MULTIOBJECTIVE OPTIMIZATION
OF AN EXTREMAL EVOLUTION MODEL

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Abstract

We propose a two-dimensional model for a co-evolving ecosystem that generalizes the extremal coupled map lattice model. The model takes into account the concept of multiobjective optimization. We find that the system self-organizes into a critical state. The distributions of the distances between subsequent mutations as well as the distribution of avalanches sizes follow power law.

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The evolutionary history of most species is characterized by long periods of stasis punctuated by relatively brief intervals of rapid evolutionary activity [1]. In recent years, there has been increasing interest that the evolution of species in an ecosystem may be a self-organized critical phenomena (SOC). Self-organized criticality refers to the tendency of large dynamical systems to organize themselves into a state, far out of equilibrium with propagating avalanches of activity of all sizes [2]. These complex systems do not need any fine tuning of a parameter to be in a critical state.

The most common interactions among species in this ecosystem are predation, competition for resources and mutualism. As a result of these interactions the evolutionary adaptation of one species must affect its nearest neighbors. Also, these interactions can lead to large evolutionary disturbances known as co-evolutionary avalanches. Each species in these evolution models is characterized by only one fitness.

Bak and Sneppen [3], proposed a self-organized model known as the BS model to explain the punctuated equilibrium of biological evolution. They considered a one-dimensional model of an ecosystem consisting of \( N \) species with periodic boundary conditions, topologically like a circle. They assigned a fitness value \( 0 < f(i) < 1 \) to each species \( i, \ i = 1, 2, \ldots, N \). At each time-step, the species \( j \) with the minimum fitness \( f(j) \), is sought, and is then replaced together with its nearest neighbors \( j \pm 1 \) by new ones that are randomly distributed. After running the system for sufficiently long time most of the fitness are greater than the certain threshold value \((0.667 \pm 0.001)\). Also, the distribution of the distance \( d \) between subsequent mutations as well as the distribution of avalanches sizes \( s \) exhibit power law \([4, 5, 6]\),

\[
P(d) \sim d^{-\tau_d}, \\
P(s) \sim s^{-\tau_s}.
\] (1)

In biology, most of real life optimization problems are multiobjective ones (MOB). For example, animals would like to get maximum resources with minimum predation. In cancer therapy, we want the optimal dose that kill maximum amount of cancer cells with killing minimum amount of normal cells. Also, humans need maximum health with saving money. Then multiobjective optimization deals with concurrent objective functions [7].

Most evolution models consider only one fitness, i.e. single objective optimization. Therefore, it is important to generalize them to multiobjective ones.

The methods of MOB optimization are intuitive, the simple and widely used method is the weighted sum of objective functions method [8]. It transform the problem to a monobjective optimization problem. It takes each objective function, associate a weight to each objective function and then, do a weighted sum of objective functions. So, we obtain a new unique objective function which has a physical meaning according to the problem. Assume that it is required to minimize the objectives \( z(i), \ i = 1, 2, \ldots, N \). Define the following quantity,

\[
Z = \sum_{i=1}^{N} w(i) \ z(i),
\] (2)
where $w(i)$'s are the weights that satisfy,

$$w(i) \geq 0 \quad \text{and} \quad \sum_{i=1}^{N} w(i) = 1 \quad (3)$$

Then the problem becomes minimization of the quantity $Z$. This method is easy to implement but has some drawbacks. The first, may give a Pareto dominated solution.

**Definition 1** A solution $z'(i)$, $i = 1, 2, ..., N$ is called a Pareto dominated solution if there is another solution $z(i)$, $i = 1, 2, ..., N$ such that $z(i) \leq z'(i)$ for all $i$ with at least one $k$ such that $z(k) < z'(k)$.

The second drawback, it is difficult to apply this method for large $N$.

We generalized the BS model to a multiobjective one [9], assigning two fitness values $x_1(i)$ and $x_2(i)$ to each site $i$ instead of only one fitness. The fitness values,

$$x(i) = \alpha x_1(i) + (1 - \alpha) x_2(i), \quad i = 1, 2, ..., N, \quad (4)$$

are computed for each species $i$, where the weight $\alpha$ satisfies $0 < \alpha < 1$. At each time-step, we look for the species with the minimum fitness, $j$, then update randomly both $x_1(j)$, $x_2(j)$ as well as $x_1(j \pm 1)$ and $x_2(j \pm 1)$. After running the system for a long time the distributions of the distance between subsequent mutations as well as the size of avalanches follow power law. Also, most fitness are above the certain threshold value ($0.57 \pm 0.01$).

An interesting way to include spatial effects in dynamical systems is the coupled map lattice (CML). It is a dynamical system with discrete-time, discrete-space and continuous states [10] and it is a simple model with the essential features of spatiotemporal chaos (STC). STC is irregular dynamics in space-time for a deterministic system that is spatially extensive. Typically, CML consists of coupled dynamical elements on a lattice. This makes it a convenient way to expand dynamical systems to spatially extended systems with dynamics in both time and space. They are also amenable to numerical simulations. Beside being mathematically interesting, it has many applications [10, 11].

