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Effect of eugenics on the evolution of populations

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Abstract. We discuss a model of population dynamics under selection pressure from a changing environment. The population, subject to mutations, is composed of diploidal organisms reproducing quasi-sexually (two parents, recombination but no sexes) and with overlapping generations. Two cases are considered – in one we do not influence the dynamics of the population, while in the other we perform eugenics, *i.e.* we eliminate all individuals which have phenotypes not conforming to the optimal one at the place where the change has been made. We show that eugenics reduces greatly genetic diversity of the population, increases the percentage of homozygotes and therefore leads to a population badly prepared to cope with the next changes of the environment. The present paper is an extension of our previous work (Ref. [9]).

PACS. 87.10.+e General theory and mathematical aspects – 02.70.Lq Monte Carlo and statistical methods

There is a number of papers devoted recently by physicists to the problems of modeling different aspects of biological evolution see *e.g.* [1–3]. One of the intriguing questions is the role of eugenics in the evolution of a population. Leaving aside moral justification of such practices, one may investigate purely biological implications.

Eugenics is a human attempt to improve the gene pool of a population. The term was coined by sir Francis Galton [4]. Although now, at least in the common knowledge, the term is linked with the Nazi practices, eugenics has been performed, in one form or another, since a long time. In Scandinavia, and especially in Sweden, it has been applied for several decades [5]. It was also present in prewar America, although in a much more subtle form of "self-improvement". The problem of eugenics is still very much alive, as may be verified by checking the appropriate Web sites presenting arguments pro and con.

In modern phraseology (see *e.g.* [6]) the arguments in favor of eugenics have more economical accents. Practicing eugenics is desirable for a nation since improving the citizens' genetic quality may lead to increasing the nation's standard of living. It also permits minimization of the means expended on welfare, as well as reduction of the crime rates. It should be up to the government to decide who is allowed to have children, so as to improve the gene pool [6]. The advocates of eugenics [7] claim that the choice of the desired traits (health, beauty, intelligence, ..., honesty) is obvious, hence there are no problems which traits are to be favored. However, even the supporters of eugenics [6] admit hat many traits are, or may be, influenced by pleiotropic genes. Hence, *e.g.* if the government bans myopic people from reproducing, there may be less children with high intelligence, since the two (myopia and high intelligence) go together [8].

In [9] we have proposed a model which permitted discussion of the role of eugenics in biological evolution. By that we mean an attempt to improve the average adaptation of the population to the environment done by eliminating individuals not conforming to the imposed pattern. We have shown in [9] that although such a procedure might be beneficial on the short run, it certainly is disastrous on a longer time scale. After just several changes of the environment the population subject to eugenics would become extinct with a very high probability.

In the present paper we would like to discuss some aspects which have not been considered in [9]. Since this paper is a sequel to [9], we shall present the model rather briefly.

We consider a population composed at time t of $n(t)$ diploidal individuals, each of them being characterized by a double chain (its *genotype*) of L sites (*loci*) which can take either a value of 0 – corresponding to a recessive or a 1 – corresponding to a dominant allele [9,10]. Two zeros at a given locus in the genotype result in a zero at the respective locus in the phenotype. Other combinations of alleles produce a one in the phenotype, which is therefore a single string of L zeros and ones.

The selection pressure is modeled by attributing a better chance of survival to individuals whose phenotypes agree better with the assumed optimal one representing here the environment. At given moments the optimal phenotype is changed by switching one, randomly chosen, bit to the opposite value (0 to 1 or 1 to 0).

