The equivocal "mean age of parents in a cohort"

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Abstract

The mean age at childbirth is an important notion in demography, ecology and evolution, where it is used as a measure of generation time. A standard way to quantify it is to compute the mean age of the parents of the offspring produced by a cohort. The resulting measure, which can be computed from life-tables or projection matrices thanks to classic formulas, is thought to represent the mean age at which a typical parent produces offspring.

In this note, I introduce a new measure of the mean age at reproduction of a typical parent. After giving a rigorous interpretation of the formulas used to estimate the mean age of parents of offspring of a cohort, I derive corresponding expressions for the mean age at reproduction and show that it can be very different from the mean age of parents of offspring of a cohort – both under simple hypotheses and in real-world applications. The mean age of parents of offspring of a cohort also systematically overestimates the mean age at reproduction, and can even be greater than the expected lifespan conditional on reproduction. Altogether, these results show that the familiar notion of "mean age of parents in a cohort" is in fact ambiguous, and that we may need to reevaluate whether we have been measuring it correctly.

1 Introduction

To gain insight into the structure and dynamics of populations, demographers and ecologists often rely on summary statistics such as the growth rate, reproductive values, etc. These statistics – or *descriptors* – are meant to quantify intuitive characteristics of populations. However, in order to formulate rigorous arguments, we need precise, unambiguous definitions – and it is not always clear what these should be.

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In this note, I illustrate this by studying in detail two quantities that reflect the typical age at which individuals reproduce, and are usually assumed to be the same: the *mean age of the parents of the offspring produced by a cohort of newborns*, a classic and widely used descriptor of populations also known as the cohort generation time; and the mean age at which a parent produces offspring, which from now on we refer to as the *mean age at reproduction*. After defining them precisely, we will see that despite being often used interchangeably these two measures of the typical age at reproduction can differ significantly, both under the most simple modelling hypotheses and in practical applications.

The rest of this note is organized as follows. First, we start by detailing a general framework in which we can formally define a measure μ_1 of the mean age of parents of offspring of a cohort, and a measure τ of the mean age at reproduction. Next, we go on to give explicit formulas for both quantities. In the case of μ_1, we recall the origin and the rigorous interpretation of the familiar expression,

$$\mu_1 \;=\; \frac{\int_0^{+\infty} t\, m(t)\, \ell(t)\, dt}{\int_0^{+\infty} m(t)\, \ell(t)\, dt}\,, \tag{1}$$

where the *survivorship function* ℓ gives the probability that an individual of the chosen cohort reaches age t, and the *age-specific fertility* m represents its rate of offspring production in such a way that, assuming the individual remains alive between ages a and b, the expected number of offspring it will produce in that interval of time is $\int_a^b m(t)\, dt$.

For the mean age at reproduction however, there does not seem to be any expression in the demographical or biological literature. We derive the following formula: letting f denote the probability density function of the lifespan of an individual,

$$\tau \;=\; \frac{1}{c} \int_0^{+\infty} \frac{\int_0^t s\, m(s)\, ds}{\int_0^t m(s)\, ds} \left(1 - e^{-\int_0^t m(s)\, ds}\right) f(t)\, dt\,, \tag{2}$$

where

$$c \;=\; \int_0^{+\infty} \left(1 - e^{-\int_0^t m(s)\, ds}\right) f(t)\, dt\,. \tag{3}$$

We also give straightforward discrete-time equivalents of formulas (1) and (2). But although an expression for μ_1 is available for general population structures, we were only able to obtain an expression of τ for age-structured populations.

Finally, we conclude by investigating the relation between μ_1 and τ, both mathematically and by means of concrete examples. In particular, we show that μ_1, the mean age of parents of offspring of a cohort, is always greater than or equal to τ, the mean age at reproduction – and that the difference between the two can be arbitrarily large.

2 An explicit model for the population

Any formula used to estimate a descriptor of a population relies on a set of assumptions, and thus on a model for the population. Yet, this underlying model is seldom made explicit, which can cause some confusion – especially when dealing

with notions that are intuitively thought to represent the same thing. Therefore, our first step in order to give clear-cut definitions of measures of the typical age at reproduction is to specify a model for the population.

The setting that we use is that of a Crump-Mode-Jagers process (Crump and Mode, 1968, 1969; Jagers, 1969), where the population consists of a discrete set of individuals such that:

(i) Each individual i has a random lifespan T_i with distribution ν and which is independent of everything else.

(ii) During their lifetime, individuals reproduce at a rate m that depends on their age only.

Formally, the fact that an individual reproduces at rate m means that the times at which it produces offspring are distributed according to a Poisson point process with intensity m. What this means exactly is explained in Section A of the Appendix, where a few useful results about Poisson point processes can also be found.

In this model, the definition and interpretation of the survivorship function and of the age-specific fertility are straightforward: the survivorship is defined by [1]

$$\ell(t) \;=\; \mathbb{P}(T_i \geqslant t) \;=\; \nu\Big([t, +\infty[\Big)\,. \tag{4}$$

Working with the measure ν is convenient because it makes it possible to treat the case where T_i is a continuous random variable and the case where it is a discrete random variable simultaneously. However, in many applications T_i will have a density f. Thus, we will do most of our calculations with ν but express our final results in terms of f or ℓ, as in formulas (1) and (2). Note that this essentially consists in replacing $d\nu(t)$ by $f(t)\,dt$ in integrals, and that either of f and ℓ can be deduced from the other, since $\ell(t) = 1 - \int_0^t f(s)\,ds$ and $f(t) = -\ell'(t)$.

The age-specific fertility is the function m. If we denote by $M_i(a, b)$ the integer-valued random variable corresponding to the number of offspring produced by i between ages a and b, then assuming that $b \leqslant T_i$ we have, as expected,

$$\mathbb{E}(M_i(a, b)) = \int_a^b m(t)\,dt\,, \tag{5}$$

The framework of Crump-Mode-Jagers processes is not meant to take into account all phenomena that shape the structure and dynamics of real-world populations. For instance, it excludes any kind of density dependence, and the fact that individuals reproduce at rate m implies that they cannot produce several offspring simultaneously. Nevertheless, this framework is close to the minimal setting containing all the ingredients needed to define most descriptors of populations, whilst being simple enough to remain tractable and make it possible to derive explicit formulas for these descriptors. Moreover, the working hypotheses of Crump-Mode-Jagers processes correspond quite well to the assumptions that are made, often implicitly, to obtain expressions for the classic descriptors of populations.

[1] In probability theory and statistics, the *survival function* almost invariably refers to the complementary cumulative distribution function of T_i, $t \mapsto \mathbb{P}(T_i > t)$. Here, however, we will stick to the convention in biology.

Finally, to obtain discrete-time equivalents of formulas (1) and (2), we consider the following version of the model, which allows simultaneous births: we keep assumption (i) under the extra hypothesis that the lifespan T_i is an integer-valued random variable, and we replace (ii) by the assumption that at each age $t = 1, \ldots, T_i$, individual i gives birth to $M_t^{(i)}$ new individuals. Again, this corresponds quite well to the usual hypotheses on which many classic formulas rely.

