Recognition games

S.G.F. Martins, T.J.P. Penna, and P.M.C. de Oliveira[a]

Instituto de Física, Universidade Federal Fluminense, Av. Litorânea s/n, 24210-340 Niterói, RJ, Brazil

Abstract. In this work we propose an evolution model based on the competition between individuals belonging to populations of neural networks, obeying the Hopfield dynamics. The selection rule adopted relies on generalization and natural classification abilities. The results obtained through computer simulation show that these populations self-organize and evolve towards equilibrium states in the region of transition between ordered and disordered phases.

PACS. 87.10+e General theory and mathematical aspects

1 Introduction

The study of complex adaptive systems has been an object of great interest in several branches of science. Biological evolution, even in the most modest organism, is certainly one of the most attractive examples of such systems. Recently, models inspired in biological evolution have received much attention in the physics research community [1].

Computer simulations of the behaviour of complex adaptive systems have shown that these systems have a tendency to accomodate themselves in a well defined transition zone between order and chaos, characterized by efficient adaptation and a power-law-governed behaviour. This situation is sometimes called the "edge of chaos" after Kauffman [2]. According to him, natural selection drives the living systems to such poised states. Normally, to confirm if a system is really at this marginal situation between order and chaos is a hard task. Suzuki and Kaneko [3] proposed an evolutionary computational model, motivated by the observed complexity of bird songs, which clearly shows this behaviour. They simulated, through imitation games, the competition between artificial birds, employing logistic maps as generators of songs. Each "bird" is a logistic map with a particular value of the control parameter, randomly chosen at the beginning. By iterating one of these maps, starting from some initial seed, a sequence of numbers is generated: this sequence is considered as the "bird song". Two competitors try to imitate each other, *i.e.* each one try to produce a sequence of numbers as near as possible to some basic sequence given by the other. An offspring of the winner, *i.e.* the one presenting a better imitation ability, replaces the looser in the population. An offspring is simply another logistic map for which the control parameter is slightly different from that of the parent. These

imitation games are repeated many times, while the population evolves. The results confirm the evolution to the "edge of chaos", *i.e.* at the end all individuals within the population correspond to control parameters near the isolated critical values where the logistic map undergoes a transition between regular and chaotic behaviours. These values of the control parameter correspond to the ones for which the Lyapunov exponent vanishes (the bifurcation points, the onset of chaos and the borders of regular windows inside the chaotic region).

In the course of biological evolution there are random changes in the genotype of every generation. They contribute to disturb the phenotype that help to decide whether an organism is viable. A case of biological evolution of great importance to contemporaneous humanity is the development of resistance to antibiotics in bacteria. A careful investigation was carried on *E. coli* species [4,5]. It was found that resistance was achieved by a change in the genotype. Through the genes, bacteria learn to recognize and to answer to this menace, guaranteeing their survival. This learning occurs during biological evolution, being transmitted through genetic inheritance [2,5]. In other words, complex living systems must "know" their environment. In this aspect, we propose an evolution model that consists in a competition between individuals belonging to populations of neural networks obeying Hopfield dynamics [6]. The adopted selection rule is based on generalization and natural classification. Natural classification means that sufficiently similar things are classified as being the same [2,7]. The results show self-organization in these populations, which evolve towards equilibrium states in the region of transition between order and chaos.

2 The Hopfield model

An attractor neural network is a model of associative memory. The state of each neuron is represented

[a] e-mail: `pmco@if.uff.br`

by a binary variable ($S_k = \pm 1$) [8]. Each neuron is connected to other neurons through synapses. The synapse intensities are represented by J_{jk}, the synaptic matrix elements. The state of a given neuron S_k is determined by the states of each other linked to it through the corresponding synapse intensity J_{jk}, which can lead to excitation or inhibition of S_k. Hence, we can express the dynamics of a neural network as [6]:

$$S_k(t+1) = \text{sgn}\left(\sum_j J_{jk}S_j(t)\right) \qquad (1)$$

i.e., the neuron S_k will be active if the sum of the received excitatory signals surpasses the inhibitory ones. This dynamics minimizes the following Hamiltonian:

$$H = -\frac{1}{2N}\sum_{j=1}^{N}\sum_{k\neq j}^{N} J_{jk}S_j S_k, \qquad (2)$$

considering a network with N neurons.

