

The pace of aging: Intrinsic time scales in demography

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Abstract

BACKGROUND

The pace of aging is a concept that captures the time-related aspect of aging. It formalizes the idea of a characteristic life span or intrinsic population time scale. In the rapidly developing field of comparative biodemography, measures that account for inter-species differences in life span are needed to compare how species age.

OBJECTIVE

We aim to provide a mathematical foundation for the concept of pace. We derive desired mathematical properties of pace measures and suggest candidates which satisfy these properties. Subsequently, we introduce the concept of pace-standardization, which reveals differences in demographic quantities that are not due to pace. Examples and consequences are discussed.

CONCLUSIONS

Mean life span (i.e., life expectancy from birth or from maturity) is intuitively appealing, theoretically justified, and the most appropriate measure of pace. Pace-standardization provides a serviceable method for comparative aging studies to explore differences in demographic patterns of aging across species, and it may considerably alter conclusions about the strength of aging.

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1. Introduction

Biodemography is a developing branch of demography that over recent decades has begun to study population dynamics and structure for non-human populations across the tree of life (Carey and Vaupel 2005; Vaupel 2010). With this development, methods to foster comparative research are increasingly sought after. For that purpose, Baudisch (2011) suggested a conceptual framework integrating approaches from life history biology that allows comparison of patterns of aging across species with vastly different life spans. The framework distinguishes between the *pace* of life on one hand and the *shape* of aging on the other. This distinction rests on the observation that different species live and die on different time scales. For example, the life course of a fruit fly is a matter of days, while the life course of humans is a matter of decades. The characteristic length of life for a species is taken as measure of the pace of life. Age and age-specific mortality are standardized by the pace of life to reveal the demographic aging pattern of a species, i.e. the shape of aging.

Pace-standardization of mortality disentangles the time scale (pace) and the change in the risk of death over the life course (shape). Thereby, the pace-shape distinction helps to unravel a problem that gerontologists face when they classify and rank species with respect to aging. Typically, gerontologists use the change in mortality to capture, on a demographic level, how organisms age. They compare rates of aging within and among species (Finch 1990). Rates, however, are given per unit time, say years, which leads to unfair comparisons when it comes to species that differ substantially in life span. Baudisch (2011) emphasizes that rates need to be pace-standardized to be meaningfully compared.

In life history biology, pace-standardization has been applied to facilitate inter-species comparison. Pearl suggested plotting survival curves over centiles of equivalent life span (Pearl 1928), and later over percentage deviation from mean duration of life (Pearl and Miner 1935; Deevey 1947, 1950). Utilizing this standardized time scale, Pearl and Miner then suggested the now classic distinction between Type I survivorship (rectangular, corresponding to increasing mortality with age), Type II survivorship (diagonal, corresponding to constant mortality with age) and Type III survivorship (L-shaped, corresponding to decreasing mortality with age), which are related to the shape of aging, as discussed by Baudisch (2011). To standardize survivorship curves, Lynch et al. (2010) used maximum life span as their measure of pace, whereas Weon and Je (2011, 2012) used the length of “characteristic life”, which they give as the age at which survival reaches a value of $\exp(-1)$ (in the Weibull model, this age equals the value of the scale parameter). Eakin (1994) suggested the use of an intrinsic time scale derived from standardizing by life expectancy and discussed its relevance to the investigation of biological populations, an approach he later expanded (Eakin and Witten 1995). Another way of accounting

for different time scales has been suggested in the context of classic demography. Lee and Goldstein (2003) investigated rescaling the life cycle by means of a proportionality assumption, which under some circumstances is justified when comparing human populations.

Demographers typically use standardization methods when it comes to comparing rates across populations that differ in population structure to avoid confounding compositional effects (Preston, Heuveline, and Guillot 2001). By contrast, pace-standardization is not concerned with age-structure. In fact, differences in population composition will be the rule rather than the exception for most applications of pace-standardization. Pace-standardization solely aims to account for differences in time scales of life that differ across species. Differences in age structure and the spread in age at death are captured by the shape of aging. Shape measures whether mortality is increasing, constant, or decreasing over age, and whether these changes are more or less pronounced. Pace and shape are two complementary concepts that help characterize the aging pattern of a species in a comparative framework (Baudisch 2011).