3 The mean age of the parents of the offspring produced by a cohort

Consider all offspring produced by a cohort $\mathcal{C}$ of newborns over its lifetime. For each of these offspring, record the age of their parents (mother, in the case of a female-based model) at the time of their birth, and compute the average of these ages: the resulting measure $Z_{\mathcal{C}}$ of the typical age at reproduction is what we call the mean age of the parents of the offspring produced by a cohort. This descriptor is ubiquitous in the demographical and biological literature, where it is frequently referred to as the cohort generation time – or, quite often, by less specific names such as the mean age at childbearing or the mean generation length.

While several well-studied other measures of generation time exist (see Ellner (2018) for a review), the mean age of parents of offspring of a cohort has the advantage of being an individual-centric measure, which makes it a popular choice for the study of the evolution of reproductive timing and of the slow-fast continuum.

The definition given above makes it straightforward to compute the mean age of parents of offspring of a cohort from detailed census data. However, to estimate it from a life-table (i.e. from the survivorship ℓ and from the age-specific fertility m), one uses the quantity μ_1 given by

$$\mu_1 \;=\; \frac{\int_0^{+\infty} t\, m(t)\, \ell(t)\, dt}{\int_0^{+\infty} m(t)\, \ell(t)\, dt}\,, \tag{6}$$

or, in discrete-time,

$$\mu_1 \;=\; \frac{\sum_{t=1}^{+\infty} t\, \ell_t\, m_t}{\sum_{t=1}^{+\infty} \ell_t\, m_t}\,, \tag{7}$$

where ℓ_t is the probability that an individual survives to age t and m_t is the expected number of offspring produced at age t by individuals who reach that age.

Formulas (6) and (7) are well-known and frequently encountered in the literature. They have been popularized by classic references such as Keyfitz (1968) and Coale (1972) in demography, and Charlesworth (1994) and Caswell (2001) in biology. They can also be found in more recent works of reference – including but not limited to Jørgensen and Fath (2008), Rockwood (2015) and Kliman (2016).

Equivalents of these formulas are also available for more general population structures. For instance, in matrix population models, if we let $\mathbf{S}$ be the survival matrix

and $\mathbf{F}$ be the fertility matrix (i.e. if we decompose the projection matrix $\mathbf{A}$ into $\mathbf{A} = \mathbf{S} + \mathbf{F}$ to separate survival probabilities from fertilities) and denote by $\mathbf{w}$ the stable distribution of the population (the dominant right-eigenvector of $\mathbf{A}$) and $\mathbf{e} = (1, \ldots, 1)$ the row vector consisting only of ones, then we can use the following modern version of the classic formula of Cochran and Ellner (1992), which can be found in Ellner (2018):

$$\mu_1 \;=\; \frac{\mathbf{eF}(\mathbf{I}-\mathbf{S})^{-2}\mathbf{Fw}}{\mathbf{eF}(\mathbf{I}-\mathbf{S})^{-1}\mathbf{Fw}}\,. \tag{8}$$

Note that $(\mathbf{I}-\mathbf{S})^{-1} = \sum_{t\geqslant 1}\mathbf{S}^{t-1}$ and that $(\mathbf{I}-\mathbf{S})^{-2} = \sum_{t\geqslant 1} t\,\mathbf{S}^{t-1}$, so that this expression closely parallels (7). Also, the entries of $\mathbf{e}$ represent the weight given to each type of offspring when computing the average age of the parents. Taking $\mathbf{e} = (1, \ldots, 1)$ thus corresponds the natural choice to weight all types of offspring equally. But, should we wish to give more importance to some offspring type, any vector with positive entries could be used in place of $\mathbf{e}$ – and in fact Cochran and Ellner (1992) suggest using the reproductive values as weights. See Steiner et al. (2014) and Ellner (2018) for more on this.

We now turn to the rigorous interpretation of μ_1. We will see that the quantity $Z_{\mathcal{C}}$ described at the beginning of this section converges to μ_1 as the size of the cohort $\mathcal{C}$ goes to infinity – even though for a finite cohort its expected value is not equal to μ_1.

First, let us give a formal definition of $Z_{\mathcal{C}}$. Let $\mathcal{C}$ denote a cohort, that is, a set of n individuals considered from the time of their birth to the time of their death. Let T_i be the lifespan of individual i, and P_i be the set of ages at which it produces offspring. Note that in our setting, conditional on T_i, P_i is a Poisson point process with rate m on $[0, T_i]$.

The average of the ages of the parents of the offspring produced by the cohort is

$$Z_{\mathcal{C}} \;=\; \frac{\sum_{i\in\mathcal{C}}\sum_{t\in P_i} t}{\sum_{i\in\mathcal{C}}\sum_{t\in P_i} 1} \;=\; \frac{\sum_{i\in\mathcal{C}} S_i}{\sum_{i\in\mathcal{C}} N_i}\,, \tag{9}$$

where $N_i = \sum_{t\in P_i} 1$ is the number of offspring produced by individual i, and $S_i = \sum_{t\in P_i} t$ is the sum of the ages at which it produces them. Note that $Z_{\mathcal{C}}$ is well-defined only when $\sum_{i\in\mathcal{C}} N_i > 0$, but that this happens with arbitrarily large probability for a large enough cohort.

As we have already seen, the expected number of offspring produced by an individual i whose lifespan is $T_i = t$ is

$$\int_0^t m(s)\,ds\,. \tag{10}$$

This quantity can be thought of as "$\mathbb{E}(N_i \mid T_i = t)$", even though this interpretation is subject to some caution. At any rate, it follows that

$$\mathbb{E}(N_i) = \int_0^{+\infty}\Big(\int_0^t m(s)\,ds\Big)d\nu(t)\,. \tag{11}$$

Moreover, using Fubini's theorem,

$$\int_0^{+\infty}\Big(\int_0^t m(s)\,ds\Big)\,d\nu(t) \;=\; \int_0^{+\infty} m(s)\Big(\int_s^{+\infty} d\nu(t)\Big)ds\,. \tag{12}$$

Using that $\int_s^{+\infty} d\nu(t) = \ell(s)$, we get the well-known expression for R_0, the *mean number of offspring produced by an individual during its lifetime*:

$$R_0 \;=\; \mathbb{E}(N_i) \;=\; \int_0^{+\infty} m(t)\,\ell(t)\,dt \tag{13}$$

Using Campbell's formula (eq. 50 in the Appendix) and the exact same reasoning, we can express the *mean sum of the ages at which an individual produces offspring* as

$$\mathbb{E}(S_i) \;=\; \int_0^{+\infty} t\,m(t)\,\ell(t)\,dt \tag{14}$$

We already see that μ_1, as given by formula (6), corresponds to the ratio of expectations $\mathbb{E}(S_i)/\mathbb{E}(N_i)$. To conclude, note that, by the law of large numbers, if we denote by $n = \mathrm{Card}(\mathcal{C})$ the size of the cohort, then as $n \to +\infty$,

$$\frac{1}{n}\sum_{i\in\mathcal{C}} N_i \to \mathbb{E}(N_i) \tag{15}$$

and

$$\frac{1}{n}\sum_{i\in\mathcal{C}} S_i \to \mathbb{E}(S_i)\,. \tag{16}$$

As a result,

$$Z_{\mathcal{C}} \;=\; \frac{\frac{1}{n}\sum_{i\in\mathcal{C}} S_i}{\frac{1}{n}\sum_{i\in\mathcal{C}} N_i} \;\xrightarrow[n\to+\infty]{}\; \mu_1\,, \tag{17}$$

where the convergence is almost sure, i.e. happens with probability 1.

