Are We Approaching the **Upper Bounds** of **Human Life Span?**

By Jack C. Yue

HE AVERAGE AGE AT DEATH continues to increase and shows no signs of slowing down. The inexorable increase in human life span has consequences across the actuarial spectrum, from insurance underwriting to lifetime income. A deeper understanding of the demographic trends at work will lead to more accurate projections and calculations. This piece studies the complex questions belied by the seemingly simple question of the headline.

Mortality improvement is a common phenomenon, but not all ages experience the same reduction in mortality rates. For example, the reductions in Taiwan's mortality rates are greatest for the elderly (ages 65

and beyond) and for the groups around ages 10 and 20 (Figure 1). As a result, the age at death will concentrate on a narrower range, an occurrence known as "mortality compression." We can use the ages-at-death probability to demonstrate mortality compression (Table 1). The median (50 percent) is the life expectancy, which keeps rising while the inter-quartile, the variance, becomes smaller.

TABLE 1 Ages of Death Probability for Taiwanese Females									
	25%	50%	75%	90%	95%				
1979-1981	69	79	86	91	93				
1989-1991	72	80	87	92	94				
1999-2001	74	83	90	95	98				
2009-2011	78	86	92	97	99				





We can look at mortality compression via the angle of survival curve as well. Figure 2 shows the survival curves of Japanese females in 1950, 1980, and 2010, based on data from the Human Mortality Database (HMD). The survival curve goes rightward and upward, and it does start to look like half of a rectangle in 2010, more so than in 1950. This is known as the "rectangularization" of the survival curve, and it shows that most people die within a certain age group—and that age group is getting smaller over time. In other words, eventually the age-specific mortality rates will converge to 0, except for the ages near the modal age.

Rectangularization is now assumed in many mortality studies, but there is no agreement on whether there is a limit to human life span. Researchers who support the premise that there is no upper limit, such as Oeppen and Vaupel (2002) and Wilmoth and Robine (2003), used historical data to show that human longevity is likely to continue increasing. On the other hand, those who support such a limit, such as Carnes et al. (2003) and Olshansky et al. (2005), thought that obesity and other biological factors would slow down and possibly restrain the incremental increases in longevity.

It is interesting to note that, depending on the methods used, researchers can arrive at different conclusions based on the same data set. For example, in exploring the issue of mortality compression, researchers do not agree on whether the variance (or standard deviation) of age-at-death distribution converges. Cheung et al. (2005) and Thatcher et al. (2010) support variance convergence, while Li et al. (2008) and Yue (2012) assert there is still not enough evidence to confirm mortality compression. In addition to the approach used, the quality of the data is also crucial in mortality studies. For example, even for the HMD, the official population counts are not available in all countries for ages 90 and beyond (Jdanov et al., 2008). Thus, the HMD needs to make adjustments (i.e., graduation) for mortality rates over age 80 using the method of extinct generations, and over age 90 using the survivor ratio method (Thatcher et al., 2002).

In this study, we propose a statistical approach for evaluating mortality compression using ungraduated mortality data. And then we apply this proposed approach to examine whether there is an upper limit to human life span. We consider optimization methods, e.g., nonlinear maximization and weighted least squares, for estimating the modal age and the standard deviation of age-at-death distribution. And finally, we use computer simulations and empirical studies to check the proposed methods.

Methodology

Mortality compression was first proposed by Fries (1980). There are quite a few ways for measuring mortality compression. Kannisto's 2000 and 2001 studies were the first to use the standard deviation, or SD(M+), to measure the compression. The SD(M+) can be defined as



$$SD(M+) = \sqrt{\frac{\sum_{x \ge M} f(x)(x - M)^2}{\sum_{x \ge M} f(x)}}$$
, (1)

where M is the modal age with the largest number of deaths.

The value of SD(M+) is derived from the formula of a sample variance and will have a lot of fluctuations, since age at death is usually recorded as the integer of age.

