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Is a limit to the median length of human life imminent?

1. INTRODUCTION

Human life expectancy at birth, that is, the average length of life, has on average roughly tripled in historical times and has steadily increased over the last century, despite some local declines in some time intervals (Wilmoth, 2000). In 2005-2010, among countries with at least one million people, Japan had the longest female life expectancy at birth, 86.1 years, and tied with Switzerland for the longest male life expectancy at birth, 79.3 years (United Nations Population Division, 2011). Over the past two centuries, the age at which the average remaining length of life was 5 years rose by about 10 years in Sweden, the United States, and Japan, and so did the age at which the average remaining life length was 10 years (Vaupel, 2010). Moreover, from 1840 to 2000, the female life expectancy at birth in the country with the highest period female life expectancy at birth in the world, $e_{max}(0)$, rose more than 0.2 years of life length per year of calendar time (Oeppen and Vaupel, 2002). In different data from 1750 to 2005, a piecewise linear model described period female maximal life expectancies $e_{max}(0)$ better than did a single straight line (Vallin and Meslé, 2009, Vallin and Meslé, 2010). Before 1790, the increase in period female maximal life expectancy at birth $e_{max}(0)$ was very slow, 0.005 year (of life length) per (calendar) year, accelerated markedly to 0.11 or 0.12 year/year during 1790-1885, accelerated further to 0.32 year/year (that is, nearly 4 months of additional life length per year of calendar time) during 1886-1960, and has been 0.23 year/year since 1960. The improvements in survival shifted from young ages to older. For these and other summary measures of human mortality, such as the median life length and the modal age of death after age 5, recent reductions of mortality at advanced ages in many countries with credible data were not less than earlier reductions (Rau *et al.*, 2008, Canudas-Romo, 2010).

Such findings contradicted some predictions of fixed limits to life expectancy (Fries, 1980). For Norway, Bourgeois-Pichat (1978) estimated that “the biological limit for life expectancy at birth is 80.3 years for females and

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73.8 years for males”. Contrary to these claims, the United Nations Population Division (2011) estimated 2005-2010 life expectancies in Norway at 82.7 years for females and 78.1 years for males. Coale (1996) concluded that “female mortality may not continue to decline when [life expectancy at birth] e_0 reaches between 84 and 85 years”, contrary to the recent experience of Japan.

Recent improvements in survival are consistent until now with conditional arguments that, for example, “life expectancy is unlikely to exceed an average [for both sexes combined] of around 85 years in the absence of radical advances in the control of the aging process – and could even decline in developed countries in this century” (Carnes and Olshansky, 2007, p. 367). They are also consistent with arguments from non-demographic data that genetic and physiological constraints could eventually limit human life expectancy (Olshansky *et al.*, 1990); and with predictions of fixed limits to life expectancy as high as 115 years (Duchene and Wunsch, 1988).

The broad question of limits to human life length remains controversial (Wilmoth, 1997, Bongaarts, 2006, Carnes and Olshansky, 2007, Vaupel, 2010, Vallin and Meslé, 2010) and deserves further analysis. Because views about future human longevity derived from evolutionary and functional biology and from the present health of younger cohorts vary widely, we addressed only one limited question: Does the human maximal median life length, where the maximum is taken over all countries with data in a given time interval, appear to be approaching a limit over the last century or two?

We used historical life tables (Human Mortality Database, 2010) to answer this question. For each life table, the median life length m is defined as the length of life at which exactly half the life-table population survived; and the remaining life expectancy $e(m)$ at the median life length m is defined as the average length of remaining life among individuals who survived to age m . Median life length m and its relation to the remaining life expectancy at the median life length have been investigated from different perspectives (Sanderson and Scherbov, 2005).

For a set s of 9 or more life tables from an individual country c in a 20-year interval indexed by its first year t , we computed the set of 9 or more data points $(m, e(m))$ (one point for each life table) to estimate an index we shall denote by $\alpha(c, t, s)$, which is measured in years of life. We shall explain below how $\alpha(c, t, s)$ is calculated. We refer to $\alpha(c, t, s)$ as the maximal median life length (MMLL) implied by the life tables of country c in time interval t in the set s . In the presence of a linear dependence of $e(m)$ on m , $\alpha(c, t, s)$ is an upper bound on median life length for country c in time interval t with set s of life tables, as explained in detail below. We examined the temporal trend, that is, the changes as t increased, of the largest value of $\alpha(c, t, s)$ over all countries c .

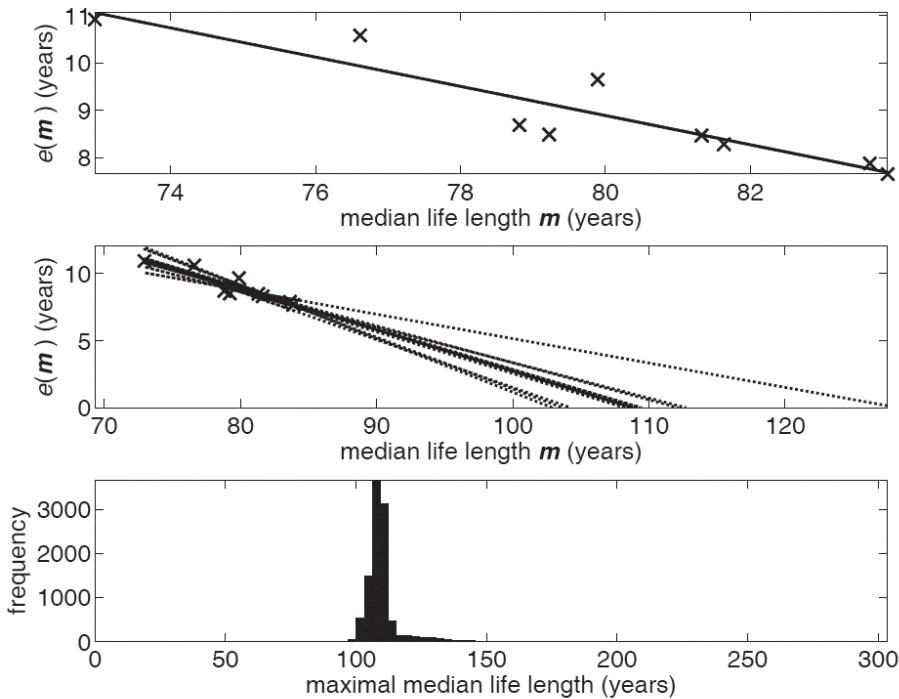
observed in time interval t . Had this index been constant over time or increasing toward an asymptote, we would have found evidence of an imminent upper limit to human MMLL. We found, on the contrary, that, for period life tables, this index increased even faster than median life length increased in the course of time, giving no evidence of an imminent upper limit to human MMLL. We now clarify the details of this procedure with an illustrative example.

1.1 Motivating example

In the life tables (Arias, 2007) of the 2004 United States population and 8 subpopulations (females, males, blacks, whites, black females, white females, black males, white males), a graph of expected remaining life $e(m)$ as a function of m was linearly decreasing (Figure 1a). At one extreme, black males had a median life length m of 72.96 years and a remaining life expectancy $e(m)$ of 10.92 years. At the other extreme, white females had $m = 83.89$ years and $e(m) = 7.65$ years. This observation (Cohen, 2010) could be interpreted as an example of the “compression of mortality” associated with greater longevity. It was consistent with many other observations using both cross-sectional (as here) and longitudinal data and many other mortality indices (Coale, 1996, Cheung and Robine, 2007). Cohen (2010) asked how generally, in sets of life tables for other countries and times and in theoretical life table functions, $e(m)$ decreased approximately linearly with increasing m . This study answers the empirical question, and then investigates the consequences of this linear relationship for the existence of an upper limit to MMLL.

When we fitted a quadratic function $e(m) = Am^2+Bm+C$ by least squares to the 9 points $(m, e(m))$ for the 2004 United States of America life tables, the point estimate of $A = 0.000023$ did not differ significantly from 0. Assuming normal theory, the 95% confidence interval (CI) for A was $(-0.036, +0.036)$. Another way to estimate the variability of the coefficients A, B, C was to use the bootstrap procedure (Efron and Tibshirani, 1993). In 10,000 bootstrap samples with replacement from these 9 data points, the median value of A was 0.00179 and the 95% CI, i.e., the (2.5 percentile, 97.5 percentile) values of A , was $(-0.096, +0.079)$. The solid line in Figure 1a superimposes the linear fitted line and quadratic fitted curve; they are indistinguishable. Thus the data offered no statistically significant evidence to reject a linear model $e(m) = am+b$ in this case.