For a small cohort however, not only can $Z_{\mathcal{C}}$ have a large variance, but its expected value (conditional on $\sum_{i\in\mathcal{C}} N_i > 0$) is actually different from μ_1. Equating the two would, roughly speaking, amount to mistake the ratio of the expectations for the expectation of the ratio.

In the next section, we define and study the descriptor that we have termed the mean age at reproduction. While μ_1 is the limit of $Z_{\mathcal{C}}$ for an infinite cohort, The mean age at reproduction corresponds to to the expectation of $Z_{\mathcal{C}}$ (conditional of this variable being well-defined) for a cohort consisting of a single individual.

4 The mean age at reproduction τ

The average age at which individual i produces offspring can be defined only if that individual does produce some offspring. In that case, it is given by

$$\bar{X}_i = \frac{1}{N_i}\sum_{t\in P_i} t\,, \tag{18}$$

where, as before, N_i is the total number of offspring produced by i and P_i is the set of ages at which it produces them. We define the *mean age at reproduction* to be

$$\tau = \mathbb{E}\Big(\bar{X}_i \,\Big|\, N_i > 0\Big)\,, \tag{19}$$

which, given our assumptions, does not depend on i or on the composition of the population. Now if we let I be a "typical parent", i.e. be uniformly sampled among the individuals that produce offspring during their lifetime, then we have

$$\mathbb{E}\Big(\bar{X}_i \,\Big|\, N_i > 0\Big) = \mathbb{E}\Big(\bar{X}_I\Big)\,. \tag{20}$$

Moreover, letting $\tilde{T}$ denote the lifespan of I, $\bar{X}_I$ is the average of a Poisson point process with intensity m on $[0, \tilde{T}]$. As explained in Section A of the Appendix, the expected value of this average is simply the expected value of a random point of $[0, \tilde{T}]$ with density $t \mapsto m(t)/\int_0^{\tilde{T}} m(s)\,ds$. The remarkable fact that it does not depend on the value of N_i is a consequence of the absence of internal structure of Poisson point processes. From this, we get

$$\mathbb{E}\Big(\bar{X}_I \,\Big|\, \tilde{T}\Big) \;=\; \frac{\int_0^{\tilde{T}} s\, m(s)\,ds}{\int_0^{\tilde{T}} m(s)\,ds}\,. \tag{21}$$

As a result,

$$\tau \;=\; \int_0^{+\infty} \frac{\int_0^t s\, m(s)\,ds}{\int_0^t m(s)\,ds}\, d\tilde{\nu}(t)\,, \tag{22}$$

where $\tilde{\nu}$ is the law of the lifespan $\tilde{T}$ of I. Note that it is different from ν, the lifespan of a fixed individual, because conditioning on the fact that an individual produces offspring biases its lifespan; for instance, if – as frequently the case in real applications – there exists an age α such that $m(t) = 0$ for $t < \alpha$, then individuals that produce offspring all live longer than α, whereas it is not necessarily the case for other individuals.

The last thing that we need to do in order to get an explicit formula for τ is thus to determine $\tilde{\nu}$. For this, note that

$$\begin{aligned} \mathbb{P}\Big(\tilde{T} \leqslant t\Big) &= \mathbb{P}(T_i \leqslant t \mid N_i > 0) \\ &= \frac{\mathbb{P}(T_i \leqslant t, N_i > 0)}{\mathbb{P}(N_i > 0)} \end{aligned} \tag{23}$$

Conditioning on T_i, using equation (42) from the Appendix for the probability that an individual with lifetime s produces some offspring, and finally integrating against ν, we get

$$\mathbb{P}(T_i \leqslant t, N_i > 0) = \int_0^t \Big(1 - e^{-\int_0^s m(r)\,dr}\Big)\, d\nu(s)\,. \tag{24}$$

As a result,

$$d\tilde{\nu}(t) \;=\; \frac{1}{c}\Big(1 - e^{-\int_0^t m(s)\,ds}\Big)\, d\nu(t)\,, \tag{25}$$

where the constant $c = \mathbb{P}(N_i > 0)$ is given by

$$c \;=\; \int_0^{+\infty} \Big(1 - e^{-\int_0^t m(s)\,ds}\Big)\, d\nu(t)\,. \tag{26}$$

Note that, by integrating by parts and using that $\ell(t) \to 0$ as $t \to +\infty$, we can also express c directly in terms of ℓ and m as

$$c \;=\; \int_0^{+\infty} e^{-\int_0^t m(s)\,ds}\, m(t)\, \ell(t)\, dt\,. \tag{27}$$

Putting the pieces together in the case where T_i has a density f, we get the expression for τ that was announced in the introduction:

$$\tau \;=\; \frac{1}{c}\int_0^{+\infty} \frac{\int_0^t s\, m(s)\, ds}{\int_0^t m(s)\, ds}\left(1 - e^{-\int_0^t m(s)\, ds}\right) f(t)\, dt\,. \tag{28}$$

This final expression is, admittedly, more complex than the corresponding formula (6) for μ_1. This of course is not a problem for real-world applications, where it is going to be evaluated numerically. For theoretical applications however, this does make exact calculations harder, if possible at all; a few examples where they can be done will be given in the next section.

When studying evolution, it is not uncommon for one to be interested in the average of a function z of the ages at which a parent produces offspring, rather than of the ages themselves [2]. By the same reasoning as above, we get the following generalization of (28): letting A denote a uniformly chosen age a which a typical parent produces offspring, for every function z we have

$$\mathbb{E}\Big(z(A)\Big) \;=\; \frac{1}{c}\int_0^{+\infty} \frac{\int_0^t z(s)\, m(s)\, ds}{\int_0^t m(s)\, ds}\left(1 - e^{-\int_0^t m(s)\, ds}\right) f(t)\, dt\,, \tag{29}$$

with the same constant c as before.

We close this section by giving an equivalent of equation (28) in discrete-time. Remember that, in that setting, individual i has integer-valued lifespan T_i and that, at each age $t = 1, \ldots, T_i$, it produces $M_t^{(i)}$ new individuals, where the variables $M_t^{(i)}$ are integer-valued and independent of everything else. Finally, we also assume that each variable $M_t^{(i)}$ is Poisson distributed with mean m_t. Under these assumptions, we have

$$\tau \;=\; \frac{1}{c}\sum_{t\geqslant 1} \frac{\sum_{s=1}^t s\, m_s}{\sum_{s=1}^t m_s}\left(1 - \prod_{s=1}^t e^{-m_s}\right) p_t\,, \tag{30}$$

where $p_t = \mathbb{P}(T_i = t) = \ell_t - \ell_{t+1}$ and

$$c \;=\; \sum_{t\geqslant 1}\left(1 - \prod_{s=1}^t e^{-m_s}\right) p_t\,. \tag{31}$$

The justification of these formulas can be found in Section B of the Appendix. It essentially consists in approaching the discrete-time model with the continuous-time one by choosing appropriate age-specific fertilities. Note that the assumption that the number of offspring produced at each age follows a Poisson distribution is necessary in order to obtain an explicit formula for τ: indeed, $\sum_{s=1}^t sM_s^{(i)} / \sum_{s=1}^t M_s^{(i)}$, the average age at which an individual with lifetime t produces offspring, has a complex behavior for generic variables $M_s^{(i)}$. Thus, although it is technically possible to use formula (30) with any life-table, this restriction of its rigorous interpretation should be kept in mind.

