



Research paper

Criticality in a dynamics ruled evolutionary model

Maneesh B. Matte, Prashant M. Gade*

Department of Physics, Rashtrasant Tukadoji Maharaj Nagpur University, Nagpur 440 033, India



ARTICLE INFO

Article history:

Received 5 February 2018

Revised 9 May 2018

Accepted 10 May 2018

Keywords:

Self organized criticality

Evolution

Critical phenomenon

ABSTRACT

We propose a model of dynamics-ruled evolution inspired by Bak–Sneppen model. We argue that the only way for the ecological system to find the least or most fit species is to infer it from dynamics. Thus, instead of punishing the species which is ‘least fit’, we punish one which ‘appears to be least fit’. We find that the model still evolves to a critical state. The detailed dynamics does not seem to affect the presence of a critical state.

© 2018 Elsevier B.V. All rights reserved.

1. Introduction

The fossil records often indicate very rapid evolutionary changes in a small period of time followed by ‘stasis’ in which there is a very little net evolutionary change. Paleontologists Eldredge and Gould termed this phenomenon of sharp, short bursts in evolution followed by gradual changes as ‘punctuated equilibrium’ [1,2]. The data was analyzed by Raup later and he modeled it using kill curve which provides an excellent fit [3,4]. Newman pointed out that this best fit implied that the size distribution of extinction events should be a power law with exponent -2 [5]. We note that this data has also been alternatively fitted by a stretched exponential [6].

An interesting model for this extinctions within the paradigm of ‘self-organized criticality’ which attracted a lot of attention was suggested by Bak and Sneppen [7]. Their simplified model was a one-dimensional lattice representing species connected to their nearest neighbors. Each species was assigned a fitness value chosen randomly in the beginning. At each time step, the species with the least fitness and its neighbors were replaced by a new species with a fitness value chosen from the same random distribution. Surprisingly, this model shows correlations in space and time and shows extinction activity with a power law. The quantities such as the first return time, return time and jump size distribution show power law behavior. Despite its simplicity, this model has not been solvable analytically.

A critical value of fitness can be defined in this model. One can define avalanche size by the number of subsequent mutations below this value. The distribution of avalanche sizes is an inverse power law and the exponent is close to 0.9 which increases in higher dimensions.

There have been several other alternative models. Sole and Marubia presented model [8–10] in which the interactions between species were defined by matrix J . The i^{th} Species became extinct when $\sum_j J_{ij} < 0$. However, its asymptotic behavior is not known reliably [11]. Manrubia-Paczuski [12], Newman [5,13], Amaral-Meyer [14], Drossel [15] and Slanina-Kotrala [16,17] introduced some further models which showed power-law distributions of extinctions with different exponents. Underlying topology of connectivity between species is not necessarily Cartesian. In some of them, even the number of species

* Corresponding author.

E-mail address: prashant.m.gade@gmail.com (P.M. Gade).

can change during evolution. These are certainly more realistic features. However, they render further difficulties in systematic analysis. One more feature in the Bak-Sneppen, Sole-Marubia, Manrunia-Paczuski and Newman models is that the species with certain low fitness become extinct in a deterministic fashion.

We argue that fitness is inferred by the environment from its dynamical indicators or ‘performance’. The idea that the fitness can be measured by absolute numeric values associated with reproductive rates has been questioned [18]. In fact, in the field studies in ‘stability versus diversity’ debate in ecology, several biologists have linked stability with variability [19]. If the level of performance fluctuates in an erratic fashion, this species will be considered ‘unfit’ by the environment and will be replaced. Naturally, its connections will be replaced. On the other hand species with a consistent performance and few fluctuations is retained. There are also few reports of negative correlation between extinction and variability due to inability of species to respond to environment. We employ this approach in this work. We employ simple well known nonlinear maps such as logistic map (which has its origin in population dynamics) to compute the performance of species. The couplings are modeled by a coupled map lattice and the fitness of a given species is characterized by parameter value of the map.

There should also be a feedback from fitness to dynamics and both should affect each other. This feature comes out well in this model.

