

# [Re] How learning can guide evolution

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## A reference implementation of

→ *How learning can guide evolution*, G. E. Hinton, and S. J. Nowlan, Complex Systems, 1 (3), 495-502, 1987.

## Introduction

Lamarckian hypothesis that experiences accumulated during the lifetime of an individual organism are directly transmitted to the next generation is considered to be incorrect. The reference paper [4] argues that this does not necessarily mean that individual learning cannot exert influence on evolution in an indirect fashion, providing a simple but convincing computational example of such interaction. The authors use an extreme scenario where optimization landscape is completely flat except for a single peak. In such environment curvature of the optimization surface does not provide any guidance and evolutionary search alone cannot find the maximum. Through a simulation the authors show that such hostile environment can be tackled by a combination of evolutionary and individual learning. If organisms can search during their lifetime in addition, those organisms whose genomes are closer to the targeted peak are going to be able to find the peak with individual search. These organisms will have higher fitness and transmit their genes to the next generation. In effect, capacity for individual learning “creates a hill” to the peak that the evolution can climb, as illustrated in Figure 1 in Hinton and Nowlan [4]<sup>1</sup>. This is one of the clearest illustrations of benefits of individual learning for evolution and interaction between the two learning processes.<sup>2</sup> This result has made a substantial impact in cognitive science literature.

The main aim of this article is to replicate the simulations reported in the reference paper [4]. I have inquired with one of the authors and the original implementation of the simulations is not available any more. I am also not aware of other implementations elsewhere. Simulations are relatively simple and I propose a replication based on description from the reference paper. Replication code relies on R programming language [5] and several R packages [6, 8, 7, 1, 2, 3].

## Methods

Description of simulations can be found in the caption of Figure 1 in the reference paper [4]. I consider the description to be detailed enough for an implementation. I have followed it closely, with two exceptions. First, I have repeated evolution many times to average out potential noise in the process. In the reference article such iterations are

<sup>1</sup>Note that captions of the figures are switched, caption of Figure 1 is incorrectly placed under Figure 2, and vice versa

<sup>2</sup>An indirect influence of individual learning on evolutionary learning is often called Baldwin effect.

not explicitly mentioned, and moreover, when interpreting their results from Figure 2, the authors state that Figure 2 presents results of “... a typical evolutionary search ...”, suggesting it is a single run of the simulation. Second, I let the population of agents evolve for 1000 generations instead of 50 generations reported in Hinton and Nowlan [4]. Reason for this will become clear in the Results section.

I describe my implementation in detail in Algorithm 1. Parameters for the simulation are summarized in Table 1.

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**Algorithm 1** Simulation description
 

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1: for  $sim = 1 : noSim$  do
2:   Generate targeted genome,  $g^* = \{a_i\}_{i=1}^{noAlleles}$ :  $a_i \sim Bernoulli(p)$ ,
3:    $p \sim Uniform(0, 1)$ 
4:   Generate initial genomes of the agents,  $G = \{g_i\}_{i=1}^{noAgents}$ :  $\forall g_i$  generate
5:    $\{a_i\}_{i=1}^{noAlleles}$  by sampling with replacement from  $\{0, 1, ?\}$  according to  $p_0, p_1, p_?$ .
6:   for  $gen = 1 : noGenerations$  do
7:     for  $ag = 1 : noAgents$  do ▷ Individual learning
8:       for  $step = 1 : lifetime$  do
9:         For all ? alleles in agent's genome:  $a_i \sim Bernoulli(0.5)$ 
10:        if  $g_i == g^*$  after individual learning then
11:          break
12:        end if
13:      end for
14:      Evaluate fitness:  $f_{ag} = 1 - 19(lifetime - step)/1000$ 
15:      Record frequency of Correct, Incorrect and Undecided alleles.
16:    end for
17:    Compute parenting probabilities:
18:     $p_{ag} = f_{ag} / \sum_{i=1}^{noAgents} f_i$ ,  $\forall ag$ 
19:    for  $i = 1 : |G|$  do ▷ Generate children genomes
20:      Choose two parents by sampling with replacement according to  $p_{ag}$ 
21:      Generate new genome,  $g_i^{child}$ : randomly choose a cross-over point,
22:      copy all alleles from the first parent up to the cross-over point,
23:      and from the second parent beyond the cross-over point.
24:    end for
25:    Update genomes:  $g_i \leftarrow g_i^{child}$ ,  $\forall i \in G$ 
26:  end for
27: end for

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**Table 1:** Simulation parameters.

Table	Value	Description
noSim	100	Number of times evolution is simulated
noGenerations	1000	Number of generations for evolutionary algorithm
noAgents	1000	Number of agents in a population
lifetime	1000	Number of cycles available for individual learning
noAlleles	20	Number of alleles in agent's genome
$p_0$	0.25	Probability that allele is of type zero
$p_1$	0.25	Probability that allele is of type one
$p_?$	0.50	Probability that allele is of type ?