Finally, to obtain an equivalent of formula (30) for more general population structures, such as those allowed by matrix population models, one would need to (1) find the law of the conditional trajectory of an individual in the life cycle given

[2] This was pointed out by Mauricio González-Forero.

that it produces offspring and (2) integrate the average of the ages at which it produces offspring against this law. While the first of these steps is feasible [3], it is unclear whether the resulting expression – if it can be obtained – would be simple enough to be useful.

We now turn to concrete examples of applications of the various formulas that we have presented. Surprisingly, these examples show that μ_1 and τ can differ greatly, even under the most simple hypotheses.

5 Examples

Let us start with a simple but fundamental example, where individuals reproduce at constant rate m. In that case,

$$\mu_1 \;=\; \frac{\mathbb{E}\Big(\int_0^T ms\,ds\Big)}{\mathbb{E}\Big(\int_0^T m\,ds\Big)} \;=\; \frac{1}{2}\frac{\mathbb{E}(T^2)}{\mathbb{E}(T)}\,, \tag{32}$$

and

$$\tau \;=\; \mathbb{E}\left(\frac{\int_0^{\tilde{T}} ms\,ds}{\int_0^{\tilde{T}} m\,ds}\right) \;=\; \frac{1}{2}\,\mathbb{E}\Big(\tilde{T}\Big)\,. \tag{33}$$

In particular, this last expression was expected because birth events are uniformly distributed on the lifetime of individuals, so on average they occur in the middle of their life. Also, since

$$\mathbb{E}\Big(\tilde{T}\Big) \;=\; \frac{\mathbb{E}\Big(T\Big(1-e^{-mT}\Big)\Big)}{\mathbb{E}(1-e^{-mT})}\,, \tag{34}$$

it follows by monotone convergence that

$$\mathbb{E}\Big(\tilde{T}\Big) \to \mathbb{E}(T) \quad \text{as } m \to +\infty\,. \tag{35}$$

We also show in Section C of the Appendix that, by the same argument,

$$\mathbb{E}\Big(\tilde{T}\Big) \to \frac{\mathbb{E}(T^2)}{\mathbb{E}(T)} \quad \text{as } m \to 0\,. \tag{36}$$

Furthermore, since $\mathbb{E}(\tilde{T})$ can also be seen to be a decreasing function of m (e.g., by coupling the Poisson point processes in their intensities), we conclude that, when individual reproduce at a constant rate,

$$\tfrac{1}{2}\mathbb{E}(T) \;\leqslant\; \tau \;\leqslant\; \mu_1\,. \tag{37}$$

In fact, the second inequality holds for general age-specific fertility functions, as shown in Section D of the Appendix.

[3] This was explained to me by Stephen Ellner.

To make this example more concrete, let us assume that individuals die at constant rate η, so that T is an exponential variable and that $\ell(t) = e^{-\eta t}$. In that case, after simplifications we get

$$\mu_1 = \frac{1}{\eta} \quad \text{and} \quad \tau = \frac{1}{2\,\eta}\left(1 + \frac{1}{1 + m/\eta}\right). \tag{38}$$

Note that here μ_1 is also equal to the expected lifespan in the population. Interpreting it as the mean age at which parents reproduce would therefore lead to a contradiction, because – in the case where the fertility m is large enough, so that the most individuals get to reproduce during their lifetime and that the lifespan of a typical parent is not very different from that of a typical individual – this would imply that, on average, the age at which an individual reproduces is the same as the age at which it dies. This is absurd, because unless individuals reproduce exactly when they die, the former has to be smaller than the latter.

We also see that for m/η large enough, $\mu_1 \approx 2\tau$. For $m = \eta$, which corresponds to the minimum ratio m/η to have a population that does not go extinct, the difference is already 33% of the true value.

Now consider the closely related discrete-time model where individual survive from one year to the other with probability p and produce Poisson(m) offspring at each age $t \geqslant 1$, so that

$$p_t = (1-p)\,p^t \quad \text{and} \quad \ell_t = p^t\,, \tag{39}$$

After straightforward calculations, we find that the numerator in formula (7), which corresponds to the mean sum of the ages at childbirth, is $mp/(1-p)^2$ and that the denominator is $R_0 = mp/(1-p)$. As a result,

$$\mu_1 = \frac{1}{1-p}\,. \tag{40}$$

Note that this model can also be seen as a 1×1 matrix population model with survival matrix $\mathbf{S} = (p)$ and fertility matrix $\mathbf{F} = (m)$, so formula (8) can also be used and gives the same result immediately.

Because $\mathbb{E}(T) = p/(1-p)$, we see that

$$\mu_1 \;=\; \mathbb{E}(T) + 1\,, \tag{41}$$

which also corresponds to the expected lifespan of individuals that reach age 1. For the same reason as before, this implies that μ_1 is not credible as an estimate for the mean age at which a typical parent produces offspring.

After standard calculations that have been relegated to Section E of the Appendix, we find that

$$\tau = \frac{1}{2}\left(\frac{1}{1-p} + \frac{1}{1 - p\,e^{-m}}\right).$$

As previously, $\frac{1}{2}\mu_1 \leqslant \tau \leqslant \mu_1$, but the difference between μ_1 and τ can be quite high, even for very reasonable values of p and m: for instance, with $p = 0.5$ and $m = 2$ the discrepancy is 30% of the true value μ_1; for $p = 0.9$ and $m = 2$, which would actually yield a model that is similar to many real-world matrix populations models, it is already 80%.

What about real-world situations? Consider the matrix population models for the tropical palm *Astrocaryum mexicanum* (Pinero et al., 1984; Cochran and Ellner, 1992), whose projection matrices can be found in Section F of the Appendix. These models have frequently been used as examples of matrix population models, as illustrated by the fact that one of them is shipped with the ULM software for studying population dynamics (Legendre and Clobert, 1995).

Table 1 lists some relevant descriptors of these models. Unfortunately, as mentioned above, we do not know how to compute τ for general matrix population models. However, it is rather straightforward to estimate it from individual-based simulations, which is what we have done here.

	High density	Medium density	Low density
T_{R_0}	197.5	169.2	153.6
$\bar{A}$	152.5	122.8	105.1
μ_1	275.2	261.8	275.5
$\hat{\tau}$	152.0	131.3	184.8
$\hat{L}$	232.2	207.6	296.0

Table 1: Comparison of several measures of reproductive timing for three real-world models for the demography of the tropical palm *Astrocaryum mexicanum*, in part taken from Table 4 of Cochran and Ellner (1992): T_{R_0} denotes the R_0 generation time, which corresponds to the time it takes for the population to grow by a factor of its net reproductive rate; $\bar{A}$ is the mean age of parents of offspring in a population that has reached its stable distribution; μ_1 is computed as in formula (8); $\hat{\tau}$ and $\hat{L}$ are estimates of the mean age at reproduction and of the expected lifespan conditional on producing offspring, respectively, that were obtained using individual-based simulations (see Section F of the Appendix). All values are expressed in years.