Analysis of shape relies on the use of intrinsic time scales based on values of characteristic life span, i.e., on pace. A sound foundation for quantifying pace is therefore required. With the present study we thus wish to contribute a systematic investigation of alternative measures of pace. We provide a general approach to the pace-standardization of demographic functions that does not hinge (in the sense specified below) on the particular choice of a measure. After deriving a list of desired mathematical properties of pace measures that enable us to evaluate the quality of each measure, we suggest different candidates. Subsequently, we formally explain the method of pace-standardization. It is a way of rescaling distributions according to their own specific pace value in order to make them comparable *beyond* the dimension of pace. We show that if two distributions are the same when standardized with respect to some pace measure, this will also be the case with respect to any other pace measure, as long as the pace measures satisfy a certain scaling property. Finally, we illustrate the significance of the procedure for comparative research on aging by showing the effect of pace-standardizing on several parametric mortality models (linear, Gompertz, Weibull). Results and implications are discussed.

It should be noted that, given our focus on studying aging as captured by increasing mortality over age, in this paper we focus solely on pace measures of death. We wish to emphasize that reproduction is an equally important factor in the demographic description of populations. Therefore it is desirable to extend this framework to account for the pace of reproduction. From that perspective and from the growing interest in evolutionary biodemography, generation time is a quantity that qualifies as an important candidate for a pace measure of reproduction (see e.g., Coale 1972; Charlesworth 1994). Other measures such as first or median age of reproduction, interbirth interval, and average or maximum number of offspring per reproductive event could further capture the pace

of reproduction, though this is beyond the scope of the current work and needs to be thoroughly investigated in future research.

A notation alert: Demographic quantities are given in continuous formulation here and follow standard demographic notation. The survival function, which gives the probability of survival up to age x , is denoted as $l(x)$. If X is a positive random variable (life spans), the corresponding survival function is denoted as l_X . The force of mortality or age-specific hazard is denoted as μ with

$$\mu(x) = -\frac{l'(x)}{l(x)}.$$

The probability density function of death is

$$f(x) = -l'(x) = \mu(x)l(x). \quad (1)$$

Remaining life expectancy at age x is given by

$$e(x) = \frac{1}{l(x)} \int_x^\infty l(a)da.$$

A summary of notation and symbols is given in Appendix B.

2. Properties and measures

What is the characteristic length of life? Previous approaches listed above apply a range of different measures commonly known to demographers, such as life expectancy, modal age at death, quantile measures of life span, or maximum life span. What measure should be preferred depends on the context. We will investigate which of the available measures is the most appropriate candidate to capture the pace of aging. As evaluation criteria we use a list of properties provided in the following, that, if fulfilled, facilitate pace-standardized analysis in demography.

2.1 Properties of pace

A pace measure M is a functional $M : l \mapsto M(l)$ that assigns a non-negative real number $M(l)$ with dimension 'time' to every survival function l . The following properties are desirable for pace measures.

P1: For all X it holds that

$$M(l_{rX}) = r M(l_X) \quad \forall r \geq 0. \quad (2)$$

This scaling property ensures that if everybody's life span changes by the factor r , then the value of pace changes by this factor as well (in more technical terms, it means that the functional M is scale-invariant).

P2: For all X it holds that

$$M(l_{X+s}) = M(l_X) + s \quad \forall s \geq 0. \quad (3)$$

If everybody gains exactly $s \geq 0$ years of life, the value of pace is the original pace value plus s . This would imply that no one dies before age s . While an age below which the probability of death is zero seems unrealistic, this property is conceptually helpful, because it follows that **P1** and **P2** can be summarized by the simple property

$$M(l_{s+rX}) = s + rM(l_X) \quad \text{for } r, s \geq 0, \quad (4)$$

which means that if X is transformed linearly, $M(l_X)$ is transformed accordingly.

Expression (4) implies that a population in which everybody lives for exactly s years has a pace value of s , because

$$M(l_s) = M(l_{s+0 \cdot s}) \stackrel{(4)}{=} s + 0 \cdot M(l_s) = s.$$

This appeals to intuition, as the concept of pace formalizes the idea of a characteristic life span.

P3:

$$\mu_1(x) \geq \mu_2(x) \quad \forall x \quad \Rightarrow \quad M(l_1) \leq M(l_2). \quad (5)$$

If two distributions are given so that the age-specific hazard of the first one is at all ages higher than or equal to the age-specific hazard of the second one, then the pace value of the first distribution is lower or equal to the pace value of the second one. This property reflects the fact that while pace captures the characteristic life span, its inverse is at the same time supposed to capture the level of the force of mortality. Thus, property **P3** is important, because it emphasizes that the concept of pace is not only one of central tendency, but has an additional focus on the force of mortality μ .

2.2 Measures of pace

The measures presented in this subsection satisfy **P1**, **P2**, and **P3**. For clarity, the (simple) proofs have been moved to Appendix A.

