Multiobjective Optimization of an Extremal Evolution Model

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Z. Naturforsch. **60a,** 335 – 342 (2005); received February 21, 2005

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 is self-organized into a critical state. The distribution of avalanche sizes follows a power law.

Key words: Self-organized Criticality; Evolution and Extinction; Bak-Sneppen Model; Multiobjective Optimization; Extremal Dynamics; Coupled Map Lattice.

1. Introduction

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 was increasing interest in the question, if the evolution of species in an ecosystem might be a self-organized critical (SOC) phenomenon. Self-organized criticality refers to the tendency of large dynamical systems to organize themselves into a state, far away from 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 an 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 evolutionary models are characterized by only one fitness.

In Section 2, we define the extremal evolution systems and the extremal coupled map lattice model. In Section 3, we review the weighted sum of the objective functions method to solve the multiobjective optimization problem. We propose a two-dimensional model that takes into account the concepts of multiobjective optimization, extremal evolution and coupled map lattice evolution, in Section 4.

2. Extremal Evolution Systems

Extremal evolution systems are systems that update themselves by identifying an active region of the system and renewing this region whilst leaving the remainder unchanged. The active subsystem is chosen according to some kind of extremal criterion; often it is centered on the location of the minimum of some spatially varying scalar variable [3]. The Bak-Sneppen model is an example of an extremal evolution model.

Bak and Sneppen [4] 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, which consists of N species, and has periodic boundary conditions, i. e., is topologically a circle. They assigned fitness values $0 < f(i) < 1$ 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 a sufficiently long time most of the fitnesses are greater than a certain threshold value (0.667 ± 0.001). Also, the distribution of avalanche sizes S approximately exhibits a power law behavior,

$$P(S) \sim S^{-\tau_S}, \tag{1}$$

where the exponent τ_S took various values in [5 – 7].

An interesting way to include spatial effects in dynamical systems is the coupled map lattice (CML) which is a dynamical system with discrete-time, discrete-space and continuous states [8]. It is a simple model with essential features of spatiotemporal chaos (STC). STC is an irregular dynamics in space-time for a deterministic system that is spatially extensive. Typically, a 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. Besides being mathematically interesting, CML has many applications [8, 9].

CML can be represented by local nonlinear dynamics as follows:

$$\begin{aligned} x^{t+1}(i) &= (1-\varepsilon)\, g(x^t(i)) \\ &\quad + \frac{\varepsilon}{2}\left[g(x^t(i-1)) + g(x^t(i+1))\right], \end{aligned} \tag{2}$$

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

Abramson and Vega [10] proposed an extremal coupled map lattice (ECML) model, 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 i 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 i and subject to nonlinear dynamics in addition to being coupled to its nearest neighbors. The logistic map is chosen for the independent evolution of the $x(i)$ with $\lambda(i)$ acting as the parameters in the nonlinear map. The evolution of each species is given by (2), where $g(x)$ is the logistic map,

$$g(x) = \lambda\, x\,(1-x). \tag{3}$$

The local coupling of strength ε models the ecological interaction between neighboring species. They proposed an extremal mechanism like the BS model. At each time-step, the species j with the minimum value of $x(j)$ is considered to be mutated at the next step. Its λ is replaced by a new value drawn from a uniform distribution $g(\lambda)$ in the range $(\lambda_0, \lambda_0 + \Delta\lambda)$ where λ_0 is any value in the range that makes the logistic equation (3) a chaotic equation. Then all elements of the system are updated using (2).

3. Multiobjective Optimization

Every day we face problems of growing complexity which appear in various fields. The problem to be solved can be frequently expressed as an optimization problem. An optimization problem is defined as the search for a minimum or a maximum of a function, this function being called *objective function*. Often, the search would not give us an unique solution but a set of solutions. These solutions are called *Pareto solutions*.

In biology, most of real life optimization problems are multiobjective ones (MOB) [11]. For example, animals would like to get maximum resources with minimum predation. In cancer therapy, we want the optimal dose that kills the maximum amount of cancer cells with killing only a minimum amount of normal cells. Also, humans need maximum health with saving money. Then multiobjective optimization deals with concurrent objective functions [12].

