Population Review

Taylor's Law and the Relationship between Life Expectancy at Birth and Variance in Age at Death in a Period Life Table

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Abstract

Mean age at death in a period life table is a major indicator of population health, as is the table's variance in age at death. Taylor's Law is a widely observed empirical pattern that relates variances to means in sets of non-negative measurements via an approximate power function. It has found application to human mortality. We add to this research by showing that Taylor's Law leads to a model that reasonably describes the relationship between mean age at death in a life table (which is the same as life expectancy at birth) and the life table's variance in age at death. We built a demonstration model, tested its accuracy, and found that it provides reasonably accurate estimates of variance in age at death in a life table. Employing independent data, the model was used to provide estimates of variance at age in death for six countries, three of which have high levels of life expectancy at birth and three of which have lower levels. The two parameters in Taylor's Law, a and b, can be interpreted, respectively, as: (1) a ≈ the product of life expectancy at birth and the sum of mean years lived and mean years remaining; and (2) b ≈ the square of life expectancy at birth. This provides Taylor's Law with a theoretical foundation when it is used to estimate variance in age at death in life tables constructed for human and other species. A significant strength of our application is that where mean age at death itself is estimated, it provides an estimate of variance in age at death that may not otherwise be available. This is useful because major agencies have produced estimates of life expectancy at birth for small areas. We illustrate this important application of the TL Method using empirical data and conclude that there is a need for a model that can produce accurate estimates of variance in age at death in a life table.

Keywords

Human Mortality Data Base, Income Inequality, Mean Age at Death, Socio-Economic Status

Background

Taylor's law (Taylor 1961) is a widely observed empirical pattern that relates the variances to the means of sets of non-negative measurements via an approximate power function: *variance$_g$ ≈ a × (mean$_g$)^b*, where g indexes the group of measurements (Reuman et al. 2017: 6788). It has found application in linguistics (Kobayashi and Tanaka-Ishii. 2018), physics (Eisler Bartos and Kertész 2008), and across a wide range of biological specialties (Azevedo and Leroi 2001, Cohen Xu and W. Schuster 2012, Cohen Xu, and Brunborg 2013, Isham 1991, Kaltz et al. 2012, Kilpatrick, Ives 2003, Taylor 2019, and Vucetich et al. 2000). Bohk, Rau and Cohen (2015) examined Taylor's law (TL) in conjunction with death rates and changes in these rates over time. They found that TL described a regular pattern in human mortality and suggested that it might be used (1) in mortality forecasting (to evaluate the quality of forecasts and to justify linear mortality assumptions) and (2) to reveal minimum mortality at some ages. In this brief report, we show for the first time that TL relates the variance of age at death in given life table to mean age at death (life expectancy at birth) in the same life table. Because of the fact that a period life table represents a stationary population, these results can be applied to the latter.

Mean age at death in a period life table is clearly a topic of interest because it is a major indicator of population health (Muszyńska and Janssen 2016). Variance in age at death in a period life table is a topic of interest because it can be used to explore substantive issues regarding health disparities (Vaupel 1986, Vaupel, Zhang, and van Raalte 2011) and provides a foundation for formal mortality analysis (Edwards and Tuljapurkar 2005, Hakkert 1987, Hill 1993, Schindler et al. 2012, Tuljapurkar and Edwards, 2011).

Wrycza (2104) shows that variance in age at death for a life table can be calculated as:

$$\sigma^2 = \int_0^w (x - e_0)^2 f(x)d(x) \qquad\qquad [1]$$

where

σ^2 = variance in age at death

x = age

e_0 = life expectancy at birth

Equation [1] represents, in continuous terms, a standard approach to calculating variance, namely, sum the squared differences between each of the measurements and their mean.

Results

This study uses a sample of 14 World Bank regional distributions of length of life in 1970 and 2000 for which e_0 and the standard deviation in e_0 are provided (Edwards 2010: Table 2) These measurements represent a group, *g*, in the TL sense as described at the beginning of this paper. Table 1 provides these 14 measurements, showing life expectancy at birth, $\boldsymbol{e_0}$ (mean age at death in each life table) and both the standard deviation (σ) and variance (σ^2) for each of seven regional populations at the two points in time.

TABLE 1. MEAN LIFE EXPECTANCY ( ) AND ITS STANDARD DEVIATION AND VARIANCE BY REGION AND YEAR			
WORLD BANK REGION	1970 e0	1970 std eo	1970 variance e0
east asia & pacific	58.3	26.5	702.25
Euope and Central Asia	67.3	21.9	479.61
high income	70.6	19	361
latin amer & caribbean	60.4	26.8	718.24
middle east & n. Africa	53.7	29.2	852.64
S. Asia	47.8	30.1	906.01
Sub-Saharan Africa	45.8	30.9	954.81
WORLD BANK REGION	2000 e0	2000 std eo	2000 variance e0
east asia & pacific	69.7	20.5	420.25
Euope and Central Asia	68.2	19.8	392.04
high income	77.7	15.9	252.81
latin amer & caribbean	71.5	21.1	445.21
middle east & n. Africa	67.7	21.5	462.25
S. Asia	60.9	25.7	660.49
Sub-Saharan Africa	50.7	28.4	806.56

