Time evolution of the Partridge-Barton model

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(Received 12 November 1999)

The time evolution of the Partridge-Barton model in the presence of the pleiotropic constraint and deleterious somatic mutations is exactly solved for arbitrary fecundity in the context of a matricial formalism. Analytical expressions for the time dependence of the mean survival probabilities are derived. Using the fact that the asymptotic behavior for large time $t$ is controlled by the largest matrix eigenvalue, we obtain the steady state values for the mean survival probabilities and the Malthusian growth exponent. The mean age of the population exhibits a $t^{-1}$ power law decay. Some Monte Carlo simulations were also performed and they corroborated our theoretical results.

PACS number(s): 87.10.+e, 87.23.Kg, 87.23.Cc

I. INTRODUCTION

Early in life we perceive that everything around us, inanimate objects, animals, and human beings undergo a variety of changes that accompany the passage of time. Everything suffers a progressive deterioration with time. This phenomenon is called aging or senescence and it is characterized by a decline in the physical capabilities of the individuals. Several theories (see [1] and references therein) have been suggested to explain why there is senescence, when it occurs, and what are the biological processes responsible for it. Usually, these theories are divided into three classes: biochemical, evolutionary, and telomeric. The first invokes damages on DNA, cells, tissues, and organs and connect senescence. The second type is concerned with the optimality theory and the mutational theory. In the optimality theory, the reproductive rate, mutation, heredity, and natural selection are considered. The third theory is based on the existence of a mechanism that controls the number of cell divisions. The replication of a normal cell is followed by a telomeric shortening. This acts as a counting mechanism which controls the number of divisions.

Evolutionary theories of aging are hypothetico-deductive in character, not inductive. They do not contain any specific genetic parameter, but only physiological factors and constraints imposed by the environment. There are two kinds: the optimality theory and the mutational theory. In the optimality theory [6], senescence is a result of searching an optimal life history where survival late in life is sacrificed for the sake of early reproduction. For the mutational theory [4,7], on the other hand, aging is a process that comes from a balance between Darwinian selection and the accumulation of mutations. The natural selection efficiency to remove harmful alleles in a population depends on when in the lifespan they come to express. Alleles responsible for lethal diseases that express late in life escape from the natural selection and accumulate in the population, provoking senescence. Nevertheless, if the natural selection is too strong then deleterious mutations might not accumulate in the population and the eternal youth could be reached. An evolutionary model with such characteristics was recently studied and solved by Onody and de Medeiros [8].

A simple evolutionary model of aging is the Partridge-Barton model [9]. It was introduced to illustrate the optimality theories of aging. Its principal feature is the inclusion of the antagonistic balance mechanism [10]. This mechanism arises out from processes that enhance the lifespan early in life, but have deleterious effects later.

In this work we find an exact solution for the whole dynamics of the Partridge-Barton model. When only deleterious somatic mutations and pleiotropy are present the time evolution of the model can be formulated in a matricial form. Explicit analytic expressions can be written for the mean survival probabilities and the growth rate. For large time $t$, the system behavior is dominated by the largest matrix eigenvalue. The existent integrals can be solved by the saddle point approximation, allowing us to determine precisely the steady state values of the survival probabilities. A time expansion for the population’s mean age shows that it converges to a constant value according to a $t^{-1}$ power law, a result that was first obtained by Ray [11]. All the results were confirmed by some Monte Carlo simulations that we performed.

II. PARTRIDGE-BARTON MODEL

In the Partridge-Barton model there are only three ages. The population consists of babies (age $=0$), juveniles (age $=1$), and adults (age $=2$). The survival probabilities from infancy to juvenile is $J_1$ and from juvenile to adulthood is $J_2$. Reproduction is permitted only to juveniles and adults, with rates $m_1$ and $m_2$, respectively. Babies do not have offspring and adults are eliminated from the population after reproduction.

