

# Model of population evolution with and without eugenics

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Received 8 April 1999

**Abstract.** We propose, and solve *via* Monte-Carlo simulation, a model describing evolution of population subject to harmful mutations. The habitat changes periodically. The evolution of two, initially identical, populations is compared. One without any external ingerence and the second in which we eliminate all individuals which are ill-fitted to the changed environment (eugenics). We show that although in the short run the individuals in the latter are better adapted and live longer, after some more changes of the environment, the populations with eugenics become extinct, while the others live on.

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

## 1 Introduction

There is a growing interest, at least in the physicists' community, in applying the statistical physics models or ways of reasoning to such complex fields as biology, economy or sociology. There are many models, constructed by physicists, which are providing interesting insights into the basis mechanisms governing dynamical processes in biology, economy etc.

In the present paper we propose a simple model describing evolution of a biological population, which is subject to mutations and selection pressure from the environment. It seems that empirically based science, such as physics or biology, could not even attempt to touch ethical or moral problems. However, we show in the considered model that elimination of ill-fitted individuals, the so-called eugenics, may improve the characteristics of the population (like average life expectancy, adaptation to the habitat) in the short run, but it may be disastrous (even deleterious) to the population at longer time scales. The term *eugenics*, which describes a human activity aimed at the improvement of the genetic pool of human population, was coined by Francis Galton [1].

Although our findings bear no direct moral message, they show that the infamous practices know from the past, like the sterilization laws enacted in several countries in the thirties, may well not have had even a biological justification.

## 2 The model

We present a simple model, solved *via* Monte-Carlo simulations, of evolution of a biological population with over-

lapping generations. The randomly mating (panmictic) population is composed of diploid organisms, each characterized by its age, genotype and resulting from it phenotype. The genotype is a double string of  $L$  two-valued (0 or 1) loci, with a zero corresponding to a recessive and a one to a dominant allele. The phenotype,  $f_j$ , of an individual  $j$ , is a chain, also of  $L$  elements, 0 or 1, constructed from the genotype in the following way. If both alleles at a given locus in the genotype are recessive, then we put a zero at the respective locus in the phenotype. Otherwise we put a one.

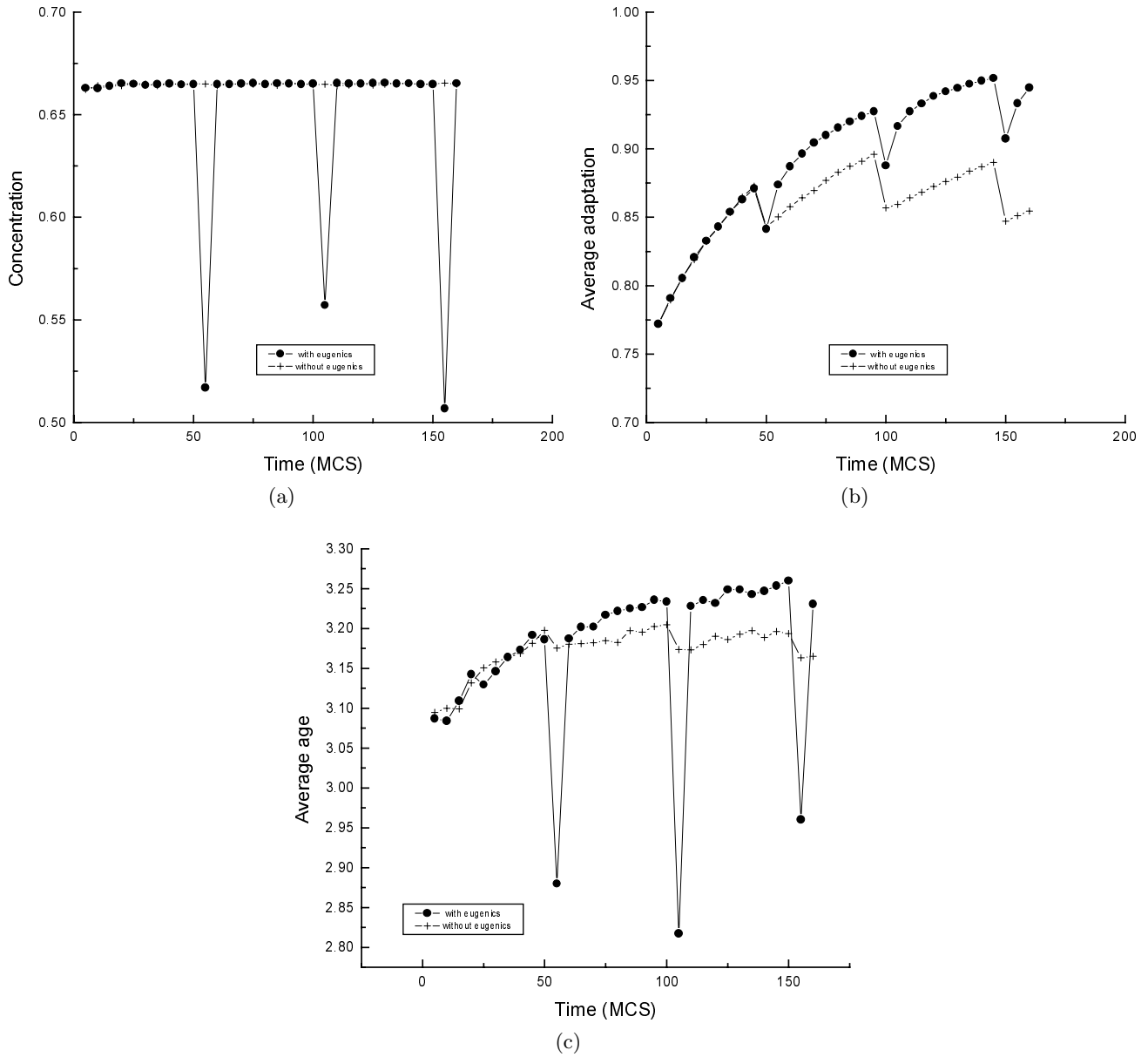
Evolution of a large population of sexual and asexual individuals characterized by genotypes and phenotypes with evaluating the role of genetic recombination has been also considered by Bernardes [2].