Hopfield proposed that some information $\xi_j^\mu = \pm 1$, $j = 1, ..., N$, is considered as learned by the neural network if it corresponds to a minimum of the Hamiltonian (2) or an attractor fixed point of (1). In this way, the recognition of a given information corresponds to a minimization process implemented by iteratively applying equation (1), one neuron after the other, until reaching convergence of the whole system. Learning is a process in which the neural network dynamically adjusts its synaptic matrix to accomodate a certain pattern ξ^μ as a new attractor, i.e., as a minimum of (2) (in this paper, we will suppress the lower index, which refers to a given neuron, when considering the complete set of neurons). Consider a network with P stored patterns in its synaptic matrix. According to Hebb's rule [9], a new information ξ^{P+1} could be learned by modifying the couplings J_{jk} according to:

$$\Delta J_{jk} = \frac{1}{N}\xi_j^{P+1}\xi_k^{P+1}, \qquad (3)$$

where ΔJ_{jk} must be added to the current value of J_{jk}.

However, this single rule does not guarantee that ξ^μ ($\mu = 1, 2, ..., P$) are fixed points of (1) (P was redefined). In order to have this model operating as an associative memory device, it is necessary that two further conditions be fulfilled. First, the information must be uncorrelated, i.e., the overlap between patterns, defined as

$$m(\mu,\nu) = \frac{1}{N}\sum_{j=1}^{N} \xi_j^\mu \xi_j^\nu \qquad (4)$$

must be statistically null for all pairs μ,ν of informations. Second, the number P of patterns stored in an N-neuron network must be smaller than $\alpha_c N$, where α_c is the critical storage capacity in the Hopfield model ($\alpha_c \sim 0.14$, for uncorrelated patterns) [10]. Besides, if those patterns are correlated (i.e., there is a large overlap) α_c is even smaller. It is worth mentioning that, even if the above conditions

are satisfied, rule (3) by itself does not guarantee that ξ^μ are the only equilibrium states of (1). Actually, there are other states that can be local minima of (2), which correspond to spurious memories.

3 Population dynamics

We consider a population with V individuals, each one being a Hopfield neural network with N neurons. In the initial step each individual i is characterized by a series of P_i patterns ξ^μ, $\mu = 1, ..., P_i$ randomly chosen. The number P_i of elements is also randomly chosen in the interval $[L,M]$. Each pattern is a word of N bits and the series of P_i patterns of each individual i, which we call "genotype", is the series of informations genetically inherited by this individual. Therefore, we take as a starting point a population of individuals characterized by different "genotypes", contrarily to reference [2], where all individuals of the species are identical, i.e., are represented by a single genotype.

At each time step we choose randomly V pairs of individuals. For each pair we proceed as follows: the individual V_1 presents all its "genotype" informations ξ^μ, $\mu = 1, ..., P_1$ to another individual V_2, also chosen randomly. Presenting an information means making it the input (stimulus) to the V_2 neural network, i.e., $S_j(t = 0) = \xi_j^\mu$, $j = 1, ..., N$, where S_j refers to the j-th neuron of V_2 and ξ^μ to the μ-th pattern memorized by V_1. This information will be processed by V_2, following the dynamics (1), until an equilibrium (stationary) state is reached (we disregard the self-interaction terms in the Hopfield dynamics and we utilize the multi-spin technique [11,12]). The equilibrium state can be either some information included in (3) for the individual V_2 or a spurious state. For each processed information, we check if the final stationary state is similar to any information contained in the "genotype" of V_2. Two patterns are considered similar if they differ by T_X genes at most (T_X is randomly chosen within the interval 0.0 to $0.5N$, for each new tossed pair of individuals). If the final stationary state is similar to any information contained in the "genotype" of V_2, we calculate the overlap between the *stimulus* and the *final stationary state*. Otherwise, we consider the overlap to be null.