Natural logarithms were calculated for each measurement in Table 1 and placed in a bivariate regression framework:

$$\ln(\sigma^2) = a + b*(\ln(e_0)) + \varepsilon \qquad [2]$$

where

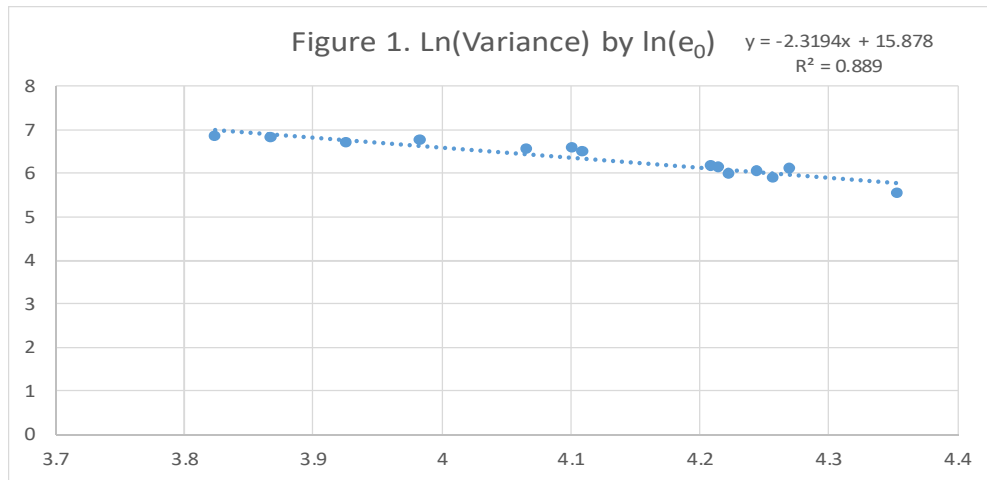σ^2 and e_0 are as defined before

and ε = error

This yielded the following model:

$$\ln(\sigma^2) = (15.878) - (2.3194*\ln(e_0)) \qquad [3]$$

$$r^2 = 0.89$$

As can be seen from the coefficient of determination ($r^2 = 0.89$) the logarithmic regression model fits the data quite nicely. Figure 1 provides a graphic view of this relationship defined by equation [3].

Figure 1. Ln(Variance) by ln(e_0)   y = -2.3194x + 15.878   R² = 0.889

The fit of the model given by equation [3] demonstrates that TL applies to the relationship between e_0 and σ^2. The sign of the model's slope parameter, $b = -2.3194$ as shown in equation [3], is consistent with findings that as life expectancy at birth increases, variance in age at death in the life table declines (Wrycza 2014), a property which also is visible in Table 1.

Test

Horiuchi, Wilmoth, and Fletcher (2008: 792) provide standard deviations for mean ages at death in life tables for Japanese females for four points in time, 1950, 1968, 1986, and 2004. These values (taken from Table 1 in their article) are, respectively, 25.91, 16.55, 13.91, and 13.59. Squaring these values yields the variances, which are, respectively, 671.33, 273.90, 193.49, and 184.69. The mean ages at death (life expectancy at birth) associated with these variances are, respectively, 60.90, 74.29, 80.98, and 85.59. Using these values in conjunction with equation [3] yields estimated variances of 570.8032, 359.9912, 294.7382, and 259.2184, respectively. The Mean Absolute Percent Error in this set of estimates is 90.60 and the Mean Algebraic Percent Error is 40.34. These two summary measures of error suggest that equation [3] is reasonably accurate for populations that have e_0 values ranging from 61 to 86 years, with the proviso that as the Mean Algebraic Percent Error shows, on average it tends to over-estimate variance in age at death for life tables.

Application

Again, using equation [3], Table 2 provides examples for three high e_0 countries using 2017 life expectancy at birth found in period life tables, followed by examples for three countries that have relatively lower e_0 levels in 2017 (Human Mortality Data Base 2021).

Table 2. Estimated Variance in e0 for Six 2017 populations		
Population	2017 e_0	Estimated 2017 Variance in e_0
Finland, Total	80.3	300.56
France, Males	79.26	309.79
Singapore, Females	85.2	261.98
Bosnia-Hergz, Total	76.76	333.69
Russian Fed., Males	67.53	449.15
Bangladesch Males	73.8	365.56