CML can be represented by local nonlinear dynamics as follows,

$$x(i) \rightarrow x'(i) = F(x(i)), \quad x'(i) \rightarrow (1 - \epsilon) F(x'(i)) + \frac{\epsilon}{2} \left[ F(x'(i - 1)) + F(x'(i + 1)) \right] \quad (5)$$

where $F(x)$ is any chaotic function of $x$, $t$ is a discrete time-step and $i$ is a lattice site.

Abramson and Vega [12] proposed an extremal coupled lattice model (ECML), that takes into account two levels of structure. The first is the microscopic level, where mutations occur (genotype), which is represented by the control parameter $\lambda(i)$ for each species in the ecosystem that consists of $N$ species arranged in a one-dimensional lattice. The second is the macroscopic level (phenotype) which is represented by $x(i)$ for each species and subjected to nonlinear dynamics in addition to being coupled to its nearest neighbors. The logistic map is chosen for
the independent evolution of \( x(i) \) with \( \lambda(i) \) acting as the nonlinear parameter in the map. The evolution of each species is given by,

\[
x^{t+1}(i) = (1 - \epsilon) F(x^t(i)) + \frac{\epsilon}{2} [F(x^t(i - 1)) + F(x^t(i + 1))]
\]

where \( F(x) \) is the logistic map,

\[
F(x) = \lambda \ x \ (1 - x)
\]

The local coupling of strength \( \epsilon \) emulates the ecological interaction between neighboring species. Abramson and Vega proposed an extremal mechanism like the BS model. At each time-step, the species with the minimum value of \( x \) is considered the candidate to mutate at the next step. Its \( \lambda \) replaced by a new value drawn from a uniform distribution \( g(\lambda) \) in the range \((\lambda_0, \lambda_0 + \Delta \lambda)\). Then update all elements of the system using equation (6).

From the definition of the extremal evolution models, it is known that not all the system elements should be updated at the same time. Therefore, we introduce a model of evolution that takes into account the above arguments, namely those of extremal dynamics, MOB optimization, CML evolution and studying that model on a two-dimensional lattice. Let us have an ecosystem consisting of \( N \times N \) species arranged on a square lattice with periodic boundary conditions, topologically like a torus. Each site \((i, j)\) corresponds to one species. It is known that there are some phenotypes that need two genotypes to be expressed. Also, there are some phenotype that need more than one gene to be expressed [13].

So, in our model, each species is characterized by two levels of structure like [12] but it differ in phenotype level. The first level is the genotype that is characterized by \( \lambda(i, j) \), where the mutations occur. The second consists of two phenotypes \( x_1(i, j) \) and \( x_2(i, j) \) that define the fitness \( x(i, j) \) of the species at site \((i, j)\) by the equation,

\[
x^{t+1}(i, j) = \alpha \ x_1^t(i, j) + (1 - \alpha) \ x_2^t(i, j), \quad i, j = 1, 2, ..., N
\]

where the weight \( \alpha \) satisfies \( 0 < \alpha < 1 \). The evolution of the system can be given by the following equations,

\[
x_1^{t+1}(i, j) = (1 - \epsilon) F(x_1^t(i, j)) + \frac{\epsilon}{4} [F(x_1^t(i \pm 1, j)) + F(x_1^t(i, j \pm 1))]
\]

\[
x_2^{t+1}(i, j) = (1 - \epsilon) F(x_2^t(i, j)) + \frac{\epsilon}{4} [F(x_2^t(i \pm 1, j)) + F(x_2^t(i, j \pm 1))]
\]

where \( F(x) \) is the nonlinear chaotic map,

\[
F(x) = \lambda \ x \ (1 - x)
\]

We propose three versions of this model. The first one uses the following rules. For each time-step, the species with the lowest fitness is sought \((k, l)\) which is known as the active site. Change the genotype of that species \( \lambda(k, l) \) randomly form the interval \((\lambda_0, \lambda_0 + \Delta \lambda)\). Then the two-phenotypes of that species \( x_1(k, l) \) and \( x_2(k, l) \) are updated as well as the phenotypes of its four nearest neighbors \( x_1(k \pm 1, l \pm 1) \), \( x_2(k \pm 1, l \pm 1) \) by using equations (9, 10).
At each time-step, in the second version, the species with the minimum fitness is sought, then the genotype $\lambda(k,l)$ as well as the genotypes of its nearest neighbors $\lambda(k \pm 1, l \pm 1)$ are updated. Also, the phenotypes of that species $x_1(k,l)$ and $x_2(k,l)$ are changed.