1. An obvious first measure is the mean age at death (or life expectancy at age 0), which captures the average life span in the population:

$$e_0 = \int_0^\infty x f(x) dx = \int_0^\infty l(x) dx = \int_0^\infty \frac{1}{\mu(x)} f(x) dx. \quad (6)$$

This is a quantity widely used in demography, and it is a natural, straightforward answer to the question about a characteristic life span.

2. A generalization of e_0 is given by the class of measures

$$M_g = \int_0^\infty g(l(x)) l(x) dx, \quad (7)$$

where g denotes any absolutely continuous and monotonically non-decreasing function

$$[0, 1] \rightarrow [0, 1]$$

with $g(1) = 1$. For $g \equiv 1$ one gets e_0 . Other choices of g can also relate M_g to known demographic quantities. For example, consider

$$g_1(x) = x.$$

Then

$$M_{g_1} = \int_0^\infty l^2(x) dx = e_0(1 - G),$$

where G denotes the Gini coefficient, a measure of inter-individual inequality - see Hanada (1983) for a proof of the right hand side of the equality above and Shkolnikov, Andreev, and Begun (2003) for an overview of the use of G in demography.

3. Another class of pace measures $\{M_p | 0 < p < 1\}$ is defined in the following way: For every fixed $0 < p < 1$ let M_p be the age (or rather the minimal age, in case it is not unique) at which the survival function reaches p :

$$M_p(l) = \inf\{x | l(x) \leq p\}.$$

$M_{0.5}$ is the median, the age up to which half of the cohort survives. For p close to 0, say $p = 0.01$, M_p corresponds to the age up to which only a small percentage of a given cohort survives (on average). Thus, in this case M_p provides a continuous approximation to a quantity frequently used in comparative aging research: ω , the longest life span observed. For some populations, this might be the only information available.

Pace measures e_0 , M_g and M_p have several advantages and disadvantages from a demographic point of view.

Pace measure e_0 has the advantage of satisfying an additional, demographically relevant property:

PA1: If l_1, \dots, l_n are survival functions and $w_1, \dots, w_n > 0$ are weights (so that $\sum_{k=1}^n w_k = 1$), then

$$l = \sum_{k=1}^n w_k l_k \quad \Rightarrow \quad M(l) = \sum_{k=1}^n w_k M(l_k), \quad (8)$$

which means that the pace value of the mixture distribution is the weighted mean of the pace values of the component distributions. For a proof see Appendix A. Depending on the application, **PA1** can be more or less desirable; in the context of frailty models for example, it may be important. e_0 is the only measure in the list above that satisfies **PA1**; in particular, **PA1** is not satisfied by M_g if g is not constant.

One disadvantage of e_0 (and more generally, of all pace measures M_g as defined above) is that the value of the integral can be infinite (for distributions where the age-specific hazard decreases strongly over age, or more generally heavy-tailed distributions), although this is unlikely to be found in demographically relevant life span distributions.

An advantage of $M_g = \int_0^\infty g(l(x))l(x)dx$ if g is not constant (i.e. if $M_g \neq e_0$) can be that - since g is increasing - the later ages contribute less to the overall value of the measure. Thus the measure is more robust with respect to life spans that are very long, i.e. to outliers.

The quantile pace measures M_p do not satisfy **PA1**. They do however satisfy a property which generalizes (4) to hold for a wider range of transformations instead of only linear ones:

PA2: If the random variable X has a continuous life span distribution and h is a nonnegative, monotonically non-decreasing function (such as - but not restricted to - $h(x) = s + rx$), then

$$M(l_{h(X)}) = h(M(l_X)).$$

For a measure satisfying **PA2** it therefore holds that if X is transformed via h , the value of the pace measure transforms accordingly. It can be shown that the quantile measures M_p are the only quantities to satisfy **PA2** (see Appendix A). The property is interesting from a theoretical point of view, but it might not have an immediate relevance for demography.

An advantage of M_p (for any $0 < p < 1$) is that it is defined even for some distributions with infinite mean, and generally requires less data to be computed. A disadvantage is the lack of sensitivity - adding an arbitrary number of members to a population does not change the pace value as long as their life spans exceed this pace value. Thus, long

life spans not only contribute less to the value of the measure (which might be desired if the value is supposed to be less sensitive to outliers), they do not change its value at all.

