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Short Communication

A model for ageing with hereditary mutations

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Abstract. — We show that a simple model that incorporates a balance of helpful and deleterious mutations inherited by future generations, leads to an ‘explanation’ of biological ageing. We also investigate the stability limit beyond which the populations decay to zero.

For ages, biologists and ecologists have been trying to explain why living beings age and why the populations of some species show interesting temporal behaviour (e.g., remain constant) [1]. Recently, it has been found that in this connection it is also very helpful to take recourse to the techniques of computational physics, mainly those suited for systems made of a huge number of interacting elements. In one of such works, Stauffer and Jan [2] have shown that a simple ‘discrete’ model incorporating somatic mutations can reproduce some ageing effects. Ray [3] continued this approach by investigating the dynamics.

The present communication aims at certain investigations related to this work. We present some results which can be the subject of future research. In a nutshell, the work by Stauffer and Jan [2] can be summarized as follows: following the two-age model of Partridge and Barton [1] they deal with a population consisting of individuals of ages 0 (‘babies’), 1 (‘juveniles’), 2 (‘adults’). At each time step (‘generation’) the adults just die off and babies (juveniles) mature to juveniles (adults) with survival probability $J(A)$ and give birth to babies, the number of babies being distributed exponentially with one average baby per parent. (This means that there is no birth in half of the cases, one birth with probability $1/2$, two births with probability $1/4$, etc.). At every generation each individual also receives mutations — somatic mutations which alter the $J$ value of each individual to $J \exp(-ne)$ were considered, with $n$ distributed exponentially with average equal to $u$. A baby survives to a juvenile with probability $J \exp(-ne)$ but since the mutations are somatic (i.e. non-heritable) it gives birth to babies having survival probability $J$ and not $J \exp(-ne)$. The probability $A$ with which this juvenile grows to an adult is determined first from Partridge–Barton assumption $J + A^4 = 1$ with the unmutated value of $J$ and then it is altered by mutations to $A \exp(-pe)$ where $p$

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is distributed, again exponentially, but now with average $uv$. After growing up to an adult, it again gives birth to a baby having survival probability $J$. The final result is that, starting from some $10^5$ babies (with $J$ distributed between 0 and 1 with equal probability), after several hundred of generations, one has an almost time-invariant ratio of babies, juveniles and adults. Also such behaviour is observed for a range of values for $u$, $v$ and $\epsilon$, which are the only three parameters of the model. It does not matter much whether or not initially all $J$ and $A$ are the same. This, Stauffer and Jan claim, explains the basic feature of population and ageing of living organisms subject to mutations.

Our first comment on this work is that although it produces interesting results from a surprisingly simple model, it incorporates only very weak hereditary mutations and in order to be meaningful, it must include hereditary mutations. Therefore, we first included hereditary mutations in their model and found that the previous results are qualitatively reproduced.

The hereditary mutations were added over the somatic mutations by replacing permanently (at every generation) $J$ values by $J_n = J \exp(-\epsilon_h)$. Thus, the new $J$ value is now changed, as before, to $J_n \exp(-\nu e)$ by somatic mutations and the babies survive to juveniles with probability $J_n \exp(-\nu e)$ and then give birth to new babies having a juvenile survival probability equal to $J_n$. The adult survival probabilities are given as before by $A_n \exp(-\nu e)$ where $A_n$ is related to $J$ via the Partridge–Barton equation. We have worked with two versions. In version a we take the Partridge–Barton equation as $J + A_2^1 = 1$ and in version b we take it as $J_n + A_2^1 = 1$. Thus in version b the hereditary mutation affects the adult survival probability in the same generation, while in version a one more generation is needed for this effect as $A_n$ sees the effect of hereditary mutations that has changed $J$ in the previous generation. The parameter $\epsilon_h$ was taken to be positive ('good' mutations) and negative ('bad' mutations) with equal probability. When it is positive (negative) its precise value was chosen randomly as any number between 0 and $\epsilon_u (-\epsilon_l)$. Thus our model now has five parameters: $u$, $v$, $\epsilon$, $\epsilon_u$, $\epsilon_l$, and we have studied several values, keeping $\epsilon = 0.01$. We have always started with $J$ values that were distributed homogeneously between 0 and 1. Results are as follows:

1) If one varies $\epsilon_l$ and keeps all other parameters constant, then for low values of $\epsilon_l$ the population becomes stationary after several hundred generations, but for high values of $\epsilon_l$ it decays to zero. The boundary between these two types of behaviour is shown in figure 1 which looks like a 'phase diagram'. (Versions a and b differ only quantitatively.)

2) The adult survival probabilities (Fig. 2b) depend only on the product $uv$ and not on the individual factors $u$ and $v$ for fixed values of $\epsilon$, $\epsilon_u$, $\epsilon_l$, but this is not the case for the juvenile survival probabilities (Fig. 2a). The phase diagram (Fig. 1) also depends on the individual factors $u$ and $v$.