The same procedure is performed, considering now that the individual V_2 is the one that presents the information to V_1. For each processing individual i, we calculate the average overlap ϕ_i defined as:

$$\phi_i = \frac{1}{N_s}\sum_{s=1}^{N_s} m(i,s) \qquad (5)$$

where N_s is the number of the stimuli received by the individual i and $m(i,s)$ is the overlap (4) between the stimuli and their respective final stationary states. The individual with the smaller average overlap dies, and is replaced by a descendent of the other. In our simulations we performed
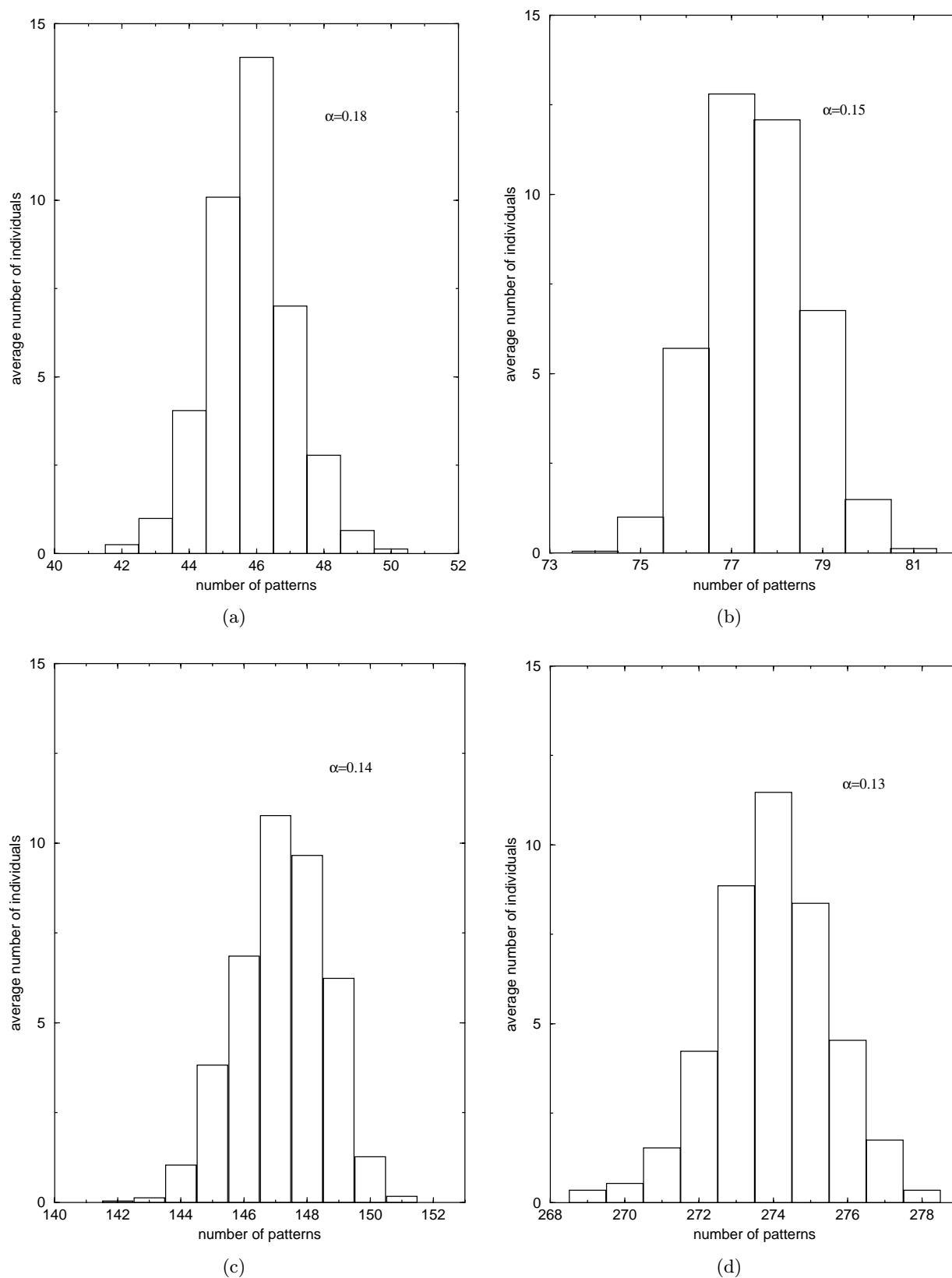