As we can see, the difference between μ_1 and τ is significant in all three scenarios – and a factor 2 in the *Medium density* model. Moreover, μ_1 is also consistently much greater than $\bar{A}$, the mean age of the parents of the offspring produced by the population when it has reached its stable distribution, and than T_{R_0}, the R_0 generation time. This is intriguing, because these three quantities are all supposed to give a measure of generation time. Overall, τ seems to be in much better agreement with T_{R_0} and $\bar{A}$ than μ_1. Finally, and most surprisingly, we see that in the *High density* case, μ_1 is greater than the expected lifespan conditional on reproduction. This counter-intuitive fact raises questions regarding the interpretation and relevance of μ_1 as a measure of reproductive timing in the life-cycle.

6 Discussion

The expressions of μ_1 and τ and the examples of the previous section make it clear that the mean age of the parents of the offspring produced by a cohort and the mean age at reproduction are two genuinely different notions. It is thus natural to wonder why they have not been recognized as such before. Part of the answer probably comes from the fact that precise definitions of these quantities are seldom

given. For instance, in the references given above – which are or have been among the most influential in the field – μ_1 is variously described as the "mean age at childbearing in the stationary population[4]" by Keyfitz (1968); as the "mean age of childbearing in a cohort" by Coale (1972, eq. (2.10) p. 19); as the "mean age at reproduction of a cohort of females" by Charlesworth (1994, eq. (1.47a) p. 30); and as the "mean age of the mothers at the time of their daughter's birth" by Rockwood (2015, eq. (4.12) p. 98). Yet these four definitions fail to mention explicitly the crucial fact that each offspring produced by the cohort should be considered when computing the average. In particular, these definitions are all compatible with the idea of sampling an individual uniformly at random among the parents of a cohort and computing the mean age at which it produces offspring – and thus apply just as well to τ.

It is not obvious from the definitions of μ_1 and τ how these two quantities are related – or indeed why they should differ at all. One helpful way to think about it is the following: μ_1 can be seen as an *offspring-centric* measure of the mean age of parents, whereas τ is a *parent-centric* measure of it. Indeed, to compute μ_1 we ask each newborn produced by a cohort "how old is your parent?", while for τ we ask a parent "how old are you going to be when you have children?" These questions have distinct answers because they correspond to two different ways to sample a parent. In particular, this explains why μ_1 is greater than τ: indeed, parents that live longer tend to have more offspring, and thus have a higher probability of being sampled via their offspring than when the sampling is done uniformly at random. As a result, they contribute more to μ_1 than to τ. Since these parents with longer lifespans are also those that tend to have a higher mean age at reproduction, this biases μ_1 upward compared to τ.

This also explains why the difference $\mu_1 - \tau$ goes to zero as the fertility becomes vanishingly small: in that case, the proportion of parents that give birth to more than one offspring during their lifetime goes to zero, and as the result the two parent-sampling schemes become equivalent.

Now that we better understand the link between μ_1 and τ, two important questions arise: does the difference matter in practice? And which descriptor should be used in which context?

There are strong arguments in favor of a positive answer to the first question. First, observe that, from a purely mathematical point of view, the difference between μ_1 and τ can be made arbitrarily large. Indeed, recall that, when individuals reproduce at a constant rate m, $\mu_1 = \mathbb{E}(T^2)/\mathbb{E}(T)$ and $\tau \to \frac{1}{2}\mathbb{E}(T)$ as $m \to +\infty$. Thus, by choosing an appropriate distribution for the lifespan T and taking m large enough, we can make μ_1 arbitrarily large and τ arbitrarily small. Although this requires using biologically unrealistic lifespans with large variances, this is informative because it shows conclusively that μ_1 and τ are not just two slightly different formalizations of the same concept. Second, the examples of Section 5 show that, both under very standard modelling hypotheses and in real-world applications, μ_1 can easily be roughly twice as large as τ. Of course, this is does not mean that the difference is going to be significant in typical real-world situations – and, in fact, since $\mu_1 = \tau$ when the lifespan of individuals is deterministic, it seems

[4] What Keyfitz calls the *stationary population* is actually a cohort.

likely that μ_1 and τ will be similar in situations where there is little variation in the lifespan of individuals – but this at least indicates that special caution should be taken when interpreting μ_1.

Finally, it is unclear which of μ_1 or τ should be favored in which context. From a practical point of view, the fact that μ_1 has a simpler expression and has become a well-established measure of reproductive timing means that it is unlikely to be replaced by τ anytime soon. Nevertheless, judging from the phrasing used by several authors, it seems that it is sometimes τ they have in mind, even when working with μ_1. Moreover, μ_1 might not be as intuitive as we usually assume; notably, the fact that it can be greater not only than the expected lifespan but also than the expected lifespan conditional on reproduction (as illustrated by the *Medium density* scenario for *Astrocaryum mexicanum* in Table 1) is likely to come as a surprise to many researchers.

In conclusion, it seems that the descriptor τ can be added as a separate entry to the list of existing measures of reproductive timing / generation time, and that some more work will be needed to understand in which context it is more appropriate than the classic descriptor μ_1.

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A Basic facts about Poisson point processes

In this section we recall basic results about Poisson point processes, focusing on the properties on which our calculations rely. Thus no attempt is made to state the results in full generality, and we do not preoccupy ourselves with technical conditions such as measurability. For a detailed presentation of Poisson point processes, see e.g. Kingman (1992) or Daley and Vere-Jones (2003).

It is common in modelling to assume that an event *occurs at rate* $r(t)$ *at time* t. Loosely speaking, this means that the probability that the event happens between t and $t + dt$ is independent of its previous occurrences, and is approximately $r(t)\,dt$. The rigorous way to formalize this is to say that the events are distributed according to an (inhomogeneous) Poisson point process with intensity r. Such a process can be seen as a random set of points characterized by the following properties: writing $N(I)$ for the number of points that fall in a fixed set $I \subset \mathbb{R}$,

(i) $N(I)$ is a Poisson random variable with mean $\int_I r(t)\,dt$.

(ii) $N(I)$ and $N(J)$ are independent whenever I and J are disjoint.

Note that the following useful fact is an immediate consequence of (i):

$$\mathbb{P}(N(I) = 0) = \exp\Big(-\int_I r(t)\,dt\Big)\,. \tag{42}$$

Property (ii), often known as the *independent scattering* property, essentially says that Poisson point processes have a "completely random" structure.