The environment the population lives in is introduced *via* the model phenotype  $F(t)$ , which guarantees the best adaptation to the existing conditions, at time  $t$ , for an individual characterized by the same phenotype. Similar ideas of an optimal phenotype have been already introduced before (see *e.g.* [3–6]). For simplicity, at the beginning  $F(t)$  contains only 1's. Hence as long as  $F(t)$  is not changed, a 1 at a locus in an individual's phenotype will correspond to a "good gene" and a 0 to a "bad gene". Harmful mutations appear in the genotypes of offspring.

Our Monte-Carlo algorithm is as follows:

1. An individual  $j$  is chosen at random.
2. Its adaptation,  $a_j$ , to the environment is calculated as the degree of similarity between the individual's phenotype and the model one, *i.e.*  $a_i$  is the number of bit positions in which the two bitstrings  $f_j$  and  $F$  agree. This adaptation is used to estimate the survival

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**Fig. 1.** Short time evolution of the population with (circles) and without (crosses) eugenics.  $L = 20$ ,  $m_{\max} = 3$ ,  $\alpha = 0.1$ ,  $N = 1000$ ,  $p_m = 5 \times 10^{-5}$ , model phenotype changed every 50 MCS, 50 runs. Reduced size of the population is shown in Figure 1a, average adaptation in Figure 1b and average age in Figure 1c.

probability,  $p_j$ , of the individual

$$p_j = \exp\left(-\frac{L\alpha w_j}{a_j}\right), \quad (1)$$

where  $\alpha$  is a parameter and  $w_j$  is the individual's age. A random number  $r \in [0, 1]$  is generated. If  $r > p_j$  the individual is removed from the population and the process returns to 1.