As an observation, notice that the arithmetic average of any finite number of pace measures that satisfy **P1** and **P2** satisfies **P1** and **P2** itself. For if M_1, \dots, M_n satisfy (4), then for

$$M = \frac{1}{n} \sum_{k=1}^n M_k$$

it holds that

$$M(l_{s+rX}) = \frac{1}{n} \sum_{k=1}^n M_k(l_{s+rX}) = \frac{1}{n} \sum_{k=1}^n (rM_k(l_X) + s) = rM(l_X) + s.$$

If M_1, \dots, M_n satisfy **P3** in addition, then so does M .

A classical measure of central tendency is the mode of a distribution, i.e. the age at which most deaths occur. However, while the mode can be useful in demographic context (see e.g. Canudas Romo 2008, 2010; Cheung and Robine 2007), it is not a good measure of pace. Even provided that it is unique (as is certainly the case for human populations if infant ages are omitted, but might not be the case for other species), the mode does not satisfy crucial property **P3** - see the appendix for a counterexample. Thus, this measure is not listed here.

3. Pace-standardization

3.1 Method

Any pace measure M can be used to introduce a population-specific intrinsic time scale. Let x^s denote standardized age, which is a dimensionless number measuring age in units of pace. It is therefore defined by dividing chronological age x by the value of pace:

$$x^s = \frac{x}{M}. \quad (9)$$

Standardized survival curves - functions of standardized age - can then be defined via

$$l^s(x^s) := l(x) = l(M x^s). \quad (10)$$

The value of standardized survival at any standardized age is defined as the value of survival at the corresponding unstandardized age. This corresponds to a scaling (shrinking/stretching) along the x-axis with scaling factor $\frac{1}{M}$. Expressions (9) and (10) can be

used to derive an expression for the standardized hazard

$$\mu^s(x^s) = -\frac{1}{l^s(x^s)} \frac{dl^s(x^s)}{dx^s} = -M \frac{1}{l(x)} \frac{dl(x)}{dx} = M\mu(x) (= M\mu(Mx^s)), \quad (11)$$

which corresponds to a scaling along both the x- and the y-axis, with the scaling factors being M for the y-axis and $\frac{1}{M}$ for the x-axis. These standardized functions are time-independent.

Note that the pace measure e_0 can be interpreted as the reciprocal of the population average of the force of mortality in a twofold sense: Firstly, because

$$\bar{\mu} = \int_0^\infty \mu(x)c(x)dx = \int_0^\infty \mu(x) \frac{l(x)}{e_0} dx \stackrel{(1)}{=} \frac{1}{e_0},$$

where $c(x) = \frac{l(x)}{e_0}$ denotes the age distribution in the stationary population. Secondly, because

$$\frac{1}{e_0} = \frac{\int_0^\infty f(x)dx}{\int_0^\infty \frac{1}{\mu(x)} f(x)dx}$$

and the right hand side of the equation is the weighted harmonic mean of μ with the weights given by the pdf f . Therefore, standardizing μ with $M = e_0$ is conveniently accomplished by dividing age by average life span and mortality by average mortality,

$$x^s = \frac{x}{e_0}, \quad \mu^s(x^s) = \frac{\mu(x)}{\bar{\mu}}, \quad (12)$$

which appeals to intuition.

Within the standardized framework, all mortality patterns have the same pace value (namely 1), because

$$\begin{aligned} l_X^s(x^s) &= l_X(M(l_X)x^s) = l_{\frac{X}{M(l_X)}}(x^s) \quad \forall x^s \\ &\stackrel{\mathbf{PI}}{\implies} \\ M(l_X^s) &= M(l_{\frac{1}{M(l_X)}}X) = \frac{1}{M(l_X)} \cdot M(l_X) = 1. \end{aligned}$$

This property justifies the name 'standardization'.

As each demographic function can be expressed in terms of survival l , standardized in (10), one can derive standardized expressions for these functions as well:

$$f^s(x^s) = Mf(x), \quad e^s(x^s) = \frac{e(x)}{M}. \quad (13)$$

3.2 Equivalence of pace measures with respect to standardizing

Assume two pace measures M_1 and M_2 , both satisfying **P1**. Denote standardization with respect to M_1 and M_2 with the upper indices s_1 and s_2 respectively. Assume further two positive random variables with survival functions l_{X_1} and l_{X_2} so that

$$l_{X_1}^{s_1} = l_{X_2}^{s_1}. \quad (14)$$

Then it also holds that

$$l_{X_1}^{s_2} = l_{X_2}^{s_2}.$$

This means that if two distributions of ages at death give the same standardized distribution with respect to measure M_1 , they also give the same standardized distribution with respect to measure M_2 .