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In order to breed, an individual j is chosen randomly, its probability of survival is calculated as

$$p_j = \exp\left(-\frac{\alpha w_j}{a_j}\right),$$

where w_j is the age of the individual, increased after each Monte Carlo step, a_j is the adaptation of the individual to the environment, *i.e.* the rate of agreement between the individual's and optimal phenotypes. $a_j \in [0,1]$. α is a parameter controlling the speed of the process. The calculated p_j is compared with a random number $r \in [0,1]$. If $r > p_j$ the individual is removed, otherwise a second partner is chosen, its survival checked and if successful the two produce m offspring

$$m = E\left[M\left(1 - \frac{n(t)}{N}\right)\right]$$

where $E[..]$ is the integer part of $[..]$, M is the maximum number of offspring the pair may have (*physiological birth rate*), and $(1 - \frac{n(t)}{N})$ is the Verhulst factor. The progeny receive independently their genotypes and phenotypes following the recombination procedure [9]. The offspring's genotypes may be affected by (harmful only) mutations with the probability p_{mut}.

As before [9], we shall consider two cases – in one the population will be left to itself to evolve according to the above described procedure. On the second one we shall perform eugenics. After changing the optimal phenotype at a given locus, say from 1 to 0, each selected individual is removed if it is a (11) homozygote at the same locus. If we change a 0 into a 1 in the optimal phenotype, all (00) homozygotes are eliminated.

The dynamics of these two processes, averaged over 50 populations have been presented in [9]. Here we would like to focus on the following questions:

1. What will happen if the initial optimal phenotype would contain not only 1 but also 0?
2. How proceeds the evolution (*e.g.* concentration) of a single population?
3. How eugenics changes the genetic pool of the population?

In order to address the last two questions we have to introduce two quantities. The first one is the *genetic diversity, GD,* of the population, defined in the following way. An individual is picked up and we check its genotype, locus by locus, against the genotypes of all other individuals in the population. Each time the two genes are different a counter is increased by one. This checking is done for all pairs of individuals and the result normalized by the number of combinations and the length of the genotype. Hence $GD \in [0,1]$ and $GD = 0$ corresponds to the population of identical individuals.

Second quantity is the percentage of homozygotes of both types (recessive and dominant) present in the population.

The initial value of the optimal phenotype will contain now a certain percentage γ of zeros. In [9] $\gamma = 0$.

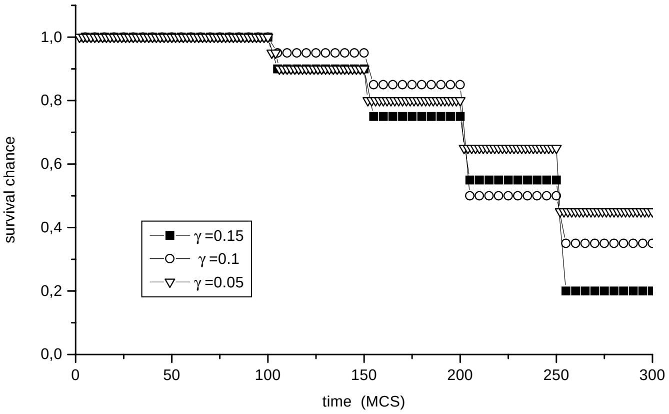

Fig. 1. Survival chances for populations subject to eugenics. The percentage of zeros in the initial optimal phenotype is given by γ. All investigated populations without eugenics survived.

Typical values of the parameters taken in the simulations are: carrying capacity of the habitat $N = 1\,000$, length of the phenotype $L = 20$, interval at which changes of the optimal phenotype are made $t_{\mathrm{ch}} = 50$ MCS, maximum number of offspring $M = 3$, parameter controlling the speed of the process $\alpha = 0.1$, probability of mutation per gene $p_{\mathrm{mut}} = 5 \times 10^{-4}$.

Performing a series of simulations we have found that γ plays an important role. In Figure 1 we present the survival chances for a population with eugenics as a function of time, for three values of γ. In the considered time interval only populations without eugenics survived all. It is therefore clear that eugenics is harmful in a changing environment. The optimal phenotype containing only 1's is the least restrictive since a 1 in the phenotype may come from three combinations of alleles in the genotype $(10, 01, 11)$, whereas a 0 comes only from a pair (00). Therefore if we start with the optimal phenotype containing already some 0's ($\gamma > 0$) the negative effects of eugenics are more pronounced and the populations die out sooner. This is especially evident at later stages of the evolution.