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

The methods of MOB optimization are intuitive. A simple and widely used method is the weighted sum of objective functions method [13]. It transforms the problem to a singleobjective optimization problem. It takes each objective function, associates a weight to each objective function and then, takes a weighted sum of all objective functions under consideration. 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 objective functions $f_i, i = 1, 2, \ldots, N$. Define the following quantity,

$$Z = \sum_{i=1}^{N} w_i\, f_i, \tag{4}$$

where the w_i's are the weights which satisfy

$$0 \le w_i \le 1 \text{ and } \sum_{i=1}^{N} w_i = 1.$$

Then the problem becomes to minimize the quantity Z. This method is easy to implement but has some drawbacks. The first one is, that it is difficult to apply this method for large N. The second drawback is, that it may give a Pareto dominated solution.

Definition 1. *A solution* f_i^*, $\quad i = 1, 2, \ldots, N$ *is called a Pareto dominated solution, if there is another solution* f_i, $\quad i = 1, 2, \ldots, N$ *such that* $f_i \le f_i^*$ *for all* i *with at least one* k *such that* $f_k < f_k^*$.

We generalized the BS model to a multiobjective one in [14]. In particular, we assigned two fitness values $f_1(i)$ and $f_2(i)$ instead of only one fitness to each site i. The weighted fitness value then is

$$f(i) = w_1 f_1(i) + w_2 f_2(i), \quad i = 1,2,\dots,N.$$

Since $w_1 + w_2 = 1$, let $w_1 = w$ and $w_2 = 1 - w$. Then the fitness values

$$f(i) = w f_1(i) + (1-w) f_2(i), \quad i = 1,2,\dots,N \tag{5}$$

are computed for each species i, where the weight w satisfies $0 \le w \le 1$. At each time-step, we look for the species with the minimum fitness, j. Then we update randomly both $f_1(j)$, $f_2(j)$ as well as $f_1(j \pm 1)$ and $f_2(j \pm 1)$. After running the system for a long time the distributions of the distances between subsequent mutations as well as the size of avalanches follow power law. Also, the best fit is above the certain threshold value $(0.57 \pm .01)$.

4. The Model

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 now study a model of evolution on a two-dimensional lattice that takes into account the above arguments, namely those of extremal dynamics, MOB optimization and CML evolution. Let us consider an ecosystem consisting of $N \times N$ species arranged on a square lattice with periodic boundary conditions, i. e., 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 genes that contribute in more than one phenotype [15].

So, in our model, each species is characterized by two levels of structures in a similar way as in [10] but it differs on the phenotype level. The first level is the genotype that is characterized by $\lambda(i, j)$, where the mutations occur. The second level consists of two phenotypes $f_1(i, j)$ and $f_2(i, j)$ that define the weighted fitness $F(i, j)$ of the species at site (i, j) by the equation

$$\begin{aligned} &F^{t+1}(i,j) = w\ f_1^t(i,j) + (1-w)\ f_2^t(i,j), \\ &i,j = 1,2,\dots,N, \end{aligned} \tag{6}$$

where the weight w satisfies $0 \le w \le 1$. The evolution of the system is defined by the following equations:

$$\begin{aligned} f_1^{t+1}(i,j) &= (1-\varepsilon)\ g(f_1^t(i,j)) \\ &+ \frac{\varepsilon}{4}\ [g(f_1^t(i \pm 1, j)) + g(f_1^t(i, j \pm 1))], \\ f_2^{t+1}(i,j) &= (1-\varepsilon)\ g(f_2^t(i,j)) \\ &+ \frac{\varepsilon}{4}\ [g(f_2^t(i \pm 1, j)) + g(f_2^t(i, j \pm 1))], \end{aligned} \tag{7}$$

where $g(x)$ is the nonlinear chaotic map (3).

We propose three versions of this model. The first one uses the following rules. For each time-step, the species (k,l) with the lowest fitness is looked for. This is denoted as the active site. We then change the genotype $\lambda(k,l)$ of that species randomly with a new λ from the interval $(\lambda_0, \lambda_0 + \Delta\lambda)$. Then the pair of phenotypes of that species $f_1(k,l)$ and $f_2(k,l)$ is updated as well as the phenotypes of its four nearest neighbors $f_1(k \pm 1, l \pm 1)$, $f_2(k \pm 1, l \pm 1)$ by using (3) and (7).

