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Human Lifetimes: Finite But Not Necessarily Bounded

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Abstract

Is the human life span intrinsically finite or potentially unlimited? We build on previously validated research and analyses in order to suggest a statistical model in which human lifetimes are viewed as *individually finite* but *unbounded in aggregate*. In the model, lifetimes are theoretically unbounded but the probability of living to an extreme age is negligible, so lifetimes are *effectively limited*. Our model incorporates a *mortality hazard rate plateau* and a *late-life mortality deceleration effect* in conjunction with a newly observed *advanced age mortality acceleration*, thereby resolving apparent contradictions in earlier discussions.

1 Introduction

Based on detailed analyses of high-quality data in Huang, Maller and Ning [1], Dong, Milholland & Vijg [2] and others, we suggested in [3] a new way of modelling the distribution of the length of human lifetimes. In [1] we fitted to the life-lengths recorded in each year-of-birth cohort of the data a model

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consisting of a Gompertz distribution up till a data determined age, followed by an extreme value distribution for greater ages. This model, which fitted the data well, described each cohort in [1] individually. Using the insights gained from this analysis, we constructed in [3] a "mixture model" for the lifetime distribution of the whole population.

In later sections we review briefly how this model informs published discussions relating to the possible existence of an upper limit to human lifetimes, how advanced age mortality "acceleration and deceleration" effects are included in it, and how the "three laws of biodemography" are satisfied by it.

The analysis in [1] used a high-quality Netherlands dataset including mortality data from adults aged 65+ (231,129 females and 73,788 males). Life tables were constructed separately for females and males born in each 1-year, year-at-birth, cohort from 1893 to 1908. The data extends to 112 years of age for females and 110 years for males (maxima over all cohorts) and contains a substantial number of individuals aged more than 95 years at death. A model consisting of a traditional Gompertz distribution up till a data determined threshold age N, followed by an extreme value distribution (a generalized Pareto distribution, GPD) for ages greater than N was fitted to the data.

The mathematical formulation of the GPD contains a parameter which determines whether the right extreme of the fitted distribution is finite or not. This effectively constitutes a test for whether the data indicates a finite or unbounded lifetime for the individuals in the population. In each of the 32 cohorts of the Netherlands data, and for both females and males, the fitted model strongly suggested a finite upper limit to individuals' lifetimes, around 110 years for males and slightly higher for females, around 114 years. The same analysis on a smaller Australian data set (18 5-year cohorts, 1860-1900) came to the same conclusion: finite lifetimes with upper bound varying randomly over the cohorts.

Assuming a finite lifetime model applied overall to the population would raise the objection that there is, in current biological understanding, no evidence for such a "hard" upper limit to human lifetimes. We finesse this problem by allowing a finite lifetime for each person individually but introduce a measure to randomise that finite upper limit over the population. This idea is related to the "frailty" concept introduced in Vaupel et al. [4].

Altogether, this suggests a super-population model in which *the lifetime distribution for an individual is bounded above (finite) but with an upper limit which itself varies randomly over the population according to some distribu-*

tion. A population model describing this situation can be constructed by randomising over the finite upper limit of an assumed generalised Pareto lifetime distribution for each person. The resulting "mixture model" has the intuitively appealing feature that each individual has a finite lifetime but a small though non-zero probability of living to an arbitrary life length.

Potentially, such a distribution may be unbounded or may have a definite upper bound. But the observed distributions of the cohort lifetimes in [1] suggest no such definite upper bound.

The mixture model resolves contradictions which have bedevilled earlier discussions. The paradox of finding a finite upper lifespan limit (in [1], [2] and other studies discussed below), and the late-life mortality deceleration effect with its accompanying mortality plateau observed in earlier studies (Barbi *et al.* [5]), is resolved by our observation of the existence of an *advanced age mortality acceleration*, in addition to those other effects. See [3] for detailed discussion.

