Simulated self-organization of death by inherited mutations

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ABSTRACT

An agent-based computer simulation of death by inheritable mutations in a changing environment shows a maxim[um?]
population, or avoids extinction, at some intermediate mutation rate of the individuals. Our results indicate that dea[th]
seems needed to allow for evolution of the fittest, as required by a changing environment.

**Key words:** changing environment, computer modeling, evolution, mutation, selection.

INTRODUCTION

More than a century ago, Weissmann argued that aging
and death are needed to make place for our children;
and children are, in turn, needed to allow for Darwinian
evolution through survival of the fittest. Kirkwood
(2005) summarized this theory of aging and many other
ones, and specific computer models of aging and death
were reviewed (Moss de Oliveira et al. 1999, Stauffer et
al. 2001, 2006), such as the Penna model (Penna 1995,
Moss de Oliveira et al. 1996, Stauffer 2007), and the
oldest-old effect (de Oliveira et al. 1998, 1999). A math-
ematical argument against immortality was recently
given in this sense (de Oliveira 2007a, 2009).

Now we want to understand the need for death
through Monte Carlo simulations of individuals. We
distinguish between newborns and adults, and take into
account environmental changes. They may come from
climate change, like ice ages and warmer periods during
the existence of *Homo sapiens*, or they may be caused by

migrations of people from one environment to ano[ther. A]
single environmental change was already used to [show?]
sexual over asexual reproduction (Sá Martins an[d]
de Oliveira 1998) or to account for geographic va[riation?]
(Cebrat and Pekalski 2004). Thus, we may all[ow the]
mutation rate of individuals to change in order [to find?]
its optimal value. Here "optimal" either means a [maxi-]
mum of the population in a fixed environmental c[arrying]
capacity, or survival instead of extinction, depend[ing on]
which of our two models (A and B) were used.

In these two models, by using sexual reprod[uction]
the genome is represented by two strings of L bit[s each,]
i.e. L loci. They represent the L most serious gene[tic dis-]
eases. Each mutation damaging the phenotype ([i.e. the]
health of the individual) reduces the survival prob[ability]
per iteration by a factor x. As genetic load, we [count]
those bit positions that differ from an ideal bit[-string.]
This latter bit-string is initially zeroed, with c[hanges]
happening at each iteration with a probability p[...]
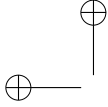
crossed-over at one randomly selected bit position, the same happening for the mother, and then one of the two resulting bit-strings from the father (the gamete) is combined with one of the two from the mother to give the child genome. Mutations are also inherited from the parents, and m new mutations are introduced at birth to each gamete (if $m \geq 1$; for $m < 1$, one new mutation is added with probability m). The genetic load N is the number of loci (bit positions) where the genome is not adapted (i.e., it is not the same as the ideal string) to the current environment. All the changes in the individuals and the environmental bit-strings are reversible.

Model A's population is not constant and finds as an optimal m – a mutation rate for which the equilibrium population reaches a maximum. Model B follows a tradition of theoretical biology and keeps the population constant except if all adults die out during one iteration; then, we check which mutation rate avoids the extinction of the whole population. Further details of the two models will be discussed in the corresponding sections.

MODEL A WITH CHANGING POPULATION

In model A, each of the individuals survives the next time step (iteration involving all survivors) with probability $x^N(1 - P/K)$, in which P is the current total population and K is a fixed input parameter, sometimes called the carrying capacity, representing limitations [due to the lack of food and space] for the population growth. Here, N is the genetic load, the number of bits that are not adapted to the current requirement of the environment. The Verhulst factor $1 - P/K$ applies to all individuals, differently from Sá Martins and Cebrat (2000).

Recessiveness is defined differently in two different versions A1 and A2 of model A, implying in a different computational procedure to determine the genetic load N in each one. For A1, the computational procedure is to take the logical *and* of the two bit-strings of the individual, and then count as N the number of bit positions where the result of the *and* operation differs from the ideal string. This procedure is close to (Stauffer and Cebrat 2006), and means that heterozygous loci do not count for the genetic load N if the

agree with each other (homozygous loci) and disagree with the ideal bit-string. In biological terms, for A1 the allele 0 is always dominant over the recessive allele 1. For A2, in contrast, allele 1 becomes dominant and allele 0 recessive when the environmental bit is 1 instead of 0.

