Model of Interaction between Learning and Evolution: Mechanisms of Interaction

Vladimir G. Red'ko

Scientific Research Institute for System Analysis, Russian Academy of Sciences, Moscow, 117218, Russia
vgredko@gmail.com

Abstract. The model of interaction between learning and evolution is designed and investigated. The evolving population of modeled organisms is considered. The mechanism of the genetic assimilation of the acquired features during a number of generations of Darwinian evolution is studied. It is shown that the genetic assimilation takes place as follows: phenotypes of modeled organisms move towards the optimum at learning; then the selection takes place; genotypes of selected organisms also move towards the optimum. The hiding effect is also studied; this effect means that strong learning can inhibit the evolutionary search for the optimal genotype. The mechanism of influence of the learning load on the interaction between learning and evolution is analyzed. It is shown that the learning load can lead to a significant acceleration of evolution.

Keywords: Speed and efficiency of evolutionary search, genetic assimilation, hiding effect, learning load.

1   Introduction

A number of authors analyzed interactions between learning and evolution by means of computer simulations [1-4]. In particular, Hinton and Nowlan [3] demonstrated that learning can guide an evolutionary process to find the optimum. Mayley [4] investigated different aspects of the interaction between learning and evolution and demonstrated that the hiding effect can take place, if the learning is sufficiently strong. The essence of the hiding effect is as follows: if the learning is enough strong to change the phenotype of the organism and organisms are selected at the evolution in accordance with the phenotype, then the selection can weakly depend on the genotype. The hiding effect significantly reduces the role of the genotype at the evolutionary selection, and the genetic assimilation becomes less pronounced.

In addition, the influence of the learning load (the cost of learning) on the interaction between learning and evolution was investigated in [4]. The learning load means that the process of learning has an additional load for the organism and its fitness is reduced under the influence of this load.

The current research uses works [3,4] as background. However, that works used rather complex forms of the genetic algorithm (with crossovers), so it was difficult to

analyze quantitatively mechanisms of influence of learning on evolutionary optimization. In contrast to [3,4], the current work uses the quasispecies model proposed by Manfred Eigen [5,6] and our estimations of the evolutionary rate and the efficiency of evolutionary algorithms [7,8]. The quasispecies model considers the evolution that is based on the selection and mutations of organism genotypes (without crossovers) and describes main properties of the evolutionary process. The use of models and methods of works [5-8] allows getting a better understanding of mechanisms of interaction between learning and evolution.

The current work analyzes quantitatively the following main properties of interaction between learning and evolution: 1) the mechanism of the genetic assimilation, 2) the hiding effect, 3) the role of the learning load at investigated processes of learning and evolution.

Additionally, the current paper analyzes the scheme by Hinton and Nowlan [3] by means of the quasispecies model and characterizes mentioned main properties of interaction between learning and evolution for this scheme.

Section 2 describes the main model. Section 3 contains the results of computer simulation for this model. Analysis of interaction between learning and evolution within the framework of the scheme by Hinton and Nowlan [3] by means of the quasispecies model is represented in Section 4.

2   Description of the Model

The evolving population of modeled organisms is considered. Similar to [3], we assume that there is a strong correlation between the genotype and the phenotype of modeled organisms. We assume that the genotype and the phenotype of the organism have the same form, namely, they are chains; symbols of both chains are equal to 0 or 1. The length of these chains is equal to N. For example, we can assume that the genotype encodes a modeled DNA chain, "letters" of which are equal to 0 or 1, and the phenotype determines the neural network of organisms, the synaptic weights of the neural network are equal to 0 or 1 too. The initial synaptic weights (at the birth of the organism) are determined by the genotype (for example, the initial synaptic weights can be equal to the genotype symbols). These weights are adjusted by means of learning during the organism's life.

The evolving population consists of n organisms, genotypes of organisms are $\mathbf{S}_{\mathbf{G}k}$, $k = 1,...,n$. The organism genotype $\mathbf{S}_{\mathbf{G}k}$ is a chain of symbols, S_{Gki}, $i = 1,...,N$. We assume that the length of chains N and the number of organisms in the population n are large: $N, n \gg 1$. The values N and n do not change in the course of evolution. Symbols S_{Gki} are equal to 0 or 1. We assume that N is so large that only a small part of possible 2^N genotypes can be presented in a particular population: $2^N \gg n$. Typical values N and n in our computer simulations are as follows: $N \sim n \sim 100$.

The evolutionary process is a sequence of generations. The new generation is obtained from the old one by means of selection and mutations. Genotypes of organisms of the initial generation are random. Organisms inherit the genotypes from their parents, these genotypes do not change during the organism life and are transmitted (with small mutations) to their descendants. Mutations are random changes of symbols S_{Gki}.

