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Unidimensional games, propitious environments, and maximum diversity

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Cellular automata have been extensively used in the modeling of complexity. In biological phenomena complexity is directly related to the intuitive concept of diversity, which manifests itself in several forms. Particularly, the game Life [E. R. Berlekamp, J. H. Conway, and R. K. Guy, *Winning Ways for Your Mathematical Plays* (Academic, New York, 1982), Vol. 2] may be viewed as a picture of nonlinear open biological systems acting cooperatively. However, it has been shown that, in Life, diversity (defined in terms of different clusters) decreases with time. We derive an alternative game introducing the concept of a propitious environment which confers longevity to live sites in time evolution. It is shown that the game self-organizes in a configuration of maximum diversity exhibiting a high geometrical complexity. This game is considered in one dimension and has some connections with the unidimensional Life.

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It is rather remarkable to see how really simple cellular automata models may simulate a great variety of complex phenomena [1] which are very difficult to approach extensively with usual analytical techniques. Such "games" are well known for the richness of properties they present, ranging from the purely geometrical to the computational level, and have been used to understand at least metaphorically essential features of real biological processes. In this context the game Life invented by Conway [2,3] offers attractive connections such as the existence of propagating and self-reproducing structures. It is famous for its capacity to generate very complex configurations from a few simple rules. Earlier attempts to study Life were restricted to taxonomic classification, where one looks for specific forms capable of executing definite tasks. With its local properties understood to a certain extent, recently some attention has been devoted to the investigation of Life as an universe of globally interacting clusters [4–7]. Bak, Chen, and Creutz have suggested [5] that Life would evolve to a self-organized critical state. Their results would reinforce the image of Life as a biological model. However, Bennet and Bourzutschky carried some experiments [8] which seemed to contradict Bak and collaborators' results. The question has proven controversial and is not defined yet [9]. Another very interesting elaboration is the one-dimensional version of Life proposed by Millen (1GL) [10,11]. This game incorporates all essential features of Conway's version (2GL) and so may be considered as a valid construction with the advantage of low dimensionality. Computational implementations on relatively large lattices are then possible. From now on, when saying Life we will be referring indistinctly to the 1GL or 2GL. The 1GL is defined on a lattice of L sites s_i, $i=1,\ldots,L$, with possible states 1 (live site) or 0 (disoccupied site), whose fate is determined by the four nearest neighbors and the following rules: (i) a disoccupied site (0) with either two or three live neighbors will be occupied ($0\rightarrow 1$, birth) in the next generation; (ii) a live site (1) with either two or four live neighbors will survive in the next generation, otherwise it will die ($1\rightarrow 0$). Local properties of the 1GL are very similar to those of the 2GL [10]. From a global point of view there are some differences but the qualitative behavior is also very similar [12]. In all that follows we will be thinking of Life as a model for interacting populations in some evolutionary universe. As the rules are applied animals are created and animals disappear so that after a long time the most fit populations and animals will remain. Obviously, Life understood as a model is only pictorial and must not be taken so far. We will always bear this in mind when comparing real phenomena with results from Life.

A distinguishing characteristic of real life is its fascinating diversity, which is manifested in many different ways. Diversity and complexity are intimately related. In fact, diversity is a major feature of biological phenomena and expresses in an intuitive way the extreme variety of behavior found in nature. By using a simple model of diversity Sales *et al.* [7] were able to investigate and derive interesting properties of the fauna in Life. This physically appealing idea successfully applied in the context of fragmentation [13–16], yields the somewhat frustrating result that, in Life, diversity is a decreasing function of time. It was noticed that for any initial configuration of the game it always evolved decreasing diversity, whereas it has been observed [17,18] that real life tends to maximize diversity. Here we introduce an alternative game which solves this question and is more physically reasonable as a biological picture. Consider a lattice populated of beings that can live or die as in a Life game. The constraints defining a birth can be modeled in many possible ways. On the other hand, differently from Life, the environment may turn out to be favorable to live sites and they exist for an average lifetime T_0 independent of their neighborhood. This longevity can be formally expressed by the probability distribution $P(t)$ giving the chance that a live site will still be alive at time step t. Generally $P(t)$ may assume an arbitrary dependence on time so that $\langle t\rangle = T_0$. We choose here our rules in the following way: (i) a disoccupied site (0) with