The effect of increasing γ on the populations without eugenics is much smaller. Since we decided that there are no reverse changes in the optimal phenotype, like $1 \to 0 \to 1$, and at large time there is a good possibility of a change $0 \to 1$ in the optimal phenotype, the population may even benefit from such a change. Provided of course that it survived till that time.

The evolution of a single population with and without eugenics for $\gamma = 0.05$ is shown in Figure 2. We see from it that the population without eugenics survives without any marked problems till 8 changes of the environment, when 40% of the original optimal phenotype has been changed. The population with eugenics experienced severe drops in its concentration after each "climate" change. The depletion after 350 MCS was so radical that the population died out. This means that the size of the population dropped below the minimum which is regarded by biologists as safe against statistical fluctuations [11].

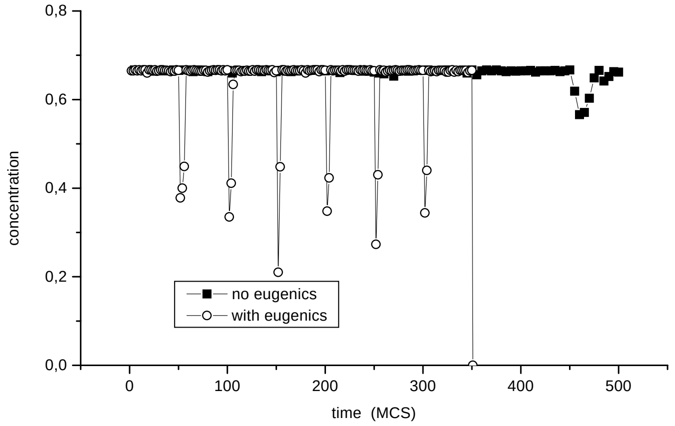

Fig. 2. Time evolution of concentration for two, initially identical populations – one on which eugenics has been applied and the second without it. In all subsequent figures $\gamma = 0.05$ and the population with eugenics died out after 350 MCS.

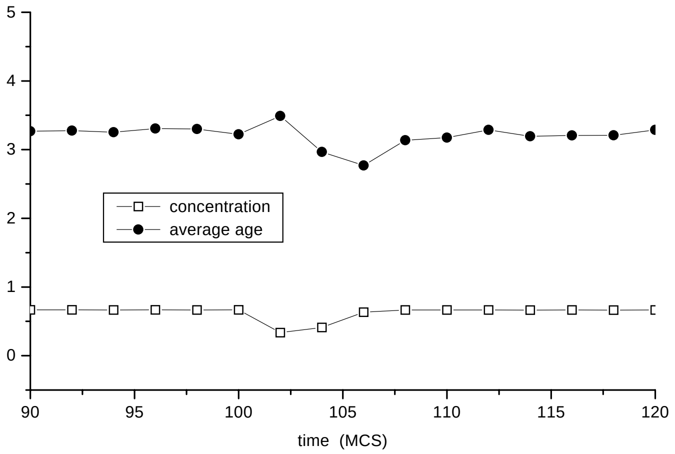

Fig. 3. Average age and concentration *versus* time for a population with eugenics. Time segment around the moment the optimal phenotype has been changed (100 MCS).

The effect of eugenics is clearly seen in Figure 3, where we plot the average age and concentration around the time when the environment has been changed and eugenics applied. The following steps could be distinguished:

1. ill-fitted individuals are eliminated – the concentration drops. Better-fitted individuals live longer – the average age increases.
2. there is more room in the system after elimination of some individuals, more babies are born. The concentration grows, average age drops down.
3. system approaches stabilization. Concentration still grows, there is less room for babies – average age grows too.

In Figure 4 we show the percentage of populations eliminated by eugenics. We see that the process is quite significant just after each change of the environment, when it may affect even a majority of the population. As seen from Figure 1, it results in drastic decreasing of the survival chances after each change of the environment.