Fig. 1. Distribution of the number of patterns per individual for (a) $N = 256$ (b) $N = 512$ (c) $N = 1024$, in $t = 1100$ and (d) $N = 2048$ in $t = 500$. We observe a process of self-organization. The distributions are symmetrical with regard to a value that apparently tends to α_c.
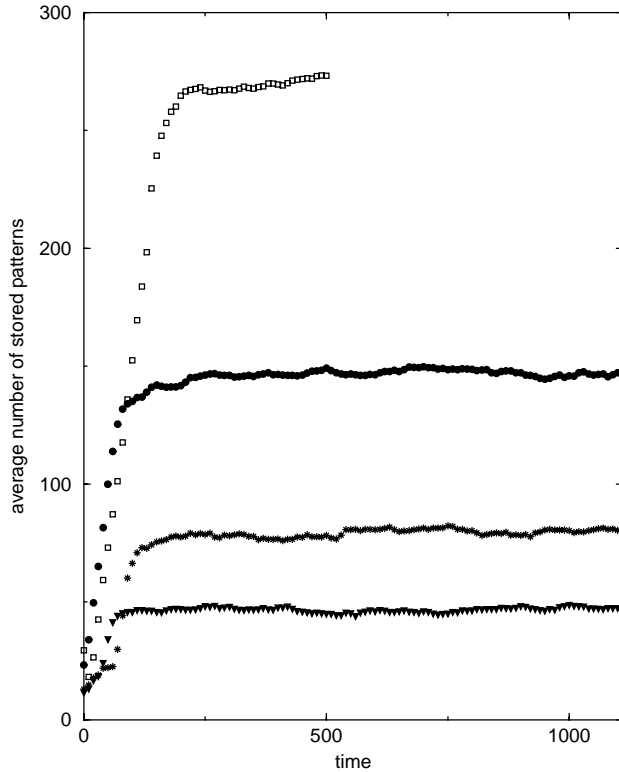
Fig. 2. Time evolution of the average number of stored patterns for each simulated population. (a) $N = 256$ (triangle), $N = 512$ (star), $N = 1024$ (circle) until $t = 1100$ and $N = 2048$ (square) until $t = 500$. We verified that, after many time steps, the average number of patterns fluctuates around an average value. This average value tends to $\alpha_c N$ ($\alpha_c \sim 0.14$), as the network dimension increases.
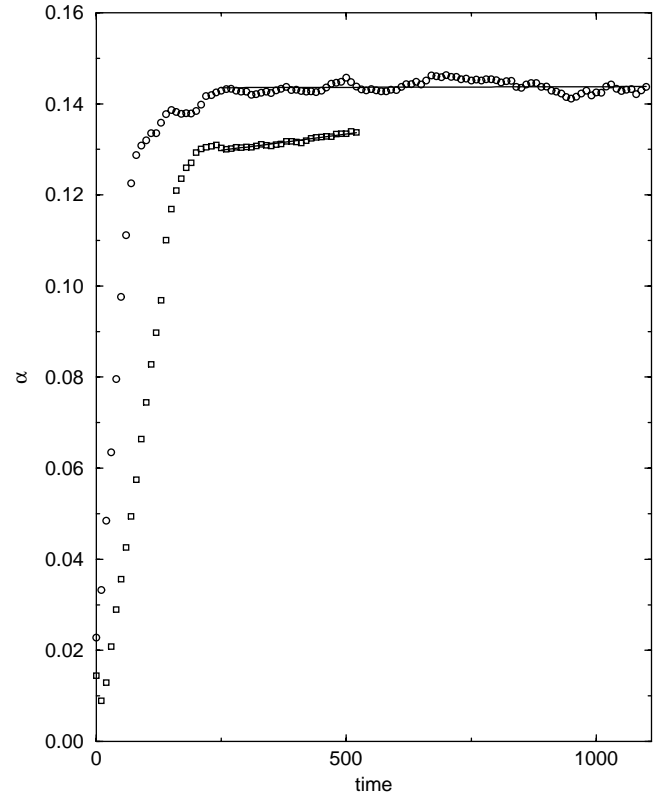