Our K is mostly 2 million, the initial population is $K/5$, and the resulting equilibrium population is mostly of the order of one million if it does not die out. The two individual bit-strings are mutated independently, each one with a mutation rate m. Each surviving female adult at each iteration gives birth to B babies, which become adult at the next iteration; we used $B = 4$. Mostly 10,000 iterations were made (100,000 for most cases with $m < 0.001$), and averages were taken from the second half of this time interval.

CASE A1

Figure 1 shows our main result: the population P has a maximum as a function of m at some intermediate m value. Thus, neither very small m ("eugenics") nor very large m ("instability") are optimal; an intermediate mutation rate leads to the largest P or the lowest $\langle N \rangle$, and, in all cases, to a finite lifespan.

Instead of applying the Verhulst deaths to all ages, Figure 2 shows the correlation between *genetic* deaths only and genetic load by applying the Verhulst deaths only to the births (Sá Martins and Cebrat 2000). Data are taken from averages calculated at different time steps of a single run for each value of x.

CASE A2

The modified recessiveness defined above for model A2 reduces N and makes survival possible for a changing environment even for an unrealistically small x. For $x \geq 0.8$ we see in Figure 3 top a plateau for small mutation rates m, followed by a decay for a larger m. Thus, there is no longer the clear population maximum as it was seen in model A1. A similar result was obtained for model A1 in a stable environment (not shown).
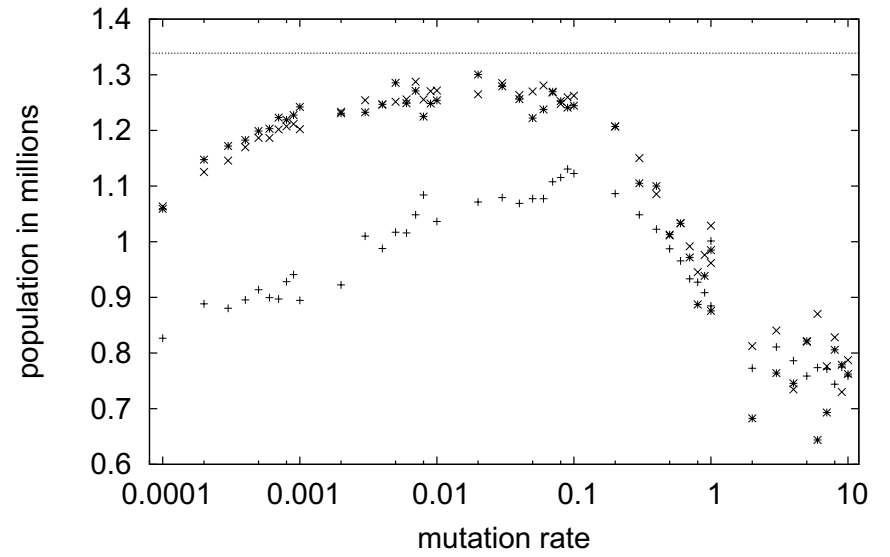
MODEL B WITH CONSTANT POPULATION

In this version, there are no random deaths by the Ver-
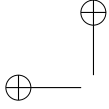
SELF-ORGANIZATION OF DEATHS

(L,x,p) = (64,.98,.1:+), (64,.98,.01:x); (8,.84,.01:*)

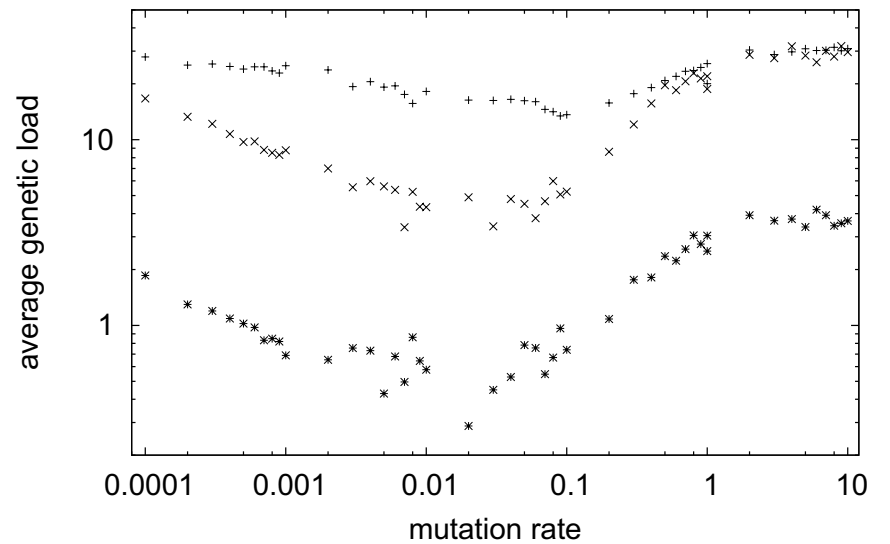(L,x,p) = (64,.98,.1:+), (64,.98,.01:x); (8,.84,.01:*)