The population grows at a steady rate $r$. The Malthusian growth exponent $r$ is related to the other parameters of the model through a discrete version of the Euler-Lotka equation [12].
The antagonistic pleiotropy [10] arises when the same gene is responsible for multiple effects. For example, genes enhancing early survival by the promotion of bone hardening might reduce later survival by promoting arterial hardening. Partridge and Barton implemented the basic ideas of the antagonistic pleiotropy by adopting the constraint, $J_1 + J_2 = 1$, between the survival probabilities $J_1$ and $J_2$. The parameter $x$ is a real positive number whose value depends on the kind of population we are dealing with. The pleiotropic condition states that it is impossible to sustain simultaneously both high juvenile and adult survivals. For the particular case in which $m_1 = m_2 = 1$ and $x = 4$, Partridge and Barton found $J_1 = 0.935$ and $J_2 = 0.505$ as the values that maximize the growth rate $r$.

Also the action of deleterious or helpful mutations can be added to the model. Using Monte Carlo simulations, Stauffer [13] studied the case in which the pleiotropic constraint $J_1 + J_2 = 1$ is accompanied by random somatic mutations. His results clearly show that the survival probabilities $J_1$ and $J_2$ move rapidly to stationary values with $J_1 > J_2$. This fact means that the model exhibits senescence, in the sense that the adult survival is lower than the juvenile. In the absence of mutations, $J_1$ and $J_2$ tend towards 0.935 and 0.505 in accord with the Partridge-Barton conclusions. However, it is not clear how the system drives itself towards these optimal values.

### III. ANALYTICAL SOLUTION

In this section we obtain the exact time solution of the Partridge-Barton model in the presence of pleiotropy and somatic mutations. Let $N_i(J_1, t)$ be the number of individuals at age $i$ ($i = 0, 1, 2$) with survival probability between $J_1$ and $J_1 + dJ_1$ at time $t$. We choose, as the initial condition, a population with the profile

$$N_i(J_1, 0) = N_0 \delta_{i, 0},$$

that is, in $t = 0$ there are only $N_0$ babies with the survival probabilities $J_0$ uniformly distributed in the interval $[0, 1]$.

At time $t$, all babies are equally submitted to somatic and deleterious mutations with strength $\alpha$ ($\alpha < 1$). Their survival probabilities $J_0$ are changed to $J_1 = \alpha J_0$. Subsequently, all these babies pass through natural selection in a such way that, on average, the number of juveniles with survival probability $J_1$ at the instant $t + 1$ is given by

$$N_1(J_1, t + 1) = J_1 N_0(J_0, t).$$

Since the mutation is restricted to be somatic, each one of the $N_1(J_1, t + 1)$ juveniles will give birth to exactly $m_1$ offspring with survival probability $J_0$.

Now, the probability with which a juvenile will reach adulthood must take into account the antagonistic pleiotropy and the somatic deleterious mutations. As pleiotropy is not affected by the somatic mutations, a juvenile with survival probability $J_1$ (formerly, a baby with survival probability $J_0$) will change its survival probability to $(1 - J_0)^{1/2}$, where $\lambda$ is a real positive number and a measurement of the pleiotropic constraint. Under the action of a deleterious somatic mutation, described by a parameter $\beta$ ($\beta < 1$, fixed), the new survival probability can be written as $J_2 = \beta(1 - J_0)^{1/2}$. By submitting all juveniles to natural selection we get, on average, the number of adults with survival probability $J_2$, which is given by

$$N_2(J_2, t + 1) = J_2 N_1(J_1, t).$$

Each one of these adults will generate $m_2$ descendants with survival probability $J_2$ since the mutations are not inherited.