Figure 1 – (a) Remaining life expectancy $e(m)$ at the median life length m , and least-squares fitted linear and quadratic functions, for the United States of America in 2004 and 8 subpopulations. (b) Straight line is fitted to the first 10 of 10,000 bootstrap samples. For each sample s , the median life length $a(\text{USA}, 2004, s)$ at which remaining life expectancy would be 0 is the age where the fitted straight line intersects the horizontal axis. (c) Frequency histogram of the values of $a(\text{USA}, 2004, s)$ estimated from 10,000 bootstrap samples s .



Therefore we fitted a linear model $e(m) = am + b$ to these 9 points by least squares. The point estimate of the slope was $a = -0.3085$ year/year, with 95% CI (-0.4286, -0.1884) using normal theory. Each increase in median age m by one year was associated, on the average, with 0.3085 year decrease in the remaining life expectancy $e(m)$. The median bootstrap estimate of the slope (based on 10,000 samples) was -0.31 with 95% CI (-0.41, -0.18).

Based on this linear relationship, we constructed a useful, albeit hypothetical, index of implications of the data. Among the many demographic precedents for constructing a hypothetical index to summarize the implications of demographic data, two familiar examples are the period total fertility rate (TFR) and the intrinsic rate of natural increase r (Spiegelman, 1968, pp.

255, 288 respectively). The TFR is the sum of the current period's age-specific birth rates. It represents the average number of children a newborn female child would have during her lifetime if the current age-specific birth rates remained valid throughout her lifetime (no temporal change) and if she survived to the end of the child-bearing interval (no mortality). The assumptions of unchanging birth rates and no mortality are clearly hypothetical. Nonetheless, the period TFR is so widely used that its assumptions are often forgotten. The intrinsic rate of natural increase r of an age-structured population with given age-schedules of fertility and mortality describes the long-run rate of change of the size of what is known as the stable population implied by those schedules, and r is the root of Lotka's integral equation of population renewal. The calculation of r assumes the given age-schedules of fertility and mortality are constant in time for an indefinite period. Despite these assumptions, stable population theory and the measure r of a population's long-run implied growth rate are useful.

In the spirit of these and other useful indices based on counter-factual hypotheses, we now define the maximal median life length (MMLL) $\alpha(c,t,s)$. Later we define three summary quantities $\beta(t)$, $\chi(t)$ and $\gamma(t)$ derived from MMLL.

If the linear relationship $e(m) = am + b$ with $a < 0$, $b > 0$, remained valid as m increased over the range where $e(m)$ remained non-negative, including values of m greater than the observed range of m , then when the median life length increased to $m = -b/a$, we would have $e(m) = 0$. The hypothetical situation in which this limit is attained is an extreme idealization of the compression of mortality. It is an unrealistic idealization because, when $m = -b/a$, all individuals who survived to age m would die instantaneously, i.e., $e(-b/a) = 0$ implies $\ell(x) = 0$ for all $x \geq -b/a$. We define this median life length as the MMLL:

$$\alpha(c,t,s) = -b/a, \text{ "maximal median life length" or MMLL.}$$

It is an index of the hypothetical consequences of a decreasing linear trend $e(m) = am + b$ with $a < 0$ and $b > 0$ in country c and time interval t and set s of life tables. Graphically, $\alpha(c,t,s) = -b/a$ is the value of m where the straight line fitted to $(m, e(m))$ data intersects the m axis (Figure 1b, solid line).

In this example, as the linear model was not rejected statistically, we estimated the MMLL $\alpha(\text{USA}, 2004, \{\text{all 9 life tables}\}) = b/a$ using the estimates of a and b from normal theory. The point estimate of MMLL was $\alpha(\text{USA}, 2004, \{\text{all 9 life tables}\}) = 108.8$ years. In 10,000 bootstrap samples s sampled from the 9 observed pairs of values $(m, e(m))$, the median, $\alpha(\text{USA}, 2004, s)$ was 108.8 years (i.e., the same as the point estimate, to four significant figures) with 95% CI (102.0, 127.5) and the range of $\alpha(\text{USA}, 2004, s)$ was from near 0 to more than 300 years. A value of $\alpha(\text{USA}, 2004, s) = -b/a$ was calcu-

lated from the values of a and b from each bootstrap sample s , and the percentiles of α came from that sampled distribution. Figure 1b shows the straight lines fitted to the first 10 of the bootstrap samples s of the $(m, e(m))$ pairs. Figure 1c shows the frequency histogram of the 10,000 sampled estimates of $\alpha(\text{USA}, 2004, s)$.

These results suggested that for the United States in 2004, the MMLL was nearly 109 years. This interpretation was not contradicted by the survival of some U.S. individuals to validated ages beyond 109 years, as the point estimate lies within an interval of uncertainty from 102 to 127.5 years.

1.2 Approach of this study

Step 1 is to show that the linear relationship $e(m) = am + b$ cannot be rejected statistically for almost all countries in nearly all 20-year time intervals, in cohort and period life tables for females and males separately. This empirical result appears to be new to demography.

Given this empirical pattern, step 2 is to estimate the distribution of MMLL using 10,000 bootstrap samples s of country c 's life tables in time interval t . We then summarize the sampled distribution of MMLL with three derived measures, defined as

$$\begin{aligned}\beta(t) &= \max_c \text{median}_s \alpha(c, t, s), \text{“best-country median life length” or BMLL,} \\ \chi(t, s) &= \max_c \alpha(c, t, s), \text{“country-maximal median life length” or CMLL,} \\ \text{and } \gamma(t) &= \text{median}_s \chi(t, s), \text{“greatest median life length” or GMLL.}\end{aligned}$$

What is the difference in demographic meaning between $\beta(t) = \max_c \text{median}_s \alpha(c, t, s)$ and $\gamma(t) = \max_c \text{median}_s \alpha(c, t, s)$? To compute $\beta(t)$, we consider each country c separately, find the median bootstrapped value of MMLL for country c , and then take the maximum of those median bootstrapped values over all countries. Thus $\beta(t)$ reflects a typical largest MMLL country by country. By contrast, to compute $\gamma(t)$, we generate a bootstrap sample s for all countries simultaneously. Then we pick the maximal $\alpha(c, t, s)$ over all countries, whichever country happens to have the maximal $\alpha(c, t, s)$ for that bootstrap sample s ; we call this value the CMLL $\chi(t, s) = \max_c \alpha(c, t, s)$. In different bootstrap samples s , $\chi(t, s)$ may come from different countries. After we do this repeatedly, $\beta(t)$ is the median of $\chi(t, s)$ over all samples s . Thus $\gamma(t)$ is a typical largest MMLL regardless of country. As $\gamma(t)$ is calculated directly from bootstrap samples, we may easily find its confidence intervals from the values of $\chi(t, s)$. If a ceiling on MMLL is imminent, $\gamma(t)$ should level off first since $\gamma(t) \geq \beta(t)$ (Cohen, 2012). Hence we examined the trends over time in GMLL $\gamma(t)$ and we sampled the variability of these trends using CMLL $\chi(t, s)$.

We subjected our results to several sensitivity analyses. We estimated m

and $e(m)$ using both linear and cubic spline interpolation in the life tables. The analysis reported in detail here used 20-year time intervals, but we also analyzed results using 10-year and 30-year time intervals, and both the median life length m and the upper quartile of life length. Our detailed analyses used life tables with single years of age and single years of time, but sensitivity analyses used life tables with single years of age and mortality data from five consecutive years. The details of our data, methods and sensitivity analyses are in the Appendix.

2. RESULTS

In these Results, when a point estimate is followed by a pair of numbers in parentheses, the pair gives the lower and upper 98% confidence limits of the point estimate, based on bootstrap sampling. When a point estimate is given without a following pair of numbers in parentheses, it is based on the least-squares estimate of the coefficients in a quadratic equation.

2.1 Step 1

In 312 of the 322 sets of 9 or more life tables in 20-year time intervals, $e(m)$ decreased as m increased, and in 10 sets $e(m)$ increased as m increased, according to the sign of the median of the slope a in bootstrap samples. Among cohort life tables, $e(m)$ increased as m increased only for New Zealand males born in 1900-1912. These men attained an age equal to their median life length in roughly the last third of the 20th century. The 9 remaining sets were period life tables, 5 for females, 4 for males, and all from 1960 or later. These 10 sets of life tables illustrated a rapid increase in survival at older ages in recent decades.

In most cases, m accounted for much of the variation in $e(m)$. The median value of the adjusted R^2 values of the quadratic regression of $e(m)$ on m for all 322 sets of life tables was 0.904. Adjusted R^2 ranged from a low of 0.012 for period female life tables from the Netherlands, 1960-1979, to a high of 0.999 for cohort female life tables from Switzerland, 1900-1916. For the linear model fitted by least squares, the median value of the adjusted R^2 values for all 322 sets of life tables was 0.888 (range 0.001 to 0.999).