Fig. 1 – Model A1. Search for the optimal mutation rate, in which the population (top) reaches the maximal value and the number $\langle N \rangle$ of u
loci (genetic load, bottom) gets the minimal, at $x = 0.98$. For $x = 0.99$, $L = 64$, $p = 0.01$, the results are similar; for $x = 0.96$, the po
die out for some values of these parameters.

an individual with zero load can still die with a prob-
ability $1 - x$. This selection mechanism may lead to
the extinction of the whole population for some values

for the next time step. There is no distinction b
males and females, and the population may be re
as one of hermaphrodites.

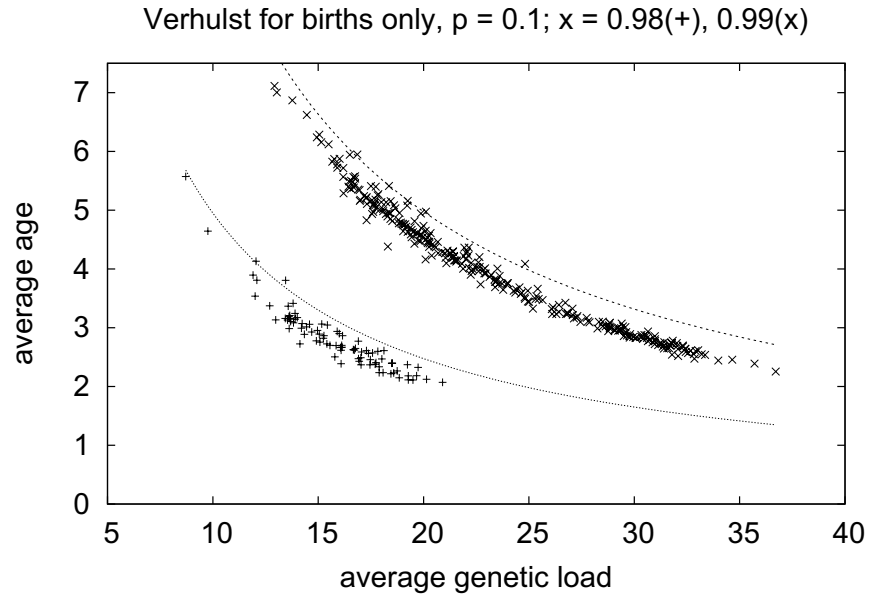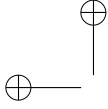Verhulst for births only, p = 0.1; x = 0.98(+), 0.99(x)

Fig. 2 – Model A1. Average age of survivors *versus* the number of unadapted loci, when the Verhulst death probability applies to the births only; the individuals are represented by pairs of 64-bit strings and results are shown for various values of *m* after some simulation time. The curves show $1/(|lnx|N)$.

tions extracted from a uniform distribution in the interval $[0, 2m)$ is then introduced in this genome, each one at a random location of a randomly chosen gamete. Thus, $m = 2$ in this model (B) corresponds to $m = 1$ in model A. If M is not an integer, then $int(M)$ mutations are added, where $int(x)$ is the largest integer contained in x, and an extra mutation is added with probability $M − int(M)$. As a result of this strategy, m new mutations are added to each offspring genome on average.

The model treats heterozygous loci in the same way as model A2, that is, they never contribute to the genetic load. A slightly different version of this model, in which x was recalculated at each time step to keep constant the fraction of deaths, was presented in de Oliveira (2001) and de Oliveira et al. (2008).

The results for this model shown in Figure 4 should be compared to Figure 1. We keep the mutation rate of the environment as $p = 0.01$, the selection strength as a fixed $x = 0.98$ and then compute the average genetic load $\langle N \rangle$, the fraction of the population that dies per time step, and the fraction of perfect, or ideal, genomes

be present at the individual's genome). We find that there is an intermediate range of values of the mutation rate for which both the genetic load and the death rate go through minima, while the fraction of perfects reaches a maximum. This result matches with what was found, in similar situations, in our model A1. (For $L = 3200$ in Fig. 4, extinction happens for mutation rates below 0.1 or above 1.2.).