From now on, we consider a fixed set $I \subset \mathbb{R}$ such that $\int_I r(t)\,dt < +\infty$. We let P be a Poisson point process with intensity r on I and denote by $N = \mathrm{Card}(P)$ its number of points. Let X be a random point of I with density $t \mapsto r(t)/\int_I r(t)\,dt$, i.e. whose distribution is characterized by

$$\forall A \subset I, \quad \mathbb{P}(X \in A) = \frac{\int_A r(t)\,dt}{\int_I r(t)\,dt}\,, \tag{43}$$

and note in passing that

$$\mathbb{E}(X) = \frac{\int_I t\,r(t)\,dt}{\int_I r(t)\,dt}\,. \tag{44}$$

Then, conditional on $N = n$, P consists of n independent copies of X – that is, for every function φ,

$$\mathbb{E}(\varphi(P) \mid N = n) = \mathbb{E}\Big(\varphi(\{X_i : i = 1, \dots, n\})\Big)\,, \tag{45}$$

where X_i, $i = 1, \dots, n$, are independent copies of X.

A consequence of this is that the expected value of the average of the points in P is $\mathbb{E}(X)$. Formally, if $N > 0$ then we can define a random variable $\bar{X}$ by

$$\bar{X} = \frac{1}{N}\sum_{t \in P} t\,. \tag{46}$$

We then have

$$\mathbb{E}\Big(\bar{X} \,\Big|\, N > 0\Big) = \mathbb{E}(X)\,. \tag{47}$$

Indeed,

$$\mathbb{E}\Big(\bar{X}\,\Big|\,N>0\Big) \;=\; \frac{1}{\mathbb{P}(N>0)}\sum_{n\geqslant 1}\mathbb{E}\Big(\bar{X}\,\Big|\,N=n\Big)\mathbb{P}(N=n)\,, \tag{48}$$

and, for every $n \geqslant 1$,

$$\mathbb{E}\Big(\bar{X}\,\Big|\,N=n\Big) \;=\; \mathbb{E}\Big(\frac{X_1+\cdots+X_n}{n}\Big) \;=\; \mathbb{E}(X)\,. \tag{49}$$

We close this short overview with a fundamental result known as Campbell's formula. This formula states that, for every function f,

$$\mathbb{E}\Big(\sum_{t\in P} f(t)\Big) \;=\; \int_I f(t)\,r(t)\,dt\,. \tag{50}$$

In contrast to (47), which is a consequence of the independent scattering property, Campbell's formula is not specific to Poisson point processes.

B Expression of τ for discrete age structures

In the discrete-time setting, individual i has an integer-valued lifespan T_i and, at each age $t = 1,\ldots,T_i$, produces $M_t^{(i)}$ new individuals. The variables $M_t^{(i)}$ are integer-valued and independent of everything else. Finally, we assume that each variable $M_t^{(i)}$ is a Poisson random variable with mean m_t.

In that setting, the average $\bar{X}_i$ of the ages at which individual i produces offspring is to be defined as

$$\bar{X}_i = \frac{1}{N_i}\sum_{t=1}^{T_i} t\,M_t^{(i)}\,, \tag{51}$$

this definition being valid only when $N_i = \sum_{t=1}^{T_i} M_t^{(i)} > 0$. Note that, in this expression, each age at which i produces offspring is weighted by the number of offspring produced. This is similar to what is done for μ_1, where each offspring contributes to the average age of the parents. Another possibility would be to weight all ages equally, that is, use the variable

$$\bar{Y}_i = \frac{\sum_{t=1}^{T_i} t\,I_t^{(i)}}{\sum_{t=1}^{T_i} I_t^{(i)}}\,, \tag{52}$$

where $I_t^{(i)} = 1$ if $M_t^{(i)} > 0$ and 0 otherwise. Since $\bar{X}_i = \bar{Y}_i$ when individuals cannot give birth to several offspring simultaneously (or, more generally, when the number of offspring produced is either 0 or some constant m), which definition we used did not matter in the continuous-time setting. But now $\bar{X}_i$ and $\bar{Y}_i$ are two acceptable definitions for the average age at which i produces offspring. However, $\bar{Y}_i$ does not lend itself to analysis as easily as $\bar{X}_i$ and, to obtain formula (30) – which is arguably the "natural" discrete-time equivalent of formula (28) – it is $\bar{X}_i$ that should be used. Therefore, we define τ to be $\mathbb{E}\Big(\bar{X}_i\,\Big|\,N_i>0\Big)$.

The reasoning that lead to (28) could be adapted to obtain an expression for τ. However, it is also possible to deduce this expression directly from our results in continuous time. Indeed, our previous calculations are valid for general lifespans, including discrete ones. In that case, for any function φ,

$$\int_0^{+\infty} \varphi(t)\, d\nu(t) \;=\; \sum_{t\geqslant 1} \varphi(t)\, p_t\,, \tag{53}$$

where $p_t = \mathbb{P}(T_i = t)$.

Moreover, observe that if we let the age-specific fertility m be the piecewise constant function defined by

$$m(t) = \sum_{s\geqslant 1} m_s \mathbb{1}_{]s-1,s]}(t)\,, \tag{54}$$

where $\mathbb{1}_{]s-1,s]}$ is the function that evaluates to 1 if $t \in\,]s-1, s]$ and 0 otherwise, then the number of offspring produced by an individual between ages $(t-1)$ and t is a Poisson variable with parameter m_t. Thus, the only difference with the discrete setting is that the ages at which these offspring are produced are uniformly distributed in $]t-1, t]$ instead of all equal to t.

Now, if we take the age-specific fertility to be the function $m^{(\varepsilon)}$ defined by

$$m^{(\varepsilon)}(t) = \sum_{s\geqslant 1} \frac{m_s}{\varepsilon} \mathbb{1}_{]s-\varepsilon,s]}(t)\,, \tag{55}$$

then the number of offspring produced between ages $(t-1)$ and t is still a Poisson variable with parameter m_t, but this time the ages at which these offspring are produced are uniformly distributed in $]t-\varepsilon, t]$. Taking ε to zero, the mean age at childbirth will therefore tend to that of the discrete-time model. We spare the reader the straightforward but somewhat technical argument by which this can be made rigorous. Noting that, for continuous functions g,

$$\int_0^t g(s)\, m^{(\varepsilon)}(s)\, ds \;\xrightarrow[\varepsilon\to 0]{}\; \sum_{s=1}^{t} g(s)\, m_s\,, \tag{56}$$

we obtain the following discrete-time equivalent of (28):

$$\mu_1 \;=\; \frac{1}{c} \sum_{t\geqslant 1} \frac{\sum_{s=1}^t s m_s}{\sum_{s=1}^t m_s} \left(1 - \prod_{s=1}^{t} e^{-m_s}\right) p_t\,, \tag{57}$$

where $p_t = \mathbb{P}(T_i = t) = \ell_t - \ell_{t+1}$, and

$$c = \sum_{t\geqslant 1} \left(1 - \prod_{s=1}^{t} e^{-m_s}\right) p_t\,. \tag{58}$$

C Proof of $\mathbb{E}(\tilde{T}) \to \mathbb{E}(T^2)/\mathbb{E}(T)$ as $m \to 0$

In this section we prove that, when the lifespan T of a fixed individual has a second moment – a condition that is always met in practice – and the age-specific fertility is constant and equal to m, then the expected lifespan of individuals that produce offspring during their lifetime converges to $\mathbb{E}(T^2)/\mathbb{E}(T)$ as $m \to 0$. As seen in the main text, if follows immediately that $\tau \to \mu_1$, both in the continuous setting where offspring production occurs at a constant rate m during the lifetime of individuals and in the discrete setting where individuals produce a Poisson(m) number of offspring at each integer-valued age $t \geqslant 1$.