Phenotypes of organisms $\mathbf{S}_{Pk}$ are chains of symbols S_{Pki}, $k = 1,...,n$, $i = 1,...,N$; $S_{Pki} = 0$ or 1. The organism receives the genotype at its birth, the phenotype $\mathbf{S}_{Pk}$ at this time moment is equal to the genotype: $\mathbf{S}_{Pk}(t = 1) = \mathbf{S}_{Gk}$. The lifetime of any organism is equal to T. The time is discrete: $t = 1,...,T$. T is the duration of the generation. The phenotype $\mathbf{S}_{Pk}$ is modified during the organism life by means of learning.

It is assumed that there is the certain optimal chain $\mathbf{S}_M$. Symbols S_{Mi} of this chain are also equal to 0 or 1; the length of the chain $\mathbf{S}_M$ is N. For a particular computer simulation, the chain $\mathbf{S}_M$ is fixed; symbols of this chain are chosen randomly. The optimal chain $\mathbf{S}_M$ is searched for by means of learning and evolution.

Learning is performed by means of the following method of trial and error. Every time moment t each symbol of the phenotype $\mathbf{S}_{Pk}$ of any organism is randomly changed to 0 or 1, and if this new symbol S_{Pki} coincides with the corresponding symbol S_{Mi} of the optimal chain $\mathbf{S}_M$, then this symbol is fixed in the phenotype $\mathbf{S}_{Pk}$, otherwise, the old symbol of the phenotype $\mathbf{S}_{Pk}$ is restored. So, during learning, the phenotype $\mathbf{S}_{Pk}$ moves towards the optimal chain $\mathbf{S}_M$.

At the end of the generation, the selection of organisms in accordance with their fitness takes place. The fitness of k-th organism is determined by the final phenotype $\mathbf{S}_{Pk}$ at the time moment $t = T$. We denote this chain $\mathbf{S}_{Fk}$, i.e. we set $\mathbf{S}_{Fk} = \mathbf{S}_{Pk}(t = T)$. The fitness of k-th organism is determined by the Hamming distance $\rho = \rho(\mathbf{S}_{Fk},\mathbf{S}_M)$ between the chains $\mathbf{S}_{Fk}$ and $\mathbf{S}_M$:

$$f_k = \exp[-\beta\rho(\mathbf{S}_{Fk},\mathbf{S}_M)] + \varepsilon , \qquad (1)$$

where β is the positive parameter, which characterizes the intensity of selection, $0 < \varepsilon \ll 1$. The role of the value ε in (1) can be considered as the influence of random factors of the environment on the fitness of organisms.

The selection of organisms into a new generation is made by means of the well-known method of fitness proportionate selection (or roulette wheel selection). In this method, organisms are selected into a new generation probabilistically. The choice of an organism into the next generation takes place n times, so the number of organisms in the population at all generations is equal to n. At any choice, the probability of the selection of a particular organism into the next generation is proportional to its fitness.

Thus, organisms are selected at the end of a generation in accordance with their final phenotypes $\mathbf{S}_{Fk} = \mathbf{S}_{Pk}(t = T)$, i.e. in accordance with the final result of learning, whereas genotypes $\mathbf{S}_{Gk}$ (modified by small mutations) are transmitted from parents to descendants.

As descendants of organisms obtain genotypes $\mathbf{S}_{Gk}$ that organisms received from their parents and not phenotypes $\mathbf{S}_{Pk}$, the evolutionary process has Darwinian character.

Additionally, similar to [4], we take into account the learning load (the cost of learning), namely, we assume that the learning process has a certain burden on the organism and the fitness of the organism may be reduced under the influence of the load. For this purpose, we consider the modified fitness of organisms:

$$f_{mk} = \exp(-\alpha d) \{\exp[-\beta\rho(\mathbf{S}_{Fk},\mathbf{S}_M)] + \varepsilon\} , \qquad (2)$$

where α is the positive parameter, $d = \rho(\mathbf{S}_{Gk}, \mathbf{S}_{Fk})$ is the Hamming distance between the initial $\mathbf{S}_{Pk}(t = 1) = \mathbf{S}_{Gk}$ and the final phenotype $\mathbf{S}_{Pk}(t = T) = \mathbf{S}_{Fk}$ of the organism, i.e. the value that characterizes the intensity of the whole learning process of the organism during its life.

It should be noted that since genotypes $\mathbf{S}_{Gk}$ of organisms in the initial population are random, the average Hamming distance between these chains and the optimal one $\mathbf{S}_M$ is equal to $N/2$. The chains $\mathbf{S}_k$ should overcome this distance at learning and evolution in order to reach $\mathbf{S}_M$.

3 Results of Computer Simulation

3.1 Parameters of Simulation

The parameters of the model at simulation are chosen in such manner that the evolutionary search is effective; the experience of the work [7] for the case of the evolution without learning is used at this choice. The fitness of the organisms in that work was determined analogously to the expression (1), only the influence of random factors did not taken into account (formally this means that the value ε was equal to 0).