2 The mixture model for lifetimes

In the model proposed by Huang et al.[6] the lifetime T of a person in the population is written as $T = N + Y$, where N is a data-determined age (typically around 96-98 years in the Netherlands and Australian cohorts) at which the lifetime distribution transitions from a Gompertz to a generalized Pareto distribution (GPD). Thus random variable Y has the generalized Pareto density

$$f_Y(y, \kappa, \theta) = \frac{1}{\theta}(1 - \kappa y/\theta)^{1/\kappa - 1},\ 0 \le y \le \theta/\kappa, \tag{1}$$

where κ and θ are positive parameters. The positivity of κ (and θ) signals that the lifetime distribution has the finite upper bound θ/κ. Our main innovation is to regard κ as an observation on a random variable K, specific to the individual person, to be randomised over the population as a whole. Assuming a density $f_K(\kappa)$, $\kappa > 0$, for K, the marginal density for a typical member of the population is then

$$f_Y(y, \theta) = \frac{1}{\theta} \int_{0 \le \kappa \le \theta/y} (1 - \kappa y/\theta)^{1/\kappa - 1} f_K(\kappa) \mathrm{d}\kappa,\ y > 0. \tag{2}$$

In Huang et al. [6] the distribution of K over the Netherlands and Australian cohorts was found to be reasonably well described by a gamma distribution with parameters $a, b > 0$ and density

$$f_K(\kappa; a, b) = \frac{b^a \kappa^{a-1} e^{-b\kappa}}{\Gamma(a)},\ \kappa > 0. \tag{3}$$

Consequently, overall, observations on Y are taken to be independent and identically distributed with marginal density

$$f_Y(y; a, b, \theta) = \frac{b^a}{\theta\Gamma(a)} \int_{0<\kappa\le\theta/y} (1 - \kappa y/\theta)^{1/\kappa - 1}\, \kappa^{a-1} e^{-b\kappa}\, \mathrm{d}\kappa,\ y > 0. \tag{4}$$

A change of variables puts this in the form

$$f_Y(y; a, b, \theta) = \frac{b^a \theta^{a-1}}{y^a \Gamma(a)} \int_{z=0}^{1} (1 - z)^{1/\kappa - 1}\, z^{a-1} e^{-bz\theta/y}\, \mathrm{d}z,\ y > 0, \tag{5}$$

which is a beta-gamma mixture, easily amenable to further analysis. Parameters θ and N (the age of transition to the GPD, hence, from N to $T = N + Y$) are specific to the individual or cohort under consideration. A density of the form (5) occurs in many areas, e.g., it is the density of the stationary distribution for the Wright-Fisher diffusion in special cases, and occurs in a network model of Sun et al. [7], for example. But its derivation in (5), by mixing over the right endpoint of a GPD, is quite different.

The conditional expectation calculated from (2) is $E(Y|K = \kappa) = \theta(\kappa + 1)^{-1}$, showing that, as κ increases, the expected lifetime decreases. Persons with higher values of κ have shorter lifetimes, on average. As κ approaches 0 lifetimes become longer and would be unbounded for $\kappa = 0$.