Fig. 3. Time evolution of storage capacity of the network for $N = 1024$ (circle) until $t = 1100$ and $N = 2048$ (square) until $t = 500$. In the second case, the results only were tested until $t = 500$, because the machine time is very large (2.5 months in the Digital Workstation 400).

a "canonical" version of the population, *i.e.*, we kept the number of individuals constant. The rule described above selects from a pair the individual with the best recognition performance, and we call it a *natural selection rule*.

Let us describe now the birth step (asexual reproduction). The individual at birth will inherit all the parent's patterns, except one pattern, randomly chosen, which will be replaced by another pattern, randomly generated at birth. Moreover, there is a probability of 1/3 that one of the following cases happen:

(a) the offspring stays with the same number P_i of patterns as the parent;

(b) the offspring has one pattern less than the parent (we erase another random one);

(c) the offspring has one (randomly generated) pattern more than the parent (we include another one).

We call *mutations* these modifications in the inherited "genotype" of the parent. Our model only allows genetic evolution. No information can be learned during the individual's life. The "genotype" is defined at birth and remains unchanged during the individual's lifetime. In this sense, the present model is completely distinct from reference [13], where "cultural" aspects are treated. A time step ends after the same procedure has been performed on V randomly chosen pairs of individuals.

4 Simulations and results

In our simulations we consider populations of neural networks with dimensions $N = 256$, $N = 512$, $N = 1024$ and $N = 2048$. All individuals of a population are represented by neural networks of the same dimension N. We consider a "mean-field" version of the population, *i.e.*, each individual can exchange information with all others. We simulate evolution between individuals of the same species. Here we do not consider the coevolution case. The results were tested using several initial configurations and different values for L (minimum number of informations contained in the "genotype" of each individual), M (maximum number of informations contained in the "genotype" of each individual) and V. The results that will be presented are those in that V, L and M take the following values:

$$N = 256 \Rightarrow V = 40 \Rightarrow L = 1 \Rightarrow M = 50$$
$$N = 512 \Rightarrow V = 40 \Rightarrow L = 1 \Rightarrow M = 100$$
$$N = 1024 \Rightarrow V = 40 \Rightarrow L = 1 \Rightarrow M = 200$$
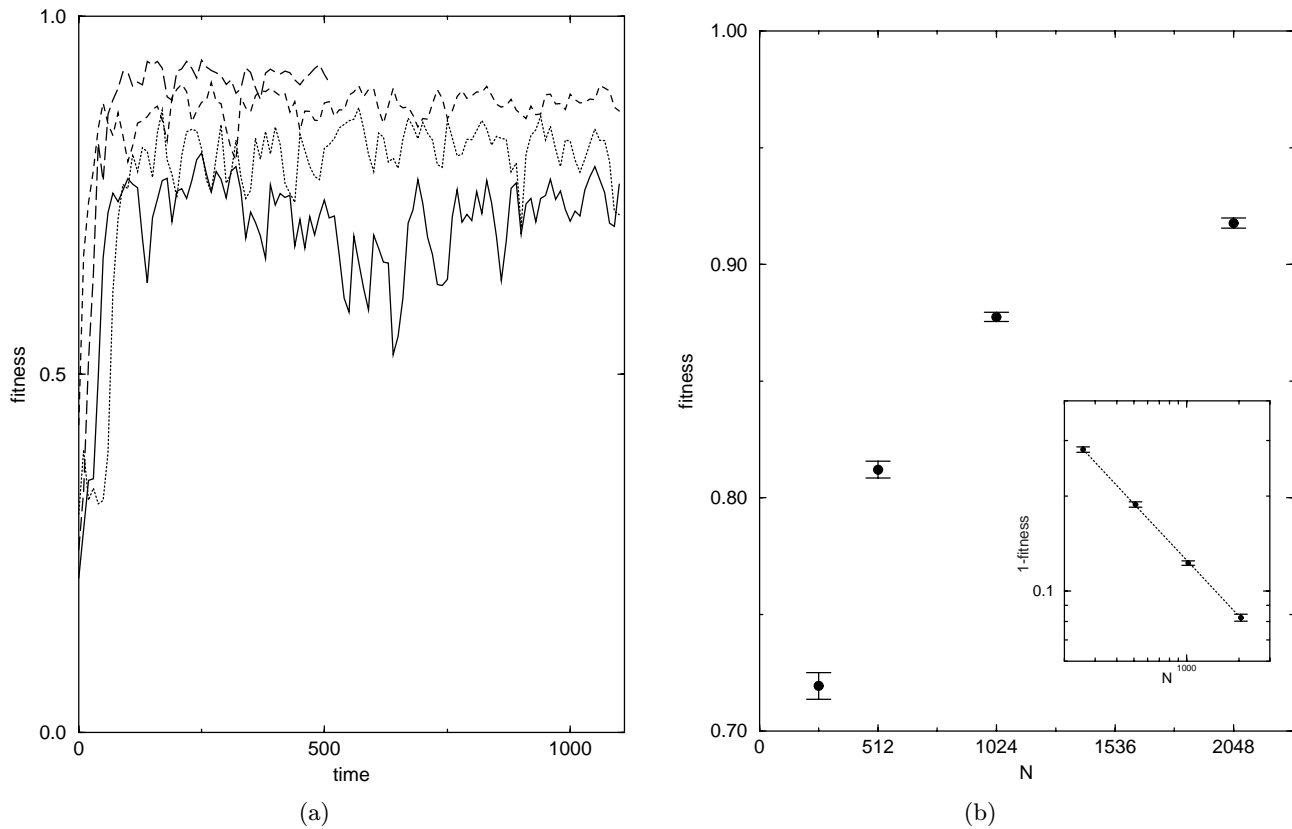$$N = 2048 \Rightarrow V = 40 \Rightarrow L = 1 \Rightarrow M = 400.$$

Fig. 4. Time evolution of the average fitness of simulated populations. (a) $N = 256$ (solid line), $N = 512$ (dotted line), $N = 1024$ (dashed line) until $t = 1100$ and $N = 2048$ (long dashed) until $t = 500$. We verified that, after many time steps, the average fitness fluctuates around an optimum value. (b) These optimum values, estimated by averaging over $t > 250$, increase with the network dimension. The inset shows how the fitness approaches the maximum conceivable value 1, suggesting a power law with exponent ~ 0.6.

In all simulations the parameter T_X was randomly chosen within the interval 0.0 to 0.5N, for each tossed pair of individuals.

In Figure 1 we show the distributions of the number of patterns per individual after some time steps. The average numbers of individuals in each class were calculated over the last $\tau = 10$ time steps. We observe that the distribution, previously uniform, after some time exhibits an organization.