In general, the number of babies with survival probability $J_0$ is given by

$$N_0(J_0, t) = m_1 N_1(J_1, t) + m_2 N_2(J_2, t)$$

for $t \geq 1$, where $J_1 = \alpha J_0$ and $J_2 = \beta(1 - J_0)^{1/2}$. If we substitute Eq. (5) into Eq. (3) we can write the following recursive matricial equation:

$$\begin{pmatrix} N_1(J_1, t + 1) \\ N_2(J_2, t + 1) \end{pmatrix} = A \begin{pmatrix} N_1(J_1, t) \\ N_2(J_2, t) \end{pmatrix},$$

where $A$ is the matrix

$$A = \begin{pmatrix} m_1 J_1 & m_2 J_2 \\ J_2 & 0 \end{pmatrix}.$$

Iterating the equation above and using the initial condition, we get for $t \geq 2$

$$\begin{pmatrix} N_1(J_1, t) \\ N_2(J_2, t) \end{pmatrix} = J_1 N_0(J_0, 0) A^{t-2} \begin{pmatrix} m_1 J_1 \\ J_2 \end{pmatrix},$$

with $A^0$ meaning the identity matrix.

The complete dynamics of the Partridge-Barton model can be obtained by diagonalizing the matrix $A$. We have, explicitly (for $t \geq 2$)

$$N_1(J_1, t) = J_1 N_0(J_0, 0) \frac{m_1 J_1 (\lambda_+^{t-1} - \lambda_-^{t-1})}{\sqrt{m_1^2 J_1^2 + 4 m_2 J_1 J_2}} + m_2 J_2 (\lambda_+^{t-2} - \lambda_-^{t-2})],$$

$$N_2(J_2, t) = J_1 N_0(J_0, 0) \frac{m_1 J_2 (\lambda_+^{t-2} - \lambda_-^{t-2})}{\sqrt{m_1^2 J_1^2 + 4 m_2 J_1 J_2}} + m_2 J_2 (\lambda_+^{t-3} - \lambda_-^{t-3})],$$

where

$$\lambda_+ = \frac{m_1 J_1 \pm \sqrt{m_1^2 J_1^2 + 4 m_2 J_1 J_2}}{2}$$

are the eigenvalues of the matrix $A$, $J_1 = \alpha J_0$, and $J_2 = \beta(1 - J_0)^{1/2}$. Let us point out that the time evolution of the babies distribution $N_0(J_0, t)$ can be calculated using Eqs. (5), (8), and (9). Having the expressions above, we can determine the evolution of many other quantities like the total number of individuals at age $i$, $N_i(t) = \int_0^t N_i(J_1, t) dJ_1$, or their mean survival probabilities.
(\langle J \rangle)(t)=\int_0^J dJ_1 N_1(J_1,t)\int_0^J dJ_1 N_1(J_1,t) dJ_1.

The given input parameters are the initial population \( N_0 \), the birth rates \( (m_1 \text{ and } m_2) \), the mutation strengths \( (\alpha \text{ and } \beta) \), and the pleiotropic constraint \( (x) \).

### IV. ASYMPTOTIC LIMIT

Before taking the asymptotic limit, we observe that \( \lambda_+ \) is the largest eigenvalue for all possible values of the input parameters. Once these parameters are fixed and \( J_2=\beta(1-J_1/\alpha)^{1/4} \), \( \lambda_+ \) is in the last instance a function of \( J_1 \). From Eq. (8) we have asymptotically

\[
N_1(J_1,t)\approx e^{t \ln[\lambda_+(J_1)]}.
\]

By integrating in \( J_1 \), the expression above, we can get the total number of juveniles \( N_1(t) \). It is convenient to change the integration variable \( J_1 \) for a new variable \( y \) (a monotonically increasing function of \( J_1 \), \( y=-\cot(\pi J_1) \), such that

\[
N_1(t)\approx \int_{-\infty}^{\infty} e^{t \ln[\lambda_+(y)]} dy.
\]

For large time \( t \), this integral can be evaluated by the saddle point approximation. We thus obtain

\[
N_1(t)=A(\tilde{y}) \frac{e^{t \ln[\lambda_+(y)]}}{\sqrt{t}},
\]

where \( \tilde{y} \) is the value that maximizes the eigenvalue \( \lambda_+ \) and \( A(\tilde{y}) = \sqrt{\pi t / (-1/2 \lambda_+)} (d^2 \lambda_+/dy^2)_{y=\tilde{y}} \).