The choice of parameters for the current simulation is as follows. We believe that the length of the chains is sufficiently large: $N = 100$. We also set $\beta = 1$, this corresponds to a sufficiently high intensity of selection, so the selection time (a number of generations) is small, thus the time of the evolutionary search is determined mainly by the intensity of mutations. On the one hand, the intensity of mutations must not be too large, in order to remove the possibility of mutational losses of already found good organisms. On the other hand, the intensity of mutations must not be too small, in order to ensure the sufficiently intensive mutational search during the evolutionary optimization. Taking this into account, we believe that the probability to change any symbol in any chain $\mathbf{S}_{Gk}$ at one generation at mutations is $p_m = N^{-1} = 0.01$. At this mutation intensity p_m approximately one symbol in the genotype of any organism is changed at one generation, i.e. during one generation, the Hamming distance ρ between genotypes $\mathbf{S}_{Gk}$ of organisms and the optimal chain $\mathbf{S}_M$ changes on average by 1 by means of mutations. The selection leads to a decrease of the distance ρ. Since the intensity of the selection is large, and the Hamming distance between genotypes $\mathbf{S}_{Gk}$ in the initial population and the optimal chain $\mathbf{S}_M$ is of the order of N, the whole process of the evolutionary optimization takes approximately $G_T \sim N$ generations. This estimation of the evolutionary rate is true, if the population size is sufficiently large and the fluctuation effects and the neutral selection of organisms (that is the selection independent on the fitness of organisms) can be neglected. To satisfy this condition, it is enough to require that the characteristic time (a number of generations) of the neutral selection, which is of the order of the population size n [9], should be greater or of the order of G_T, so we believe that $n = G_T = N$.

Thus, the parameters of simulation are: $N = 100$, $\beta = 1$, $p_m = N^{-1}$, $n = N$.

We also believe that $T = 2$, $\varepsilon = 10^{-6}$.

3.2 Comparison of Regimes of Pure Evolution and Evolution Combined with Learning

Fig. 1 shows the dependence of the average Hamming distance $\rho = \rho(\mathbf{S}_{Gk}, \mathbf{S}_M)$ between genotypes $\mathbf{S}_{Gk}$ of organisms in the population and the optimal chain $\mathbf{S}_M$ on the generation number G. The curve 1 characterizes the regime of evolution combined with learning; the curve 2 characterizes the regime of "pure evolution", that is the evolution without learning (in this case, the learning does not occur and $\mathbf{S}_{Pk} = \mathbf{S}_{Gk}$). The fitness of organisms is determined by the expression (1). We can see that the pure evolution without learning (the curve 2) does not optimize organisms $\mathbf{S}_k$ at all; whereas evolution combined with learning (the curve 1) obviously ensures the movement towards the optimal chain $\mathbf{S}_M$.

To understand, why the pure evolution does not ensure a decrease of the value ρ, let us estimate the value of the fitness (1) in the initial population. The Hamming distance $\rho = \rho(\mathbf{S}_{Gk}, \mathbf{S}_M)$ for initial genotypes is of the order of $N/2 = 50$, therefore, $\exp(-\rho) \sim 10^{-22}$ and $\exp(-\rho) \ll \varepsilon$. This means that all organisms of the population have approximately the same value of the fitness $f_k \approx \varepsilon$. Consequently, the evolutionary optimization of genotypes does not occur in the case of the pure evolution. Thus, the movement towards $\mathbf{S}_M$ occurs only in the presence of learning; this movement leads to the decrease of the value ρ. A similar influence of learning on the evolutionary optimization (though in another context) was described in [3].

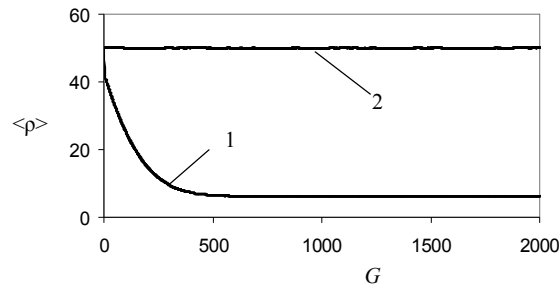**Fig. 1.** The dependence of the average Hamming distance $\langle\rho\rangle = \langle\rho(\mathbf{S}_{Gk}, \mathbf{S}_M)\rangle$ between genotypes $\mathbf{S}_{Gk}$ and the optimal chain $\mathbf{S}_M$ on the generation number G. The curve 1 characterizes the regime of evolution combined with learning; the curve 2 characterizes the regime of pure evolution. Results are averaged over 1000 calculations.