3 Observed vs expected centenarians

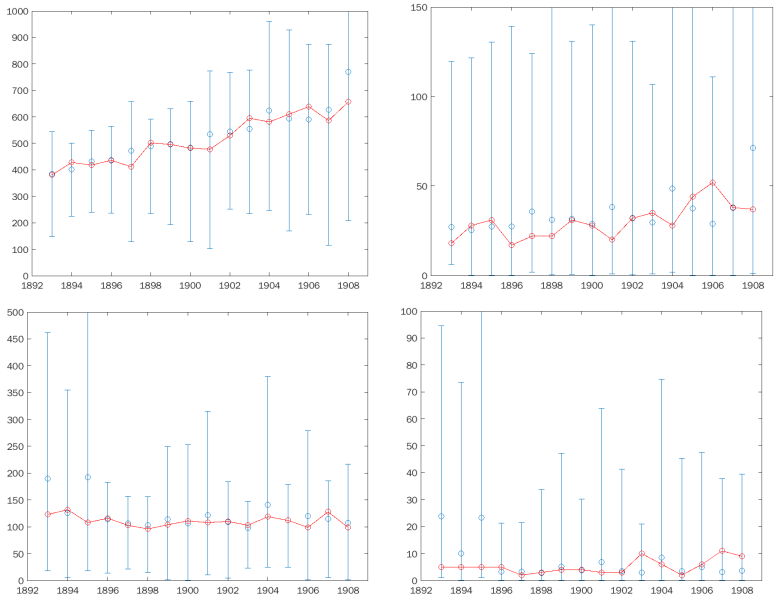
The probability of living to age $x > N$ years or more can be calculated as

$$\begin{aligned} P(T > x) &= P(T - N > x - N | T > N) \times P(T > N) \\ &= P(Y > x - N) \times P(T > N), \end{aligned} \tag{6}$$

where N is the threshold age for the cohort under consideration. Multiplying the probability $P(Y > x - N)$ in Eq. (6) by the number alive in the cohort

at age N gives the expected number in the cohort living to age x, or beyond, according to the model. These are compared in **Fig. 1** with the actual numbers for ages $x = 100$ and 105 in the Netherlands data predicted by the mixture model. (No person of either sex in the data lived longer than 115 years, and at this age model predictions were < 0.01 persons.)

Figure 1: *Numbers of observed (red) and predicted by model (blue) living to ages* ≥ 100 *(left column) and* ≥ 105 *(right column) in cohorts 1893–1906.*



Upper panel: female; lower panel: male. Approximate 95% confidence intervals around the estimated numbers were calculated by resampling. Chi-square values comparing observed with expected numbers are: Female $\geq 100, 46.18$*; male* $\geq 100, 30.68$*; female* $\geq 105, 70.42$*; male* $\geq 105, 30.59$.

Observed and expected compare fairly well but some inaccuracy is to be expected especially for the smaller numbers as we are attempting to predict in the extreme upper end of the life-table. We note an increasing trend with birth cohort year for females and males surviving to 100 years or beyond, but not for 105 years or more. We stress that the model is not fitted to the observations in **Fig. 1**; the figure just shows a comparison of values predicted by the model, with the actual values.

Table 1 gives the observed and expected numbers in the Netherlands cohorts living to ages 100+, 105+, and 110+, according to the mixture model.

Table 1: *Observed (expected) number alive, by age and cohort, Netherlands data.*

	Females			Males		
Cohort	100+	105+	110+	100+	105+	110+
1893	381 (384.8)	18 (27.2)	0 (0.6)	123 (189.7)	5 (23.7)	0 (1.7)
1894	428 (402.3)	28 (25.3)	1 (0.4)	132 (126.2)	5 (10.0)	0 (0.4)
1895	418 (431.3)	31 (27.5)	0 (0.4)	108 (192.0)	5 (23.3)	0 (1.6)
1896	436 (437.2)	17 (27.5)	1 (0.4)	116 (114.1)	5 (3.3)	0 (0.0)
1897	412 (472.5)	22 (35.7)	0 (0.8)	103 (106.8)	2 (3.3)	0 (0.0)
1898	502 (488.6)	22 (31.1)	1 (0.5)	96 (103.3)	3 (2.8)	0 (0.0)
1899	496 (498.2)	31 (31.8)	3 (0.5)	104 (113.9)	4 (5.2)	0 (0.0)
1900	482 (483.6)	28 (29.0)	1 (0.4)	111 (106.2)	4 (3.7)	0 (0.0)
1901	478 (533.8)	20 (38.3)	0 (0.8)	108 (121.8)	3 (6.8)	0 (0.1)
1902	529 (544.6)	32 (32.1)	0 (0.4)	110 (109.2)	3 (3.4)	0 (0.0)
1903	595 (554.6)	35 (29.7)	0 (0.3)	103 (97.7)	10 (3.0)	1 (0.0)
1904	581 (623.6)	28 (48.6)	1 (1.3)	119 (140.9)	6 (8.4)	0 (0.2)
1905	610 (594.3)	44 (37.4)	0 (0.7)	112 (112.1)	2 (3.5)	0 (0.0)
1906	639 (589.4)	52 (28.9)	2 (0.3)	99 (120.2)	6 (4.9)	0 (0.0)
1907	586 (627.8)	38 (37.8)	0 (0.6)	128 (114.8)	11 (3.2)	0 (0.0)
1908	657 (769.5)	37 (71.3)	0 (2.7)	99 (107.0)	9 (3.6)	0 (0.0)
All	8230 (8151.7)	483 (481.0)	10 (6.6)	1771 (1722.4)	83 (55)	1 (0.4)

