined and considered is proposed. The models with different interaction strength (0 < α ≤ 1) can self-organize to critical states.

(2) Simulations of one- and two-dimensional model of various degrees of interaction strength show that $f_c(α)$ decreases as $α$ increases. It is also shown that $γ(α)$, and two basic exponents, $τ(α)$ and $D(α)$, are $α$ dependent.

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Figure Captions:

Fig. 1: Distribution of m-event for different $α$ in the evolution of (a) one-dimensional models of size $L = 100$ and (b) two-dimensional models of size $L = 20$.

Fig. 2: Dependence of interaction strength $α$ on $α$ in the evolution of one-dimensional models of size $L = 100$ and two-dimensional models of size $L = 20$.

Fig. 3: Space-time fractal activity pattern for one-dimensional evolution model with $α = 0.8$. $S$ is the number of updated steps and $R$ is the location of updated sites.

Fig. 4: Punctuated equilibrium behavior emerges in one-dimensional evolution models of size $L = 100$ with $α = 0.5$. $G(s)$ is the gap that tracks the peaks of extremal signal, $f_{\text{min}}$, in the transient. $f_c$ in the plot is about 0.8556.

Fig. 5: Avalanche distribution for one-dimensional model of size $L = 100$ with $α = 0.7$. $S$ is the size of avalanche, is the number of subsequent mutations below the threshold 0.728. $P_{\text{aval}}(S)$ denotes the distribution of $S$. The slope of the curve is about 0.774 ± 0.001.

Fig. 6: Dependence of $f_c(α)$ on $α$ for one-dimensional evolution models of size $L = 100$ and two-dimensional models of size $L = 20$.

Fig. 7: (a) Dependence of $γ(α)$ on $α$ for one-dimensional evolution models of size $L = 100$ and two-dimensional models of size $L = 20$. (b) Dependence of $τ(α)$ on $α$ for one-dimensional evolution models of size $L = 100$ and two-dimensional models of size $L = 20$. (c) Dependence of $D(α)$ on $α$ for one-dimensional evolution models of size $L = 100$ and two-dimensional models of size $L = 20$.

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FIG. 1

(a) $d=1$
$L=100$

(b) $d=2$
$L=20$
FIG. 2

- $d=1$, $L=100$
- $d=2$, $L=20$
\[ G(S) \]

\[
\alpha = 0.8 \\
d = 1 \\
L = 100
\]
\( \alpha = 0.7 \)
\( d = 1 \)
\( L = 100 \)
FIG. 7

(a) $\gamma(\alpha)$ for $d=1$, $L=100$ (open circles) and $d=2$, $L=20$ (filled circles).

(b) $\tau(\alpha)$.

(c) $D(\alpha)$. 

Note: The figure illustrates the variation of three different quantities ($\gamma(\alpha)$, $\tau(\alpha)$, and $D(\alpha)$) with respect to $\alpha$ for two different dimensions ($d=1$ and $d=2$) and two different lengths ($L=100$ and $L=20$).