In a second version of the model, at each time-step, 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 $f_1(k,l)$ and $f_2(k,l)$ are changed.

The third version is that at each time-step, we change both the genotypes $\lambda(k,l)$ and the phenotypes $f_1(k,l)$ and $f_2(k,l)$ of the species with the lowest fitness as well as its four neighbors $\lambda(k \pm 1, l \pm 1)$, $f_1(k \pm 1, l \pm 1)$ and $f_2(k \pm 1, l \pm 1)$.

In Figs. $1-4$, 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 ($\varepsilon = 0.1$) and strong ($\varepsilon = 0.5$) interaction among the system elements. Also, we run the system for different values of the weight $w = 0.3$, 0.5, 0.9 and of the nonlinearity parameter $\lambda_0 = 3.7$, 3.8, 3.9. We find that the figures of the first and third versions are nearly identical while the second one is quite different from the former. This means that the first and the main effect is the change in the phenotype level. The change in the genotype level is important but not like the phenotype level.

In all cases the system reaches a critical state in which most of the fitnesses are above a certain threshold value. The threshold value and the shape of the distribution are not the same for all cases but depend on the nonlinearity parameter λ of the chaotic map, the weight parameter w and the strength ε of the interaction among the species in the ecosystem.

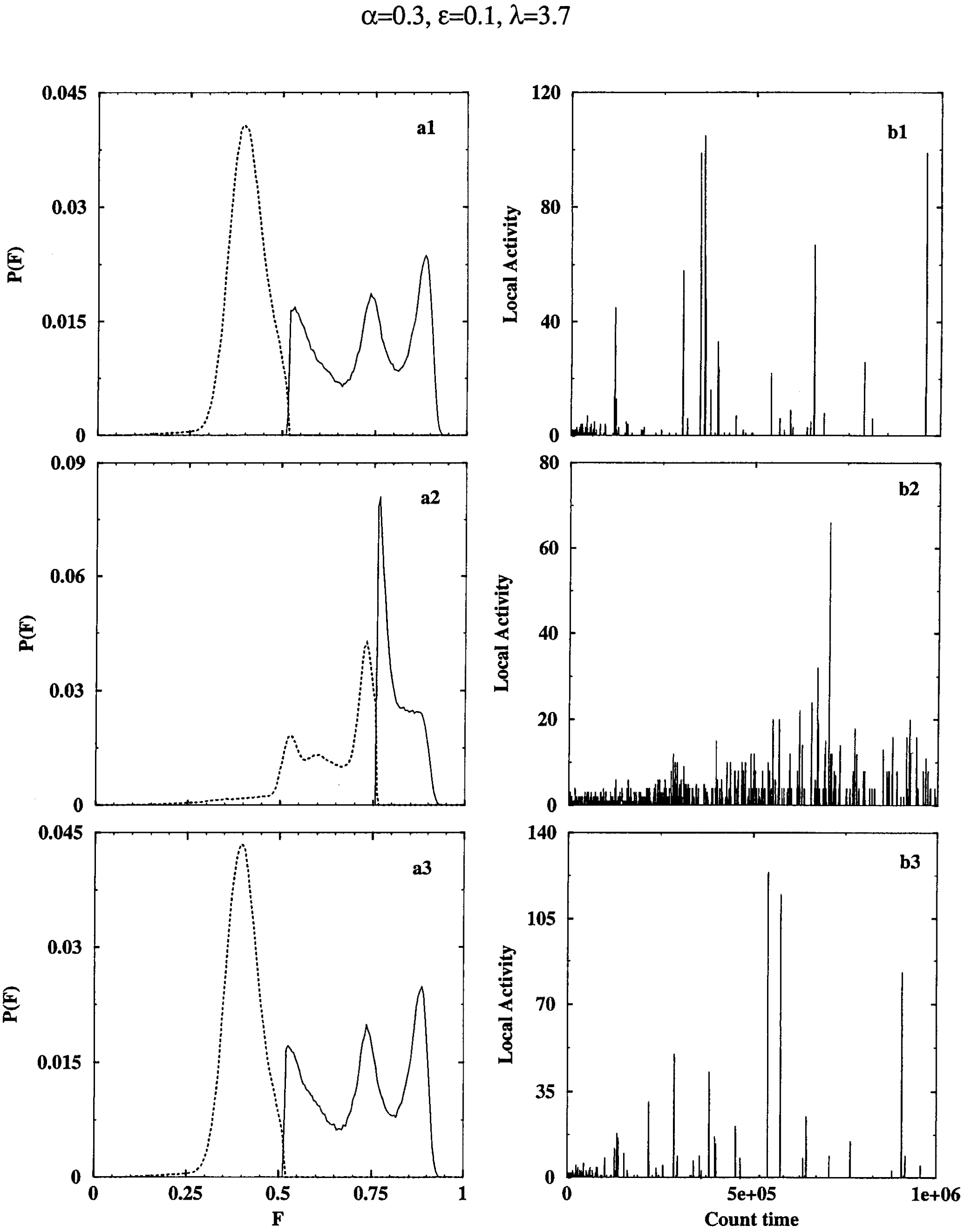

Fig. 1. System size $N = 500$, $\alpha = 0.3$, $\varepsilon = 0.1$, $\lambda_0 = 3.7$, $\Delta\lambda_0 = 0.1$, and $t = 10^7$ iteration. (a1), (a2), (a3) Distribution $P(F)$ of the fitness $F = F(i, j)$ in the critical state (right solid curve) with the distribution of minimum fitness (left doted curve)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

The effect of increasing the strength ε of the interaction among the species in the ecosystem is to decrease the range of the final fitness distribution and increase the threshold value. The change of the nonlinearity pa-