Proof: From (14) it follows that

$$l_{X_1}(zM_1(l_{X_1})) = l_{X_2}(zM_1(l_{X_2})) \quad \forall z,$$

or, with $y = zM_1(l_{X_1})$:

$$l_{X_1}(y) = l_{X_2}\left(y \frac{M_1(l_{X_2})}{M_1(l_{X_1})}\right) \quad \forall y, \quad (15)$$

which implies

$$l_{X_1} = l_{\left(\frac{M_1(l_{X_1})}{M_1(l_{X_2})}\right)X_2}.$$

Because M_2 satisfies **P1**, this implies

$$M_2(l_{X_1}) = \frac{M_1(l_{X_1})}{M_1(l_{X_2})} M_2(l_{X_2}),$$

so that

$$\frac{M_1(l_{X_2})}{M_1(l_{X_1})} = \frac{M_2(l_{X_2})}{M_2(l_{X_1})}.$$

Inserting this into (15) gives

$$l_{X_1}(y) = l_{X_2}\left(y \frac{M_2(l_{X_2})}{M_2(l_{X_1})}\right) \quad \forall y,$$

and thus with $w = \frac{y}{M_2(l_{X_1})}$

$$l_{X_1}(wM_2(l_{X_1})) = l_{X_2}(wM_2(l_{X_2})) \quad \forall w,$$

which implies

$$l_{X_1}^{s_2} = l_{X_2}^{s_2}.$$

Q.E.D.

Pace-standardization can be seen as providing an equivalence relation on life span distributions: Two distributions are equivalent if they give the same standardized distribution. The result above states that if two pace measures satisfy property **P1**, they provide the same partition into equivalence classes, regardless of how their actual values might differ.

3.3 Mortality: Standardized vs. unstandardized perspective

The age-specific force of mortality (or hazard of death) is an important quantity for biodemographic research on aging patterns of different species, and standardized depictions of mortality and other vital rates have recently been used to reveal the diversity of patterns across species (Jones et al. 2014). It is therefore instructive to see how pace-standardizing simple hazard functions can give results that drastically differ from the unstandardized perspective. For this subsection the pace measure is $M = e_0$.

First, assume a linearly increasing force of mortality

$$\mu(x) = bx + c$$

with fixed $b = 0.0001$, and let c vary between 0.001 and 0.01. Figure 1 depicts the resulting hazard functions with the 'normal' perspective (i.e. $\mu(x)$ over chronological age x) on the left and the pace-standardized perspective (i.e. $\mu^s(x^s)$ over $x^s = \frac{x}{e_0}$) on the right. Lighter color indicates higher values of c .

Comparing these two alternative views reveals a striking difference: While in the normal view all the curves have the same slope, so that a common interpretation would conclude that all the populations in question experience the same strength of aging, the pace-standardized view reveals that the higher c is, the lower the slope of the curve turns out to be, i.e. the less aging the population in question experiences.

As another example, assume Gompertz mortality defined as

$$\mu(x) = ae^{bx}$$

with fixed $b = 0.1$, and let a vary between 0.00001 and 0.0002. Figure 2 depicts the resulting hazard functions, again both from normal and pace-standardized perspective. Lighter color corresponds to higher values of a (hazard is presented on a log-scale).

Again, there is a clear difference between the two panels. Because parameter b is held constant, the logarithm of the force of mortality in the normal view always has the same

slope - and thus, the common interpretation of b as the 'rate of aging' would conclude that all the populations in question experience the same strength of aging. But the pace-standardized view reveals that the higher a is, the lower the slope of log-mortality turns out to be, i.e., that the pace-standardized rate of aging be_0 implies less aging for higher values of a .

As a last example, assume Weibull mortality defined as

$$\mu(x) = \alpha x^\beta$$

with fixed $\beta = 2$, and let α vary between 0.00005 and 0.0005. Figure 3 depicts the resulting hazard functions, again both from both normal and pace-standardized perspective. Lighter color indicates higher values of α .

In this case, it turns out that all the pace-standardized schedules fall on the same line, i.e., that parameter α does not influence the pace-standardized hazard function *at all* (this can also be shown analytically, see Appendix A). Parameter β is all that matters for the shape of the standardized curve. While Ricklefs' "rate of aging" defined as $\omega = \alpha^{\frac{1}{\beta+1}}$ (Ricklefs 1998) would have assigned different rates to each curve, no differences in shape are observed in the framework that is suggested here.