A linear relation between $e(m)$ and m was acceptable in the great majority of cases, though not universally. In 87% of the 322 sets of life tables, a linear model of $e(m)$ as a function of m was not rejected (Table 1). In 6% of the 322 sets, the data supported a concave quadratic relation and in 7% a convex quadratic relation.

In period life tables for females, the BMLL $\beta(t)$ rose from 93.3 years of age in 1800-1819 (in Sweden, the only country with enough reliable life tables in that

Table 1 – Number of sets of life tables by type (cohort, period), sex (female, male), and shape of the relation of $e(m)$ to m (concave, linear, convex).

Type of life table	Cohort	Cohort	Period	Period	Total	Per
	Female	Male	Female	Male		cent
Concave	0	3	12	4	19	6
Linear	28	26	108	117	279	87
Convex	6	5	7	6	24	7
Total	34	34	127	127	322	100

Note: A "set" of life tables was specified by a country and a 20-year interval, provided there were ≥ 9 life tables in contiguous years for that combination of country and time interval. For example, of the 127 sets of period female life tables in a specified country and 20-year interval, 108 were acceptably described by a linear relation of $e(m)$ to m .

interval) to 182 years in 2000-2008 (in Japan), an increase of 88.8 years in two centuries (discrepancy due to rounding). In period life tables for males, the BMLL rose from 99.4 years in 1800-1819 (in Sweden) to 149.7 years in 2000-2008 (in Japan), an increase of 50.3 years in two centuries. In cohort life tables for females, the BMLL rose from 90.5 years in 1800-1819 (in Sweden) to 123 in 1900-1916 (in New Zealand non-Maori), an increase of 32.5 years in one century. In cohort life tables for males, the BMLL rose from 99.8 years in 1800-1819 (in Sweden) to 175.2 years in 1900-1916 (in Scotland), an increase of 75.4 years in one century.

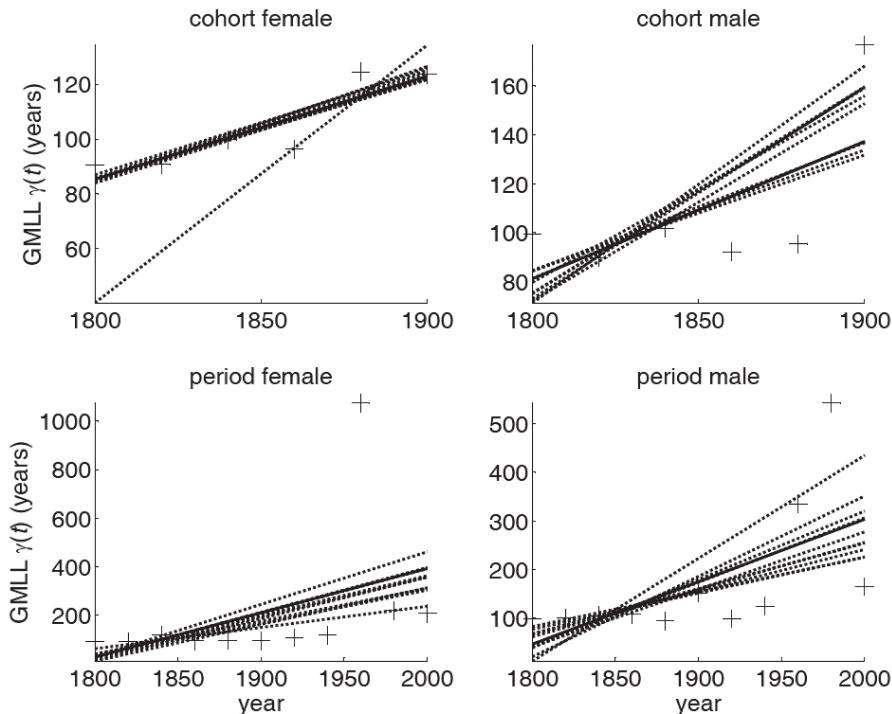
2.2 Step 2

For cohort female, cohort male, period female, and period male life tables analyzed separately, the least-squares straight line fitted to the greatest median life length (GMLL) $\gamma(t) = gt + h$ (Figure 2, solid line) had a positive slope g . The straight lines based on the first 10 bootstrap samples (Figure 2, dashed lines) also had positive slope, and so did all but three of the 40,000 bootstrapped sample slopes $g(s)$ (Table 2, Figure 3) in the least-squares fits, for each bootstrap sample s , of $\max_c \alpha(c,t,s) = g(s)t + h(s)$. The total of 40,000 bootstrap samples resulted from 10,000 samples for each of cohort female, cohort male, period female, and period male life tables.

Table 2 compares median_s $g(s)$ of the 10,000 fitted straight lines, the 98% CIs of $g(s)$, and the slopes g in the straight lines fitted to $\gamma(t) = gt + h$ as a function of t (Figure 2, solid line). For each category of life table (cohort female, cohort male, period female, and period male), median_s $g(s) > g$, and the difference is substantial for period male life tables. According to median_s $g(s)$, in period female life tables, $\max_c \alpha(c,t,s)$ increased by 2.09 (0.716, 86.5) years of age

per calendar year, and in period male life tables, $\max_c \alpha(c,t,s)$ increased by 2.11 (0.56, 85.0) years/year. For period life tables, median, $g(s)$ suggested that over 200 years $\max_c \alpha(c,t,s)$ increased by about 418 and 422 years for females and males, respectively, while g suggested that $\gamma(t)$ increased by about 365 and 258 years. The modal values of $g(s)$ suggested that $\max_c \alpha(c,t,s)$ increased by about 265 and 215 years in the same 200-year interval.

Figure 2 – Greatest median life length (GMLL) $\gamma(t) = \text{median}_s \max_c \alpha(c,t,s)$ (plotted by +) as a function of the initial year t in 20-year intervals that contained at least 9 life tables by single year of age and single year of time, for (a) cohort female life tables, (b) cohort male life tables, (c) period female life tables, (d) period male life table.



Note: The solid straight line is the linear model $\gamma(t) = gt + h$, where the units of g are years of age per calendar year. The dotted lines are linear regressions $\chi(t,s) = g(s)t + h(s)$ for 10 representative bootstrap samples s . Extreme outliers (slopes of >50 years per 20-year interval) were discarded from these plots. The solid regression lines $\gamma(t) = gt + h$ had parameter values: (a) $g = 0.38$, adjusted $R^2 = 0.80$; (b) $g = 0.56$, adjusted $R^2 = 0.40$; (c) $g = 1.83$, adjusted $R^2 = 0.174$; (d) $g = 1.29$, adjusted $R^2 = 0.38$.

Table 2 – Rates of increase in the country-maximal median life length (CMLL) and related indices.

Line	Type of life table	Cohort Female	Cohort Male	Period Female	Period Male
1	slope, median _s $g(s)$	0.380	0.580	2.09	2.11
2	slope, 1 percentile (lower CI)	0.263	0.193	0.716	0.562
3	slope, 99 percentile (upper CI)	1.07	24.9	86.5	85.0
4	$P(g(s)>0)$	100%	100%	100%	100%
5	g (years per year)	0.377	0.561	1.83	1.29
6	modal $g(s)$ (years/year)	0.375	0.475	1.33	1.08

Note: For each bootstrap sample s , the linear model $\chi(t,s) = g(s)t + h(s)$ was fitted by least squares. The unit of $g(s)$ is years of life per calendar year. For example, between 1800 and 2008, in period female life tables, the median_s $g(s)$ (line 1) indicated that CMLL typically increased by 2.09 years of age per calendar year, or 418 years of age over 200 calendar years. The 98% confidence interval of $g(s)$ (lines 2, 3) was from 0.716 to 86.5 years/year. For cohort female life tables, the median slope indicated that CMLL typically increased by 0.380 years of age per calendar year, or 38.0 years over 1800–1900. $P(g(s)>0)$ is the fraction of sampled values of $g(s)$ that were positive (line 4). The slope of the median values, i.e., g in the linear model $\gamma(t) = gt + h$ (line 5), taken from the fitted straight lines in Figure 2 and measured in years of increase in CMLL per (calendar) year, was smaller than the median slope (line 1), in some cases substantially (e.g., period male life tables). However, the slope of the median values (line 5) and the approximate modal slope (line 6) always fell within the 98% CIs (lines 2 and 3).