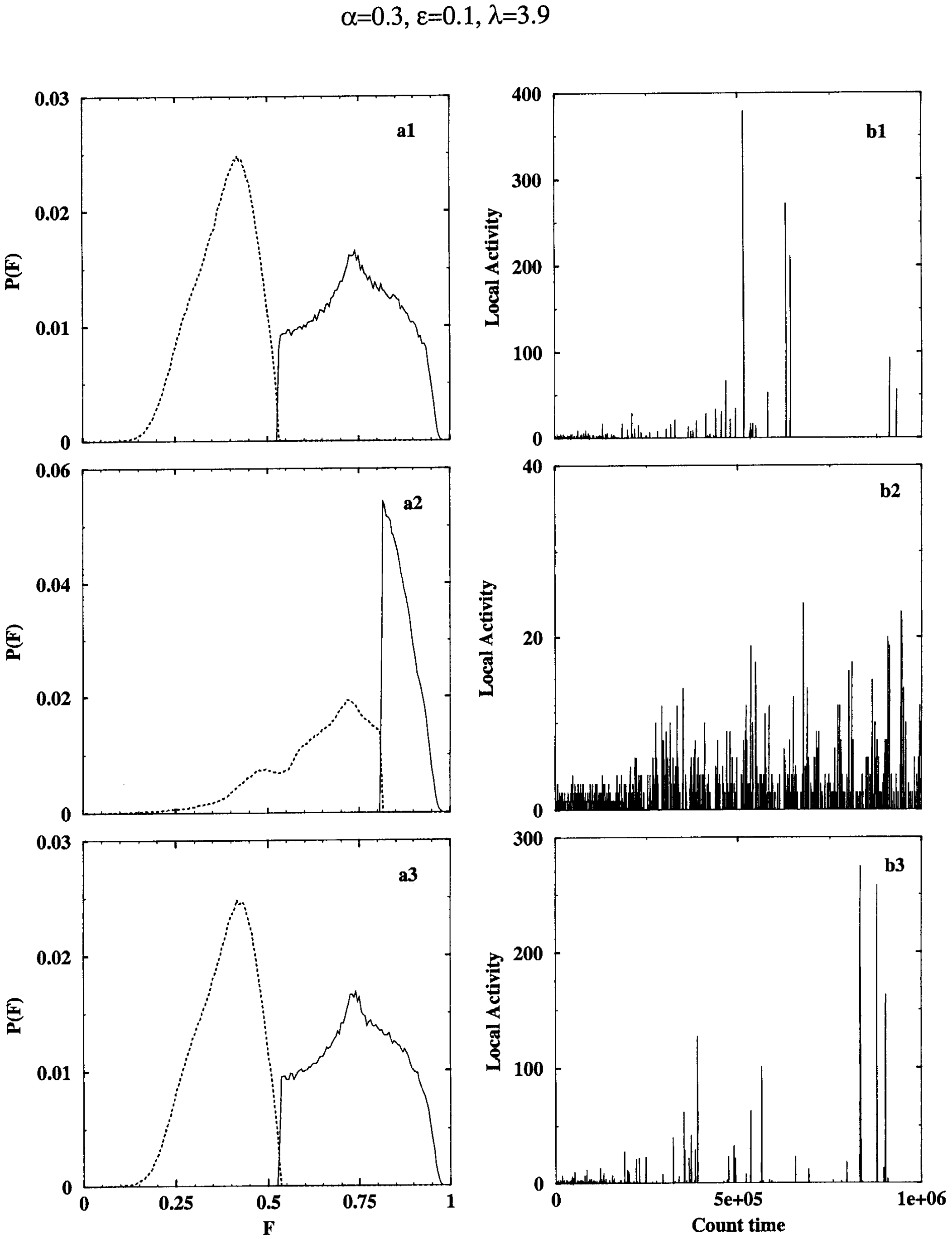

Fig. 2. Same as in Fig. 1 but $\lambda_0 = 3.9$.

rameter λ of the chaotic map 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. In Fig. 5, we