Let us consider the effect of the acceleration of the evolutionary process by learning (the curve 1 in Fig. 1). Analysis of results of simulations shows that the gradual decrease of the values $\rho = \rho(\mathbf{S}_{Gk}, \mathbf{S}_M)$ occurs as follows. First, the learning shifts the distribution of organisms $n(\rho)$ on the value ρ towards smaller ρ, so the values $\rho = \rho(\mathbf{S}_{Fk}, \mathbf{S}_M)$ become small enough, such that $\exp[-\rho(\mathbf{S}_{Fk}, \mathbf{S}_M)]$ is of the order of ε. Consequently, the fitnesses of organisms in the population in accordance with (1) become essentially different; so organisms with small values $\rho(\mathbf{S}_{Fk}, \mathbf{S}_M)$ are selected into the population of the next generation. It is intuitively clear that genotypes of $\mathbf{S}_{Gk}$ of selected organisms should be rather close to final phenotypes $\mathbf{S}_{Fk}$ (obtained as a result of the

learning) of these organisms. Thus, the result of the selection is choosing of organisms, which genotypes are also moving to the optimal chain $\mathbf{S_M}$. Therefore, values ρ in the new population decrease.

The described mechanism of the genetic assimilation is characterized by Fig. 2, which shows the distributions of the number of organisms $n(\rho)$ for given ρ in the population for different moments of the first generation. The curve 1 shows the distribution $n(\rho)$ for $\rho = \rho(\mathbf{S}_{Gk},\mathbf{S_M})$ for the initial genotypes of organisms at the beginning of the generation. The curve 2 shows the distribution $\rho = \rho(\mathbf{S}_{Fk},\mathbf{S_M})$ for organisms after the learning, but before the selection. The curve 3 shows the distribution $\rho = \rho(\mathbf{S}_{Fk},\mathbf{S_M})$ for organisms, selected in accordance with the fitness (1). The curve 4 shows the distribution $\rho = \rho(\mathbf{S}_{Gk},\mathbf{S_M})$ for the genotypes of selected organisms at the end of the generation. The genotypes of selected organisms $\mathbf{S}_{Gk}$ are sufficiently close to the final phenotypes of learned and selected organisms $\mathbf{S}_{Fk}$, therefore the distribution $\rho = \rho(\mathbf{S}_{Gk},\mathbf{S_M})$ for genotypes (the curve 4) moves towards the distribution for final phenotypes $\mathbf{S}_{Fk}$ (the curve 3). Similar displacement of the distribution $n(\rho)$ towards smaller values ρ takes place in the next generations. Errors of values $n(\rho)$ at the plots are smaller than 0.3.
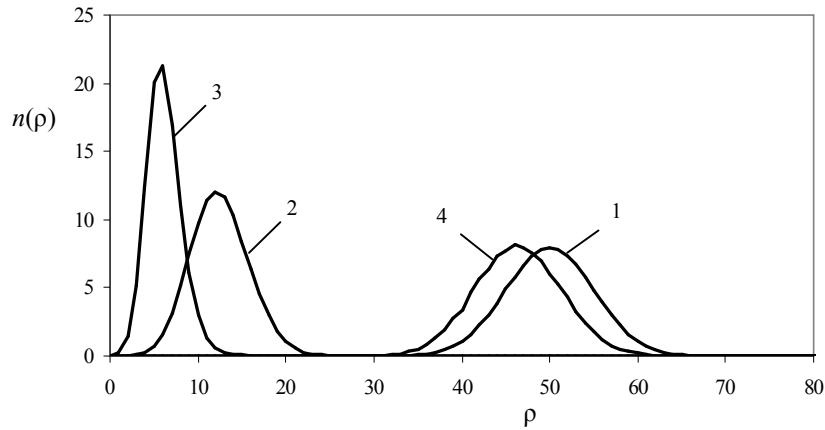

Fig. 2. The distributions $n(\rho)$ in the first generation of evolution for different moments of the generation. The curve 1 is the distribution $n(\rho)$ for $\rho = \rho(\mathbf{S}_{Gk},\mathbf{S_M})$ for the original genotypes before learning. The curve 2 is the distribution $n(\rho)$ for $\rho = \rho(\mathbf{S}_{Fk},\mathbf{S_M})$ for organisms after the learning, but before the selection. The curve 3 is the distribution $n(\rho)$ for $\rho = \rho(\mathbf{S}_{Fk},\mathbf{S_M})$ for selected organisms. The curve 4 is the distribution $n(\rho)$ for $\rho = \rho(\mathbf{S}_{Gk},\mathbf{S_M})$ for the genotypes of selected organisms at the end of the generation. Results are averaged over 10000 calculations.

Such displacement reveals the mechanism of the genetic assimilation: the selection leads to the genotypes of organisms $\mathbf{S}_{Gk}$, which are closer to the phenotypes of learned and selected organisms $\mathbf{S}_{Fk}$, than the initial genotypes of organisms at the beginning of the generation. Consequently, the transition from the curve 1 to the curve 4, i.e. the decrease of the values ρ, takes place during the generation.