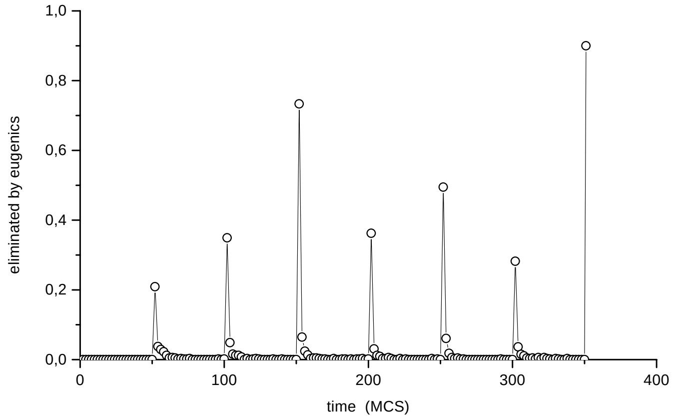

Fig. 4. Percentage of populations eliminated by eugenics *versus* time.

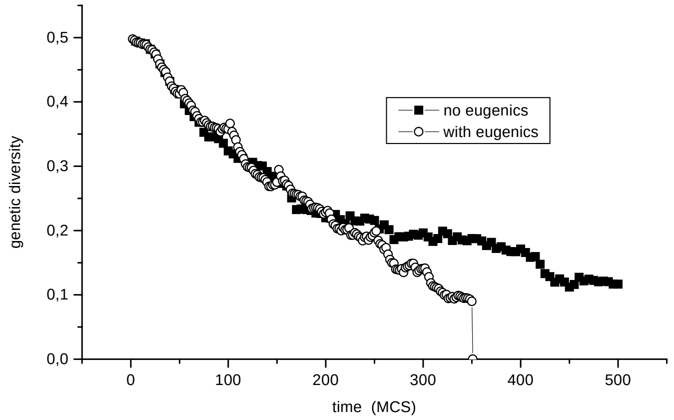

Fig. 5. Genetic diversity *versus* time in the populations with and without eugenics.

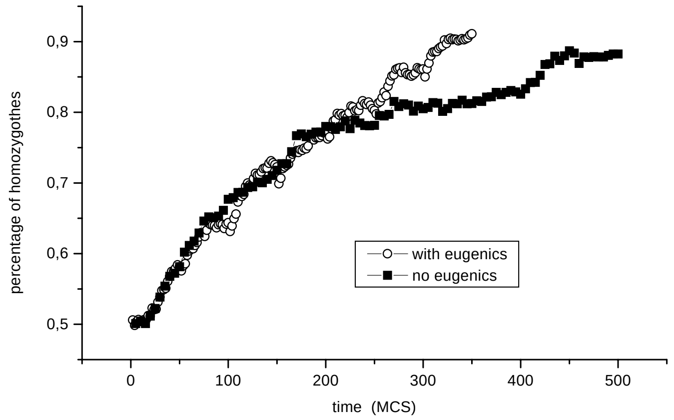

Fig. 6. Percentage of homozygotes *versus* time in the populations with and without eugenics.

Elimination by eugenics plays also a certain, decreasing, role after a change of the environment.

The disastrous role of eugenics is even better understood from the data presented in Figure 5 (genetic diversity) and Figure 6 (percentage of homozygotes). Natural selection present in our model through the adaptation and survival probability of an individual leads to a rather homogeneous population. Genetic diversity is decreasing in time and elimination of heterozygotes by eugenics clearly speeds up the process. It accelerates when there are more zeros in the initial optimal phenotype. Switching from a 1 to a 0 in the optimal phenotype results in a strong selection in favor of homozygotes (00) at that locus. This is clearly seen in Figure 6, where the percentage of homozygotes (of both kinds – (00) and (11)) raises sharply in the population with eugenics. Just before extinction the population subject to eugenics is nearly entirely homozygotic, and at all loci. Any subsequent change of the environment must then lead to a disaster. Only a high level of mutations which may introduce heterozygotes can save such a population.

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