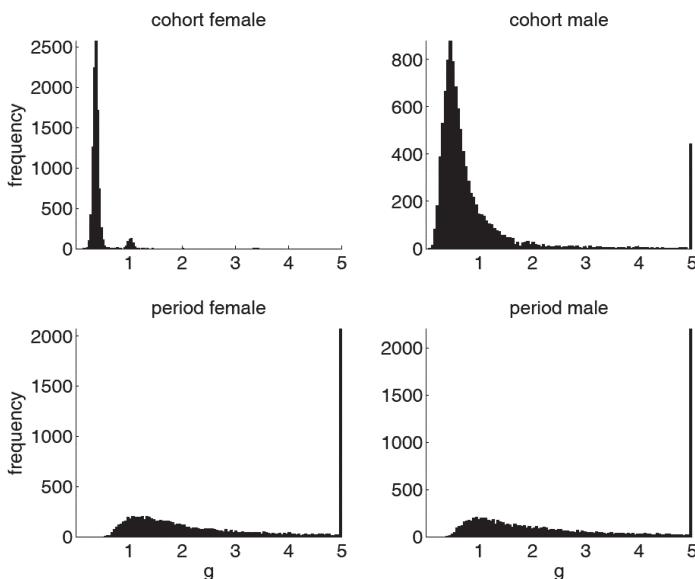
For cohort life tables, median_s $g(s)$ (Table 2) suggested that, over 100 years, the CMLL $\chi(t,s) = \max_c \alpha(c,t,s)$ increased by about 38 and 58 years for females and males, respectively, while g suggested that the GMLL $\gamma(t)$ increased by similar amounts and the modal values of $g(s)$ suggested that $\max_c \alpha(c,t,s)$ increased by about 37.5 and 47.5 years.

The large differences in the implied increases in different indices of maximal median life length among g , median_s $g(s)$, and mode_s $g(s)$ result from a very asymmetric and long-tailed distribution of $g(s)$ (Figure 3). These differences suggest caution in relying exclusively on any single index. Nevertheless, they all concur in indicating very substantial increases in MMLL. These increases are larger for period life tables than for cohort life tables, an unexpected result that is discussed below.

Visual inspection of Figure 2 suggests that, for period life tables, these slopes are influenced upward by a few exceptionally high points early in the second half of the 20th century. Similar exceptionally high points early in the second half of the 20th century occur in plots based on the median life length and 10-year time intervals and on the upper quartile of life length using 20-year and 10-year intervals (Appendix). These sensitivity analyses indicate that these high values are not artifacts of using the median and 20-year intervals, but do not resolve whether the peaks are historically unique or are early expressions of a

large potential for further increase. The possible effects of yearly statistical fluctuations in mortality were excluded by using life tables in 30-year intervals for single years of age and 5 years of time, which showed the same peak (Figure S1). Canudas-Romo (2010, his Figure 3, p. 304) displayed a similar peak early in the second half of the 20th century in his analysis of the record modal and median ages at death and the record life expectancy at birth in period life tables over the interval 1840–2005.

Figure 3 – Frequency histogram of the slopes $g(s)$ estimated (as in Figure 2) for linear models of country-maximal median life length (CMLL) as a function of the initial year t in 20-year intervals that contained at least 9 life tables by single year of age and single year of time, for 10,000 bootstrap samples s , for (a) cohort female life tables, (b) cohort male life tables, (c) period female life tables, (d) period male life tables.



Note: The horizontal $g(s)$ axis has 102 bins of width 0.05. The left boundary points of the bins are -0.05 increasing by increments of 0.05 to 5. The left bin counts the frequency of values of $g(s) < 0$. The right bin counts the frequency of all values of $g(s) \geq 5$. Values of $g(s) \geq 5$ appeared to be randomly sparsely distributed. For nearly all samples s , $g(s) \geq 0$, i.e., CMLL generally increased with time. For cohort life tables, the modal values of $g(s)$ were approximately 0.38 and 0.48 years of age per calendar year for females and males, respectively. Most commonly (among the bootstrap samples s) CMLL increased (for both sexes combined) by about 0.43 year of age per calendar year, or roughly 43 years of age over the 100-year interval of observation. For period life tables, the modal values of $g(s)$ were about 1.33 and 1.08 years per year for females and males, respectively, suggesting that most commonly (among the bootstrap samples s) CMLL increased by roughly 1.2 years of age per calendar year, or roughly 240 years of age over the 200-year interval of observation.

The results support an increasing trend in all indices of the maximal median life length, including the best-country median life length and the greatest median life length. The slopes are positive and there is no indication (Figure 2) that the maximal median life length, however its distribution may be summarized, is increasing asymptotically toward or at a finite ceiling.

2.3 *Sensitivity analyses*

To test the robustness of conclusions based on median life length and 20-year intervals, we repeated the analyses using the median life length with 10-year intervals and the upper quartile of life length U (the age at which one-quarter of a life-table population survives) with both 20-year and 10-year intervals. We also repeated the analyses using the median life length of life tables by single years of age and five years of time, in 30-year intervals. The Appendix gives detailed methods, results, and discussion of these sensitivity analyses.

In summary, the 10-year time intervals are better described by linear models than the 20-year time intervals. A linear relation between U and $e(U)$ is slightly more likely than a linear relation between m and $e(m)$ using either 20- or 10-year time intervals. There were no systematic differences between corresponding female and male estimates of $\gamma(t)$ based on the same indicator (m or U) of life length and the same duration of time, nor between 20-year and 10-year estimates of $\gamma(t)$ based on the same indicator of life length and the same sex (Table S3 gives the period $\gamma(t)$ for these comparisons). In every comparison of life tables from the same sex using the same indicator of longevity, the median slope, median, $g(s)$, was larger for period than for cohort life tables. In general, U and $e(U)$ led to higher values of the GMLL $\gamma(t)$ and to higher estimates of the median slope than did m and $e(m)$. That is, the GMLL $\gamma(t)$ was higher and rose faster according to the upper quartile U of life length than according to the median life length m . Regardless of using 20- or 10-year time intervals, both the median m and the upper quartile U of life length gave no evidence of an imminent limit to life expectancy. The analyses using the median life length of life tables by single years of age and five years of time, in 30-year intervals, gave the same result.

Over longer periods of time, using life tables by single year of age and single year of time, the relationship between m and $e(m)$ was non-linear. Alternatives to using 10- or 20-year intervals, over which m and $e(m)$ are linearly related, include fitting piecewise linear models with changes in slope at points calculated by an optimization procedure, and non-linear models. Our approach assumed the least about the data.

2.4 *Cohort versus period*

Comparisons of mortality improvements in period and cohort life tables (Wilmoth, 2005, Canudas-Romo and Schoen, 2005, Goldstein and Wachter,

2006) generally reported that in industrialized countries the period life expectancy at birth (which is based on deaths in the current year of people who were mostly born in prior years) increased more slowly than the cohort life expectancy at birth (which is based on deaths mostly in future years of people who are born in the current year), as would be expected from declining age-specific death rates. For example, Wilmoth (2005, p. 268) observed: “In a situation of sustained mortality decline, … the rise in life expectancy over time tends to be slightly faster from cohort to cohort than from period to period”. He also noted (p. 255): “the slope of the cohort trend [in life expectancy in Sweden] tends to be greater than the slope of the period trend when cohort e_0 is plotted as a function of year of birth, but less when plotted according to the period in which the cohort mean age at death actually occurs”.

Here, by contrast, the GMLL $\gamma(t)$ increased more quickly, on the average, in the 208 years of period life tables than in the 116 years of cohort life tables. In every comparison of life tables from the same sex using the same quantile of life length, the median slope, median, $g(s)$, was larger for period than for cohort life tables (Table S4).

This contrast probably resulted from comparing two different intervals, the 19th century for cohort life tables compared to the 19th and 20th century for period life tables. From 1800 to 1900, for each sex, GMLL $\gamma(t)$ rose more rapidly for cohort than for period life tables (Figure 2), as expected from the previous studies. But for either sex the rise in period GMLL in the 20th century exceeded the rise in cohort GMLL in the 19th century for that sex. Specifically, the cohort life tables (with birth years 1800-1917) had average years of death from roughly 1838 to roughly 1975 $\approx 1917 + 60$ while the period life tables, dated by year of death, had years of death from 1800 to 2008. Reductions in mortality over 1800-2008 exceeded those over 1838-1975.

3. DISCUSSION AND CONCLUSION

The absence of an apparent limit to human maximal median life length, the best-country median life length, or the greatest median life length, and consequently to the life expectancy at birth, does not entail the non-existence of such a limit, but suggests that such a limit is not imminent.

