

Model of Evolution and Learning of Kauffman's NK networks. Features of the Interaction between Learning and Evolution

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Abstract

A computer model of learning and evolution of autonomous agents, genotypes and phenotypes of which are determined by Kauffman's NK-networks, has been built and investigated. The interaction between learning and evolution for such networks has been investigated. The possibility of observing three effects of interaction between learning and evolution was analyzed. These effects are 1) the effect of genetic assimilation, 2) the hiding effect, 3) the effect of learning load. Simulations have shown that only the hiding effect is observed in the current model. However, the effect of genetic assimilation and the effect of learning load are not observed in the current model. This is due to the absence of an explicit correlation between the genotypes and phenotypes of the agents in the current model. The correlation between genotypes and phenotypes of agents can be of great importance for understanding the mechanisms of interaction between learning and evolution for biological organisms.

Keywords

Kauffman's NK-networks, learning, evolution, autonomous agents, genotypes, phenotypes

1. Introduction

In this work, a computer model of learning and evolution of autonomous agents is constructed. The genotypes and phenotypes of agents are encoded by Stuart Kauffman's NK-networks [1, 2]. A model of interaction between learning and evolution for such networks is constructed and investigated. NK-network consists of N logical elements, each of which has K inputs, $N \gg 1$. The connections between the elements and the logical elements themselves are random. There are no external inputs to the network.

At $K \sim 2$, NK-networks can be considered as a model of molecular-genetic control systems of biological cellular organisms [1, 2].

Previously, the interaction between learning and evolution in populations of autonomous agents was studied in works [3-6]. These works demonstrated the main effects of the interaction between learning and evolution:

1. The genetic assimilation of skills acquired as a result of individual learning over a number of generations of the evolutionary process.
2. The hiding effect, which means that strong learning inhibits the evolutionary search for the optimal genotype.
3. The effect of the learning load, which leads to the acceleration of the evolutionary process of finding the optimum.

In works [5, 6], the quasispecies model was used [7, 8], and simpler cases as compared with NK-networks were considered. In [5], the distance to the single optimum of the fitness function of agents was minimized, while the process of decreasing the Hamming distance to this optimum was considered.

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In [6], the energy of the spin-glass determined by the Sherrington – Kirkpatrick model [9, 10] was minimized. In these cases, the genotype and phenotype of agents were determined by simple chains of binary symbols that are equal to 0 or 1 (for the model with Hamming distance) or bipolar symbols that are equal to +1 or -1 (for the model based on spin-glasses). In the current work, a much more complex representation of the genotypes and phenotypes of agents is used. Now, both the genotype and phenotype of the agent are encoded using NK-networks. Note that in [5, 6], only one significant variable was used in the processes of evolution and learning (the Hamming distance to the optimum or the energy of the spin-glass). In the present model, one essential variable (the number of attractors M of the analyzed NK-networks) is also used.

2. Computer model of evolution and learning that is based on NK-networks

We consider the following model. There is an evolving population of self-learning agents. The number of agents in the population is n . An agent has a genotype and phenotype that have the same structure. Both genotype and phenotype are encoded by NK-networks. The number of logical elements in the network is N . The number of inputs of each element is equal to $K = 2$.

The outputs of each logical element of the network are equal to 0 or 1. During the functioning of the NK-network, the set of the outputs of its elements changes and converges to a certain attractor. We assume that the number of attractors in the NK-network characterizes the fitness of the agent (see below for details).

We believe that the genotypes of agents are optimized through evolution, and the phenotypes are optimized through learning.

The evolution of the population of agents is as follows. There are generations of evolution. In the initial generation, the genotype of each agent is encoded by a random NK-network: both logical elements and connections between elements are random. During a generation, the genotypes of agents are not changed, the phenotypes are changed via learning. In the initial moment of the generation, the genotypes of the agents are transferred from the parent agents of the previous generation to the descendant agents of the current generation. The selection of parent agents is carried out in accordance with agents' fitness. In the initial moment of the generation, the phenotypes of agents are also formed; at this moment of time, the phenotype of each agent is equal to the genotype of this agent.