Proposition 1. *Let T denote the lifespan of a fixed individual, and let $\tilde{T}$ have the distribution of T conditional on reproduction in the model where reproduction happens at constant rate (or in the model where individuals produce* Poisson(m) *offspring at each integer age $t \geqslant 1$ at which they are alive), i.e.*

$$\mathbb{E}\big(\tilde{T}\big) \;=\; \frac{\mathbb{E}\big(T(1-e^{-mT})\big)}{\mathbb{E}(1-e^{-mT})}\,. \tag{59}$$

Then, if $\mathbb{E}(T^2) < +\infty$,

$$\mathbb{E}\big(\tilde{T}\big) \to \frac{\mathbb{E}(T^2)}{\mathbb{E}(T)} \quad \text{as } m \to 0\,. \tag{60}$$

Proof. The following proof is due to Stephen P. Ellner and is a welcome simplification of my original proof.

Let $g(m,t) = (1-e^{-mt})/m$, so that

$$\mathbb{E}\big(\tilde{T}\big) \;=\; \frac{\mathbb{E}(Tg(m,T))}{\mathbb{E}(g(m,T))}\,. \tag{61}$$

Since

$$\frac{\partial}{\partial m} g(m,t) \;=\; \big(1+mt-e^{mt}\big)\frac{e^{-mt}}{m^2} \tag{62}$$

and that $1+x \leqslant e^x$ for all x, we see that $g(m,t)$ increases to t as m decreases to 0. By the monotone convergence theorem, it follows that $\mathbb{E}(g(m,T)) \uparrow \mathbb{E}(T)$ and $\mathbb{E}(Tg(m,T)) \uparrow \mathbb{E}(T^2)$ as $m \downarrow 0$. This terminates the proof. □

D Proof of $\tau \leqslant \mu_1$

In this section we prove that μ_1, as defined by formulas (6) and (7), is always greater than or equal to τ, as defined by formulas (28) and (30). This will be a simple consequence of the following lemma.

Lemma 1. *Let X be a positive random variable, and let g and h be positive functions such that $x \mapsto g(x)/x$ is nondecreasing and $x \mapsto h(x)/x$ is nonincreasing. Then,*

$$\mathbb{E}\left(\frac{g(X)h(X)}{X}\right)\mathbb{E}(X) \;\leqslant\; \mathbb{E}(g(X))\,\mathbb{E}(h(X)) \tag{63}$$

Proof. Let Y be a random variable with the same distribution as X and that is independent of X. We have to show

$$\begin{aligned}
& \mathbb{E}(g(X))\,\mathbb{E}(h(Y)) - \mathbb{E}\left(\frac{g(Y)h(Y)}{Y}\right)\mathbb{E}(X) \;\geqslant\; 0 \\
\iff \quad & \mathbb{E}\left(Xh(Y)\left(\frac{g(X)}{X} - \frac{g(Y)}{Y}\right)\right) \;\geqslant\; 0 \\
\iff \quad & \mathbb{E}\left(Xh(Y)\left(\frac{g(X)}{X} - \frac{g(Y)}{Y}\right)\mathbb{1}_{\{X>Y\}}\right) \\
& \quad + \;\; \mathbb{E}\left(Xh(Y)\left(\frac{g(X)}{X} - \frac{g(Y)}{Y}\right)\mathbb{1}_{\{X<Y\}}\right) \;\geqslant\; 0
\end{aligned} \tag{64}$$

Since $x \mapsto g(x)/x$ is nondecreasing,

$$\left(\frac{g(X)}{X} - \frac{g(Y)}{Y}\right)\mathbb{1}_{\{X<Y\}} \;\leqslant\; 0 \tag{65}$$

and since $x \mapsto h(x)/x$ is nonincreasing,

$$0 \;\leqslant\; Xh(Y)\mathbb{1}_{\{X<Y\}} \;\leqslant\; Yh(X)\mathbb{1}_{\{X<Y\}}\,. \tag{66}$$

As a result,

$$\begin{aligned}
& \mathbb{E}\left(Xh(Y)\left(\frac{g(X)}{X} - \frac{g(Y)}{Y}\right)\mathbb{1}_{\{X<Y\}}\right) \\
\geqslant\; & \mathbb{E}\left(Yh(X)\left(\frac{g(X)}{X} - \frac{g(Y)}{Y}\right)\mathbb{1}_{\{X<Y\}}\right) \\
=\; & -\mathbb{E}\left(Xh(Y)\left(\frac{g(X)}{X} - \frac{g(Y)}{Y}\right)\mathbb{1}_{\{X>Y\}}\right)
\end{aligned} \tag{67}$$

Plugging this into (64) finishes the proof. □

Proposition 2. *Let T denote the lifespan of a fixed individual. Define the random variables M and M^* by*

$$M = \int_0^T m(s)\,ds \quad \textit{and} \quad M^* = \int_0^T s\,m(s)\,ds \tag{68}$$

in the case where reproduction occurs at a constant rate, and by

$$M = \sum_{s=1}^{T} m_s \quad \textit{and} \quad M^* = \sum_{s=1}^{T} s\,m_s \tag{69}$$

in the case where it takes place at integer-valued ages $t \geqslant 1$, so that, in both cases

$$\mu_1 \;=\; \frac{\mathbb{E}(M^*)}{\mathbb{E}(M)} \quad \textit{and} \quad \tau \;=\; \frac{\mathbb{E}\left(\frac{M^*}{M}(1-e^{-M})\right)}{\mathbb{E}(1-e^{-M})}\,. \tag{70}$$

Then, $\tau \leqslant \mu_1$.

Proof. First, observe that M^* is actually a deterministic function of M. Indeed, let ψ (resp. ψ^*) denote the function such that $M = \psi(T)$ (resp. $M^* = \psi^*(T)$). Since ψ is nondecreasing, if we define θ by

$$\theta(x) = \inf\{t \geqslant 0 : \psi(t) \geqslant x\}\,, \tag{71}$$

then we have $M^* = \psi^*(\theta(M))$. To see this, note that $\theta(M) \leqslant T$ by construction and that $\theta(M) < T$ implies $\int_{\theta(M)}^T m(s)\,ds = 0$ (resp. $\sum_{s=\theta(M)}^T m_s = 0$), which in turn implies $\int_{\theta(M)}^T s\,m(s)\,ds = 0$ (resp. $\sum_{s=\theta(M)}^T s\,m_s = 0$). Thus, writing

$$g(x) = \psi^*(\theta(x)) \quad \text{and} \quad h(x) = 1 - e^{-x}\,, \tag{72}$$

we have to prove

$$\mathbb{E}(g(M))\,\mathbb{E}(h(M)) \;\geqslant\; \mathbb{E}\left(\frac{g(M)h(M)}{M}\right)\mathbb{E}(M)\,. \tag{73}$$