Figure 1: Comparison of normal (left panel) vs. pace-standardized (right panel) view of linear hazard functions

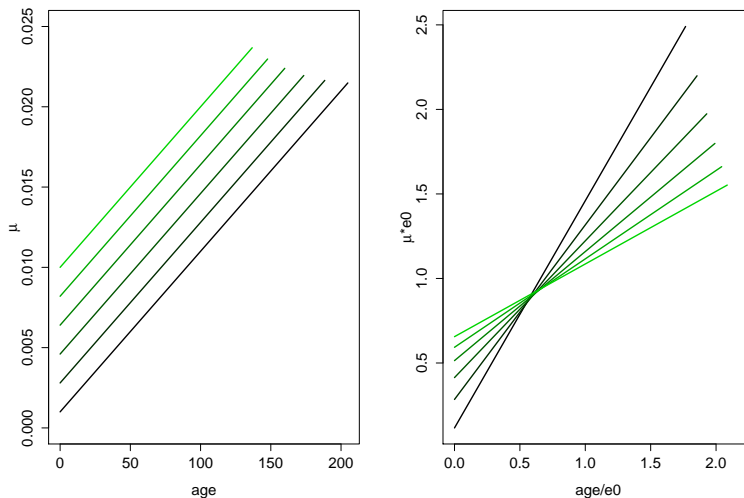


Figure 2: Comparison of normal (left panel) vs. pace-standardized (right panel) view of Gompertz hazard functions

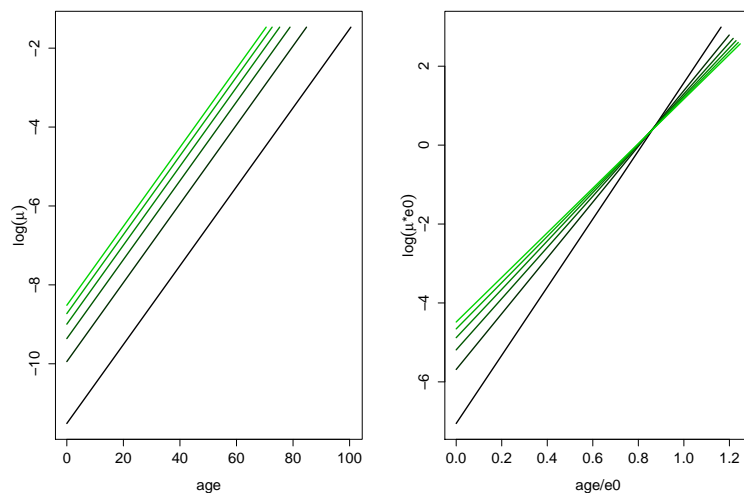
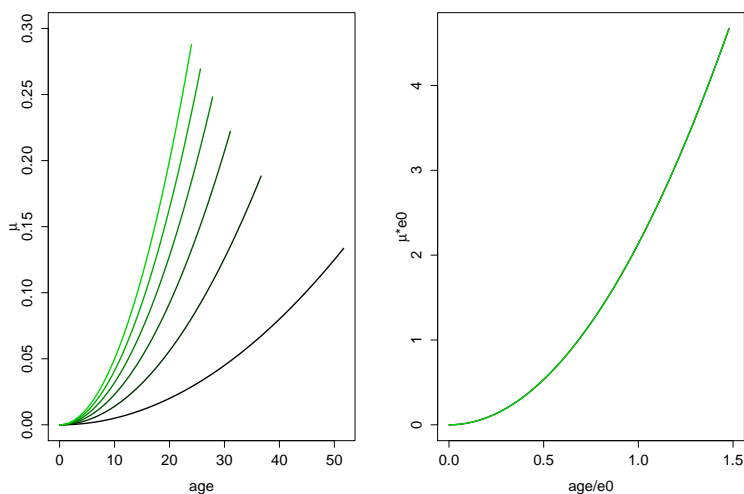


Figure 3: Comparison of normal (left panel) vs. pace-standardized (right panel) view of Weibull hazard functions



4. Conclusion

Comparative aging research that aims to find and measure differences in demographic aging patterns across species is an exciting and rapidly developing field (Baudisch and Vaupel 2012; Jones et al. 2014; Baudisch et al. 2013), and it crucially hinges on serviceable methods.

To facilitate meaningful comparison between different species, with this paper we provide a systematic discussion of 1) how the time aspect of aging can be measured, 2) how pace measures can be used as an intrinsic time scale to create pace-standardized demographic functions, and of 3) why this procedure does not hinge on the particular choice of a measure (in the sense specified in 3.2). We conclude that of all the candidates for pace measures discussed here, e_0 is the one to be preferred (if its value is available), because it additionally satisfies property **PA1** concerning mixture distributions, which is demographically relevant. All measures of life span commonly used in demographic applications have been discussed in the present analysis, although further candidates may exist.