In the original paper of Partridge and Barton, the optimization process was achieved by a direct (and not well explained) maximization of the growth rate. Here, in our formalism, it is a simple and a natural consequence of taking the asymptotic time limit in the exact evolving equations. Further, the growth rate or the Malthusian exponent is simply given by \( \ln[\lambda_+(\tilde{y})] \).

To have the deepest insight in the dynamics, let us determine the probability density \( P_1(J_1,t) \) of finding a juvenile at time \( t \) with survival probability between \( J_1 \) and \( J_1+\text{d}J_1 \). It is given by

\[
P_1(J_1,t)=\frac{N_1(J_1,t)}{\int_0^J N_1(J_1,t) dJ_1} = \frac{N_1(J_1,t)}{N_1(t)} \approx e^{t \ln[\lambda_+(J_1)/\lambda_+^+J_1]} \]

where we have used Eqs. (11) and (13) and \( \tilde{y}=-\cot(\pi J_1) \). Clearly, at the asymptotic limit, the distribution probability \( P_1(J_1,t) \) approaches the Dirac delta function \( \delta(J_1-\hat{J}_1) \) and the mean survival probability at age 1 is simply given by \( \langle J_1 \rangle=\hat{J}_1 \). Similar results can be obtained for the ages 0 and 2. Another interesting quantity that can be calculated is the population mean age \( \langle A \rangle(t) \) defined as \( \langle A \rangle(t) = \Sigma_{i=0}^2 i N_i(t)/\Sigma_{i=0}^2 N_i(t) \). It is straightforward to show that

\[
\langle A \rangle(t) = \frac{\gamma+2}{\gamma(1+m_1)+(1+m_2)} + \left\{ \frac{2 \gamma(1+m_1)+(1+m_2)}{2[\gamma(1+m_1)+(1+m_2)^2]} \right\} t^{-1} + O(t^{-2}),
\]

where \( \gamma=\lambda_+(\hat{J}_1)/J_2 \) with \( J_2=\beta(1-J_1/\alpha)^{1/4} \). So we rederive, in a quite simple way, the power law decayment first found by Ray [11].

### V. DISCUSSION

We solved exactly in this paper the Partridge-Barton model under the action of arbitrary pleiotropic constraints...
and deleterious somatic mutations. Through a matricial formalism we were able to predict the complete time evolution of the population. We derived analytic expressions for the time dependence of the mean survival probabilities and the Malthusian exponent. Since for large time $t$ the system behavior is controlled by the largest eigenvalue, it was possible to obtain the steady state values of the survival probabilities and to demonstrate, in a simple way, that the population mean age has a power law $t^{-1}$ decayment to its final constant value.

For comparison with our analytical results, we also performed some Monte Carlo simulations. In these simulations, the natural selection is implemented by discarding any individual with survival probability smaller than a random number $\sim$ generated from a uniform distribution $\theta$. The deleterious somatic mutations and the antagonistic pleiotropy can be easily incorporated into the computer program. It is more difficult to avoid an explosion of the computer’s memory due to the unlimited growth of the population. To take this problem into account, we resort to the Verhulst factor [12] which is commonly used in such circumstances.

In Fig. 1 we put together the analytical solution and the Monte Carlo result. The exact solution was plotted by inserting Eqs. (8), (9), and (10) into the expressions for the mean survival probabilities $\langle J_i \rangle(t)$ and by integrating them using the software Maple [14]. We conclude that the Monte Carlo simulations confirm the theoretical results very well.

Finally, let us point out that, unfortunately, the technique developed here cannot be applied to the case in which mutations are hereditary. The main reason for this comes from the fact that Eq. (5) is no longer valid.

ACKNOWLEDGMENT

We acknowledge CNPq (Conselho Nacional de Desenvolvimento Científico e Tecnológico) for financial support.

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