Future limits, if any, to human median life length and life expectancy at birth depend on many aspects of the future, including environmental conditions, biomedical science, public health, social, political, and economic organization, food supplies, households and individual behavior, literacy and education, and human values (Riley, 2001). These factors can be predicted to a very limited extent. Many demographers and biologists have emphasized the importance of biological factors in future limits to life expectancy, and they have reached widely divergent conclusions (Duchene and Wunsch, 1988, de Grey, 2006, Carnes and Olshansky, 2007). In light of the inconsistency of these views, we examined

whether historical mortality data indicated imminent constraints on further improvements in the median and average length of human life. We recognized that the available historical mortality data have limitations and are not the only data relevant to future life expectancy.

We organized historical life tables from the Human Mortality Database to test two hypotheses. The first hypothesis was that, within 20-year time intervals, in most countries, the expected remaining life $e(m)$ at the median life length m was a decreasing linear function of m . The data confirmed that the relation was decreasing in 97% of 322 country-specific, time-interval-specific sets of life tables, and that the relation was approximately linear in 87% of these 322 data sets.

Future research may explore whether classical and recent model life tables (e.g., Schoen and Canudas-Romo, 2005, Li and Anderson, 2009, Denton and Spencer, 2011) predict the empirical pattern that the expected remaining life $e(m)$ at the median life length m was a decreasing linear function of m . It would also be desirable to model the behavior of MMLL in the presence of sustained mortality improvements of various kinds, as Wilmoth (2005) and Canudas-Romo (2010) modeled several other indicators of longevity.

The negative linear relation of the expected remaining life $e(m)$ to the median life length m parallels results using, instead of m , the modal (commonest) age at death M and, instead of $e(m)$, $SD(M^+)$, the standard deviation of remaining length of life above M , or $e(M)$, the expected remaining life at the modal age of death M . For 16 countries at various periods from 1841 to 1980, $SD(M^+)$ was very nearly $1.25 \times e(M)$, so that trends in $SD(M^+)$ are equivalent to trends in $e(M)$. For England, Finland, the Netherlands, and Switzerland, $e(M)$ decreased nearly linearly as M increased (Kannisto, 2001). For France, Italy, Japan, and Sweden from 1980 to 2000, for females and males, $SD(M^+)$ declined as M increased, and $\log SD(M^+) = aM + b$, $a < 0$, was proposed as a model (Cheung *et al.*, 2008). Explicit statistical tests of the log-linearity of this model were not reported in this study. In Switzerland, over the last 50 years, as M increased by about 10%, $SD(M^+)$ decreased by about 10% (Cheung *et al.*, 2009). The broadly linear, nearly inverse relation between modal life length M and root-mean-squared remaining life length $SD(M^+)$ spanned the entire period studied, 1876–2005. Cheung *et al.* (2009, p. 569) concluded: “This analysis has not found any evidence suggesting that we are approaching longevity limits in term of modal or even maximum life spans”. The present study shares this conclusion.

By extrapolating the linear model $e(m) = am + b$ from a set s of life tables for a given country c in a given 20-year interval with first year t , we estimated a maximal median life length, $\alpha(c,t,s) = -b/a$, an upper bound on the life expectancy at birth, as a useful index of the consequences of the mortality conditions of country c in the time interval with first year t .

Our second null hypothesis was that the greatest median life length $\gamma(t)$ was

constant over a succession of non-overlapping 20-year intervals. The data rejected this null hypothesis. Instead, the data demonstrated increasing trends in $\gamma(t)$ (Table 2). The data offered no evidence of an imminent or impending upper asymptote or limit to $\gamma(t)$.

The index $\alpha(c,t,s)$ and the derived indices are not to be taken literally, any more than other counter-factual demographic indices such as the total fertility rate and the intrinsic rate of natural increase. Rather, MMLL, BMLL, and GMML estimate maximal median life length implied by the compression of remaining mortality with increasing median life length, for a given time interval and country.

Most values of the GMML $\gamma(t)$ for period life tables (female and male) lie in the range 90-200 years (Figure 2, Table S3). Are life expectancies in this range plausible? A rough calculation may be based on two facts. First, the highest national (Japanese) period female life expectancy at birth around 2010 was above 86 years. Second, since 1960, the estimated annual increment in the maximal (over all countries) life expectancy was 0.23 years (of age) per year (of calendar time). Chunn *et al.* (2010) posited future increases in life expectancy that are asymptotically linear at a maximum of 0.23 years (of age) per year (of calendar time). Were that rate of progress to be maintained, the maximal period female life expectancy at birth would be 106.7 years in 2100. The achievement by the end of the 21st century of a period female national life expectancy of 90 to 200 years seems plausible, though hardly assured.

Such an increase would be compatible with our estimated rates of increase in the maximal median life length. For period female life tables, if MMLL increased over the 100 years from 2000 to 2100 at the median rate of increase median, $g(s)$ estimated for the last 200 years, namely, 2.09 years of life per calendar year (Table 2), then the upper bound on life expectancy at birth would rise by about 209 years from the estimate for year 2000 of about 207 years (Table S3).

These crude calculations assume a continued progress, not significantly slower than that of the last two centuries, in scientific knowledge, practical application of knowledge, and living conditions. These assumptions seem modest compared to some “life-extension milestones” that have been posited as enabling life expectancies of 5,000 years by the end of the 21st century (de Grey, 2006). These calculations do not contradict the maximal span of life of 115 years posited by Duchene and Wunsch (1988) but they do exceed the assumption of Duchene and Wunsch that “deaths due to senescence alone would yield an average age at death of 90 ± 5 years”.

The increases in MMLL demonstrated here in cohort and period life tables for females and males suggest caution in basing public policy for pension systems and health care systems on any supposed fixed upper limits on life expectancy at birth.

The finding that, within 20-year (and 10-year) intervals, for nearly all coun-

tries, $e(m)$ almost always decreased when m increased may be viewed as a short-term, local, “compression of mortality”, a concept with various meanings (Cheung *et al.*, 2005). The finding that the GMLL implied by this decreasing linear relationship increased over one century (for cohort life tables) or two centuries (for period life tables) suggests that, under the circumstances most favorable for improvement in old-age survival (i.e., in the best country at least), as median life length increased, the compression of mortality at older ages diminished.

Beyond their interest to human demography, these empirical results have relevance to ecological and evolutionary studies of trade-offs in life histories (Charnov, 1991, Charnov, 1993, Harvey and Purvis, 1999). The dramatic rise in human life expectancy at birth globally over the past two centuries must be due more to environmental, economic, behavioral, sanitary, nutritional, and medical changes (Riley, 2001, Fogel, 2004) than to evolutionary changes, and the present disparities in life expectancy within and between countries are probably due more to environmental, economic, behavioral, sanitary, nutritional, and medical differences than to evolutionary differences within and between countries (Crimmins *et al.*, 2010a, Crimmins *et al.*, 2010b). The general association of an increasing median life length m with decreasing remaining life expectancy $e(m)$ at age m suggests the possible existence of biological constraints on the improvement of mortality at different ages (Horiuchi *et al.*, 2003).

Analyses of data on the recent past of human mortality cannot address its indefinite future. Condorcet (1795) wrote (Bourgeois-Pichat’s translation): “Of course, man will not become immortal, but is it not possible to believe that the interval between the moment man’s life begins and the time when, in a natural way, without being subjected to sickness or accident, he finds it difficult to continue to exist, will go on increasing indefinitely?”. Bourgeois-Pichat (1978) described this as “a very optimistic outlook” and posited a limit to life expectancy that has already been surpassed. Carnes and Olshansky (2007, p. 373) argued that “the mortality experience of populations today is fundamentally different from that of earlier cohorts. The mortality of the future may well depart from both of these patterns as ways to intervene in the processes of senescence are discovered and implemented”. We shall see.

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Appendix

1. DATA AND METHODS

1.1 Data, selection, and organization

Apart from the United States example, we used the data of the Human Mortality Database (HMD) on 701 cohort life tables for each sex from 1800 to 1917 from 11 countries and 2,579 period life tables for each sex from 1800 to 2008 from 26 countries, making 3,280 life tables for females and males sepa-

Table S1 – Summary of Human Mortality Database life tables used in this study (female and male, 1 year of time × 1 year of age).

Country	Subgroup	Cohort life tables		Period life tables		Years omitted	Number of life tables for each sex
		First year	Last year	First year	Last year		
Australia				1921	2007	0	87
Austria				1947	2008	0	62
Belgium				1841	2007	1914-8	0
Canada				1921	2006	0	86
Chile				1992	2005	0	14
Denmark		1835	1916	1835	2007	82	173
Finland		1878	1917	1878	2008	40	131
France	civilian	1816	1916	1816	2007	101	192
Germany				1990	2008	0	19
Great Britain - Scotland		1855	1915	1855	2006	61	152
Great Britain - England and Wales		1841	1915	1841	2006	75	166
Great Britain - total				1922	2006	0	85
Ireland				1985	2006	0	22
Israel				1983	2007	0	25
Italy		1906	1915	1906	2006	10	101
Japan				1947	2008	0	62

...Cont'd...