Our main result refers to the need for a strong selection mechanism as a means to enforce a small genetic load: death of the least adapted individuals makes way to fitter ones. In Figure 5 we show the time evolution of the average genetic load of the population for four different sets of parameters. In all four, we simulate a population of 1000 individuals, each one represented by two bit-strings of 3200 bits size, with a mutation rate at birth of $m = 1.0$. In case (a), $x = 0.98$ (weak selection) and $p = 0$, the environment does not change. The average genetic load starts at 0 (ideal individuals) and grows to a small value of order 1. The distributions of genetic loads are shown in Figure 6, averaged after the initial
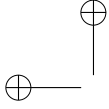
Model A2, L=64, p=0.01; x=.98(+), .96(x), .9(*), .8(sq.)
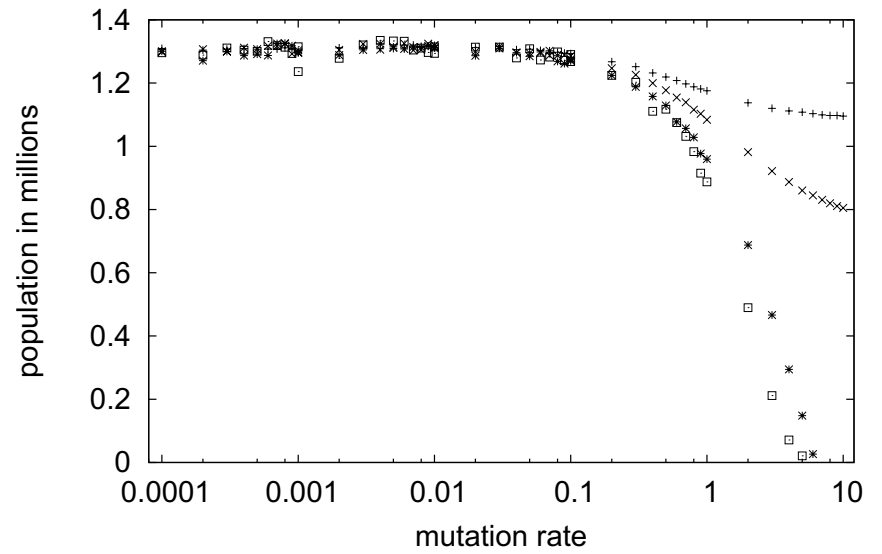
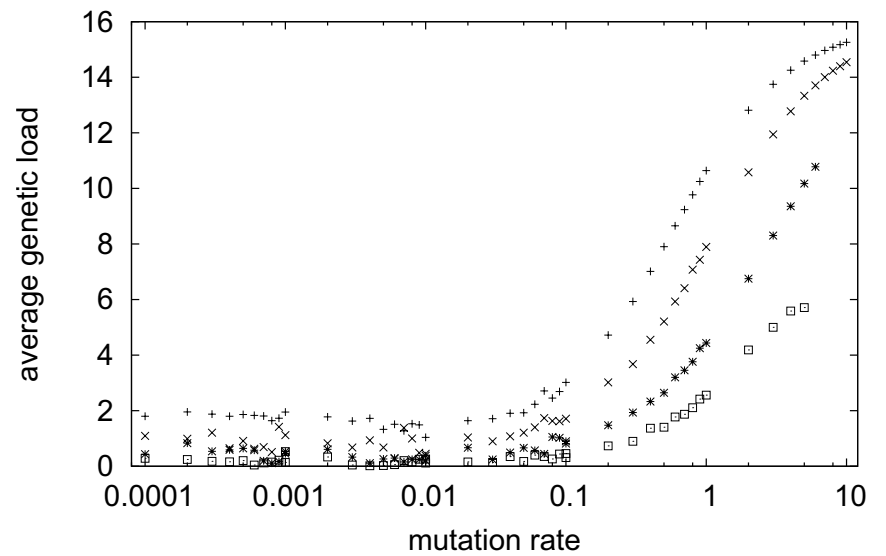Model A2, L=64, p=0.01; x=.98(+), .96(x), .9(*), .8(sq.)