3) A set of parameter values that results in higher juvenile survival probabilities than those of another set has at the same time adult survival probabilities that are lower.

4) As regards figure 2, the versions a and b give qualitatively similar results, only there is the quantitative difference that $J$ for version a is larger than that for version b (with all parameters unchanged) and for $A$ the trend is reverse.

5) For $\epsilon_h = 0$ the population dies out (see Lynch and Gabriel [4]).

Thus, we find that introducing hereditary mutations in the work of Stauffer and Jan (with reasonable values of parameters) one gets meaningful results. In view of this we attempted next to construct a simple model which reproduces all the essential features of the Stauffer and Jan model, incorporates hereditary mutations and does away with the parameter $v$ which so far has been chosen rather arbitrarily (see Lynch and Gabriel [4] for biological estimates).

Thus, we now ignore somatic mutations and fluctuations in birth (precisely one birth per generation) and assume that each individual carries one $J$ and one $A$ value. The $J$ ($A$) value is relevant only when it grows from a baby (juvenile) to a juvenile (an adult). When it
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![Graph](image)

Fig. 1. — Regions of growing and decaying populations for $\epsilon = 0.01$, $\epsilon_u = 0.01$, $uv = 16$. We start with 50000 babies and observe 400 generations.

gives birth, the baby carries the same $J$ and $A$ values. The effect of hereditary mutations is to change the $J$ and $A$ values of each individuum differently. Thus, an individuum is selected randomly from all the babies and juveniles, and either its juvenile survival probability $J$ or its adult survival probability $A$ (with probability $1/2$ each) is multiplied by $\exp(-\epsilon)$ where $\epsilon$ is chosen between the limits $\epsilon_1$ and $\epsilon_u$ as before. Such selections are made $2nu$ times (where $n$ is the total number of individuums at any stage) so that on average each individuum has its $J$ (as well as $A$) mutated $u$ times. Also we do not assume any antagonistic balance between $J$ and $A$, start with babies all having $J = A = 1$ and vary the three parameters $\epsilon_1$, $\epsilon_u$ and $u$. As before, with a given $\epsilon_u$ and $u$, for a low value of $\epsilon_1$, the population becomes stationary and as $\epsilon_1$ is increased, at some point it decays. The region of stationary behaviour is shown in figure 3. Note that as $u$ increases 10 times, the scales for $\epsilon$ values had to be reduced 10 times.
To facilitate simulations we had to incorporate 'food-restriction' following Stauffer and Jan. Thus, the juvenile survival probability $J$ is multiplied by a Verhulst factor $(1 - n_t/n_0)$ [5] where $n_t$ is some limit beyond which the population cannot grow. This factor thus incorporates the fact that when the population of some species increases too much, there is a food shortage (or some other factor unrelated to gene mutation reducing the population) which affects mainly the babies. Without this food restriction artefact, the regions of stationary population would be replaced by regions of monotonic increase of population.

An interesting behaviour is found when we look at the stationary values of $J$ and $A$ close to the boundary between stationary and decaying region. We find that these values are $J = 0.65$ to $0.70$, and $A = 0.40$ to $0.50$ independent of the parameters $u$, $\epsilon_1$ and $\epsilon_u$ and also of the starting $J$ and $A$ values. How the computer selects these numbers is still unclear to us.

Thus, the second part of this communication indicates that starting with a symmetrical situation ($J = A = 1$) and incorporating hereditary mutations in a reasonable way, we end up with $J > A$, i.e. with less health at old age. For some values of the parameters the population
Fig. 2. — Juvenile and adult survival probabilities $J$ and $A$ as a function of $uv$ for $u = 10$, $\epsilon = 0.01$, $\epsilon_1 = 0.1$. We start with $10^6$ babies and carry over to 300 generations. This plot is for type a, but type b differs only qualitatively. For $u = 2$ figure 2b would be similar but figure 2a will change (see text). $J_{\text{theor}}$ and $A_{\text{theor}}$ are the lines predicted by the formulae $J = 0.935/(1 + u\epsilon)$ and $A = 0.505/(1 + u\epsilon\epsilon_1)$ derived by Stauffer and Jan [2] on the basis of some simple arguments.
Fig. 3. — Regions of stationary and decaying population for the second part of our work. We start with $n_0$ babies, having $J = A = 1$, and perform $T$ iterations. The values $(n_0, n_t, T)$ were taken to be $(4 \times 10^5, 10^8, 2000)$. Some data points were checked with $(n_0, n_t, T) = (4 \times 10^6, 10^7, 3000)$. The number $n_t$ is the parameter which fixes the pattern of 'food restriction' (see text).
decays with generations and for the other values the population increases monotonically (without food restriction), or attains a stationary value (with food restriction). The stationary value for survival probabilities are in turn independent of the input parameters. This, we believe, might be an indication in support of some ageing theories based on mutation accumulation [6].

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References