Programming techniques for physical simulations
Exercise 9

November 11, 2009

1. Read the paper by S. Moss de Oliveira et al., Physica A 215, 298 (1995) which introduces fishing in the Penna model.

2. Implement this modified model as well and try to obtain the same time evolution of your population using fishing parameters as described in the paper.

Simulating the vanishing of northern cod fish

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Abstract

Introducing fishing in a recently presented model for biological ageing we show, through computer simulations, how a slight increase of fishing may destroy a whole stable population.

1. Introduction

The sudden disappearance of northern cod [1] and other fish at the Atlantic coast of North America, in particular off Newfoundland, has been ascribed to many reasons, only one being overfishing. More recently, a great number of new reports about the collapse of many american fisheries have appeared. The new England National Marine Fisheries Service has also been repeatedly warning about the level of their stocks of bottom-dwelling fish such as cod, haddock and flounder. In fact it is estimated that fully 45% of the fish stocks whose status is known are now overfished, and populations of some species are reduced to less than 10% of the optimum level for sustainable catch [2]. In Jamaica, many coral reefs have been strongly degraded over the past two or three decades through a combination of the effects of overfishing, hurricane and disease [3].

We present here computer simulations indicating that a slight increase of fishing may destroy an initially stable population. Of course we do not claim this to be a proof that overfishing alone was the cause of this ecological and economic catastrophe. Mathematically it is obvious that such effects are possible if we change the death

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rate from a value slightly below the birth rate to a value slightly above it in a linear differential equation for population growth; we address here the question if such effects also occur in a more realistic stochastic model.

2. The model

The bit-string [4] model of life history is an efficient way to simulate ageing in a population, using a balance of hereditary mutations and evolutionary selection pressure, but nevertheless avoiding the "mutational meltdown" due to accumulation of deleterious mutations [5]. It makes use of a bit-string algorithm based on Boolean variables [6], which allows a large number of time intervals to be incorporated into the life history of an individual (instead of only two [7]: youth and adulthood).

Consider an initial population $N(t = 0)$, where each fish is characterized by a word of 32 bits (genome) randomly chosen, half equal to one and half equal to zero. This genome contains the information when the effect of a mutation will be present during the life of a given fish. The time is a discrete variable running from 1 to 32 years. If at time $t = i$ the ith bit in the genome is equal to one, it is considered that the fish will suffer the effects of a deleterious mutation in that and all following years. There is a threshold T for the number of allowed mutations, and if at any moment the number of bits 1 in the genome is no longer smaller than this threshold, the fish dies. In this way, at each year one more bit of the genome is read, and the total number of bits 1 until that year is computed and compared to T. The effect of food and space restrictions is taken into account by an age-independent Verhulst factor, which gives to each fish a probability $(1 - N(t)/N_{max})$ of staying alive. N_{max} is typically ten times the initial $N(0)$, and represents the maximum size the population can achieve. The stability of the population is assured by a birth rate: each surviving individual with an age larger than the reproduction age R generates, with probability b, one baby per year. Since it is known that the cod maximum lifetime is 16 years and that reproduction starts after 7 years [8], we have considered $R = 7$ in our simulations. Notice that while each fish can live at most 32 years, there exists the Verhulst factor and the aging effects pulling down this age, and the maximum lifetime in our system is also something around 16 years. Therefore the idea of each step of the simulation representing one year can be considered reasonable in our case. The baby's genome will be the same as the parent (hereditarity), except by a number M of randomly chosen bits toggled at birth. These new mutations may increase the number of old bad mutations stored in the parent genome. Until now the model works with the following parameters: The initial population $N(t = 0)$, the maximum number of deleterious mutations T, the maximum number of fishes N_{max}, the minimum age R at reproduction, the probability b of generating an offspring and the mutation rate M for the babies.