There are several possible approaches to reduce the fluctuations of the observed measures. Numerical methods are a frequent choice since they often provide good results. We use three optimization methods, similar to Yue (2002), including maximal likelihood estimation (MLE), nonlinear maximization (NM), and weighted least squares (WLS), to estimate the variance of age-at-death distribution.

To simplify the analysis, we present the NM method as a demonstration. The NM and MLE methods are expected to produce similar results in parameter estimations. However, in practice, not all data are used by the MLE method, thus the NM method will produce more accurate estimates. Also, it should be noted that in order to apply the optimization methods, the age-at-death distribution is required.

If the number of deaths at age *x*, or d_x , satisfies the function f(x), then the NM estimate is found by solving the following equation M^{+2k}

$$\arg\min\sum_{x=M}^{M^{+2x}} w_x (f(x) - d_x)^2 \qquad , \qquad (2)$$

where w_x is the weight, M is the modal age, and k is the data range.

If the age of death follows the normal distribution, equation (2) can be written as

$$\arg\min_{M,\sigma} \sum_{x=M}^{M+2k} w_x \left(\frac{1}{\sqrt{2\pi\sigma}} \exp\left[\frac{-1}{2\sigma^2} (x-M)^2 \right] - d_x \right)^2$$
(3)

Note that equation (2) assumes a stationary population. However, in practice, the annual number of births may not be the same, or the radix l_0 may be different every year.

We can apply the process to mortality rates and modify equation (2) as

$$\arg\min\sum_{x=M}^{M+2k} d_x \left(f(x) - \frac{d_x}{l_0} \right) = \arg\min\sum_{x=M}^{M+2k} d_x (f(x) - x p_0 \times q_x)^2$$
(4)

where $_{x}p_{0}$ is the survival probability of age 0 to age *x*, and q_{x} is the death probability between age *x* and age *x*+1.

Similarly, we can modify SD(M+) in equation (1) to

$$SD(M+) = \sqrt{\frac{\sum_{x=M}^{M+2k} d_x (x-M)^2}{\sum_{x=M}^{M+2k} d_x}}$$
 (5)

The modal age at death can be derived from the process of optimization for the NM method, but it must be estimated separately for the SD(M+) method. The modal age is usually determined by pure observation, but it will have a lot of fluctuations and will not be unique if there are two or more modal ages at death. To deal with these problems, Kannisto (2000) suggested a modified estimate of the modal age

$$M^* = x + \frac{f(x) - f(x-1)}{[f(x) - f(x-1)] + [f(x) - f(x+1)]} , \qquad (6)$$

where *x* is the age with the largest number of deaths.

We will use equation (6) to obtain the modal age for the SD(M+) in this study.

Simulation and Empirical Analysis

We will then use a computer simulation to evaluate whether the proposed estimation method works. Before showing the simulation results, we need to add a note about the estimation of the NM method. Since age at death is usually recorded as the age on the deceased's last birthday, the age of a person aged x is between x and x+1, or [x, x+1). This means that the average age of a person aged x is x+1/2. In other words, to estimate the modal age using the NM method requires the addition of half a year.

Example 1. Suppose the age of death follows a normal distribution with modal (mean) M=80 and standard deviation σ =10. For each simulation run, we simulate 100,000 deaths whose ages at death follow a normal distribution. The idea behind this setting is similar to the radix (l_0 = 100,000) of life tables where





there are 100,000 newborns. The simulation is repeated 1,000 times.

The data used to calculate the modal age and standard deviation for the NM method are from ages M-k to M+k, and the value of k is at least 5. We want to determine if the observations used have a significant influence on the estimation result. Also, in practice, we can use the observed information or we can apply equation (3) to determine the M value for use with the NM method. It should be noted that, as mentioned by Kannisto (2000), the original setting for estimating the standard deviation for SD(M+) is to use the deaths beyond the modal age, or $[M, \infty)$. However, according to our experiment on the proposed approach, we found that the estimation results using the data aged $M-k \sim M+k$ are slightly better than those aged $M \sim M+2k$. Therefore, we use the data aged $M-k \sim M+k$ for the NM method and those of aged $M \sim M+2k$ for SD(M+) in the

TABLE 2 Coverage Probability of Normal Distribution								
	N							
	Integer Age	First Decimal	SD(M+)					
М	0.951	0.952	0.969					
σ ²	0.956	0.937	0.000					
Note: Coverage values larger than 0.964 or smaller than 0.936 are significantly different from the 95% level, and are marked in red.								

simulation study.