4 Expected survivors at extreme ages

How many individuals exceeding Jeanne Calment's record age (122 years and 164 days) might we expect to see in the remainder of this century? In our mixture model, for the Netherlands data, survival to age 115 or older is possible, but with a probability so small as to be negligible. One could speculate that, on a global scale, an increasing number of supercentenarians might result in the appearance of new longevity records. However, our findings place a robust limit on the emergence of any record-breaking individuals.

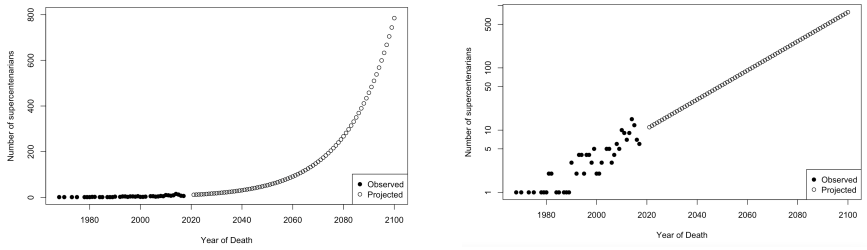
Assuming the model derived from the Netherlands and Australian data applies generally, we can estimate roughly the potential growth in the number of supercentenarians, globally, from 2022-2100. The annual growth in supercentenarians recorded in the IDL for England and Wales, 1968–2017, is well described by an exponential growth function with a doubling-time of 12.9 years. **Fig. 2** shows the raw data and regression predictions on linear

and log scales. The regression function is

$$y = \exp(-106.44042 + 0.05386x),$$

where x is calendar year above 2021 and y is the number of supercentenarians dying in that year.

Figure 2: *Regression models for centenarians. Left column, linear scale; Right column, log scale.*



From this function we extrapolated, optimistically, the supercentenarian count to be expected in England and Wales for 2022–2100. Multiplying by a factor of 100 (for the approximate proportion of the world population in England and Wales) gives an estimate of 1,476,796, or in broad terms a total of ≈ 1.5 million supercentenarians, male and female, to be expected world-wide over the period 2022–2100.

For an optimistic estimate of the number of survivors from this population expected to exceed a specified age of interest, we multiply 1.5×10^6 by the corresponding proportion surviving calculated from the model fitted distribution. The model then predicts that 8268 of those 1.5m supercentenarians would survive to age 115, and 41 would live to age 120, but less than 1 (expectation 0.23) would live past age 125. These rough estimates at the extreme upper end of the age distribution come with large standard errors, but are consistent with the small numbers of extreme-aged individuals currently observed, and suggest there is a low probability of Jeanne Calment's record being broken even once in the remainder of this century. Barring a revolutionary advance in medicine, the benchmark age of 125 appears to represent a firm limit to human longevity unlikely to be exceeded in the foreseeable future.