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## Results

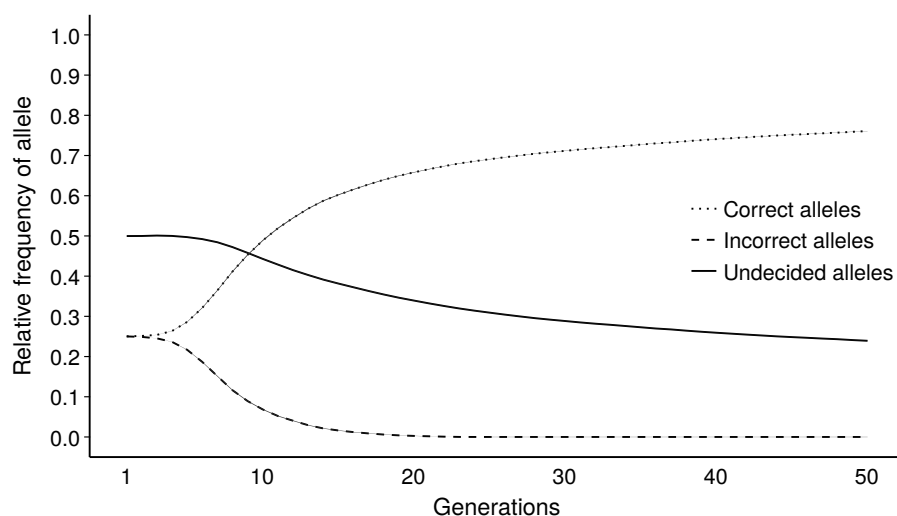
Simulation results are summarized in Figure 1, which corresponds to Figure 2 from the reference article. Qualitatively the results are very similar - there is an obvious increase in proportion of alleles correctly set by the evolution (close to 75% by generation 50) and proportion of incorrect alleles decreases to zero by generation 50. This is a clear evidence of individual learning guiding evolutionary search even though there is no direct transmission of knowledge acquired during individual learning from one generation to the next.

There is an important difference with respect to the reference paper, however. In original simulations proportion of Undecided alleles that are left to individual learning is relatively constant, close to initial 50%. The authors point out this as an interesting result - there is little selective pressure to specify last few connections by evolution because few switches are quickly set through individual learning. In contrast, results in Figure 1 show that proportion of Undecided alleles is continuously decreasing. In fact, whereas proportion of Correct alleles in the reference article flattens out in my case it continues increasing, with increase coming from proportion of Undecided alleles decreasing further. To make sure this is really a long run trend I have let populations evolve for larger number of generations than in the reference article. Results of all 1000 generations are presented in Figure 2. By generation 1000 proportion of Undecided alleles drops to 9%. Even though decrease is smaller with each generation, it does not seem to stop and flatten out by the end of the simulation.

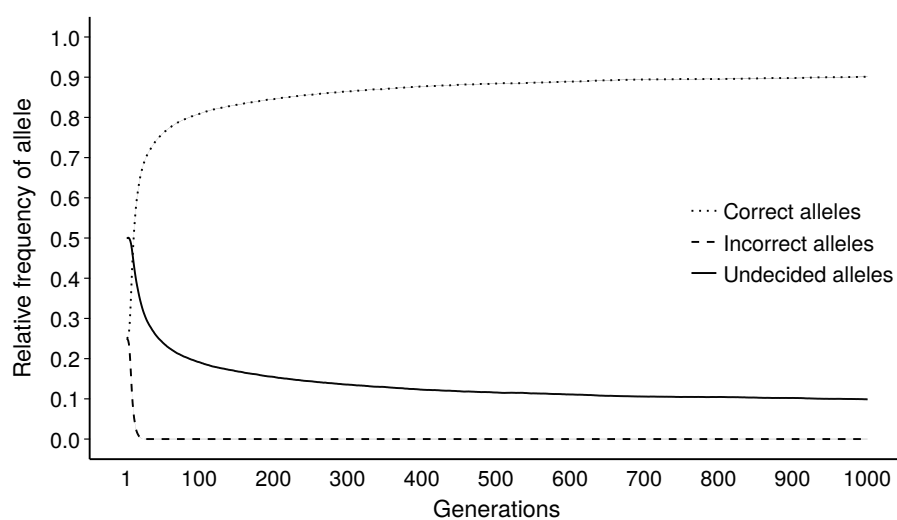
What is the source of this particular difference in results? One explanation is that results reported in Figure 2 in the reference article stem from a non-typical draw. This is unlikely as upon examining evolutionary paths of Undecided alleles in all simulation runs, they all show a strong downward trend already in first 50 generations, differing only in the exact generation when this decrease onsets. Another explanation is that original implementation is flawed as there actually is a selection pressure for eliminating individual learning after some time. The fitness function described in the reference article is such that the smaller the number of steps an agent takes in individual lifetime to reach the peak, the higher the probability of mating and transmitting the genes to the next generation. Number of steps is a direct function of number of undecided alleles in the genome. Hence, there is a selection pressure for decreasing the number of Undecided alleles. In personal correspondence, one of the authors agreed with this interpretation, stating that indeed there should be a selective pressure for decrease in number of Undecided alleles. The pressure should decrease as a power function of the mean number of steps agents need to reach the peak, which explains rapidly decreasing improvements with each generation.

## Conclusion

Qualitatively the result is comparable to that reported in the reference article, but there is relatively important quantitative difference. Proportions of Undecided alleles in implementation proposed here diminish over time, whereas in the original implementation they stay close to initial values. I attribute the difference to a flaw in the original implementation, providing arguments based on fitness function proposed in the reference article. Although the main result of the reference article - individual learning indirectly guiding evolutionary search - has been reproduced, the difference I have found suggests that individual learning would be eradicated over time.



**Figure 1:** The evolution of the relative frequencies of the three possible types of allele. Correct alleles are those that are set by evolutionary learning and correspond to the targeted pattern, Incorrect denote proportion of incorrectly set alleles, while Undecided denote proportion of alleles left for individual learning. Proportions are means of 100 simulation runs, and barely visible grey ribbons are standard errors. This is the reproduction of Figure 2 in the original article.



**Figure 2:** The evolution of the relative frequencies of the three possible types of allele, with a larger number of generations. Proportions are means of 100 simulation runs, and barely visible grey ribbons are standard errors.

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