Table S1 – *Cont'd*

Country	Subgroup	Cohort life tables		Period life tables		Years omitted	Number of life tables for each sex	
		First year	Last year	First year	Last year		Cohort	Period
Netherlands		1850	1915	1850	2006	66	157	
New Zealand	non-Maori	1876	1912	1876	2003	37	128	
New Zealand	total			1948	2003	0	56	
Norway		1846	1916	1846	2007	71	162	
Portugal				1971	2007	0	37	
Spain				1960	2006	0	47	
Sweden		1800	1916	1800	2007	117	208	
Switzerland		1876	1916	1876	2007	41	132	
Taiwan				1970	2008	0	39	
USA				1933	2006	0	74	
Total		1800	1917	1800	2008	701	2579	
Cohort & period life tables of each sex							3280	
Cohort & period life tables of both sexes								6560
Number of countries						11	26	

rately and 6,560 life tables altogether (Table S1), by single years of age and single years of time. In sensitivity analyses, we used these same life tables by single years of age and five years of time. We included cohort life tables, which prior studies of this kind excluded, for comparison with period life tables. Cohort and period life tables were analyzed separately. Because cohort and period life tables shared some basic age- and year-specific mortality rates, the two data sets were not entirely independent. The time series of cohort life tables were far shorter than those of period life tables. No cohort analysis was possible for many countries.

We excluded some countries in HMD on grounds of insufficient quality (such as former Communist countries) or quantity (e.g., where populations were so small that frequently no deaths in single years of age occurred in single years of time, or where <9 life tables from consecutive years were available in a 10- or 20-year interval). All decisions to exclude HMD data were made prior to the analyses conducted here, so no selection bias was introduced for or against the hypotheses to be tested.

Although HMD metadata advised extra caution in using Taiwanese data prior to 1980, we included Taiwanese period life tables 1970–2008. In two cases only, we preliminarily included countries and subunits (Great Britain total, Great Britain – Scotland, and Great Britain – England and Wales; New Zealand total, New Zealand non-Maori) to see whether the subunits differed materially from the larger aggregation. They did not and the “total” life tables were dropped thereafter. None of these cases affected our conclusions regarding trends in BMLL because they were not among the countries with the largest MMLL in the time intervals in which they were observed.

The four sets of life tables (cohort and period, for each sex, female and male) were organized by countries, indexed by c , and by time intervals, indexed by t . A country was included in the analyses for a time interval only if it had ≥ 9 one-year life tables in that 10- or 20- year interval, and only when it had at least 5 five-year life tables in that 30-year interval. For the period life tables, we divided 1800-2008 into 11 disjoint intervals: ten intervals 20 years long, 1800-1819, 1820-1839, ..., 1980-1999, plus the residual 9 years, 2000-2008. No cohort life tables were available after 1917, so we allocated them to 6 intervals of 20 years, namely, the five 20-year intervals in the 19th century plus 1900-1917.

The choice of 20 years as the duration of time intervals was a compromise between two opposing desires: on one hand, to increase the number of data points (beyond the required minimum of 9) within each interval for greater statistical stability in estimating the relation between m and $e(m)$ (or between the upper quartile U of life length and $e(U)$, in a sensitivity analysis), and, on the other hand, to keep each interval as short as possible so that the life tables for each country included represented a snapshot of an unchanging or slowly changing mortality regime during the interval. The aim was to reveal long-term trends in the relation between m and $e(m)$ by simple relationships in successive short intervals rather than by a complex pattern within long intervals. The choice of 9 life tables as the minimum required for a country to be represented in a time interval was motivated by the example from the USA, the limited number of years of data available from the 21st century (2000-2008, 9 years), the ability to bootstrap (the smaller the number of values, the higher the likelihood of singular bootstrap samples), and the desire to have a minimum number of life tables compatible with a sensitivity analysis that used 10-year intervals.

1.2 *Statistical methods, step 1*

A “set” of life tables was specified by a country c and a time interval t , provided there were ≥ 9 life tables in contiguous years for that combination of country and time interval. When time intervals were 20 years long, there were 322 sets.

To test whether $e(m)$ was a linear function of m , independently for each set, life tables in a set were bootstrap sampled 10,000 times. By definition, each bootstrap sample was a sample with replacement in which each life table was included with equal probability and the total size of the sample equaled the number of life tables observed for the given country c and time interval t .

For each sample of life tables in the set, a quadratic function $e(m) = Am^2+Bm+C$ was fitted by least squares to the data points $(m, e(m))$ in the sample. This yielded 10,000 estimates of each coefficient A , B , and C , for each c and t . Matlab function ‘bootstrp’ applied the bootstrap operation to the linear and quadratic coefficient estimates obtained from Matlab function ‘regress’.

To obtain the 98% confidence interval (CI) of A , the 10,000 values of A

were sorted from smallest to largest. In this sorted list of A values, the lower limit of the CI was the 100th value from the low end, and the upper limit of the CI was the 9900th value from the low end. The hypothesis of linearity was not rejected if the 98% CI, estimated by the bootstrap, of the quadratic coefficient A included 0. If the lower limit of the CI exceeded 0, we classified $e(m)$ as a convex function of m for this c and t . If the upper limit of the CI was less than 0, we classified $e(m)$ as a concave function of m for this c and t . Even when this analysis rejected linearity for a set, some of the bootstrap samples of life tables from the set may have been consistent with a linear relation of $e(m)$ to m according to normal theory for the confidence interval of A for the particular bootstrap sample. Such samples are included in the analysis of step 2.

1.3 Statistical methods, step 2

For each time interval t and for each country c with ≥ 9 life tables in successive years in time interval t , we constructed a bootstrap sample s_c as above. We let s represent one sample for each country simultaneously, i.e., $s = \{s_c \mid c = 1, 2, \dots\}$. We constructed 10,000 bootstrap samples s .

For the life tables in time interval t , country c , and bootstrap sample s_c , we tested the hypothesis that $e(m)$ changed linearly with m , against the alternative hypotheses that $e(m)$ was a quadratic function of m , concave or convex, using the normal theory of the distribution of the coefficient A in the regression of $e(m)$ on m and a 95% significance level. The significance level 95% was conservative because, for example, a 99% significance level would have yielded a wider CI and the null hypothesis of linearity would have been rejected less frequently. When linearity was rejected for sample s of country c in interval t , we discarded sample s_c for country c in interval t . When linearity was not rejected for sample s_c , i.e., when the 95% CI of A by normal theory included 0, we calculated the MMLL $\alpha(c,t,s_c) = -b(c,t,s_c)/a(c,t,s_c)$, where we estimated the coefficients of $e(m) = a(c,t,s_c)m + b(c,t,s_c)$ by least squares. Thus we may have generated fewer than 10,000 bootstrapped estimates of $\alpha(c,t,s_c)$ for country c in interval t . Then, for each t and each s , we computed the CMLL $\chi(t) = \max_c \alpha(c,t,s_c)$ separately for cohort and period life tables, female and male life tables. For every t , there were 10,000 values of CMLL because at least one country c in every time interval t and every sample s had an acceptably linear relation of $e(m)$ to m and therefore generated a value of $\alpha(c,t,s_c)$. For each s , we then fitted a linear relationship $\chi(t) = g(s)t + h(s)$. This procedure produced 10,000 samples of the slope $g(s)$ to describe the variability of the trend of $\chi(t)$ as a function of t . We also plotted the frequency distribution (histogram) of $g(s)$. If $g(s) > 0$ for most samples s , then CMLL usually increased. This straightforward approach was chosen instead of using a fixed- or random-effects model to avoid the sometimes arbitrary decisions about which effects to consider fixed or random.

To estimate a typical largest value of MMLL as a function of time, we com-

puted $\gamma(t)$ from those bootstrap samples for which linearity was not rejected by the normal theory of the quadratic coefficient A . We then fitted a linear relationship $\gamma(t) = gt + h$ to describe the time trend of the typical largest MMLL.

1.4 Sensitivity analyses

To test the robustness of our conclusions based on 20-year intervals, we repeated step 2 using 10-year intervals 1800-1809, 1810-1819, To test the robustness of our conclusions based on median life length, we repeated steps 1 (testing for linearity) and 2 (testing for trends in GMLL) using instead of m the upper quartile U of life length (U is the age at which one-quarter of a life-table population survives, $\ell(U) = 1/4$) and the expectation $e(U)$ of remaining life at age U , with both 20-year and 10-year intervals.

Cubic spline and linear interpolation were used to obtain U and $e(U)$. For m , $e(m)$ and U , the two interpolations differed by >0.1 year in one life table only, and for $e(U)$ they differed by >0.1 year in no life tables.

