Search for bottleneck effects in Penna ageing and Schulze language model

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No influence was seen when in two models with memory effects the populations were drastically decreased after equilibrium was established, and then allowed to increase again.

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I. INTRODUCTION

In reversible models like the Ising paramagnet above the Curie temperature, the equilibrium distribution is independent of the initial distribution. This is not always the case in systems with memory, for example if a small fraction of elements always remains at the initial states. In biology, at a “bottleneck” (see e.g. [1]) most of the population dies out e.g. due to an environmental catastrophe, and then the population grows back to about its old size. Immediately after this bottleneck, the distribution of genes then is an equilibrium distribution, which in general differs from both a random distribution and the case where all genomes are identical. Then, if the system has long-time memory, the final genetic distribution long after the bottleneck can be different from the one immediately before the bottleneck.

The present note searches unsuccessfully for such bottleneck effects in the Penna model for biological ageing and the Schulze model for human languages. Though both models are reviewed e.g. in [2] we define them in Section II and present our simulations in Section III with conclusions in Section IV.

II. MODELS

In the Penna model [2, 3], individuals age according to a bit-string representing their genome. A bit set to zero represents health, a bit set to one represents an inherited disease which starts at the age corresponding to the position of this 1 within the 32 bits of the string. Three or more active diseases kill the individual. And above the reproductive age of eight (in time units of bit positions) each individual has three offspring having the same genome except that one randomly selected bit is set to one. If it is already one it stays at one. This latter assumption makes the model irreversible: Bits set to one never can become zero again. Initially, all bits are set to zero.

The Schulze model also started with bit-strings, but later [4] it was generalized to $F$ features each of which can be $1, 2, 3, \ldots, Q$, with $F = 8, Q = 5$ in our simulations below. This string of small integers represents the language (or grammar) of the individual. Each site of a square lattice carries one individual, which on each sweep through the lattice is replaced by a child having the same language except for one mutation. And also at each such iteration each individual switches to the language of a randomly selected neighbour with probability $0.9(1-x)^2$ where $x$ is the fraction of people in the whole population speaking the individual’s language. The mutations happen for each of the $F$ features with probability $p$; if a mutation happens, then with probability $1/2$ the feature gets a random value between 1 and $Q$, or gets the value of a randomly selected nearest neighbour on the lattice. These mutations, in contrast to those of the Penna ageing model, are reversible. However, the model shows a strong first-order phase transition with hysteresis, between dominance of one language and fragmentation of the population into numerous languages. Due to this hysteresis the results also in this language model may depend on the initial conditions or more generally on history.

III. SIMULATION

In both models we made 10,000 iterations (sweeps through the population), then simulated a bottleneck by reducing the population to ten randomly selected individuals, and then made another 10,000 iterations to find the new equilibrium. Then we compare the results after the second half with those after the first half (before the bottleneck).

Fig. II shows for the Penna ageing model that the effects of the bottleneck vanish after several dozen iterations, before even the total population gets its equilibrium value. Also in the age distribution of the population and the distribution of 1 bits among the 32 bit positions no significant difference was found (not shown.)

Fig. II shows the size distribution of languages, i.e. we count how many languages exist which are spoken by a given number of people. Again, no effect of the bottleneck is seen. The same holds for the time development of the size of the largest language (not shown). (The bot-
FIG. 1: Penna ageing model: Total population for short (part a) and long (part b) times, with final agreement before (+) and after (x) the bottleneck.

FIG. 2: Schulze language model: Histogram of language sizes on 1000 × 1000 lattice at mutation probability \( p = 0.1 \). The lines give data binned by powers of two in the language size = number of people speaking one language.

tleneck consisted in randomly selecting ten survivors and to let them randomly populate the whole lattice again.

IV. SUMMARY

These simulations showed no long-time bottleneck effects. This does not exclude that with other parameters or in other models such effects exist. And for short times the bottleneck effects are clearly visible, Fig. 1(a). Thus, if for example the species *Homo Sapiens* survived a bottleneck \( 10^5 \) years ago, it could be that some genes mutate with a probability of less than \( 1/10^5 \) per year and thus we are not yet in genetic equilibrium.

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[1] J. S. Sá Martins and S. Moss de Oliveira, Why sex? – Monte Carlo simulations of survival after catastrophes, Int. J. Mod. Phys. C 9, 421-432 (1998); J. P. Radomski and S. Moss de Oliveira, Simulating the mitochondrial DNA bottleneck, Int. J. Mod. Phys. C 11, 1297-1304 (2000).

[2] D. Stauffer, S. Moss de Oliveira, P. M. C. de Oliveira and J. S. Sá Martins, *Biology, Sociology, Geology by Computational Physicists*, Elsevier, Amsterdam 2006.

[3] T. J. P. Penna, A bit-string model for biological aging, J. Stat. Phys. 78, 1629-1633 (1995).

[4] C. Schulze and D. Stauffer, Computer simulation of language competition by physicists, in: B.K. Chakrabarti, A. Chakraborti and A. Chatterjee, eds., *Econophysics and Sociophysics: Trends and Perspectives*, Wiley-VCH, Weinheim 2006, chapter 11, 307-332; Recent developments in computer simulations of language competition, Computing in Science and Engineering 8, 86-93 (May/June 2006); Monte Carlo simulation of survival for minority languages, Adv. Compl. Syst., in press.