Fig. 3 – Model A2. As Figure 1 but with modified recessiveness and smaller x.

a probability of $p = 0.01$ at each time step (case (b)), the average genetic load increases to a value of order 10 and its distribution peaks at a small non-zero value of the same order. Further increase in the rate of environmental change to $p = 0.02$ leads the population to

tation rate at birth and a fast environmental chang even with a weak selection, leads eventually to tion. The need for a strong selection is now show the same parameters (p and m) but smaller x (case (d)), the population resists and the distribu
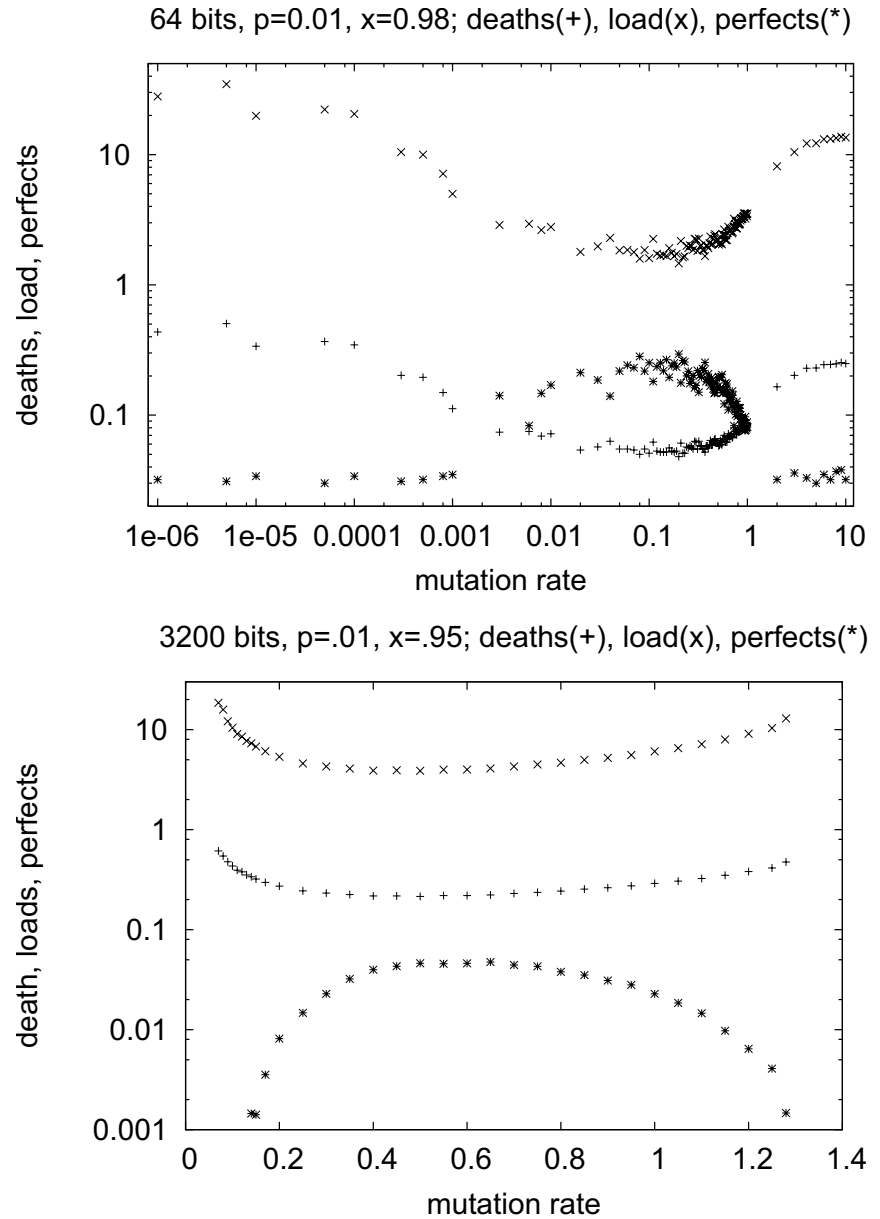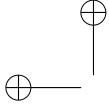
64 bits, p=0.01, x=0.98; deaths(+), load(x), perfects(*)

3200 bits, p=.01, x=.95; deaths(+), load(x), perfects(*)

Fig. 4 – Average genetic load $\langle N \rangle$, deaths and number of perfect individuals as a fraction of the population. Top figure for bit-strings of size 64, and bottom figure for 3200. Simulations running for 10^6 time steps.

for larger populations and stronger selection pressure, similar to de Oliveira (2007b).