The examples in 3.3 show that the difference between unstandardized and standardized perspectives can be immense if one compares mortality curves. Conclusions about the strength of aging may change and even reverse when switching perspectives. Therefore, the methods discussed here may prove useful to researchers who investigate differences in demographic aging patterns between different populations/species - in particular if the populations in question differ significantly with respect to how long they live, i.e., in their pace values.

5. Acknowledgments

We thank Trifon Missov, James W. Vaupel, and two anonymous reviewers for providing comments and helpful suggestions on the manuscript. We also thank Ruth Archer for thorough language editing.

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Appendix

A Properties and measures

Note that

$$l_{s+rX}(x) = \begin{cases} 1 & x \leq s, \\ l_X\left(\frac{x-s}{r}\right) & x > s. \end{cases} \quad (16)$$

This relationship is needed for the following proofs.

Proof that M_g satisfies (4) for any absolutely continuous and monotonically non-decreasing

$$g : [0, 1] \rightarrow [0, 1]$$

with $g(1) = 1$:

$$\begin{aligned} M_g(l_{s+rX}) &= \int_0^\infty g(l_{s+rX}(x)) l_{s+rX}(x) dx = \\ &\stackrel{(16)}{=} \int_0^s g(1) dx + \int_s^\infty g\left(l_X\left(\frac{x-s}{r}\right)\right) l_X\left(\frac{x-s}{r}\right) dx = \\ &\stackrel{z=\frac{x-s}{r}}{=} s + r \int_0^\infty g(l_X(z)) l_X(z) dz = s + r M_g(l_X). \end{aligned}$$

Q.E.D.

Proof that for each p , M_p satisfies (4):

Let $0 < p < 1$ be fixed. For every x with

$$l_X(x) \leq p$$

it holds that

$$l_{s+rX}(s+rx) \stackrel{(16)}{=} l_X(x) \leq p.$$

Conversely, any y with $l_{s+rX}(y) \leq p < 1$ has to be $> s$ and for $x = \frac{y-s}{r}$ it holds that

$$l_X(x) = l_{s+rX}(y) \leq p.$$

It follows that

$$\{y | l_{s+rX}(y) \leq p\} = \{s+rx | l_X(x) \leq p\},$$

and thus the infimum of both sets is also the same.

Q.E.D.

Proof that M_g satisfies **P3** for any absolutely continuous and monotonically non-decreasing

$$g : [0, 1] \rightarrow [0, 1]$$

with $g(1) = 1$:

Because

$$\mu_1(x) \geq \mu_2(x) \quad \forall x \quad \Rightarrow \quad l_1(x) \leq l_2(x) \quad \forall x,$$

and, because g is monotonically non-decreasing, also

$$g(l_1(x)) \leq g(l_2(x)) \quad \forall x,$$

it follows that

$$M_g(l_1) = \int_0^\infty g(l_1(x))l_1(x)dx \leq \int_0^\infty g(l_2(x))l_2(x)dx = M_g(l_2).$$

Q.E.D.

For the quantile measures M_p , **P3** follows directly from the fact that

$$\mu_1(x) \geq \mu_2(x) \quad \forall x \quad \Rightarrow \quad l_1(x) \leq l_2(x) \quad \forall x.$$

Proof that the mode of a distribution does not satisfy **P3**:

Assume linearly increasing mortality $\mu(x) = bx + c$. By setting $f'(x) = l(x)(\mu'(x) - \mu^2(x)) = 0$ in order to find the maximum of f , one finds that the mode is $\frac{1}{\sqrt{b}} - \frac{c}{b}$. If $c > 0$ is kept fixed, this value is 0 when $b = c^2$, then increases with b as long as $b \leq 4c^2$, and afterwards decreases as b increases. For example, if $c = 0.01$, for $b_1 = 3c^2 = 0.0003$ the mode is ≈ 24.4 , while for $b_2 = 4c^2 = 0.0004$, the mode is 25 and thus bigger than for b_1 . But $b_1 \leq b_2$ means that $\mu_1(x) \leq \mu_2(x) \quad \forall x$, which according to **P3** would imply $M(l_1) \geq M(l_2)$, which is not the case. Thus the mode does not in general satisfy **P3**.
Q.E.D.