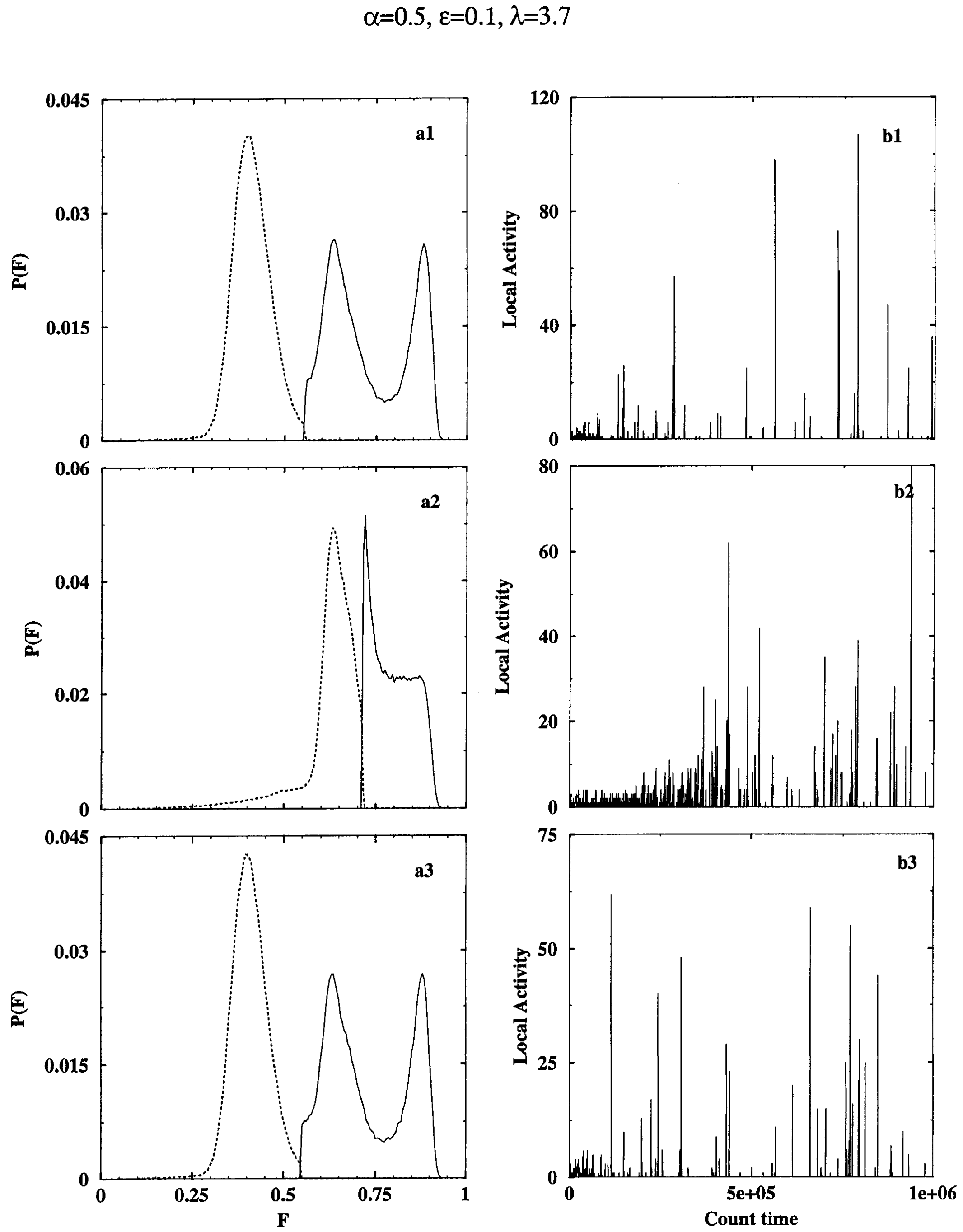

Fig. 3. Same as in Fig. 1 but $\alpha = 0.5$.

draw, in a log-log plot, the distribution of avalanche sizes S in the first version for some values of the above parameters. The plot approximately follows the power law (1) with exponents $\tau_S \approx 2.3$ (a, b), $\tau_S \approx 1.5$ (c), and $\tau_S \approx 2.6$ (d).