Extinction can then be correlated to features of the distribution of genetic load. It is avoided as long

in Figure 7, where we plot the results of simulations of populations with each individual represented by two bit-strings of 2048 bits size, with $x = 0.9$ (strong se-
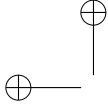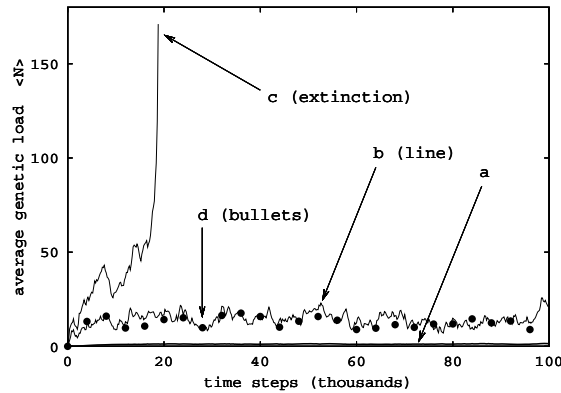
SELF-ORGANIZATION OF DEATHS

Fig. 5 – Time evolution of average genetic load for the four cases ((a)-(d)) described in the text. Case (c) leads to extinction, while case (d) shows survival when selection is increased.
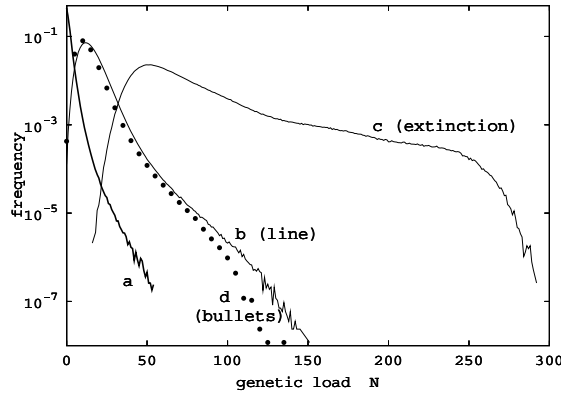

Fig. 6 – Distribution of genetic load for the four cases ((a)-(d)) described in the text.

Fig. 7 – Average genetic load – open circles – and width o: tribution of load – error bars – (y scale on the left), fractio population with no genetic load and fraction of deaths per t (y scale on the right). Values correspond to averages taken a initial time steps, up to 10^6. Similar results are obtained for L ;

parison between its genetic strings and the ideal type. This genetic load determines the death prob of each individual.

Our results come from simulations with rate of environmental change and a fixed value parameter that measures selection strength x. W that population fitness, determined by its size, rea broad maximum, while the average genetic load r a minimum, for some intermediate range of the m rate at birth (model A1). So, nature has self-organ cellular error correction machinery to ensure a m rate within some range.

On the other hand, when the rate of enviro tal change increases, our results are consistent w interpretation that selection has to get stronger to population extinction (model B).

A more realistic approach would assign a d selective value for each different bit position, sir ferent inherited diseases differ in their danger to su However, since these values would have to be f rameters, their introduction in the model would it almost useless.

tion of individuals with zero load decreases. Beyond $p = 0.35$, this fraction vanishes and extinction is the outcome of the simulation. In the same plot, we also show the fraction of individuals that die (for genetic reasons only, in this model) at each time step. As p increases, survival of the population becomes more difficult and causes this fraction to be ever increasing.

CONCLUSION

In all our models, the genetic heritage of a diploid individual is represented by a pair of bit-strings, which undergo mutations at birth, while the ideal phenotype is
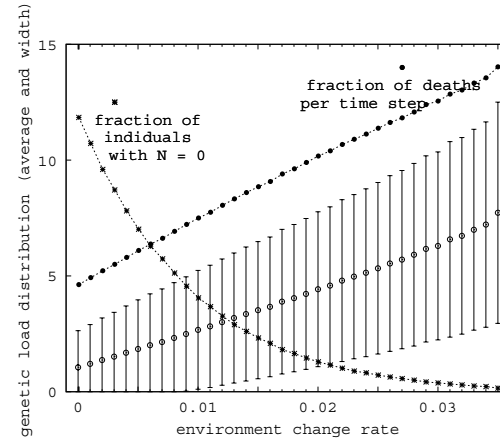
714   JORGE S. SÁ MARTINS et al.

RESUMO

Simulação computacional de agentes individuais que se repro-
duzem e morrem por acúmulo de mutações herdadas mostra
um máximo da população ou evita extinção, para taxas de mu-
tação intermediárias. Assim, as mortes parecem necessárias
para a evolução dos mais adaptados a um ambiente mutante.

Palavras-chave: ambiente mutante, evolução, modelagem
computacional, mutação, seleção.

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