In Figure 2 we show the time evolution of the average number of stored patterns per individual, for each simulated population. These average numbers were calculated at each $\tau = 10$ time steps and are defined as:

$$\langle P(\tau t)\rangle = \frac{1}{\tau} \sum_{t'=\tau t+1}^{\tau(t+1)} \wp(t') \tag{6}$$

where $t \geq 0$ and $\wp(t')$ is the average number of patterns of the population at time step t'. We observe that after some time the average number of patterns fluctuates around an average value (P_m). Considering the definition $\alpha = \frac{P}{N}$, we obtained for each simulated population the following results:

$$\begin{aligned}
N &= 256 \Rightarrow P_m = 47 \Rightarrow \alpha = 0.18 \\
N &= 512 \Rightarrow P_m = 78 \Rightarrow \alpha = 0.15 \\
N &= 1024 \Rightarrow P_m = 146 \Rightarrow \alpha = 0.14 \\
N &= 2048 \Rightarrow P_m = 269 \Rightarrow \alpha = 0.13.
\end{aligned}$$

As the network dimension increases, we verify that the values P_m around which the populations self organize, tend to the transition value. This is so because the average values of α tend to $\alpha_c \sim 0.14$, the critical storage capacity in the Hopfield model. In Figure 3 one can see that a complete saturation was not yet reached for $N = 2048$ and $t = 500$. This explains why the value $\alpha = 0.13$ is still smaller than α_c.

Evolution is a process of fitness optimization. The fitness is not a property of a genotype alone, but depends upon its environment. With the inclusion of population dynamics, the fitness of each individual depend on the population at that moment. Therefore, in this work, the fitness landscape is not given in advance, in contrast with many theoretical models [2]. According to reference [3], the fitness landscape emerges naturally through evolution. In this work the average fitness of a population is
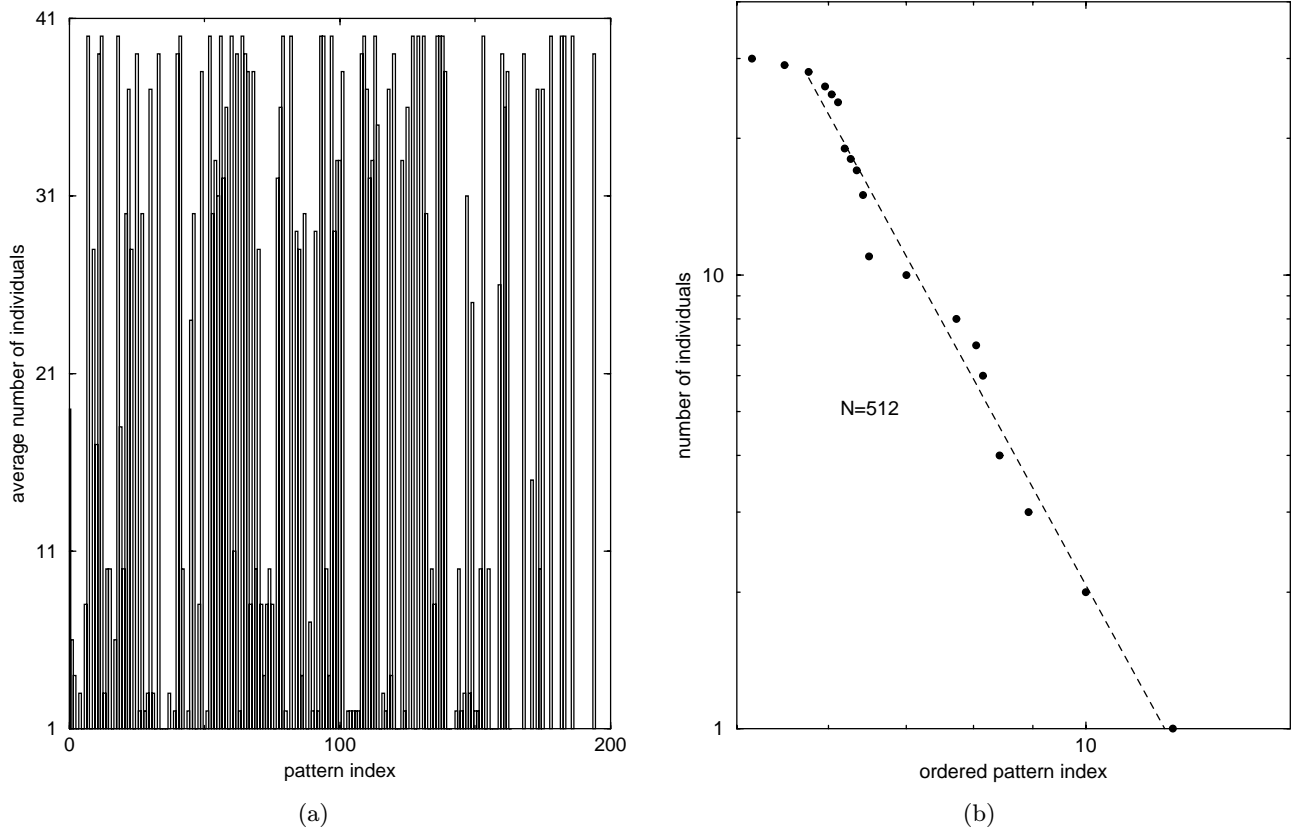
Fig. 5. (a) Number of individuals sharing the same pattern in the final step of the simulation ($t = 1100$) by $N = 512$. (b) The same as in (a), now with a new ordering: the patterns are ranked according to decreasing numbers of individuals sharing the same pattern. In this curve the first points where saturation occurs were not plotted. The distribution suggests a power law.