We will use the bias and the variance, or mean squared error (MSE), which is the sum of $(bias)^2$ and variance, of the estimate to evaluate the proposed method. We will use the logarithm of MSE (Figure 3) since it is easy to distinguish the differences. In addition, we want to know whether the estimates for ages to one decimal place are better than the estimates for integer ages.

It seems that the estimate of the NM method has a smaller MSE and the MSE decreases as the value k increases. Interestingly, using the format of integer age is slightly better than using the data of ages to first decimal, which indicates data up to integer ages would be sufficient. Also, the MSE of the estimate from equation (4) looks like a constant no matter how many data are used.

The results of σ estimate are similar and show more obvious differences between the NM method and SD(M+). The NM method can obtain an accurate estimate for σ , for different *k* values (Figure 4). On the other hand, the SD(M+) is underbiased, and the bias becomes smaller as the data range *k* increases. However, the bias is still noticeable when more than 30 data points (different ages) are used, or *k* = 15. Based on these simulation results, it seems that the NM method is reliable in providing the estimates of M and σ , and data in the form of integer age are preferred.

We further use the coverage probability of the estimate of modal age to evaluate the estimation methods. Together with the estimate of modal age and σ for every simulation replication, we can use the variance to construct the confidence intervals. Table 2 shows the coverage probabilities of the modal age and σ for the NM method and SD(M+). The NM method meets expectations when the data are recorded in integer age or are accurate up to the first decimal. On the other hand, the SD(M+) is underbiased for estimating σ and cannot achieve its significance level. Note that, in practice, the variances and confidence intervals of the parameters M and σ can be acquired from a bootstrap simulation.

In addition to the empirical study of mortality data from the HMD, we examine whether the graduation method would influence the estimates of modal age and standard deviation σ .

TABLE 3 Parameter Estimates for Various Graduation Methods

σ	NM			SD(M+)		
k	Raw	W1	W2	Raw	W1	W2
5	9.99	10.00	9.73	5.47	5.47	5.50
6	10.00	10.00	9.70	6.34	6.34	6.39
7	9.99	10.00	9.67	7.10	7.09	7.19
8	10.00	10.00	9.67	7.71	7.71	7.89
9	10.00	10.00	9.66	8.31	8.31	8.46
10	10.01	10.01	9.66	8.69	8.69	8.91

Note: The W1 and W2 are the results under Whittaker graduation.

Example 2. Similar to Example 1, we assume that the age at death follows the normal distribution with modal age 80 and standard deviation 10. Also, there are 100,000 deaths in every simulation run. We chose the Whittaker-Henderson method (London, 1985) to graduate the raw data, by minimizing the following objective function,

$$F = \sum_{x=1}^{n} w_{x} (v_{x} - u_{x})^{2} + h \sum_{x=1}^{n-z} (\Delta^{z} v_{x})^{2} , \qquad (7)$$

where w_x is the weight of age, *h* is the weight of smoothness, and u_x and v_x are the raw and graduated data of age *x*, respectively. The value of *z* is usually set to 3, and w_x is the sample size of age *x*.

In this study, we consider two different values of h (W1 and W2): One is the average sample size of all ages (Yue, 1997), and the other is 10,000 times the average sample size. The purpose of 10,000 times the average sample size is to allow the graduated values to be close to a polynomial of degree z–1.

Table 3 shows the averages of the σ estimate from the raw data and two types of graduated data for various data range *k*. The NM method has less bias for all types of data used, but the σ estimates from SD(M+) are obviously underbiased. On the other hand, the estimates based on Whittaker graduation W1 are close to those based on raw data, for both NM and SD(M+) methods; but those based on Whittaker graduation W2 are somewhat different. The results of the model estimate are similar and are omitted. Thus, we suggest using the raw data to explore mortality compression, although most past work on mortality compression was based on graduated (or life table) data. Next, we will continue exploring mortality compression using the empirical data.