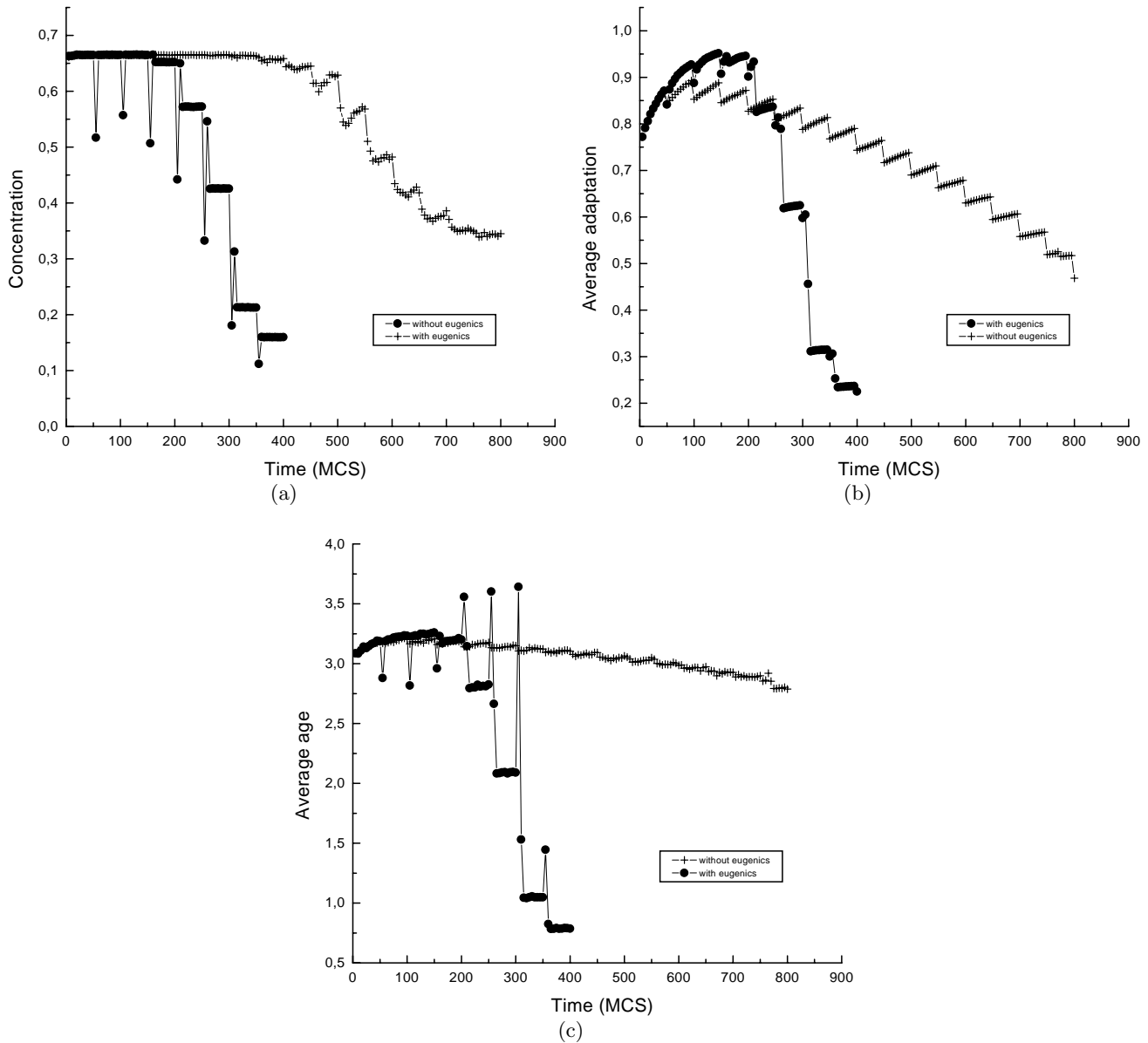
3. If the individual survived, a mate is chosen at random, its survival probability is constructed and checked against a new random number. If the mate survived,

$m$  offspring are produced:

$$m = E\left[m_{\max}\left(1 - \frac{n(t)}{N}\right)\right], \quad (2)$$

where  $E[\dots]$  means the integer part of  $[\dots]$  and  $m_{\max}$  is the maximum number of offspring allowed in the model,  $n(t)$  is the size of the population at time  $t$ , and  $N$  is the carrying capacity of the system.

4. Each offspring receives independently its genotype. The parents' genotypes are copied, each copy is cut at a random locus and then cross-connected, forming two gametes. From each parent one gamete is chosen



**Fig. 2.** Long time evolution of the same population as in Figure 1. Same data and same notation.

randomly to produce the offspring's genotype, from which the phenotype is constructed, following the steps described above. With a probability  $p_m$  an allele is changed, if the change would produce a "bad gene". Otherwise the mutation does not take place – there are no reversions of defected genes.