It should be underlined that the decrease of values ρ at learning should be sufficiently large in order to ensure the small role of the parameter ε and the significant difference of the fitnesses (1) of organisms after the learning, and therefore, the effective selection of organisms with small values $\rho(\mathbf{S}_{Fk},\mathbf{S_M})$. This selection corresponds to the essential decrease of values ρ at the transition from the curve 2 to the curve 3 in Fig. 2. In order to guarantee the effective operation this mechanism, the learning should be enough strong. The other role of strong learning is characterized in the next subsection.

It should be noted that the displacement of the distribution $n(\rho)$ at learning in the first generation can be estimated as follows. Before learning, the value $\rho(\mathbf{S}_{Pk},\mathbf{S_M})$ (the number of symbols of phenotype $\mathbf{S}_{Pk}$ that do not coincide with corresponding symbols of the optimal chain $\mathbf{S_M}$) is approximately equal to $N/2 = 50$. After the first step of learning approximately a half of non-coinciding symbols are changed, so the value $\rho(\mathbf{S}_{Pk},\mathbf{S_M})$ becomes to be approximately equal to $N/4 = 25$. After the second step of learning (at the end of the generation) the next half of non-coinciding symbols are changed, so the value $\rho(\mathbf{S}_{Pk},\mathbf{S_M})$ diminishes to $N/8 = 12.5$. This is in agreement with the curve 2 in Fig. 2.

The described results show that learning can lead to the effective genetic assimilation and to the radical acceleration of the evolutionary search.

3.3 Hiding Effect

Thus, the strong learning can accelerate the evolutionary search. However, the strong learning can also prevent a finding of the optimal genotype. The curve 1 in Fig. 1 shows that at large G the decrease of values $\langle\rho\rangle = \langle\rho(\mathbf{S}_{Gk},\mathbf{S_M})\rangle$ is limited: the asymptotic value $\langle\rho\rangle$ is approximately equal to 6.2. This is due to the fact that at large G ($G \sim 1000$) the strong learning results in finding the optimal phenotype $\mathbf{S}_{Popt} = \mathbf{S_M}$ independently on the genotype $\mathbf{S}_{Gk}$. Therefore, at final stages of the evolutionary process, the genotypes $\mathbf{S}_{Gk}$ do not move towards the optimum $\mathbf{S_M}$. So, the hiding effect [4] is observed.

Fig. 3 characterizes the mechanism of the hiding effect. This figure represents the distributions $n(\rho)$ at the end of the evolutionary process (at $G = 2000$) for different moments of the generation. The results are for the described case of simulation for the regime of evolution combined with learning. Fig. 3 shows that the distribution $n(\rho)$ after the learning includes organisms, for which $\rho(\mathbf{S}_{Fk},\mathbf{S_M}) = 0$, i.e. the optimal phenotype $\mathbf{S}_{Popt} = \mathbf{S_M}$ is found by means of the learning. Though the selection in accordance with values $\rho(\mathbf{S}_{Fk},\mathbf{S_M})$ occurs, the distance between the initial genotype distribution (the curve 1) and the final genotype distribution (the curve 4) is sufficiently small. Therefore, further reduction of $\rho = \rho(\mathbf{S}_{Gk},\mathbf{S_M})$ at the end of the evolutionary process does not occur. The hiding effect is confirmed by the fact that at the end of the evolution the curves (that are shown in Fig. 3) do not shift for successive generations. This effect is also consistent with the fact that the value $\langle\rho\rangle = \langle\rho(\mathbf{S}_{Gk},\mathbf{S_M})\rangle$ becomes constant at large G (see the curve 1 in Fig. 1). The distributions $n(\rho)$ for genotypes at the beginning of the generation and after the selection (curves 1 and 4 in Fig. 3) differ slightly, this is due to mutations that lead to a small increase of ρ in the beginning of a

generation as compared with the distribution after selection. Thus, at the end of the evolutionary process, the strong learning results in finding of the optimal phenotype; hence a further optimization of genotypes does not occur.
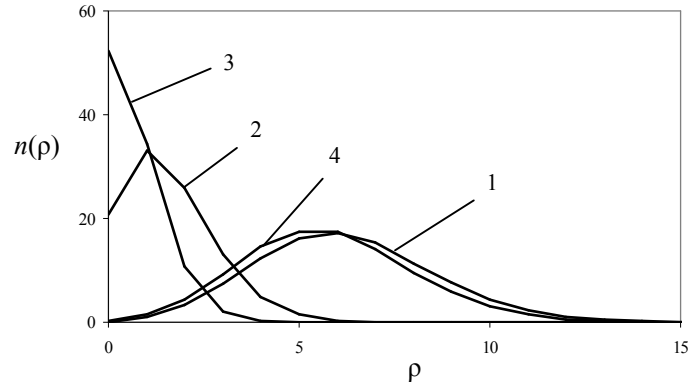