Clearly, M is a positive random variable, and the functions g and h are positive. Therefore, all we have to do to finish the proof is to show that $x \mapsto h(x)/x$ is nonincreasing and that $x \mapsto g(x)/x$ is nondecreasing, so that we can apply Lemma 1. First,

$$\frac{d}{dx}\left(\frac{h(x)}{x}\right) \;=\; \frac{e^{-x}(1+x)-1}{x^2} \;\leqslant\; 0\,, \tag{74}$$

since $1 + x \leqslant e^x$. Second,

$$\frac{g(x)}{x} \;=\; \frac{\psi^*(\theta(x))}{\psi(\theta(x))} \;=\; F(\theta(x)) \tag{75}$$

where $F\colon t \mapsto \psi^*(t)/\psi(t)$. The function θ is nondecreasing by construction. The fact that F is nondecreasing can be shown by straightforward calculations, e.g., in the continuous case,

$$\frac{d}{dt}F(t) \;=\; \frac{m(t)\Big(\int_0^t (t-s)m(s)\,ds\Big)}{\Big(\int_0^t m(s)\,ds\Big)^2} \;\geqslant\; 0\,. \tag{76}$$

However, it is more satisfying to see that $F(t)$ can be interpreted as the expectation of a random variable X_t with density $f_t(s) = m(s)\mathbb{1}_{[0,t]}(s)/\psi(t)$ in the continuous case, and with probability mass function $p_s^{(t)} = m_s/\psi(t)$ for $s = 1, \ldots, t$ in the discrete case. It then is easy to see that X_t is stochastically dominated by $X_{t'}$ for $t < t'$, and so if follows immediately that $F(t) = \mathbb{E}(X_t) \leqslant \mathbb{E}(X_{t'}) = F(t')$. □

E Example of calculation of τ

In this section we detail the calculations of τ in the case where the lifespan T of a fixed individual is a geometric variable such that for all $t \geqslant 0$, $\mathbb{P}(T_i = t) = (1-p)p^t$, and the age-specific fertility is constant and equal to m for all ages $t \geqslant 1$.

First, since

$$\frac{\sum_{s=1}^{t} s\, m}{\sum_{s=1}^{t} m} = \frac{t+1}{2} \tag{77}$$

we see that, writing $\tilde{T}$ for the lifespan conditional on reproduction,

$$\tau \;=\; \frac{1}{2}\left(\mathbb{E}\left(\tilde{T}\right)+1\right), \tag{78}$$

where

$$\mathbb{E}\left(\tilde{T}\right) \;=\; \frac{\mathbb{E}\left(T(1-e^{-mT})\right)}{\mathbb{E}(1-e^{-mT})}. \tag{79}$$

Now,

$$\begin{aligned}\mathbb{E}\left(1-e^{-mT}\right) &= 1-\sum_{t\geqslant 0} e^{-mt}\,(1-p)\,p^t \\ &= 1-\frac{1-p}{1-p\,e^{-m}} \\ &= \frac{p\,(1-e^{-m})}{(1-pe^{-m})}\,.\end{aligned} \tag{80}$$

Similarly,

$$\begin{aligned}\mathbb{E}\left(T(1-e^{-mT})\right) &= \sum_{t\geqslant 0} t\,(1-p)\,p^t - \sum_{t\geqslant 0} t\,e^{-mt}\,(1-p)\,p^t \\ &= \frac{p}{1-p} - \frac{(1-p)\,p\,e^{-m}}{(1-p\,e^{-m})^2} \\ &= \frac{p\,(1-e^{-m})(1-p^2e^{-m})}{(1-p)(1-p\,e^{-m})^2}\,.\end{aligned} \tag{81}$$

As a result,

$$\mathbb{E}\left(\tilde{T}\right) = \frac{1-p^2e^{-m}}{(1-p)(1-p\,e^{-m})} \tag{82}$$

and finally,

$$\tau = \frac{1}{2}\left(\frac{1}{1-p}+\frac{1}{1-p\,e^{-m}}\right). \tag{83}$$

F Projection matrices for *A. mexicanum*

In this section we give the projection matrices for *Astrocaryum mexicanum* that are behind Table 1. These matrices are taken from Appendix 6 of Cochran and Ellner (1992), who averaged them from several projection matrices of Pinero et al. (1984). Note that there is a small typo in the projection matrix for the *Low density* model given by Cochran and Ellner (1992): the entry $(9, 8)$ of the projection matrix given is 0.8775, when it should be 0.08775. Correcting this, we find the same descriptors as in their Table 4.

The model is mostly size-based. Stage 1 corresponds to seedlings; stages 2–4 to non-reproducing juveniles and stages 5–10 to full-grown adults. In the matrices below, entries in bold correspond to reproductive transitions.

$$\mathbf{A}^{\text{high}} = \begin{pmatrix} 0 & 0 & 0 & 0 & 0 & \mathbf{1.4792} & \mathbf{8.1560} & \mathbf{9.9513} & \mathbf{14.259} & \mathbf{23.594} \\ 0.037349 & 0.83093 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 \\ 0 & 0.015881 & 0.89666 & 0 & 0 & 0 & 0 & 0 & 0 & 0 \\ 0 & 0 & 0.048969 & 0.95944 & 0 & 0 & 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0.029778 & 0.90496 & 0 & 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 & 0.082074 & 0.91348 & 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 & 0 & 0.086520 & 0.90553 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 & 0 & 0 & 0.094467 & 0.87733 & 0 & 0 \\ 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0.088200 & 0.88642 & 0 \\ 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0.11358 & 0.9950 \end{pmatrix}$$

$$\mathbf{A}^{\text{med.}} = \begin{pmatrix} 0 & 0 & 0 & 0 & \mathbf{0.18385} & \mathbf{4.222} & \mathbf{8.41} & \mathbf{8.8405} & \mathbf{16.676} & \mathbf{19.904} \\ 0.03629 & 0.84127 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 \\ 0 & 0.014582 & 0.91636 & 0 & 0 & 0 & 0 & 0 & 0 & 0 \\ 0 & 0 & 0.058131 & 0.93735 & 0 & 0 & 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0.051565 & 0.91462 & 0 & 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 & 0.065923 & 0.8468 & 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 & 0 & 0.1424 & 0.8725 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 & 0 & 0 & 0.1200 & 0.84332 & 0 & 0 \\ 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0.14800 & 0.913030 & 0 \\ 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0.086966 & 0.9950 \end{pmatrix}$$

$$\mathbf{A}^{\text{low}} = \begin{pmatrix} 0 & 0 & 0 & 0 & \mathbf{0.33} & \mathbf{0.918} & \mathbf{8.0875} & \mathbf{16.606} & \mathbf{13.068} & \mathbf{16.875} \\ 0.030332 & 0.850010 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 \\ 0 & 0.026738 & 0.93928 & 0 & 0 & 0 & 0 & 0 & 0 & 0 \\ 0 & 0 & 0.04966 & 0.94548 & 0 & 0 & 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0.04804 & 0.9185 & 0 & 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 & 0.0815 & 0.9313 & 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 & 0 & 0.0687 & 0.86362 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 & 0 & 0 & 0.13637 & 0.91225 & 0 & 0 \\ 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0.08775 & 0.87867 & 0 \\ 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0.12133 & 0.9950 \end{pmatrix}$$

The estimates of τ and L (the expected lifespan conditional on reproduction) presented in Table 1 were obtained from these matrices using straightforward individual-based simulations. The code is available as an online enhancement to the manuscript.