The phenotypes are changed over a generation via a trial and error method of learning. The phenotype of the agent is modified and this modification is checked every step of the agent's lifetime, during the entire generation. The modification is the trial. The trial is carried out for each logical element. During the trial, the considered logical element of the NK-network of the phenotype is replaced by another random logical element, and the input connections of this logical element are also randomly changed. If after the trial, the number of attractors of the phenotype NK-network is increased, then the new logical element and its new connections in the phenotype NK-network are conserved. If after the trial, the number of attractors of the NK-network of the phenotype is decreased, then the old logical element and its connections are restored. Thus, during learning, the number of attractors of the NK-network of the phenotype gradually increases.

At the end of a generation, the fitness of agents is determined by the number of attractors of NK-networks of final phenotypes. The fitness of the k -th agent is

$$f_k = \exp(\beta M_k) \quad (1)$$

where β is the selection intensity parameter, M_k is the number of attractors of the NK-network of the phenotype of the k -th agent at the end of the generation (after learning), $k = 1, 2, \dots, n$. The selection of agents for the new generation is carried out by the well-known roulette method. The probability to select the k -th agent into the new generation is proportional to its fitness f_k . As a result of this selection, the number of agents of the population in all generations is constant and is equal to n .

The genotypes of agents selected for the new generation mutate. Mutations are carried out in the same way as learning trials. With probability P_M , a logical element of the NK-network of the agent's genotype is selected and this element is replaced with another random logical element, and the input connections of this logical element are also randomly changed. P_M is mutation intensity.

3. Results of computer simulation

The simulation included the following computer experiments. Initially, the simulation was carried out separately for 1) the processes of evolution of the population of agents and 2) the processes of learning of one agent. After that, the interaction between learning and evolution was analyzed.

The following parameters were used in the simulation: the number of logical elements in the NK-network $N = 10$, the number of inputs of each logical element $K = 2$, the population size $n = 10$, the selection intensity parameter $\beta = 1$, the mutation intensity $P_M = 0.1$.

The simulation results showed that evolution without learning and learning of one agent lead to qualitatively similar results: the number of attractors of NK-networks of genotypes (for evolutionary processes) or phenotypes (for learning processes) changes from values M_k that are approximately equal to 1.5 to values M_k that are approximately equal 6-8. The characteristic time of evolutionary optimization was 100 generations, the characteristic time of optimization by learning one agent was 1000 time moments.

After checking evolution and learning separately, we simulated the interaction between learning and evolution. Attempts have been made to demonstrate all three effects observed in [3-6]: 1) the effect of genetic assimilation, 2) the hiding effect, 3) the effect of the learning load. It turned out that only the hiding effect was observed in our simulation. The effects of genetic assimilation and learning load were not observed in our simulation. The obtained simulation results are demonstrated in Figures 1-4.

3.1. Attempt to model genetic assimilation

As in the works [5,6], the fitness function was modified to model genetic assimilation. To the fitness function, defined by expression (1), a large term was added, which suppresses evolutionary selection:

$$f_k = \exp(\beta M_k) + D_L \quad (2)$$

where $D_L = 1000$. As shown in [5,6], without learning, such a term leads to the suppression of evolution, and learning leads to the fact that at the end of a generation the number of attractors of phenotypes increases, and due to this, the role of the first term in expression (1) increases.

The results of the works [5, 6] demonstrate that a) agents with good phenotypes are selected for the next generation, and b) because genotypes are close enough to phenotypes, then good agent genotypes are selected into the next generation. However, the simulation for the current model showed that condition b) poorly fulfilled in our model, and therefore genetic assimilation is not observed. This fact is illustrated in Figures 1 and 2.

Figure 1 shows the dependence of the number of attractors M_k for NK-networks of phenotypes on the learning time T_L during the first generation of evolution. It can be seen that the number of attractors for phenotypes during learning clearly grows, and the first term in (2) makes a significant contribution to the fitness of agents.