Fig. 3. The distributions $n(\rho)$ at the end of the evolutionary process (at $G = 2000$) for different moments of the generation. The curve 1 is the distribution of $\rho = \rho(\mathbf{S}_{Gk}, \mathbf{S_M})$ for the initial genotypes before learning. The curve 2 is the distribution of $\rho = \rho(\mathbf{S}_{Fk}, \mathbf{S_M})$ for organisms after the learning, but before the selection. The curve 3 is the distribution of $\rho = \rho(\mathbf{S}_{Fk}, \mathbf{S_M})$ for selected organisms. The curve 4 is the distribution of $\rho = \rho(\mathbf{S}_{Gk}, \mathbf{S_M})$ for the genotypes of selected organisms at the end of the generation. Results are averaged over 1000 calculations.

Thus, the mechanism of the hiding effect is analyzed. This effect means that the strong leaning prevents a finding of the optimal genotype, as such learning increases the chances of finding a good phenotype independently on the genotype of the organism. In our case, the hiding effect is observed at the end of the evolutionary process.

3.4 Influence of Learning Load on Modeled Processes

We also analyzed the influence of the learning load on modeled processes. For this case, the fitness of organisms is determined by the expression (2). The simulation is performed for the mentioned parameters ($N = n = 100$, $\beta = 1$, $p_m = 0.01$, $T = 2$, $\varepsilon = 10^{-6}$), the value α is equal to 1. The simulation results are represented in Figs. 4,5. Fig. 4 shows the dependence of the average Hamming distance $\langle\rho\rangle = \langle\rho(\mathbf{S}_{Gk}, \mathbf{S_M})\rangle$ between genotypes $\mathbf{S}_{Gk}$ and the optimal chain $\mathbf{S_M}$ on the generation number G. Fig. 5 shows the distributions $n(\rho)$ of values ρ for different moments of the first generation of the evolution.

The comparison of Figs. 1,2 and Figs. 4,5 shows that the learning load leads to the considerable acceleration of the evolutionary search for the optimal chain $\mathbf{S_M}$. This acceleration is due to the fact that the learning load results in the more strong selection of organisms that have small distance $\rho(\mathbf{S}_{Gk}, \mathbf{S}_{Fk})$ between the initial $\mathbf{S}_{Pk}(t = 1) = \mathbf{S}_{Gk}$ and the final $\mathbf{S}_{Pk}(t = T) = \mathbf{S}_{Fk}$ phenotypes, than for the case of the fitness (1).
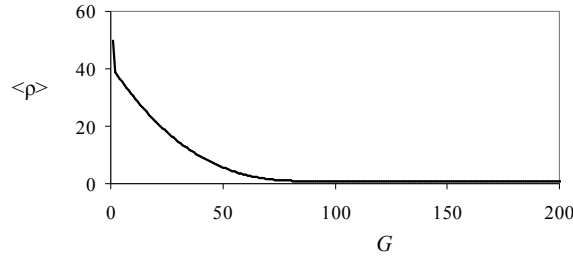
Fig. 4. The dependence of $\langle\rho\rangle = \langle\rho(\mathbf{S}_{Gk},\mathbf{S_M})\rangle$ on generation number G; the influence of the learning load is considered; the fitness of organisms is determined by the expression (2); the decrease of values $\langle\rho\rangle$ is much faster than in Fig. 1 (results are averaged over 1000 calculations).
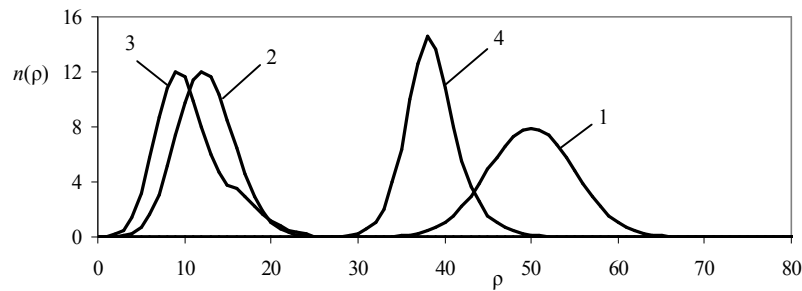

Fig. 5. The distributions $n(\rho)$ for different moments of the first generation of evolution; the learning load is taken into account; the fitness of organisms is determined by the expression (2). The curve 1 is the distribution of $\rho = \rho(\mathbf{S}_{Gk},\mathbf{S_M})$ for the original genotypes before learning. The curve 2 is the distribution of $\rho = \rho(\mathbf{S}_{Fk},\mathbf{S_M})$ for organisms after the learning, but before the selection. The curve 3 is the distribution of $\rho = \rho(\mathbf{S}_{Fk},\mathbf{S_M})$ for selected organisms. The curve 4 is the distribution of $\rho = \rho(\mathbf{S}_{Gk},\mathbf{S_M})$ for the genotypes of selected organisms at the end of the generation. The displacement of the distribution 4 to smaller values ρ is significantly larger than in Fig. 2. Results are averaged over 10000 calculations.

