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# Self-organisation of female menopause in populations with child-care and reproductive risk

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**Abstract.** In this paper, by using a computer model for the evolution of age-structured populations, we show that in a sexual population subject to: (i) senescence, (ii) age-increasing reproductive risks, and (iii) long juvenile dependence, menopause arises spontaneously, in order to guarantee the survival of the offspring.

**PACS.** 87.10.+e General, theoretical, and mathematical biophysics (including logic of biosystems, quantum biology, and relevant aspects of thermodynamics, information theory, cybernetics, and bionics) – 02.70.Lq Monte-Carlo and statistical methods – 07.05.Rm Data presentation and visualization: algorithms and implementation

## 1 Introduction

The existence of post-reproductive periods observed in several species of mammals is one of the most challenging mysteries of Biology. The basic problem is that cessation of reproduction (menopause) and post-reproductive periods seem to contradict the assumption that, from an evolutionary point of view, sterility is the selective equivalent of death [1]. Different hypotheses have been proposed to solve this puzzle, and they can be gathered in two groups, corresponding to either an adaptive or a non-adaptive approach [2].

The evolutionary theory of senescence predicts that selection becomes weaker as soon as reproduction finishes. This means that the harmful genetic mutations which would lead to genetic diseases acting at older ages will spread in the population, thus causing senescence and death. This is known as the mutation-accumulation hypothesis [3–5]. Thus, cessation of reproduction and senescence/death are strongly connected. The best example of this connection is the catastrophic senescence observed in semelparous populations (as the Pacific salmon, which reproduces only once and dies soon after reproduction) [6]. Although it is often claimed that menopause observed in women is a byproduct of recent advances of civilization, references to this phenomenon can be found in very old texts, as in this well known citation from the Bible: "Abraham and Sarah were already old and well advanced in years, and Sarah was past the age of childbearing." (Gen 9:11). If menopause is not a product of domestication and/or civilization, as may be concluded also from the observations of its occurrence in non-technological human populations, and several mammals species living in the wild [7,8], it must be a product of natural selection and evolution [2]. Williams pointed out 40 years ago that menopause "may have arisen as a reproductive adaptation to a life-cycle already characterized by senescence, unusual hazards in pregnancy and childbirth, and a long period of juvenile dependence" [1]. The fundamental idea is that menopause is part of a reproductive strategy selected by evolution, in order to allow a female to devote her remaining energy to her living offspring. This argument explains the non-existence of synchronization between cessation of reproduction and ageing processes observed in those females who have menopause [3].

Evolutionary hypotheses are very difficult to be tested experimentally [3], since it is not possible to recreate past scenarios. So, solutions derived from mathematical and/or computational models are a way to deal with those hypotheses. However, as far as we know, up to now there are no computer simulations dealing with this problem. Among the many computer models introduced to describe the evolution of populations [9], the Penna model [10] is the most widespread microscopic model for computer simulations of the evolution of age-structured populations. Many problems have been studied using this model, in qualitative agreement with experimental results [11].

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## 2 The model

The Penna model describes the time evolution of a population of $N(t)$ organisms: $N_f(t)$ females and $N_m(t)$ males. Each diploid organism is represented by two computer words of 32 bits, which contain the life-story of the individual and are read in parallel. Each bit position represents a given time interval (which could be a day or a year, depending on the species). In our simulations one time interval corresponds to one time step in evolution. Just one breeding season occurs at each time step.

If at age $i$ the two $i$th bits in the two strings are set to one, the individual suffers the effect of a deleterious mutation (which causes a genetic disease) from this age on until death; if they are both zero no disease occurs. In order to compute the number of accumulated diseases, dominant and recessive mutations are distinguished. In the latter case, a new disease is counted only if both strings have a deleterious mutation at the same position; in the former, a new disease happens even if present in just one string. The $d$ dominant positions are randomly selected at the beginning of the simulation and remain fixed throughout time evolution. When the total number of accumulated diseases reaches a value greater than or equal to a limit $T$, the individual dies. The individual can also die for lack of food and space. This is taken into account through the Verhulst factor $V = 1 - N(t)/K_{max}$, where $N(t)$ is the current population and $K_{max}$ is the maximum carrying capacity of the environment, defined at the beginning of the simulation. At each time step and for each individual a random number between 0 and 1 is generated and compared with $V$; if it is greater than $V$, the individual dies independently of its age or the diseases expressed up to that time.