Interestingly, this is rather close to a certain earlier estimate: *"... yet his days shall be one hundred and twenty years"* (Genesis 6:3).

5 Is there an upper limit to human lifetimes?

Recent vigorous discussion centered around the paper of Dong, Milholland & Vijg [2], where data from 40 countries in the Human Mortality Database [8] was used to illustrate a continuing increase in human life expectancy since 1900, but with a rate of improvement in survival which peaks and then declines for very old ages. In this data, the time series of the estimates of the age with greatest improvement in survival appeared to level off around 1980, rather than continuing to increase with calendar year. It was inferred from this in Dong *et al.* [2] that human lifespan may have a natural limit. The authors went on to analyse the yearly maximum reported ages at death of individuals aged 110 years or more ("supercentenarians") from France, Japan, the UK and the US in the International Database on Longevity [9]; a total of 534 individuals over the years 1968–2006. They used linear regression techniques to bolster their conclusion that the increase in ages at death occurring between the 1970s and early 1990s stopped around 1995.

Lively commentary on this paper and its conclusions, much of it critical, occurred in Brown *et al.* [10], Hughes and Hekimi [11], Rozing *et al.* [12] and Lenart and Vaupel [13]. The negative criticism revolved mainly around the statistical techniques employed. Most of those writers argued for the contrary conclusion – for no upper limit to human lifespan. Rootzen [14], using longevity data from Japan and Western countries, rejected the notion of a hard limit to human life, and predicted it would be possible in the next quarter-century for someone to reach the age of 128. de Beer *et al.* [15], using a logistic model, argued that someone will live to 125 years within the next century. In replies to these discussions, Dong et al. defended their methods and conclusions and remained of the view that human lifespan has a finite natural limit.

More recently, Barbi *et al.* [5] tracked every person born in Italy between 1896 and 1910 who lived to age 105 or beyond; a total of 3,836 individuals (3,373 women and 463 men). Their hazard rate analysis suggested a "mortality hazard rate plateau" between ages 105 and 110 and a consequent "late-life mortality deceleration effect"; that is, that the rate of increase in mortality with advanced age becomes slower than it is in the Gompertz law. This effect is usually understood to imply a model with a potentially infinite life span. The existence of a late-life mortality hazard rate plateau is also argued by Greenwood and Irwin [16] and Gavrilov and Gavrilova [17].

In the Gompertz/GPD model fitted to the Netherlands and Australian

data by Huang, Maller and Ning [1], a late-life mortality deceleration is indeed observed, but, remarkably, in conjunction with the previously mentioned finite upper limit to the lifespan. These conclusions appear at first to be inconsistent but the apparent paradox vanishes when we notice that the model also implies an *advanced age mortality acceleration* rate following the late life mortality deceleration. The final acceleration results in estimated finite limits to the life spans. This is discussed in more detail in [3].

6 The three laws of biodemography

The compensation law of mortality ([18], [19], [20]), states that for a given species, differences in death rates between different sub-populations (cohorts, in our case) decrease with age — because higher or lower initial death rates are accompanied by a lower or higher rate of mortality increase with age, such that mortality rates for different cohorts tend to equalise after some high age.

This tendency exists in the Netherlands data and is captured in the Huang et al. [1] model. The threshold ages N at which the convergence takes place are around 98 years for females and (with somewhat greater variability) around 96 years for males. These are close to the estimate of around 95 years made in [19] on quite different grounds.

The three *laws of biodemography* have been stated as:

- the Gompertz-Makeham law of mortality;
- the compensation law of mortality, and
- the existence of a late-life mortality deceleration.

The Netherlands and Australian data and the model fitted to them are consistent with the compensation law, so all three laws are satisfied. The model also allows for, and for those data, predicts, via an advanced age mortality acceleration, a finite limit to human life span. The Huang et al. [1] model seems to be unique in possessing all of these properties, and the mixture model, which incorporates the Huang et al. [1] as a sub-model, inherits them too.

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