Fig. 6 represents the distributions $n(\rho)$ at the end of the evolutionary process (at $G = 200$) for different moments of the generation. This figure shows that the optimal genotype $\mathbf{S}_{Gopt} = \mathbf{S_M}$ in the considered case is found. The hiding effect is absent in this case.

It should be underlined that the genetic assimilation for cases of the fitness, which is determined by the expression (1) and the expression (2), has the same nature. In both cases, genotypes of selected organisms $\mathbf{S}_{Gk}$ approach to final phenotypes $\mathbf{S}_{Fk}$ of learned and selected organisms. That is in both Fig. 2 and Fig. 5 the curve 4 moves towards the curve 3. A significant difference consists only in the fact that the learning load makes this movement more evident and more effective. Thus, the learning load leads to more effective optimization of genotypes of $\mathbf{S}_{Gk}$; and consequently, the evolu-

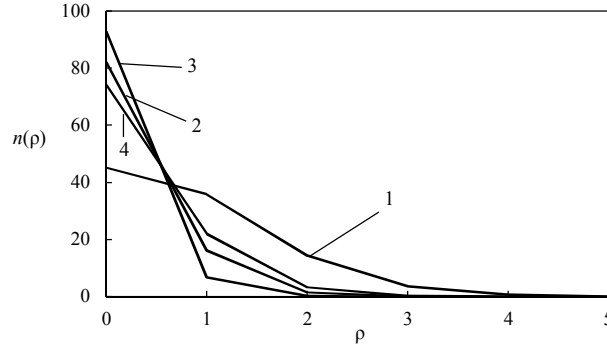tion process is significantly accelerated. The learning load makes the genetic assimilation more profound.

Fig. 6. The distributions $n(\rho)$ at the end of evolution (at $G = 200$) for different moments of the generation; the learning load is taken into account; the fitness of organisms is determined by the expression (2). The curve 1 is the distribution of $\rho = \rho(\mathbf{S}_{Gk}, \mathbf{S_M})$ for the initial genotypes before learning. The curve 2 is the distribution of $\rho = \rho(\mathbf{S}_{Fk}, \mathbf{S_M})$ for organisms after the learning, but before the selection. The curve 3 is the distribution of $\rho = \rho(\mathbf{S}_{Fk}, \mathbf{S_M})$ for selected organisms. The curve 4 is the distribution of $\rho = \rho(\mathbf{S}_{Gk}, \mathbf{S_M})$ for the genotypes of selected organisms at the end of the generation. Results are averaged over 1000 calculations.

Thus, the computer simulation shows that the genetic assimilation, the hiding effect, and the significant acceleration of the genetic assimilation and the evolutionary process under the influence of the learning load are observed in the current model.

4 Comparison with the Approach by Hinton and Nowlan

This section uses the approach by Hinton and Nowlan [3] as well as the quasispecies model [5,6]. We consider the additional model that is very similar to the main model described above. The additional model is based on the approach of the work [3]. Almost all assumptions of the additional model are the same as in the main model. In the additional model, we suppose that organisms of the evolving population have genotypes $\mathbf{S}_{Gk}$ and phenotypes $\mathbf{S}_{Pk}$, $k = 1,...,n$. $\mathbf{S}_{Gk}$ and $\mathbf{S}_{Pk}$ are chains of symbols, S_{Gki}, S_{Pki}, $i = 1,...,N$, N, $n \gg 1$. Symbols S_{Gki}, S_{Pki} are equal to 0 or 1. $\mathbf{S}_{Pk}(t = 1) = \mathbf{S}_{Gk}$, $t = 1,...,T$. T is the duration of the generation. There is the certain optimal chain $\mathbf{S_M}$ (components of which S_{Mi} are equal to 0 or 1, $i = 1,...,N$), which is searched for in the process of evolution and learning. Learning is performed by means of the method of trial and error (as described above). At the end of the generation, the selection of organisms in accordance with their fitness takes place; the method of fitness proportionate selection is used.

Only the fitness of organisms in the additional model is defined in another way, as follows.

If learning takes place, the fitness of k-th organism is determined by the final phenotype $\mathbf{S}_{Pk}$ at $t = T$:

$$f_k = \exp[-\beta\rho(\mathbf{S}_{Fk},\mathbf{S}_M)] , \qquad (3)$$

where $\mathbf{S}_{Fk} = \mathbf{S}_{Pk}(t = T)$, $\rho = \rho(\mathbf{S}_{Fk},\mathbf{S}_M)$ is the Hamming distance between $\mathbf{S}_{Fk}$ and $\mathbf{S}_M$.