2. RESULTS OF THE SENSITIVITY ANALYSES

To compare the usefulness of a linear model of the relation between m and $e(m)$ and between U and $e(U)$ using 20- and 10-year time intervals, Table S2 shows the numbers of sets of life tables classified as convex, concave, and linear for all four alternatives. This table extends Table 1. The 10-year time intervals are better described by linear models (98% for m , 99% for U) than the 20-year time intervals (87% for m , 91% for U). This result is not surprising as the smaller number of observations in 10-year intervals may have smaller power to reject the null hypothesis of linearity. A linear relation between U and $e(U)$ is slightly more likely than a linear relation between m and $e(m)$ using 20- and 10-year time intervals, respectively. The cases where linearity was rejected are nearly evenly distributed between convexity and concavity. At least for the two quantiles m and U , a linear relation between the quantile of life length and the expectation of remaining life is robust.

Table S3 compares the GMLL $\gamma(t)$ for period female and male life tables using the median and upper quartile for 20- and 10-year time intervals. For either m or U and for either 20- or 10-year intervals, GMLL for males was sometimes longer and sometimes shorter than GMLL for females; no systematic pattern of difference by sex was obvious. Similarly, comparison of 20-year and 10-year estimates of GMLL based on the same quantile of life length for the same sex revealed no systematic pattern of difference. Sometimes the 20-year estimate of GMLL fell between the two 10-year estimates in the same time interval, but sometimes the 20-year estimate fell above or below both 10-year estimates.

However, in general, U and $e(U)$ led to higher values of GMLL than did m and $e(m)$ for the same duration of time intervals and the same sex. Of the 11 pos-

Table S2 – Number of sets of life tables by type (cohort, period), sex (female, male), and concavity, linearity, and convexity in the relation of $e(m)$ to m and in the relation of U to $e(U)$ using 20- and 10-year time intervals.

Type	Sex	Median, 20-year time intervals				Median, 10-year time intervals			
		Concave	Linear	Convex	Total	Concave	Linear	Convex	Total
Cohort	Female	0	28	6	34	0	66	2	68
Cohort	Male	3	26	5	34	0	66	2	68
Period	Female	12	108	7	127	2	272	0	274
Period	Male	4	117	6	127	4	268	2	274
Total		19	279	24	322	6	672	6	684
Percent		6	87	7	100	1	98	1	100
Upper quartile, 20-year time intervals									
Cohort	Female	3	26	5	34	2	64	2	68
Cohort	Male	4	26	4	34	0	67	1	68
Period	Female	4	121	2	127	1	271	2	274
Period	Male	2	121	4	127	0	274	0	274
Total		13	294	15	322	3	676	5	684
Percent		4	91	5	100	0	99	1	100

Table S3 – Values of the greatest median life length ($GMLL$) $\gamma(t) = \text{median}_s \max_c \alpha(c, t, s)$ based on the linear relation of $e(m)$ to m and of U to $e(U)$ using 20- and 10-year time intervals, for those bootstrap samples that did not reject linearity (see Appendix Methods).

Initial year	$m, e(m)$	Period female $\gamma(t)$ using				Period male $\gamma(t)$ using			
		$U, e(U)$		$m, e(m)$		$U, e(U)$		$m, e(m)$	
		20 years	10 years	20 years	10 years	20 years	10 years	20 years	10 years
1800	92.8	93.6	97.1	95.7	98.9	101.0	95.5	94.8	
1810		92.2		101.3		95.4		97.8	
1820	92.1	88.8	106.2	113.1	100.4	99.0	100.6	122.9	
1830		94.1		102.6		101.8		96.5	
1840	116.9	127.0	139.5	126.5	105.4	111.2	116.9	133.7	
1850		113.3		153.5		104.1		131.5	
1860	93.6	104.4	117.7	121.2	108.0	99.9	108.8	112.2	
1870		96.1		161.0		113.9		163.9	
1880	95.3	95.8	205.3	121.3	94.8	94.4	142.8	121.0	
1890		122.2		283.8		122.3		156.4	
1900	94.7	109.4	151.4	186.5	152.2	97.8	117.8	140.2	
1910		101.8		228.0		169.0		168.2	
1920	107.3	159.2	173.9	358.6	99.1	124.2	191.1	259.3	
1930		128.6		456.1		130.3		311.5	
1940	117.2	177.6	167.0	421.9	124.7	181.7	246.1	454.9	
1950		263.8		505.3		367.8		484.9	
1960	1074.3	587.0	1280.5	410.9	335.3	434.5	754.7	417.1	
1970		383.0		783.6		547.9		523.9	
1980	220.0	479.5	234.6	412.8	542.3	437.2	182.0	382.2	
1990		182.6		266.8		234.2		235.9	
2000	207.2	206.8	251.1	252.4	165.0	165.8	282.9	281.1	

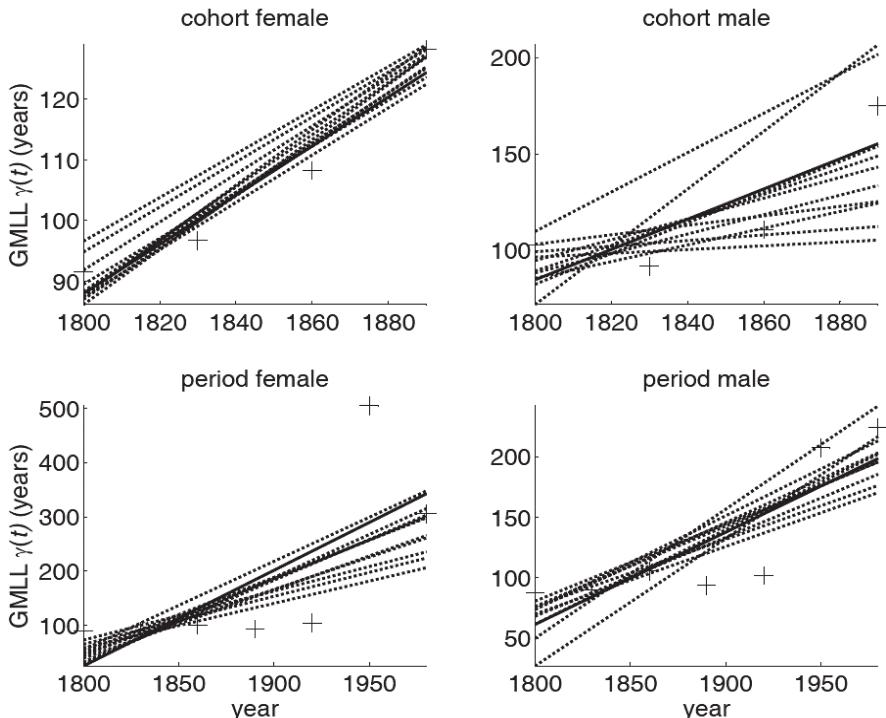
sible comparisons using 20-year intervals, GMLL from U exceeded those from m 11 times for period female life tables and 8 times for period male life tables. Of the 21 possible comparisons using 10-year intervals, GMLL from U exceeded those from m 18 times for period female life tables and 15 times for period

Table S4 – *Rates of increase in the country-maximal median life length (CMLL) $\chi(t,s) = \max_c \alpha(c,t,s)$ for life tables by type (cohort, period) and sex (female, male), based on the median m and upper quartile U of life length using 20- and 10-year time intervals.*

Type of life table	Cohort Female	Cohort Male	Period Female	Period Male
<i>Based on median m and expected remaining life $e(m)$ using 20-year intervals</i>				
Slope, median _s $g(s)$	0.38	0.58	2.09	2.11
Slope, 1 percentile (lower CI)	0.263	0.193	0.716	0.562
Slope, 99 percentile (upper CI)	1.07	24.9	86.5	85.0
$P(g(s)>0)$	1.0000	1.0000	1.0000	1.0000
<i>Based on median m and expected remaining life $e(m)$ using 10-year intervals</i>				
Slope, median _s $g(s)$	0.497	0.35	2.56	3.08
Slope, 1 percentile (lower CI)	0.331	0.126	0.804	0.888
Slope, 99 percentile (upper CI)	1.27	19.5	79.3	82
$P(g(s)>0)$	0.9999	0.9964	0.9987	0.9996
<i>Based on upper quartile U and expected remaining life $e(U)$ using 20-year intervals</i>				
Slope, median _s $g(s)$	0.940	1.79	1.66	2.06
Slope, 1 percentile (lower CI)	0.413	0.576	-4.18	0.613
Slope, 99 percentile (upper CI)	22.4	116	91.5	95
$P(g(s)>0)$	0.9995	1.0000	0.9585	0.9980
<i>Based on upper quartile U and expected remaining life $e(U)$ using 10-year intervals</i>				
Slope, median _s $g(s)$	1.52	1.62	4.54	3.77
Slope, 1 percentile (lower CI)	0.205	-2.61	0.619	3.77
Slope, 99 percentile (upper CI)	56.3	42.9	163	134
$P(g(s)>0)$	0.9927	0.9732	0.9931	0.9893

Note: All life tables in this tabulation use single years of age and single years of time. For each bootstrap sample s , $g(s)$ is the slope in the linear model $\chi(t,s) = g(s)t + h(s)$. Line 1 shows the median slope, median_s $g(s)$, in years of life per calendar year, over all bootstrap samples s . Lines 2, 3 show the bootstrapped 98% confidence interval (CI) of $g(s)$. Line 4 is the fraction of sampled values of $g(s)$ that were positive, $P(g(s)>0)$.