The fishing is introduced in the following way: We define the step $M1$ where the fishing starts (after a stable population is reached), and the step $M2$ where an extra fishing is included in addition to the first one ($M2 > M1$). Both fishing rates are also
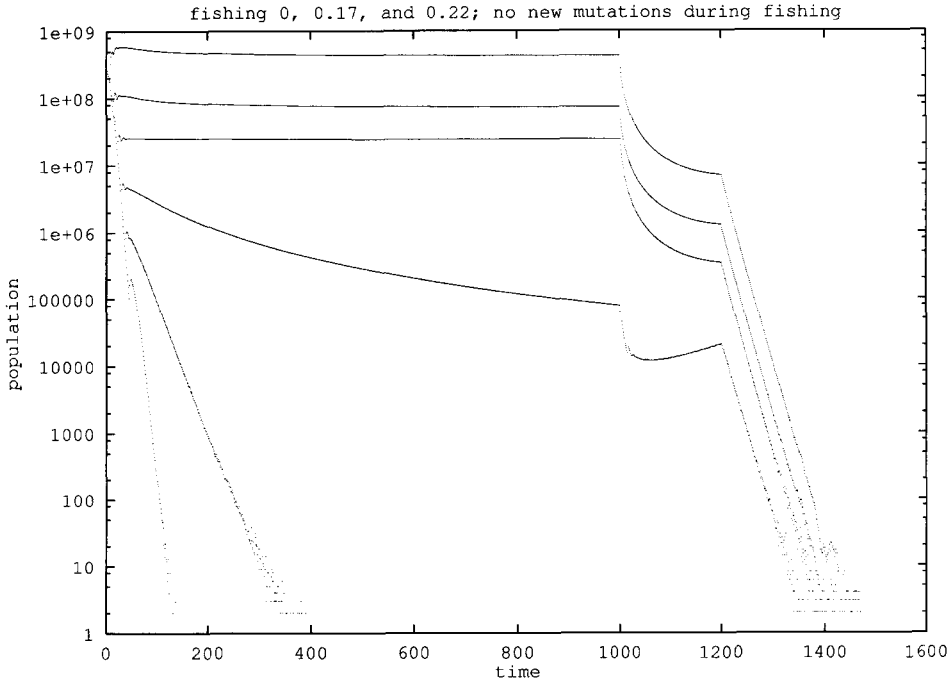
Fig. 1. Development of the population in time. Starting with 313 million babies, increasing to 519 million, stabilizing without fishing near 419 million and a Gompertz-like [9] age distribution. Thereafter fishing first reduces, then kills the whole population. The top curve shows this total population, then (from top to bottom) those of ages 1, 8, 16, 24, and 32.

defined: *death* and *diff*, respectively. Therefore a *death* of ten percent means that in each year one out of ten fishes is killed by fishing, in addition to the natural death. A *diff* of one percent means that in some moment the fishing rate is increased from 10 to 11 percent. It is also possible to define the step $M0$ where bad mutations stop, if we don't want to carry them for the whole process. Therefore the parameters for fishing are: The step $M1$ when it starts, the step $M2$ when extra fishing is included, and their respective probabilities *death* and *diff*.

As a final remark, it is interesting to say that it is also possible to start the whole process with genomes free of mutations (only zero bits) and wait a convenient number of steps to achieve a stable population. The final age distribution obtained is the same for both strategies.

3. Results

Fig. 1 shows one of our Monte Carlo simulations, with hundreds of millions of fish, performed on an Intel Paragon computer, for the following parameters:

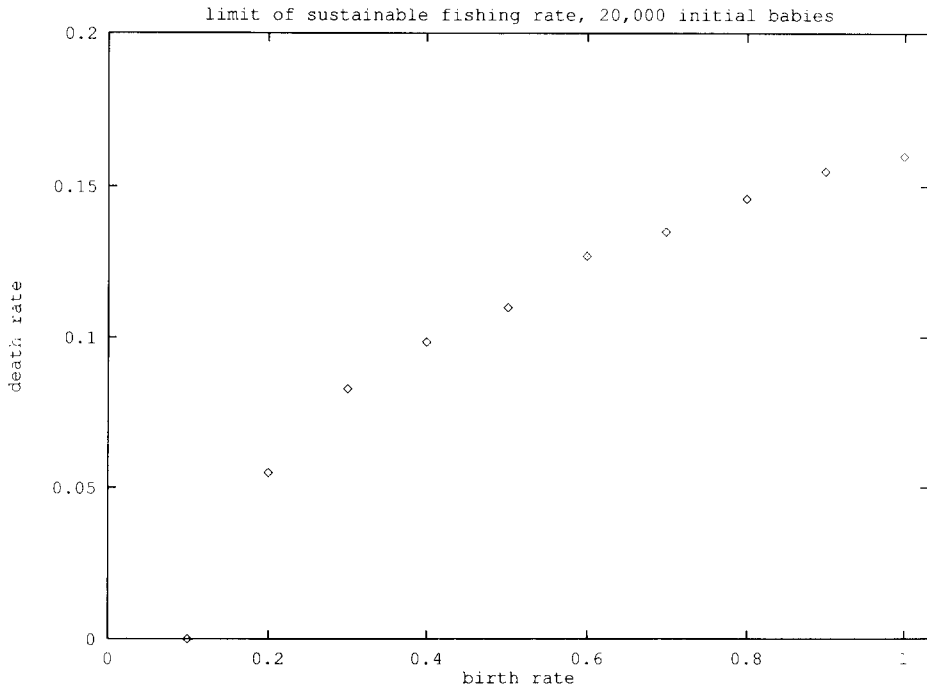(i) $M = 1 \longrightarrow$ number of toggled bits in the parents genome, defining the baby genome;

Fig. 2. Variation of the death rate with the birth rate obtained for small systems.

(ii) $M0 = 1000 \longrightarrow$ step when mutations stop;
(iii) $M1 = 1000 \longrightarrow$ step when fishing starts;
(iv) $M2 = 1200 \longrightarrow$ step when additional fishing is introduced;
(v) $death = 0.17 \longrightarrow$ the fishing rate;
(vi) $diff = 0.05 \longrightarrow$ the additional fishing rate;
(vii) $T = 3 \longrightarrow$ the maximum number of allowed mutations;
(viii) $R = 7 \longrightarrow$ the minimum age at reproduction;
(ix) $b = 1 \longrightarrow$ the probability of generating one baby per year.