Proof that of all the measures presented, only e_0 satisfies **PA1**:
For the measures M_g assume

$$l_1(x) = \begin{cases} 1 & 0 \leq x \leq 2, \\ 0 & x > 2, \end{cases}$$

$$l_2(x) = \begin{cases} 1 & 0 \leq x \leq 1, \\ 0 & x > 1, \end{cases}$$

Then for any given $0 < w < 1$ consider $l_w = wl_1 + (1 - w)l_2$, so that

$$l_w(x) = \begin{cases} 1 & 0 \leq x \leq 1, \\ w & 1 < x \leq 2, \\ 0 & x > 2. \end{cases}$$

Since $M_g(l_1) = 2$ and $M_g(l_2) = 1$, it holds that

$$wM_g(l_1) + (1 - w)M_g(l_2) = 1 + w.$$

On the other hand,

$$M_g(l_w) = \int_0^1 g(1) dx + \int_1^2 g(w)w dx = 1 + wg(w),$$

so that if **PA1** holds, $g(w) = 1$. But this is true for *any* $0 < w < 1$, so that $g \equiv 1$ is the only function for which M_g gives a measure satisfying **PA1**.

For the quantile measures M_p assume $l_1(x) = e^{-x}$, $l_2(x) = e^{-2x}$, $w_1 = w_2 = 0.5$ and a $0 < p < 1$ fixed. Then $M_p(l_1) = -\log(p)$ and $M_p(l_2) = -\frac{1}{2}\log(p)$. For $l(x) = 0.5(l_1(x) + l_2(x))$ it holds that

$$l\left(\frac{1}{2}(M_p(l_1) + M_p(l_2))\right) = l\left(-\frac{3}{4}\log(p)\right) = \frac{1}{2}(p^{\frac{3}{4}} + p^{\frac{3}{2}}) \neq p,$$

so that

$$M_p(l) \neq w_1M_p(l_1) + w_2M_p(l_2).$$

Q.E.D.

Proof that if a measure M satisfies **PA2**, then there exists a $0 < p < 1$ with $M = M_p$ (with M_p referring to the quantile measures as defined in subsection 2.2):

The proof relies on the probability integral transform. If F_Y is the cumulative distribution function of the random life span variable Y , then the random variable $Z = F_Y(Y) = 1 - l_Y(Y)$ is uniformly distributed on $[0, 1]$, and the cumulative distribution function of $F_Y^{-1}(Z)$ is F_Y . $F_Y^{-1}(u) = \inf\{y | F_Y(y) \geq u\}$ is a monotone non-decreasing function, so that **PA2** with $h = F_Y^{-1}$ and $X = Z$ gives

$$M(l_Y) = F_Y^{-1}(M(l_Z)),$$

and thus

$$F_Y(M(l_Y)) = F_Y(F_Y^{-1}(M(l_Z))) = M(l_Z),$$

where $p = M(l_Z)$ is a fixed value not depending on Y , so that $M(l_Y) = M_p(l_Y)$.
Q.E.D.

Proof that for the Weibull mortality $\mu(x) = \alpha x^\beta$, parameter α does not influence the standardized distribution, i.e., that $\mu_1(x) = \alpha_1 x^\beta$, $\mu_2(x) = \alpha_2 x^\beta$ implies $\mu_1^s = \mu_2^s$:

We choose e_0 as the pace measure (as shown in 3.2, the particular choice of a pace measure does not matter). If $\omega = \alpha^{\frac{1}{\beta+1}}$, then

$$\mu(x) = \omega(\omega x)^\beta \text{ and } l(x) = e^{-\frac{1}{\beta+1}(\omega x)^{\beta+1}}.$$

This implies

$$e_0 = \int_0^\infty l(x) dx \stackrel{z=\omega x}{=} \frac{1}{\omega} \int_0^\infty e^{-\frac{z^{\beta+1}}{\beta+1}} dz = \frac{C(\beta)}{\omega}$$

with a function $C(\beta)$ depending only on β . This means

$$l^s(x^s) = l(x^s e_0) = e^{-\frac{1}{\beta+1}(C(\beta)x^s)^{\beta+1}},$$

which does not depend on α . Thus μ^s also does not depend on α .

Q.E.D.

B Overview of notation

Symbol	Meaning
x	age
ω	maximum life span
X, Y	random variables (of age at death)
M_g	Pace Measure (specified by subscript)
$l(x)$	Survival function
$l_X(x)$	Survival function corresponding to rand. var. X
$\mu(x)$	Force of mortality, age-specific hazard
$f(x)$	Probability density function of age at death
$e(x)$	Remaining life expectancy (as function of x)
e_0	Life expectancy at age zero
$x^s, l^s, \mu^s, f^s, e^s$	Quantities standardized
a, b, c, α, β	parameters of mortality functions

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