Figure S1 – Greatest median life length (GMLL) $\gamma(t) = \text{median}_s \max_c \alpha(c, t, s)$ (plotted by +) as a function of the initial year t in 30-year time intervals that contained at least 5 life tables by single year of age and 5 years of time, for (a) cohort female life tables, (b) cohort male life tables, (c) period female life tables, (d) period male life tables.



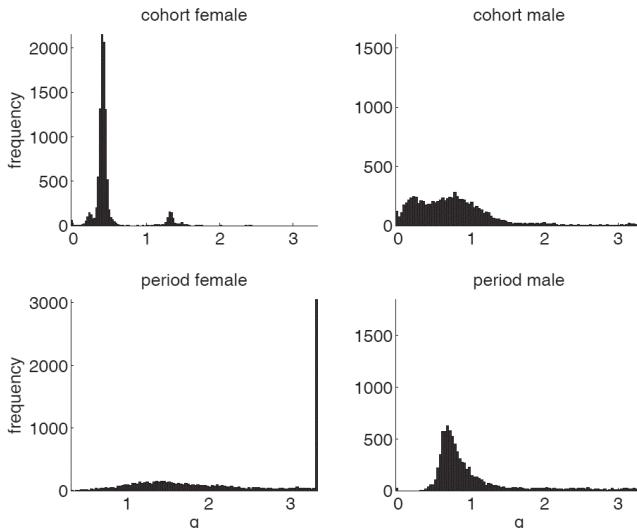
Note: The solid straight line is the linear model $\gamma(t) = gt + h$. The units of g are years of age per calendar year. The dotted lines are linear regressions $\chi(t, s) = g(s)t + h(s)$ for 10 representative bootstrap samples s . Extreme outliers (slopes of >50 years per 30-year interval) were discarded from these plots. The solid regression lines $\gamma(t) = gt + h$ had parameter values: (a) $g = 0.41$, adjusted $R^2 = 0.93$; (b) $g = 0.79$, adjusted $R^2 = 0.66$; (c) $g = 1.80$, adjusted $R^2 = 0.49$; (d) $g = 0.76$, adjusted $R^2 = 0.70$.

male life tables. These differences may seem unsurprising since $m < U$ in every life table, so the straight lines relating $e(m)$ to m were mostly placed to the left of the straight lines relating U to $e(U)$. However, it was not a priori predictable that the values of $e(U)$ would place the values of GMLL to the right of those derived from $e(m)$. This is an empirical finding, not a tautology.

Table S4 compares the rates of increase in the CMLL (i.e., the distribution of the slope $g(s)$ of $\chi(t, s)$ as a function of time t) for life tables by type (cohort, period) and sex (female, male), based on the median m and upper quartile U of life length using 20- and 10-year time intervals. In every comparison of corre-

sponding life tables by sex and quantile of longevity, the median slope was larger for period than for cohort life tables. In every comparison of life tables of the same type, sex, and time interval, the median slope was larger for estimates based on the upper quartile than for estimates based on the median. That is, the upper bound rose faster according to the upper quartile than according to the median. This behavior reflects the improvements in health at the oldest ages and is consistent with the prior observation (Vallin and Meslé, 2009, Vallin and Meslé, 2010) that recent improvements in mortality occurred mostly in age groups at or above the upper quartile of life length. In every case, $P(g(s)>0) >$

Figure S2 – Frequency histogram of the slopes $g(s)$ estimated (as in Figure S1) for linear models of country-maximal median life length (CMLL) as a function of the initial year t in 30-year intervals that contained at least 5 life tables by single year of age and five years of time, for 10,000 bootstrap samples s , for (a) cohort female life tables, (b) cohort male life tables, (c) period female life tables, (d) period male life tables.



Note: The horizontal $g(s)$ axis has 102 bins of unit width with left boundary points from $-1/30$ to $100/30$. The left bin counts the frequency of values of $g(s) < 0$. The right bin counts the frequency of all values of $g(s) \geq 100/30$. Values of $g(s) \geq 100/30$ appeared to be randomly sparsely distributed. For nearly all samples s , $g(s) \geq 0$, i.e., CMLL generally increased with time. For cohort life tables, the modal values of $g(s)$ were about 0.47 and 0.73 years of age per calendar year for females and males, respectively, suggesting that most commonly (among the bootstrap samples s) CMLL increased by about 47 and 73 years of age over the 100-year interval of observation for females and males, respectively. For period life tables, the modal values of $g(s)$ were about 1.33 and 0.73 years of age per calendar year for females and males, respectively, suggesting that most commonly (among the bootstrap samples s) CMLL increased by about 266 and 146 years of age over the 200-year interval of observation for females and males, respectively.

0.95, i.e., the trend in CMLL was increasing in at least 95% of bootstrap samples, regardless of life table type, sex, duration of time interval, or median or upper quartile of life length.

As life tables by single year of age and single year of time may have some small numbers of deaths and may therefore be vulnerable to statistical fluctuations, we also analyzed life tables by single year of age and five years of time. (We retained the requirement of single year of age to estimate accurately the median life length and remaining life expectancy). Life tables were then separated by five years, so we binned the life tables into 30-year intervals, 1800-1829, 1830-1859, ..., 1980-2009. We required a minimum of five life tables within each 30-year interval to reduce the risk that bootstrap samples of life tables within an interval would consist entirely of repetitions of a single life table. Our results remained qualitatively and quantitatively similar, though noisier, with more extreme values of slope $g(s)$, albeit more conservative median values (Figures S1 and S2, which are equivalent to Figures 2 and 3). In cohort life tables, median, $g(s)$ increased by 0.402 (0.153, 1.45) years per calendar year for females, and 0.792 (-0.0137, 63.6) years per calendar year for males, values comparable with those (Table 2) from the life tables by single year of time. For the period data, female and male median, $g(s)$ increased by 2.08 (0.565, 77.6) and 0.869 (0.432, 117) years per calendar year, respectively. The period female median rate of increase using five years of time, 2.08 years per year, was very close to that, 2.09 years per year, using single years of time. For males, the rate of increase was substantially lower, 0.869 instead of 2.11, but the broader confidence interval from the life tables based on five years of time, namely, (0.432, 117), included the estimate and the confidence interval from the life tables based on single years of time (Table 2).

3. DISCUSSION

Whether the linear models of $e(m)$ versus m and of $e(U)$ versus U were influenced substantially by regularities created by the Human Mortality Database Protocol will become clearer as more and better mortality data at advanced ages are assembled. For now, there are two reasons for tentative confidence in the linear models. First, the linear relationship was clear in the U.S. life tables, which were not subject to this Protocol. Second, for many countries and time intervals, the median life length was well below the advanced ages at which the Protocol imputed mortality rates.

3.1 Time interval

These sensitivity analyses indicated that the choice of time interval, 20-years or 10-years, hardly affected the results. Exploratory work prior to these

calculations, not reported here in detail, showed that significantly longer time intervals, e.g., 50 or 100 years, would have more frequently displayed curvilinear, usually convex, relations between $e(m)$ and m and between $e(U)$ and U for an individual country, among those few countries with long enough series of life tables. Since most countries did not have such long series of life tables, an approach using short time intervals was preferred, because it could be applied uniformly to countries with long or relatively short series of life tables. The sensitivity analysis shows that the particular choice of short time interval mattered little.

3.2 *Indicator of longevity: median or upper quartile*

The choice of a quantile of life length, m or U , may affect the results obtained, depending on the question being asked. U gave a larger value of GMLL than the m did for most time intervals (Table S3). U also gave a larger value of the median slope, median_s $g(s)$, than did m (Table S4). This finding is consistent with the observation by many demographers that in recent decades the improvements in survival at older ages have been more rapid than the improvements in survival in early or middle life in the wealthy countries that produced most HMD data. But both m and U concurred in giving no evidence of an imminent limit to life expectancy.