After reaching the minimum reproduction age $R$, a female generates $B$ offspring in that and all following ages. Random mating is assumed, and only males also older than $R$ can mate. The bit-strings which will represent the zygote are constructed as follows: at the moment of reproduction, the mother's strings are broken at a random position, and two complementary pieces (one from each string) are joined (mimicking the process of crossover and recombination). This process creates the string of the offspring that contains the genetic inheritance from the mother. The same steps are repeated for the father's strings. Then, $M$ mutations are randomly introduced (for some simulations we produced $M/2$ mutations in the mother inherited string and $M/2$ in the father strings; the results did not change). Only deleterious mutations are allowed: if a selected bit is equal to zero, it is now set to one; otherwise, if already one, it will remain set to one in the offspring's strings. The gender of the offspring is selected at random.

In order to simulate the evolution of populations with maternal care and at the same time females subjected to reproductive risk, we introduced the following ingredients in the model.

- Maternal Care: if at a time step a female (mother) dies, all her offspring that are younger than or at age $A_{mc}$ automatically die. Those that are older than $A_{mc}$ remain alive. In our simulations we did not include any type of group or clan protection of the young orphans.

- Reproductive Risk: at the moment of giving birth, we calculate the reproductive risk of a female. This is done through the expression Risk $= \alpha G_d/T$, where $\alpha$ is a predefined factor, which can reduce or increase the whole risk function, and $G_d$ is the actual number of diseases which have already arisen in that female at the current age.

- Age of cessation of female reproduction (menopause) $A_m$. For both, males and females, we define a maximum age of reproduction at the beginning of the simulation. In all the cases we are going to discuss, this maximum age is set equal to 32. It means that – at the beginning of the simulation – males and females can reproduce until the end of their lifes (there is no menopause at the beginning). When a female with a given value of $A_m$ gives birth to a daughter, the daughter's value of $A_m$ is the same as its mother with a probability $P_m$, or is equal to $A_m \pm 1$ with probability $(1 - P_m)/2$ ($A_m$ also does not change if a number greater than 32 or less than $R$ is generated).

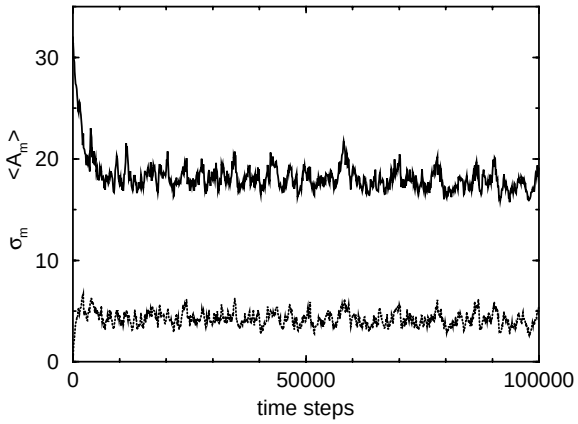


**Fig. 1.** Time evolution of the cessation of reproduction (menopause) age for female population: average (upper curve) and standard deviation (lower curve). Initially this age has been set as 32 time intervals for all the females (maximum possible value in our simulations). After a few thousand time steps the age of menopause is spontaneously organised by the dynamics of the system: both the average and the standard deviation fluctuate around a given value. Initial population $N_0 = 1600$ (800 males and 800 females); mutation rate is $M = 2$; limit of genetic diseases that kill an individual $T = 4$; dominance is $d = 5$; minimum age of reproduction is $R = 10$; juvenile dependence (period of required maternal care) is $A_{mc} = 5$ time steps after birth; reproductive risk parameter $\alpha = 0.25$; and maximum environmental carrying capacity $K_{max} = 160\,000$.

## 3 Results and discussion

Figure 1 shows the results obtained for the average value of the menopause age, $\langle A_m \rangle$, and its standard deviation,

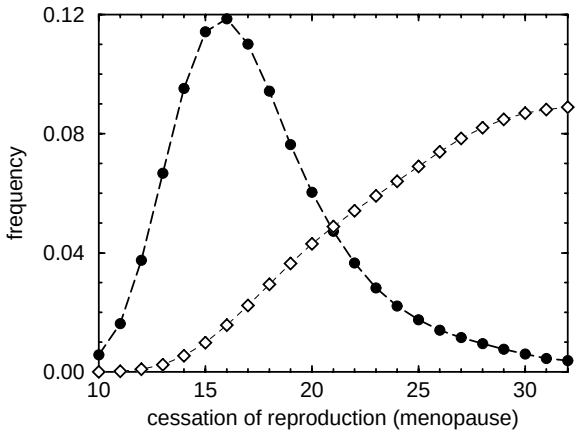


**Fig. 2.** Distributions of female menopause age for two distinct simulations: with reproductive risk and maternal care (filled circles); and neither reproductive risk nor maternal care (open diamonds). For the first case one observes that the age of menopause self-organises showing a peak around 16 time intervals ($\sim$ 80% of the females have menopause within the interval 11 to 21). The distribution in the second case is an artifact of the random choice of the menopause ages and the impossibility to chose an age greater than 32 time intervals. Simulations with several values of $A_{mc}$ have been performed. For $A_{mc}$ up to 3 (meaning the need for a short period of maternal care) the distributions are similar to those represented by open diamonds. For $A_{mc} = 4$ the curve is similar to the one with $A_{mc} = 5$. These distributions correspond to the average of the data obtained within the last 5000 time steps.