If there is no learning, then the fitness is:

$$f_k = 1 \text{ at } \mathbf{S}_{Gk} = \mathbf{S}_M ; \quad f_k = 0 \text{ at } \mathbf{S}_{Gk} \neq \mathbf{S}_M . \qquad (4)$$

Additionally, the influence of the leaning load is taken into account. In this case, the fitness is modified:

$$f_{mk} = \exp(-\alpha d) \exp[-\beta\rho(\mathbf{S}_{Fk},\mathbf{S}_M)] , \qquad (5)$$

where $d = \rho(\mathbf{S}_{Gk},\mathbf{S}_{Fk})$.

The additional model has been analyzed by means of computer simulation. All simulations have been made for the case, when the learning takes place; that is the fitness is determined by expressions (3), (5). The results for the additional model are almost the same as the described results for the main model. The genetic assimilation, the hiding effect, and the influence of the leaning load are observed in the case of the additional model.

The coincidence of the essential results for the main and additional models shows that the role of the parameter ε (see expressions (1) and (2)) in the main model is rather small. This parameter is essentially significant only for clear comparison of regimes of pure evolution and evolution combined with learning (see Fig. 1).

Thus, the comparison demonstrates that in the framework of the approach of the work [3], we can design the model, which reveals actually the same properties of interaction between learning and evolution as the main model.

The analysis of both models shows that a) the genetic assimilation, b) the hiding effect, and c) the significant acceleration of the genetic assimilation and the evolutionary process under the influence of the leaning load are observed in these models under the following assumptions:

1) Each organism of the evolving population has a genotype and a phenotype.

2) The genotype and the phenotype are chains of symbols; the both chains have the same form.

3) Genotypes of organisms are transmitted from parents to descendants with small mutations. The genotype of the organism is not changed during its life.

4) The initial phenotype of the organism at its birth is equal to the organism genotype.

5) There is a certain optimal chain, which is searched for by means of learning and evolution. The optimal chain has the same form as the genotype and the phenotype.

6) The phenotype is essentially adjusted by means of learning during the organism lifetime. During learning, the phenotype moves towards the optimal chain.

7) The selection of organisms into a new generation occurs in accordance with final phenotypes of organisms.

5   Conclusion

Thus, the model of interaction between learning and evolution has been constructed and investigated.

The mechanism of the genetic assimilation is studied. It is shown that the genetic assimilation takes place as follows. The phenotypes of modeled organisms move towards the optimum at learning; then the selection in accordance with final phenotypes takes place; the genotypes of selected organisms also move towards the optimum.

The mechanism of the hiding effect is analyzed. This effect means that strong learning inhibits the evolutionary search for the optimal genotype, if this learning increases the chances of finding a good phenotype regardless of the genotype.

The influence of the learning load on the interaction between learning and evolution is studied. It is shown that the learning load leads to the effective genetic assimilation and to a considerable acceleration of evolution.

It should be underlined that our analysis essentially uses the quasispecies model [5,6]. Basing on this model, it is sufficient to consider only single significant variable, the distance to the optimum ρ. This ensures the clear understanding of mechanisms of interaction between learning and evolution.

References

[1] Belew, R.K., Mitchell, M. (eds.): Adaptive Organisms in Evolving Populations: Models and Algorithms. Addison-Wesley, Massachusetts (1996)

[2] Turney, P., Whitley, D., Anderson, R. (eds.): Evolution, Learning, and Instinct: 100 Years of the Baldwin Effect. Special Issue of Evolutionary Computation on the Baldwin Effect (Vol. 4. No. 3). (1996)

[3] Hinton, G.E., Nowlan, S.J.: How Learning Can Guide Evolution. Complex Systems, 1, 495-502 (1987)

[4] Mayley, G.: Guiding or Hiding: Explorations into the Effects of Learning on the Rate of Evolution. In: P. Husbands and I. Harvey (eds.) Proceedings of the Fourth European Conference on Artificial Life, pp. 135-144. The MIT Press, Cambridge, Massachusetts (1997)

[5] Eigen, M.: Selforganization of Matter and the Evolution of Biological Macromolecules. Naturwissenschaften, 58, 465–523 (1971)

[6] Eigen, M., Schuster, P.: The Hypercycle: A Principle of Natural Self-Organization. Springer Verlag, Berlin et al. (1979)

[7] Red'ko, V.G., Tsoy, Yu.R.: Estimation of the Efficiency of Evolution Algorithms, Doklady Mathematics, 72, 810-813 (2005)

[8] Red'ko V.G., Tsoy Yu.R.: Estimation of the Evolution Speed for the Quasispecies Model: Arbitrary Alphabet Case. In: L. Rutkowski, R. Tadeusiewicz, L. Zadeh, and J. Zurada (eds.) Artificial Intelligence and Soft Computing, 8th International Conference, Proceedings, pp. 460-469, Springer, Berlin et al. (2006)

[9] Kimura, M.: The Neutral Theory of Molecular Evolution. Cambridge University Press (1983)