The third version is that at each time-step, we change both the genotypes $\lambda(k,l)$ and the phenotypes $x_1(k,l)$ and $x_2(k,l)$ of the species with the lowest fitness as well as its four neighbors $\lambda(k \pm 1, l \pm 1), x_1(k \pm 1, l \pm 1)$ and $x_2(k \pm 1, l \pm 1)$.

In all figures, the index numbers 1, 2, 3 refer to the version number, also the letter $a$ means the left box and the letter $b$ means the right box in the same figure. We run the system with $N = 500$ species for a weak $\epsilon = 0.1$ and strong $\epsilon = 0.5$ interaction among the system elements. Also, we run the system for different values of weight $\alpha = 0.3, 0.5, 0.9$ and of nonlinear parameter $\lambda = 3.7, 3.8, 3.9$. We find that the figures of the first and third versions are nearly identical while the second one is of great difference from the former. This means that the change in the lowest fitness species affects its nearest neighbors not only in the phenotype level but also in the genotype level.

In all cases the system reaches a critical state in which most of the fitness are above a threshold value. The threshold value and the shape of the distribution are not the same for all cases but depend on the nonlinear parameter of the chaotic map $\lambda$, the weight parameter of the multiobjective optimization $\alpha$ and the strength of the interaction among the species in the ecosystem $\epsilon$.

The effect of increasing the strength of the interaction among the species in the ecosystem $\epsilon$ is to decrease the range of the final fitness distribution and increase the threshold value, while the change of the nonlinear parameter of the chaotic map $\lambda$ affects the smoothness of the curve of the fitness distribution. The figures show the activity versus time in a local segment of twenty consecutive species. We observe long periods of stasis interrupted by sudden bursts of activity in the first and third versions at weak interactions.

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References


Figure Caption

Figure 1 System of size $N = 500$, $\alpha = 0.3$, $\epsilon = 0.1$, $\lambda_0 = 3.7$, $\Delta \lambda_0 = 0.1$, and $t = 10^7$ iteration. (a1, a2, a3) Distribution $P(F)$ of the fitness $F$ in the critical state (right curve) with the distribution of minimum fitness (left dotted curve) in the three versions. (b1, b2, b3) Punctuated equilibrium behavior, activity vs time in a local segment of twenty consecutive species.

Figure 2 System of size $N = 500$, $\alpha = 0.3$, $\epsilon = 0.1$, $\lambda_0 = 3.9$, $\Delta \lambda_0 = 0.1$, and $t = 10^7$ iteration. (a1, a2, a3) Distribution $P(F)$ of the fitness $F$ in the critical state (right curve) with the distribution of minimum fitness (left dotted curve) in the three versions. (b1, b2, b3) Punctuated equilibrium behavior, activity vs time in a local segment of twenty consecutive species.

Figure 3 System of size $N = 500$, $\alpha = 0.5$, $\epsilon = 0.1$, $\lambda_0 = 3.7$, $\Delta \lambda_0 = 0.1$, and $t = 10^7$ iteration. (a1, a2, a3) Distribution $P(F)$ of the fitness $F$ in the critical state (right curve) with the distribution of minimum fitness (left dotted curve) in the three versions. (b1, b2, b3) Punctuated equilibrium behavior, activity vs time in a local segment of twenty consecutive species.

Figure 4 System of size $N = 500$, $\alpha = 0.5$, $\epsilon = 0.5$, $\lambda_0 = 3.7$, $\Delta \lambda_0 = 0.1$, and $t = 10^7$ iteration. (a1, a2, a3) Distribution $P(F)$ of the fitness $F$ in the critical state (right curve) with the distribution of minimum fitness (left dotted curve) in the three versions. (b1, b2, b3) Punctuated equilibrium behavior, activity vs time in a local segment of twenty consecutive species.

Figure 5 The distribution $P(S)$ of avalanches sizes $S$ in the critical state of a system with $N = 500$, $\Delta \lambda_0 = 0.1$ and $t = 10^7$ iteration in a log-log plot. (a) $\alpha = 0.3$, $\epsilon = 0.1$, $\lambda_0 = 3.7$, (b) $\alpha = 0.5$, $\epsilon = 0.1$, $\lambda_0 = 3.7$, (c) $\alpha = 0.3$, $\epsilon = 0.1$, $\lambda_0 = 3.9$, (d) $\alpha = 0.5$, $\epsilon = 0.5$, $\lambda_0 = 3.7$. 

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$\alpha=0.3, \varepsilon=0.1, \lambda=3.7$

Figure (1)
\( \alpha = 0.3, \epsilon = 0.1, \lambda = 3.9 \)

![Graphs depicting different distributions and activity over time.](image)

**Figure (2)**
\( \alpha = 0.5, \varepsilon = 0.1, \lambda = 3.7 \)

**Figure (3)**
$\alpha=0.5, \epsilon=0.5, \lambda=3.7$

Figure (4)
Figure (5)