In this figure, the top curve represents the total population. The curves bellow correspond to the populations at ages 1, 8, 16, 24 and 32, respectively. we see that moderate fishing reduces the population but lets some fish survive, whereas the later slight increase of fishing eventually kills all fish. The ageing effect can also be clearly noticed in this figure.

Although the birth rate b was fixed in our big runs, it is also possible to verify how it varies with the death rate if we adjust both rates such that the population barely survives. The result for small systems ($N(t = 0) = 20\,000$ fishes) is shown in Fig. 2 for $M = 1$, $M0 = M1 = 1000$, $diff = 0$, $T = 3$, $R = 8$. Another feature of the model which was also verified is that the sum, $death + diff$, is a constant for each birth rate under this balancing condition.

This constancy of the sum $death + diff$ seems due to the mutations. The mutations allow the genome to adjust slowly to any changes in the environment, and so after some
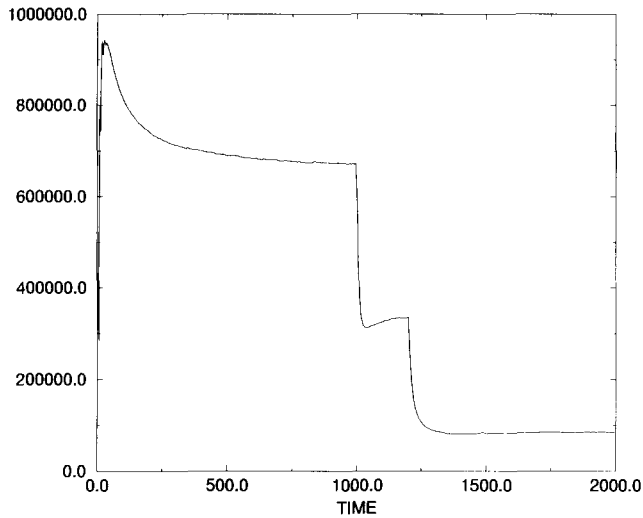
Fig. 3. Evolution of the population in time, for the case that caught fish below reproduction age is returned. The values of the fishing rates are to be compared to those of Fig. 1. Note the linear scales, instead of the logarithmic scale in Fig. 1.

time the memory of earlier conditions is forgotten. Thus after some time only the total fishing rate is relevant for the ratio of populations and different ages and for the ratio of populations at two consecutive time steps. Only the absolute value of the population depends on the history of how fishing rates were varied: When no fish were killed at earlier times then the number of fish is greater.

Similarly, also the initial conditions for the genes seem important only for the absolute numbers, not for the population ratios like the age distribution. When we start with no bad mutations, the populations develop smoothly as during the first iterations in Fig. 1. If, on the other hand, the initial genome is random with half of the genes mutated, then (as illustrated by Penna and Stauffer [4]) the populations first decays drastically since the age distribution of the mutations is unfavorable; afterwards most mutations are concentrated in the old age, and the population may rise again if it was not destroyed completely due to finite-size effects. In the end, however, the age distribution is about the same, whether the initial genes are random or free from mutations. (Also otherwise the age distribution does not depend strongly on the various parameters as long as the minimum age of reproduction is much smaller than 32.)

In many countries it is forbidden to catch fish that are below a given size. To investigate this effect, we performed some simulations in which a caught fish that is below the reproduction age is returned, and another one is fished in its place. In Fig. 3 we present the result of one of these simulations, for an initial population $N(0) = 500\,000$, *death* = 0.30 and *diff* = 0.15. The other parameters are the same of Fig. 1. It can be noticed, if compared to Fig. 1, that the fishing rate can be strongly raised, if such a kind of protection law is obeyed. In fact we obtained that, for $R = 8$ (as in Fig. 2) and $b = 1$, the maximum death rate raises from 0.16 to 0.55 when this rule is taken into account.

A primitive mean field theory is only partially in agreement with our Monte Carlo simulations. Neglecting all age structure, the total population $N(t)$ as a function of the time is now assumed to obey

$$N(t) = bN(t')(1 - N(t)) - dN(t) ,\tag{1}$$

with a birth rate b and a death rate d averaging over the effects of mutations etc. The delay $t' = t - R$ takes into account that reproduction sets in only at age R. This equation has the stationary solution

$$N = 0 \quad (d > b) \qquad \text{and} \qquad N = 1 - d/b \quad (d < b)\tag{2}$$

and thus gives

$$d = b\tag{3}$$

as the borderline between survival and extinction of the population. Simulations in a typical case confirm nicely the linear variation with d of the final population N, at fixed b, as predicted in Eq. (2). However, Fig. 2 already showed that the relation between d and b is nonlinear, contradicting prediction (3).

4. Conclusions

We present a modified version of the bit-string model for aging, where we introduce two stages of fishing and allow bad mutations only during a fixed number of steps. Through computer simulations, we show that in some parameter range, a small cause can have big effects in this ecological model. We also show that simple rules, when obeyed, can easily avoid such a kind of disaster.

Acknowledgements

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