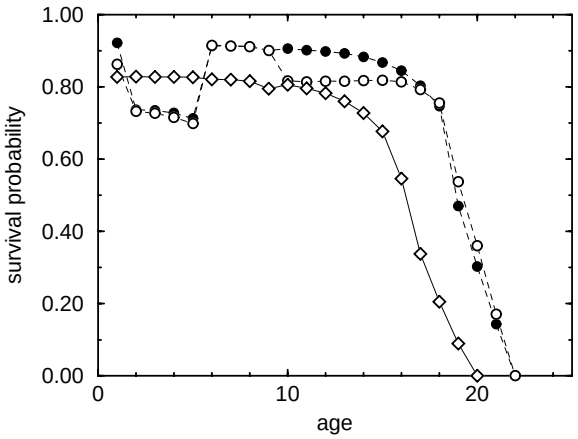


**Fig. 3.** Survival probabilities $N(t)_i/N(t)_{(i-1)}$ – where $N(t)_i$ represents the number of individuals with age $i$ at time $t$ – for two populations: with reproductive risk and maternal care (filled circles represent males and open circles females); and neither reproductive risk nor maternal care (open diamonds represent males; survival probabilities are about the same for the female population). The first dip observed for both – males and females – when reproductive risk and maternal care are considered, is caused by the death of offspring that loose maternal care. The second one (for female population at age = 10), is due to the reproductive risk. Despite these dips, the population submitted to parental care and reproduction risk lives longer and generally presents a higher survival probability than the population without these restrictions.

$\sigma_m$, for a population with reproductive risk and maternal care. The values of the parameters used in our simulations are described in the figure caption. In a few thousand time steps the value of $\langle A_m \rangle$ decreases from its initial value, 32, and now fluctuates around $\sim 17.4$, while $\sigma_m$ fluctuates around $\sim 4.0$. After 100 000 time steps the distribution of $A_m$ looks like a Gaussian one, as can be seen in Figure 2. There we show two distributions obtained in two different simulations. The first one – represented by the filled circles – corresponds to the case described in Figure 1. The second case (open diamonds) represents the final distribution of $A_m$ for a population without reproductive risk and without child-care. In the first case it is clear that the age of menopause self-organises in a population with risk and child-care. This occurs in order to guarantee the survival of the offspring. The profile of the distribution for the second case is merely due to an artifact: the initial distribution is an impulse at age 32, and there is a probability for this age to decrease, but not to increase, since 32 is the maximum allowed age. In this case there is no self-organisation. Moreover, the choice of the limit 32 has no influence in the population dynamics, since the maximum life expectancy is much lower than that, as shown in Figure 3.

Figure 3 shows the values of the survival probabilities for the two cases discussed above. The case of reproductive risk and maternal care is represented by circles, while that without restrictions is represented by diamonds. The dips observed in the first case are caused by the death of females: the first dip concerns maternal care (death of juveniles) and the second one (present only in the female survival rate) to the reproductive risk. Even so, the populations with these restrictions live longer. Furthermore, 20% of the fertile female population has post-reproductive life. Williams also pointed out that "no one is post-reproductive until its youngest child is self-sufficient" [1]. The maximum age observed in our simulations is 21 to 22 time intervals and therefore 5 time intervals above the peak observed in the menopause distribution.

We performed simulations also for systems with only maternal care or with only reproductive risk. With only reproductive risk [12], the females reproduce during a shorter interval than without reproductive risk due to the fact that they die sooner, but the distribution of $A_m$ shows the same profile as that of the diamonds in Figure 2. It means that reproductive risk alone reduces the reproductive interval but does not lead the system to self-organisation. On the other hand, populations with only maternal care (without reproductive risk) have a higher survival rate, but the $A_m$ distribution is again similar to the open diamonds one. Finally, we performed simulations with different periods of maternal care. For short periods (meaning that the offspring need a short period of maternal care to survive) the distribution is the same as without care.

In summary, our simulations show that a sexual population evolving under those restrictions suggested by Williams presents a self-organised cessation of female reproduction, in order to guarantee the survival

of the youngest offspring. The non-synchronization between cessation of reproduction and senescence is clearly seen here. It can be explained by the fact that the difference between the menopause age and life expectancy is about the time needed to the youngest offspring be self-sufficient.

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