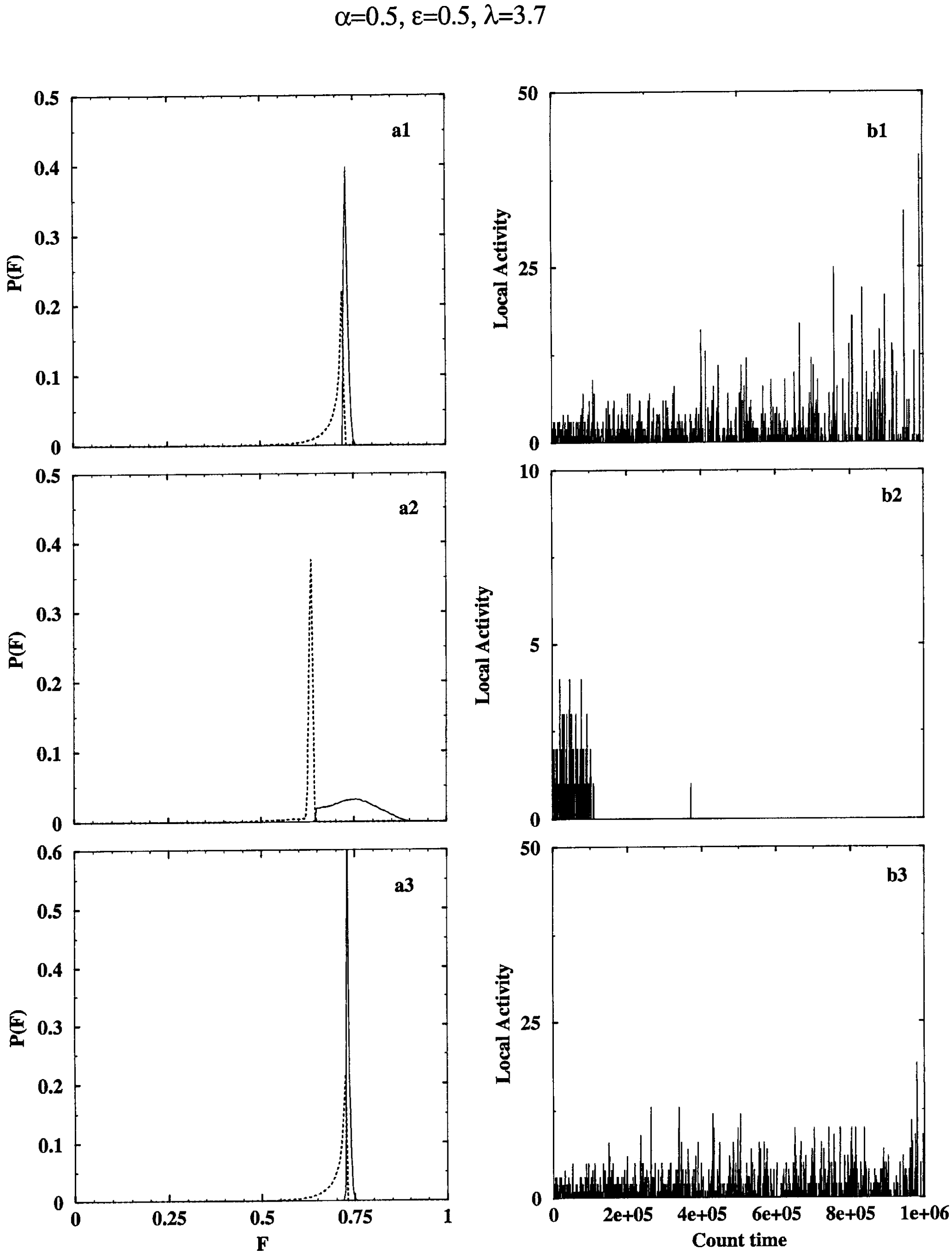

Fig. 4. Same as in Fig. 3 but $\varepsilon = 0.5$.

Acknowledgements

This work was done within the framework of Associateship Scheme of the Abdus Salam International Center for Theoretical Physics, Trieste, Italy. The author acknowledges the academic support of Prof. E. Ahmed for useful discussion and comments.

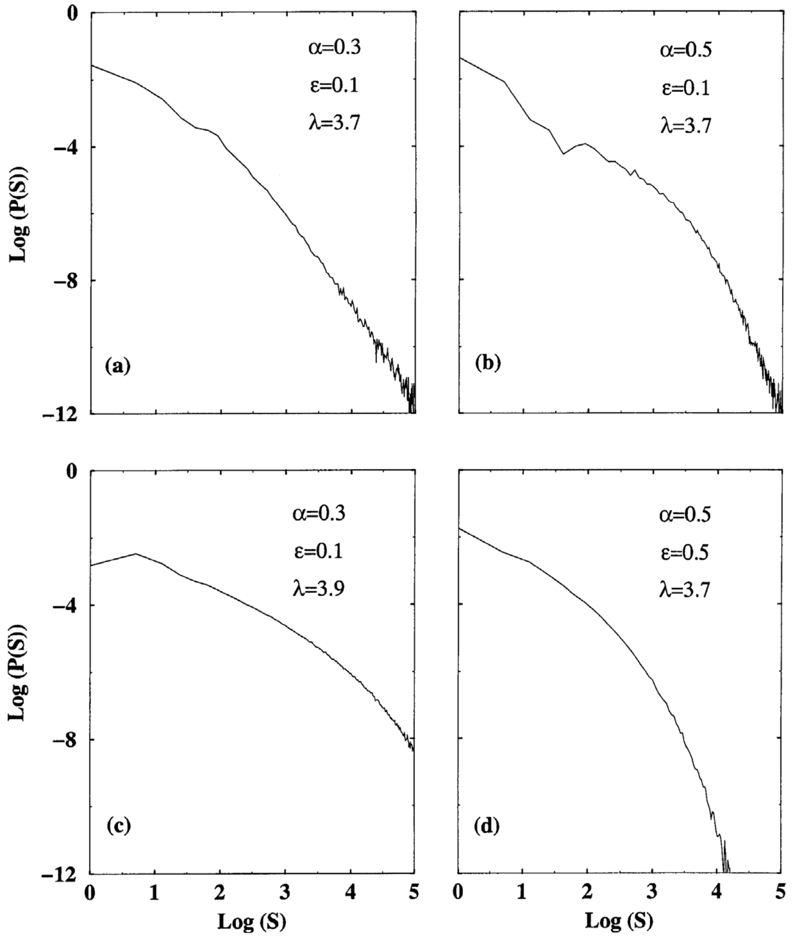

Fig. 5. The distribution $P(S)$ of avalanches sizes S in the critical state of a system with $N = 500$, $\Delta\lambda_0 = 0.1$ and $t = 10^7$ iterations in a log-log plot. (a) $\alpha = 0.3$, $\varepsilon = 0.1$, $\lambda_0 = 3.7$. (b) $\alpha = 0.5$, $\varepsilon = 0.1$, $\lambda_0 = 3.7$. (c) $\alpha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

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