5. After choosing, as first partners, as many individuals as is the size of the population at that time, one Monte-Carlo step (MCS) has been made. After completing each MCS, the age of all individuals is increased by one.

The populations will be subject to periodic changes of the environment, every  $t_{ch}$  MCS, realized as a change at a random locus in the model phenotype  $F$  of a 1 into a 0. We shall compare two situations – in the first one we do not manipulate with the genetic pool of the population, while on the second one we perform eugenics. By that we mean that we eliminate, after each change of the environment, individuals possessing genes which do not conform to the introduced change in the model phenotype. A similar model, but without eugenics, has been recently published by one of us [7].

### 3 Results

During the simulations we recorded the following quantities: size of the population (reduced by the carrying capacity of the system), average adaptation to the environment of the individuals in the population, and their average age. The model has the following external parameters: carrying capacity  $N$ , number of loci in the genotypes  $L$ , maximum number of offspring  $m_{\max}$ , probability of a mutation (per genom)  $p_m$ , the rate at which the environment is changed  $t_{\text{ch}}$  and the parameter controlling the strength of selection  $\alpha$ . For the simulations we took the values  $N = 1000$ ,  $L = 20$ ,  $m_{\max} = 3$ ,  $p_m = 2 \times 10^{-3}$ ,  $t_{\text{ch}} = 50$  MCS,  $\alpha = 0.1$ . We have checked that changing the parameters around those values does not alter qualitatively the final results.

In Figures 1 and 2 we compare the fate of two, initially identical, populations, one with and the second without eugenics.

Reduced size of the population, its average adaptation and the average age of the individuals, are shown in Figures 1a–c for the evolution up to 160 MCS, *i.e.*, after 3 changes of the environment. Evidently, the population on which eugenics has been applied, does much better. Apart from drastic drops after each change of the environment, the size of the population is the same as that without eugenics. An average individual from the population with eugenics is better adapted and it lives longer. It seems therefore that in our model the populations with eugenics are preferred. If we let however the population evolve longer (Figs. 2a–c; Fig. 1 is plotted from the same data) we see that the benefits of the eugenics are truly short-ranged. The population has more and more problems in adaptation to the next changes of the environment. All the recorded quantities are dropping down dramatically after each change. Detailed analysis shows that after a change in the environment there is, in the population with eugenics, a kind of transition period, before the population, *i.e.* its size and average age, stabilize again. During that period the size of the population decreases (elimination of ill-fitted individuals) and next the age increases sharply (well-fitted individuals live longer). Then there is a “baby-boom”, which results in lowering of the average age and increase of the size of the population.

With each change of the environment more and more populations with eugenics are dying out. After 300 MCS, *i.e.* 6 changes, only about 1/3 of all populations survived, and none lived till 10 changes. In contrast, all populations without eugenics survived 10 changes.

Increasing the mutation probability by two orders of magnitude makes the data more “noisy” and reduces the effect of eugenics.

### 4 Conclusions

It is therefore clear that in our model the benefits brought at the beginning of the process by eugenics are disastrous

at a longer time scale. This is understandable, since by eliminating certain individuals we are restricting the genetic pool of the population, hence we reduce its chances in accommodating to the next changes of the environment. It should also be noted that in our model the genes are completely independent, hence elimination of one of them has no effect on the others. This is not necessarily true in nature, therefore the effect of eugenics in real life could be even more pronounced than in our simple model.

One can argue that it is hard to find an example of the environment change which changes drastically the value of an allele, although similar modifications of the environment based on changing a single bit in the optimal phenotype have been applied in [8]. Nevertheless, there are some examples in the human population genetics which could fit to the described situation. It is known that the obesity is at least partially determined by the genetic background of the individual. In the past, genes determining obesity could be very advantageous, allowing the storage of the occasional surplus of energetic resources. Nowadays, there is even economical pressure to eliminate these genes from the genetic pool by rising the insurance costs of their carriers. The positive role of these genes in determining higher fertility is not even considered. We have not simulated in our model two overlapping populations for which the same allele could be deleterious or advantageous depending on environment conditions like in case of sickle cell anaemia. In European population this recessive allele is much more rare than in African populations exposed to malaria. It would be very interesting to simulate the effect of eugenics in case of alleles being in linkage disequilibrium. In fact we can expect the linkage disequilibrium in ethnic groups living in more or less hermetically separated populations.

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