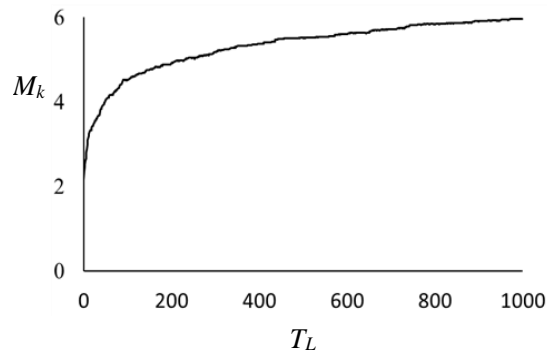


Figure 1: The dependence of the number of attractors M_k for NK-networks of phenotypes during the first generation of evolution on the learning time T_L . The results are averaged over 10 different calculations

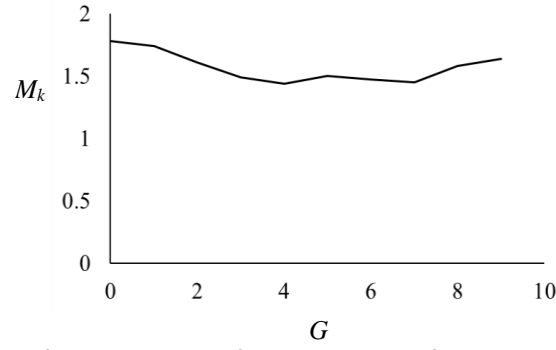


Figure 2: The dependence of the number of attractors M_k for NK-networks of genotypes on the generation number G . The results are averaged over 10 different calculations

Figure 2 shows the dependence of the number of attractors M_k for NK networks of genotypes on the generation number G . It can be seen that the number of attractors for genotypes does not increase, i.e. genetic assimilation is not observed.

Note that the considered approach to modeling genetic assimilation is exactly the same as in [5, 6], only in that works, learning of phenotypes led to a shift in the space of genotypes to an area in which the optimization of genotypes via selection occurs. So, learning shifts the population into an area of effective selection. A similar shift to the area of efficient selection by means of learning was observed in [3]. However, in the current model, the shift to an area of effective selection via learning is not observed. In our opinion, this is due to the weak correlation between genotypes and phenotypes that are encoded by NK-networks.

Let us note that in works [5,6], a strong correlation between genotypes and phenotypes is clearly visible: both genotypes and phenotypes are encoded by simple strings of binary or bipolar symbols. This is significantly different from the coding of genotypes and phenotypes by means of NK-networks.

3.2. Modeling of the hiding effect

The meaning of the hiding effect is the following. If the selection of agents is made in accordance with the final phenotypes obtained as a result of learning, then strong learning can inhibit the evolutionary optimization of genotypes. Strong learning leads to the fact that the final phenotype may be weakly dependent on the genotype, so a good genotype is not very important for optimizing phenotypes. The hiding effect in this model is demonstrated in Figure 3, which shows the dependence of the number of attractors M_k for NK networks of genotypes on the generation number of evolution in the absence (curve 1) and in the presence (curve 2) of learning. The fitness of agents is determined by expression (1). The agents' lifetime is equal to 100 time moments, i.e. the learning is strong enough.

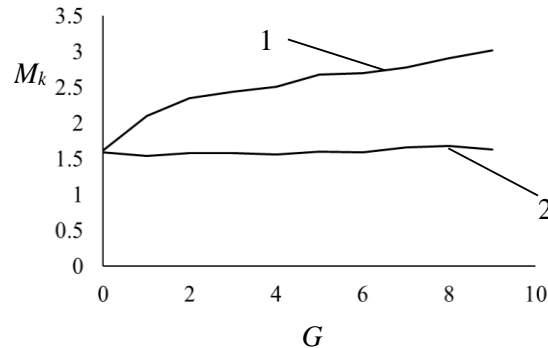


Figure 3: Dependence of the number of attractors M_k for NK-networks of genotypes on the generation number G . The evolution without learning (curve 1) and the evolution combined with learning (curve 2) are considered. The results are averaged over 100 different calculations

It can be seen that in the presence of learning, the genotypes of agents are not optimized: successful phenotypes during learning are formed for different genotypes, i.e. optimization of genotypes is not required for agents. Note that a strong correlation between genotypes and phenotypes is not essential for this effect. The only important thing is that the selection is carried out in accordance with the final phenotypes obtained by learning.