Example 3. Here we apply the mortality data from the HMD (Years 1950-2009) and check for mortality compression by



estimating the standard deviation σ , using the NM method and SD(M+). In addition, we want to examine the influence of using graduated data.

Note that the modal age increases annually, like the life expectancy, and the results are virtually the same in almost all countries. We can use the Japanese mortality data to show the common pattern. Figure 5 shows the estimated modal ages for the NM method and pure observation, assuming the ages at death follow normal and logistic distribution. The reason for applying different distribution is to test whether the distribution would influence the estimates of the NM method. The increase in the modal age is about the same for three different approaches, and the estimates of the NM method are smoother for both genders.

There are 37 countries in the HMD; the patterns of σ estimates can be roughly separated into two groups. For the period 1950-1980 the σ estimates decrease annually but do not always decrease after 1980. We can use the female data from Australia, France, Italy, Japan, and the U.S. for a more detailed analysis. As shown in Figures 6 and 7, the σ estimates are smoother for the NM method and thus it is easy to determine if there is mortality compression by using the NM method. The σ estimates of Australia, France, and Italy continue the decreasing pattern, and it seems mortality compression is a reasonable assumption. However, for Japan and the U.S., the σ estimates fluctuate and do not continue the rate of decrease seen before 1980. The σ estimates of SD(M+) do not have an obvious sign of decreasing.

This is an interesting finding. Intuitively, we would expect that mortality compression is more plausible for countries with a greater life expectancy. Among these five countries, the life



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expectancy is greatest in Japan and lowest in the U.S. It seems there are no strict connections between life expectancy (or modal age) and mortality compression. Still, although the results are not shown here, we found that the shortest interval of covering 50 percent of deaths continues its decreasing pattern for the HMD countries. There is still no decisive evidence to support or reject mortality compression.

Similar to Example 2, in this example we can also use the empirical data to verify the influence of graduated data. Since the results of σ estimates are about the same as using the raw data, we should look at the estimate of the 95th percentile, i.e., 95 percent of deaths by this age. Figure 8 shows the results of the Japanese data. Although the graduation is intended to reduce the fluctuation in mortality rates, quite the opposite is true: The estimates of the 95th percentile show larger fluctuations for both genders. If possible, we would choose using the raw data over the graduated data.

Still Not Enough Evidence

Mortality compression is a common conjecture. Although many studies support this theory, there still is not enough evidence to draw a valid conclusion. In fact, some recent studies show quite the opposite result. In addition to the data quality (including the insufficient amount of data at the higher ages), the compression measures and their estimation methods are one of the reasons why the study of mortality compression is difficult.

In this study, we propose the nonlinear maximization (NM) method to estimate the standard deviation σ for the age-atdeath distribution. We showed that the proposed NM method does provide a reliable and more stable estimate for the standard



FIGURE 8



deviation σ . Unfortunately, there exists estimate discrepancy in the standard deviation σ among different countries even using the NM method. Perhaps there are not enough data on the elderly population, and applying different estimation methods (for the standard deviation σ) alone cannot help us to conclude mortality compression.

Another piece of evidence against mortality compression (and thus the theory that life span has an upper bound) is the fact that estimates of the 95th percentile for the age at death distribution show no signs of slowing down. This finding indicates the mean (or life expectancy) of the age-at-death distribution is likely not converging, and neither are its standard deviation and therefore its maximum (i.e., life limit).

Although the distribution of age-at-death is well studied below the 95th percentile, one cannot determine the mortality rates of the oldest population—people 85 and beyond—merely by extrapolating the mortality trend. And so using simple extrapolation to estimate the life span limit is questionable at best. (Note that this method is used by most of the current models.) We need more mortality data if we are to accurately study the theory of mortality compression—and if we hope to answer the question of whether human life span has an upper bound.

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