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either two or three live neighbors will be occupied in the next generation (birth); (ii) a live site (1) will die in the next generation with constant probability, irrespective of its neighborhood. Note that the birth rule is the same as in 1GL. The important noise component introduced by this alternative game solves a major deficiency in Life considered as a model, which is that it is a deterministic game, while biological processes, especially evolutionary ones, have a strong factor of indeterminism.

Probably the best way to probe the evolution of our model is through computer simulations. It is possible, however, to develop some basic calculations on a mean-field level in the same spirit of those conducted by Schulman and Seiden [4]. If s_i^t denotes the state of site i at time t, then its state at time $t+1$ will be given by

$$s_i^{t+1}=\begin{cases}\delta\left[2,\sum{}' s^t\right]+\delta\left[3,\sum{}' s^t\right] & \text{if } s_i^t=0\\ 0 \text{ with probability } 1-P(t) & \text{if } s_i^t=1\ ,\end{cases} \tag{1}$$

where the prime on the summation indicates that only the four nearest neighbors are to be considered. $\delta(i,j)$ is the Kronecker delta; $\delta(i,j)=1$ when $i=j$ and 0 otherwise. The macroscopic density ρ is expressed by $\rho_t=\sum_i \langle s_i^t\rangle /N$. If at time $t=0$ an uncorrelated random distribution of live and disoccupied sites yelding a density ρ_0 is given we may write based on simple combinatorial considerations that

$$\rho_{t+1}=2\rho_t^2(1-\rho_t)(3-\rho_t)[1-P(t)\rho_t]+P(t)\rho_t\ . \tag{2}$$

This equation is exactly correct only for $t=1$ but it may give some general trends about the evolution of density. In what follows we concentrate in the case where T_0 tends to infinity, or simply $P(t)=1$, so that the environment provides condition for long lifetimes. As a result, Eq. (2) will be written as

$$\rho_{t+1}=\rho_t(-2\rho_t^4+10\rho_t^3-14\rho_t^2+6\rho_t+1)\ , \tag{3}$$

which has three fixed points: 0 (stable), 0.276 48 (unstable), and 1 (stable). Every configuration with initial occupation lower than 0.276 48 would evolve to complete extinction, while a higher density would lead to complete population of the Universe. As it is clear from the statement of the game the fixed points 0 and 1 do exist but from computer simulations we have found that the unstable point 0.276 48 is not present and furthermore the fixed point 0 is unstable. As we could expect, since all individuals are very healthy any not too small, initial density should lead to a high populational density. This was indeed found and the results are shown in Fig. 1. Note that, differently from Life [6], where in the region of interesting initial densities the asymptotic population does not retain any information of ρ_0, in our model history is somehow encoded in the $t\rightarrow\infty$ states.

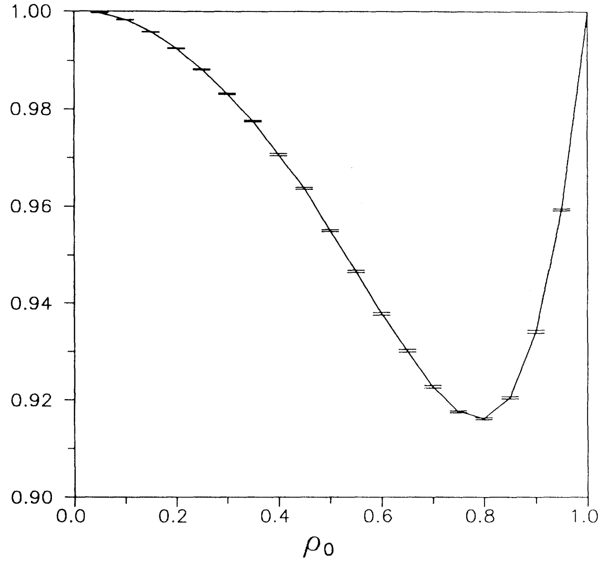

FIG. 1. Asymptotic populational density ρ_∞ as a function of initial random density ρ_0. A total of 20 experiments in a lattice of 10^6 available sites were performed in each case.