3.3. Attempt to model a learning load

An attempt was also made to simulate the effect of the learning load. For this, it is assumed that the learning of agents does not necessarily occur every time moment for all logical elements of phenotypes, but such learning is carried out with a certain probability P_L every time moment.

The learning load is determined by the total number of trials N_T that occurred for the considered agent during learning. It is assumed that the more the number of trials N_T is, the greater the learning load is. The fitness of the k -th agent is determined by the expression:

$$f_k = \exp(\beta M_k) \exp(-\gamma N_T) \quad (3)$$

where γ is a parameter that takes into account the learning load, N_T is the number of trials that took place for the k -th agent during learning. If $\gamma = 1$, then the learning load is taken into account, if $\gamma = 0$, then this load is not taken into account. The results taking into account the load ($\gamma = 1$) and not taking into account the load ($\gamma = 0$) are shown in Figure 4. The small difference in curves in Figure 4 is due to small errors during simulation (errors were approximately 3%). The probability of learning in both cases was $P_L = 0.1$. Figure 4 shows that the effect of the influence of learning load in the current model is not observed. Figure 4 also shows that the hiding effect is significantly weakened in comparison with Figure 3; this is due to the fact that for the results shown in Figure 4, learning is significantly weakened ($P_L = 0.1$). The possibility of detection of the learning load was also analyzed at an increased probability of learning, at $P_L = 0.5$. However, in this case, the effect of the influence of the learning load was not observed too.

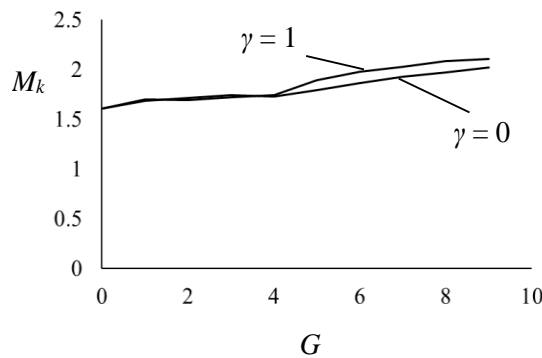


Figure 4: Dependence of the number of attractors M_k for NK-networks of genotypes on the generation number G . The possible effect of the learning load is analyzed. The results are averaged over 100 different calculations

4. Conclusion

Thus, we have analyzed a model of evolution and learning of agents whose genotypes and phenotypes are encoded by Kaufman's NK-networks. The specificity of the interaction effects between learning and evolution for such agents was also analyzed. The possibility of observing three main effects of interaction between learning and evolution was analyzed. These effects are 1) the effect of genetic assimilation, 2) the hiding effect, 3) the effect of learning load.

The performed simulations demonstrated that only the hiding effect is observed in the current model. However, the effect of genetic assimilation and the effect of the learning load for the current model, in which the genotypes and phenotypes of agents are encoded by Kaufman's NK-networks, are not

observed. This sharply distinguishes the results of this work and the results of our previous works [5, 6], in which all three indicated effects were observed. Apparently, this difference is due to the fact that the structure of the genotype and phenotype in [5, 6] was encoded by simple chains of binary (in [5]) or bipolar (in [6]) symbols, and there was a clear correlation between the genotypes and phenotypes of agents. In the present model, there is no such clear correlation between the genotypes and phenotypes of agents; therefore, the effects of genetic assimilation and the effect of the learning load are not observed. This dependence on the correlation between genotypes and phenotypes of agents can be of great importance for understanding the mechanisms of interaction between learning and evolution for biological organisms. Therefore, this question deserves a more detailed further study.

Note that for the hiding effect, the correlation between genotype and phenotype is not significant. It is only important that the selection is carried out according to the final phenotypes obtained as a result of learning. Strong learning leads to the fact that the final phenotype can be weakly dependent on the genotype, so a good genotype is not very important for optimizing phenotypes. As a result, strong learning inhibits the evolutionary optimization of genotypes.

Also, note that genetic assimilation can depend on the ecological niche that organisms fall into. Learning can help to find a certain good niche for organisms. Then, over many generations, evolution can rediscover this successful niche, as a result of this rediscovery, organisms can be adapted to this niche from birth, and this is beneficial for organisms [11]. Of course, this question also deserves further study.

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