2. Dynamical evolutionary model

We define a dynamical evolutionary model as a variant of coupled map lattice (CML). We have N sites on a one-dimensional lattice. Let $x_i(t)$ be a variable value at site i at time t and let the time evolution be dictated by

$$x_i(t+1) = (1-\epsilon)f_i(x_i(t)) + \frac{\epsilon}{2}(f_{i-1}(x_{i-1}(t)) + f_{i+1}(x_{i+1}(t))) \quad (1)$$

where $\epsilon \in [0, 1]$. We assume periodic boundary conditions. The functions $f_i(x)$ belong to a family of chaotic tent maps, i.e

$$\begin{aligned} f_i(x) &= a_i x & \text{if } x \in [0, 1/2) \\ f_i(x) &= a_i (1-x) & \text{if } x \in [1/2, 1] \end{aligned} \quad (2)$$

The difference with a usual CML model is that we change these a_i 's dynamically. Initially, we set them to maximal value 2 and initial conditions $x_i(0)$ are random. We carry out simulations for $N = 4096$ and $\epsilon = 0.1$.

The manner in which a_i 's are changed is as follows. We evolve the system for τ time interval. We note the maximum and minimum value taken by the variable for each site i . We denote the difference between the maximum and minimum by $d(i)$, i.e. $d(i) = \max(x_i(1), x_i(2) \dots x_i(\tau)) - \min(x_i(1), x_i(2) \dots x_i(\tau))$. The variable $d(i)$ is indicator of variability of site i . Now we note a site m for which $d(m) < d(i)$, $i \neq m$, i.e $d(m)$ is minimum. This site m has minimum fluctuations in the period τ .

We change the parameter value a_m of m 'th site and its neighbors a_{m+1} and a_{m-1} by new random parameter values in the range $[0, 2]$. We repeat this process of checking maximum and minimum and replacing the fluctuating sites after every τ steps. The evolution reaches some kind of steady state which is our object of interest.

The first quantity we analyze is the jump size distribution. Let m^{th} site be found most fluctuating at time $t\tau$ and m'^{th} site is most fluctuating at time $(t+1)\tau$, and thus parameters a_m , a_{m-1} and a_{m+1} are replaced at time $t\tau$ and parameters $a_{m'}$, $a_{m'+1}$ and $a_{m'-1}$ are replaced at time $(t+1)\tau$. Now the jump size J is the shortest distance between the sites m and m' . The probability distribution $P(J)$ is plotted in Fig. 1(a) for various lattice sizes. It shows a clear power law. The behavior can be modeled by $P(J) \sim J^{-2.26}$ and it is far from -3.15 observed in Bak-Sneppen model. Thus this variant of our model shows a higher probability of mutations in the vicinity of previous mutations than Bak-Sneppen model. However, this exponent changes with specific nature of map used as we will demonstrate later.

If we consider a patch of sites, say, first 100 sites and consider the distribution of successive time-steps during which active site belonged to this patch, it shows a power law as well. This behavior is expected from the behavior of jump size in which smaller jumps are more probable.

We investigate first passage time in these systems. We define first passage time T_i as the time at which a site i changed its parameter from a_i from initial conditions for the first time. The distribution of first passage times T shows a clean power law behavior. (We have binned it in units of 10.) The probability distribution of first passage times $P(T)$ is plotted in Fig. 1(b). We can fit it with an inverse power-law with exponent 0.62.

Another quantity of interest is first return times. This is the time interval between two successive updates at the same site. Let $T'(i, k)$ be the time at which site i is updated k th time and $T'(i, k+1)$ be the time at which it is updated $k+1$ th time. Now let $\Delta T(i, k) = T'(i, k+1) - T'(i, k)$. This quantity ΔT (on averaging over i and k on discarding certain transients) is investigated. We obtain the distribution of return times $P(\Delta T)$ and an excellent inverse power law with exponent 1.60 is obtained in this case which is slightly higher than 1.58 obtained for Bak-Sneppen model.

We must mention that the results do not seem to be model specific, though there is variation in exponents. We investigated logistic map $f(x) = a_i x(1-x)$ for the above scheme. We begin with random initial conditions for x and $a_i = 4$ initially. Using d_i as a measure, we replace sites which display most variability by new parameter values of a_i between $[3, 4]$. We obtain jump size distribution with power-law decay, though the decay is not as clean as in case of tent map.

We also investigate the distribution of first passage times. Here we obtain a clean inverse power law with exponent 0.61. The distribution of return times shows an inverse power law with exponent 1.60. One may argue that this model is clearly

Download English Version:

<https://daneshyari.com/en/article/7154454>

Download Persian Version:

<https://daneshyari.com/article/7154454>

[Daneshyari.com](https://daneshyari.com)