As in Ref. [7], diversity is defined in terms of cluster size. A cluster is a set of live sites connected by a nearest-neighbor relation. Diversity is then the number of different clusters found in the system at a given time. This can be made more explicit by saying that if $n(s,t)$ denotes the number of clusters of size s at time t than the diversity $\Delta(t)=\sum_s \theta[n(s,t)]$, with $\theta(x)=1$ for $x>0$ and 0 otherwise. This definition of diversity is particularly appropriate for computational implementations and suitable for problems defined on a lattice. With the high densities attained by the game as shown in Fig. 1 one could expect low values of diversity. Nevertheless, we see in Fig. 2 that as t increases the system goes from a condition

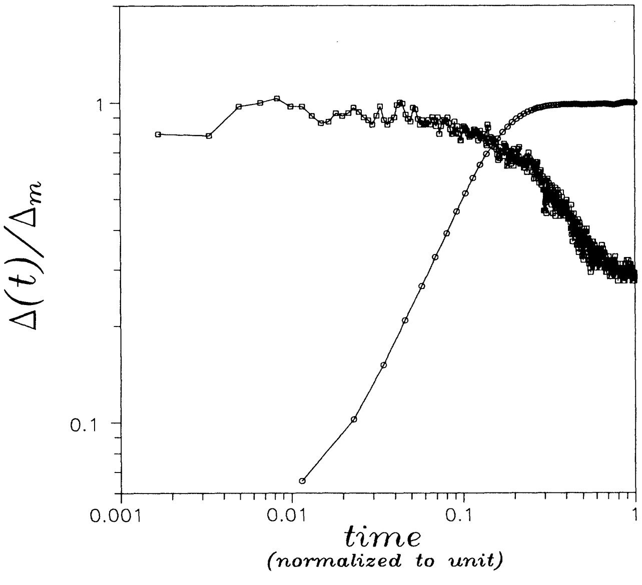

FIG. 2. Typical evolution of diversity in time for the model described in the text (○) and for the unidimensional Life (□). The curves shown refer specifically to $\rho_0=0.2$ and $L=2\times10^5$. An arbitrary normalization is introduced in the time axis to allow a clear comparison of both cases, while the diversity is normalized by the maximum diversity value Δ_m exhibited by the system. The time scales of the unidimensional Life for reaching stable configurations are about 10^2 times greater than that in our model.

of lower to higher diversity. For comparison we include a curve illustrating the typical dependence of diversity with time in the 1GL (a similar comparison can be made with the 2GL [7]). As a consequence, our model is able to account for the idea that in an evolutionary environment the best fit will survive with high probability and yet high biodiversity will result.

Another quantity that may be measured is the cluster population denoted by $N(t)$. Define $N_1=N(1)$ and $N_\infty=N(t\rightarrow\infty)$ and also $\Delta_1=\Delta(1)$ and $\Delta_\infty=\Delta(t\rightarrow\infty)$, where $t=1$ means the first time the dynamical rules are applied from an initial random configuration at $t=0$ and Δ_∞ is the maximal diversity state. From numerical simulations in lattices of sizes up to $L=10^6$ we have found that

$$\epsilon=\frac{\Delta_\infty/N_\infty}{\Delta_1/N_1} \tag{4}$$

is a constant and equals 1.000±0.022 independent of initial state or lattice size. We call ϵ the population-diversity parameter. We believe that ϵ may satisfy such a simple relation even when the site lifetime is finite as long as it is not too small. This turns out to be a remarkable fact because for the type of automata discussed here the time evolution may lead to rather unpredictable structures. The fact that some quantity link in a very definite way initial and long-term states may be very useful because one would need not to carry extensive simulations of the game to learn some information *a priori.*