calculated at each $\tau = 10$ time steps and is defined as

$$\langle \Phi(\tau t) \rangle = \frac{1}{\tau} \sum_{t'=\tau t+1}^{\tau(t+1)} \phi(t') \qquad (7)$$

where $t \geq 0$ and $\phi(t')$ is the average overlap (5) of population at time step t' (taken after all V pairs of individuals were processed).

In Figure 4a we show the time evolution of the average fitness, $\langle \Phi(t) \rangle$, of different populations of neural networks. We verified that after some time steps the average fitness fluctuates around the optimum value. In Figure 4b we show the average of the values $\langle \Phi(t) \rangle$, over $t > 250$, as a function of the network dimension. We verified that these averages increases with the network dimension.

In Figure 5a we show the distributions of the number of individuals sharing the same pattern as a function of these patterns after several time steps. We observe that a population is composed of distinct individuals with a few common patterns. In contrast, at the beginning ($t = 0$), each pattern was present in only one individual. In Figure 5b we show the frequency of individuals with a given pattern *versus* their ranking. The regularity expressed by straight lines in the logarithmic plot of rank *versus* frequency suggest a "Zipf law" [14] with exponent bigger than one.

We also verified that starting from populations of individuals with different genotypes, all individuals of the self-organized populations have the same ancestor, *i.e.*, all are originated from the same "Eve" (this result was tested also for populations with $V > 40$). This is in accordance with the result obtained in references [15,16] for other completely distinct systems, and with the "coalescence theory" [17].

5 Conclusions

Motivated by the work in reference [3], where the proposed model for the evolution considers the competition between individuals which are simple logistic maps, we propose an evolution model where the individuals of the population are themselves complex systems. With a simple evolution model, we find that the populations adapt under the patronage of natural selection at the transition region between ordered (presence of recognition) and disordered (absence of recognition) phases. In this region the average number of stored patterns by the populations fluctuates around $\alpha_c N$ and the average fitness of populations attain optimum values. Therefore the adopted selection rule drives and supports the equilibrium states in the region of transition between order and chaos.

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