We have shown previously that as the rules are applied initial random states converge to equilibrium configurations with high mass density (>0.91). As a consequence it is not surprising that the fractal dimension D of the system is equal to 1. However, combined with great occupancy one finds maximum diversity. This means that the system organizes itself so as to yield a high level of complexity even if it tends to overpopulation. It is possible to conclude that the structure of "gaps" (disoccupied sites separating clusters) are nonuniformly distributed such that the requirement massiveness-diversity is satisfied. We have found that the gaps determine a geometric multifractal [19] in the limit of $t\rightarrow\infty$ by calculating the generalized dimensions D_q defined from the scaling relation $\langle(m(R)/m_\infty)^{q-1}\rangle\sim(R/L)^{(q-1)D_q}$, where $m(R)$ gives the number of disoccupied sites within a radius R centered on a point of the gap structure and $m_\infty=L(1-\rho_\infty)$. The brackets $\langle\,\rangle$ denote an average over randomly chosen center points. The curve D_q vs q is shown in Fig. 3 for lattices of size $L=10^6$.

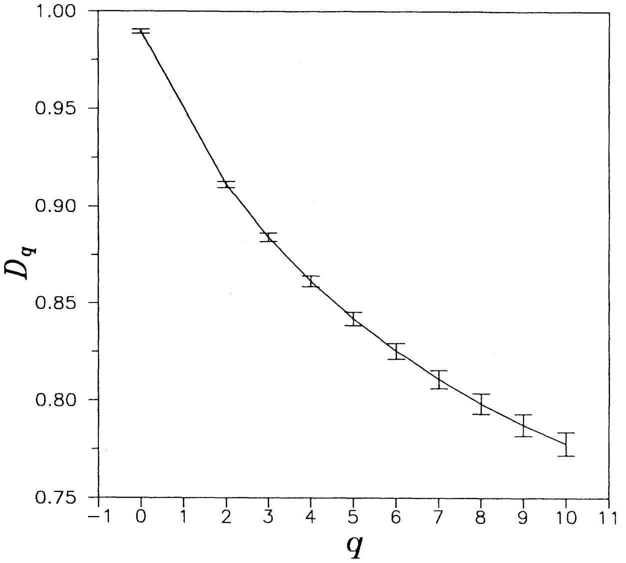

FIG. 3. Generalized dimensions D_q vs q for the geometric distribution of gaps separating clusters in the time of maximum diversity.

In conclusion, we have presented an alternative unidimensional game, which may be useful as a metaphor for biological phenomena, especially population dynamics and evolution. Only the unidimensional case was considered here although extension to higher dimensionality seems straightforward albeit computationally demanding. Live and disoccupied sites are defined on a line and births can occur from definite fixed neighborhood relations. A stochastic factor affecting births can also be introduced but we have disregarded such complication in the present approach. Each live site has a longevity characterized by a probability distribution $P(t)$ yielding an average lifetime T_0 possibly independent of neighborhood. The same birth rule of Millen's unidimensional version of Life was chosen. In the case where $P(t)=\delta(2,\sum_i' s_i^{t-1})+\delta(4,\sum_i' s_i^{t-1})$, Life dynamics is recovered. For general longevity functions the local properties of our model may be very different from Life in that no stable structures exist in average for a time greater than T_0 and propagating animals have a limited range of action ("mortal gliders"). We have analyzed the case where $P(t)$ is a constant and the site lifetime is large, showing that the game evolved to final configurations of maximum diversity and high geometrical complexity. Also, the cluster population and its diversity may be very simply related through the parameter ϵ connecting initial and asymptotic states.

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