Discussion

In this section, we provide an interpretation of the parameters found in TL. As background, we start with Kim and Aron (1989) provide a proof that mean age in a stationary population, μa, is equal to mean expected years remaining, μr :

$$\mu a = \mu r \qquad\qquad [4]$$

Moving on, Vaupel (2009) demonstrated that that the mean number of years lived in a stationary population, μl, is equal to the mean expected years remaining, μr :

$$\mu a = \mu l \qquad\qquad [5]$$

Finally, Pressat (1972: 479-480) examined the relationship between mean age of a stationary population and life expectancy at birth and found (in the notation we use):

$$\mu a = 0.5(e_0 + (\sigma^2/e_0)) \qquad\qquad [6]$$

 where

 μa, is the mean age of the stationary population

 e_0 = life expectancy at birth

 σ^2 = variance in age at death

Re-arranging the terms in [6] yields

$$\sigma^2 = [e_0(2\mu_a)] - e_0^2 \qquad\qquad [7]$$

Per equations [4] and [5], we see that equation [7] can be re-expressed as

$$\sigma^2 = [e_0(\mu l + \mu r)] - e_0^2 \qquad\qquad [8]$$

Taking logarithms of [7], we have

$$\ln(\sigma^2) = \ln([e_0(\mu l + \mu r)] - \ln(e_0^2) =$$
$$2\ln(\sigma) = \ln(e_0) + \ln((\mu l + \mu r)) - 2\ln(e_0) \qquad\qquad [9]$$

Using my "group" and its notation, TL can be expressed as

$$\sigma^2 \quad \approx \quad a(e_0)^b \qquad\qquad [10]$$

By using equation [7] we see that equation [10] can also be expressed as

$$[e_0(2\mu a_{,})] - e_0^2 \quad \approx \quad a(e_0)^b \qquad\qquad [11]$$

And further using equation [8], equation [11] can be expressed as

$$[e_0(\mu l + \mu r)] - e_0^2 \quad \approx \quad a(e_0)^b \qquad\qquad [12]$$

Using equation [9] to reduce the left side of [12] and taking logarithms of both sides yields

$$\ln(e_0) + \ln((\mu l + \mu r)) - 2\ln(e_0) \quad \approx \quad \ln(a) + (b)(\ln(e_0)) \qquad\qquad [13]$$

From [13] we can see that the intercept, a, of the logarithmic TL regression model is equivalent to multiplying e_0 by the sum of mean years lived and mean years remaining and that the (unsigned) slope coefficient, b, is equivalent to 2. That is, squaring e_0. Thus, in the case of variance in mean age at death in a stationary population, the two parameters in Taylor's Law, a and b, can be interpreted, respectively, as approximating the product of life expectancy at birth and the sum of mean years lived and mean years remaining and as approximating the square of life expectancy at birth. In the model constructed in this paper, equation [3], we see that, unsigned, b = 2.3194, which approximates 2. As observed earlier, the fact that b is negative (b= -2.3194) is consistent with findings that as life expectancy at birth increases, variance in age at death in the life table declines (Wrycza 2014), a property which also is visible in Table 1.

The substantive interpretation of the two parameters provided here is also a useful feature in that TL clearly has a theoretical basis and is more than just an empirical "law" when applied to variance in age at death in a life table.

A useful feature of the TL method is that it can be used to estimate the Gompertz age slope (β) of log mortality. Tuljapurkar and Edwards (2011: 7) show that $\sigma^2 \approx 1/\beta^2$, with a high level of accuracy. We easily can re-arrange the terms to show that $\beta \approx (1/\sigma^2)^{\frac{1}{2}}$. Thus, once we have estimated σ^2 via the TL method from an estimated e_0, we can, in turn, use σ^2 to estimate β, the Gompertz slope of log mortality for those over the age of ten in the population associated with the estimated e_0.

Conclusion

The evidence presented in this pilot study suggests that the TL method can be used to generate reasonably accurate estimates of variance in age at death for a life table from life expectancy at birth (e_0). The TL method also can be used where e_0 itself is estimated (Arias et al., 2014; Congdon, 2014; Dwyer-Lindgren et al. 2017, Swanson, 1989; Swanson and Stockwell, 1986, 1988; Swanson and Sanford, 2012; Swanson, McGehee, and Hoque, 2009), given that it is within this same range. This is a significant strength of the TL method because, with it, variance in age at death can be estimated where it may otherwise not be available. As two examples, the TL method could be used to estimate variance in age at death from the census tract e_0 estimates produced by the Centers for Disease Control (Arias et al., 2018) and those at the county level produced by the Institute for Health Metrics and Evaluation (2017). These small areas are important because health inequalities are distributed geographically, as is found in the study (Swanson and Sanford, 2012) from which we take data to illustrate this application of the TL Model shown as equation [3].

The results of applying this TL Model to the estimated e_0 values for counties in Washington stratified by SES level taken from Swanson and Sanford (2012: Table 9a) are shown in Table 3, where we can see, as expected, when e_0 increases, variance in age at death declines. For the low SES county populations, going from a mean e_0 of 71.12 in 1990 to a mean e_0 of 76.03 in 2010 resulted in a decline of nearly 15 percent in the mean of variance in age at death (where $15\% \approx ((340.91 - 398.90)/398.90)*100$). For the high SES counties, going from a mean e_0 of 72.78 in 1990 to a mean e_0 of 77.24 in 2010 resulted in a decline of nearly 13 percent in the mean of variance in age at death (where $13\% \approx ((328.91 - 377.07)/377.07)*100$). Importantly, the estimated variances by county now provide us with a view of the life expectancy differentials within each county.

As an illustration of how rigorous analyses might proceed in terms of examining life expectancy differentials within a geographic unit, we provide a quick sketch comparing two counties, Asotin and Pacific (Table 3). Swanson and Sanford (2012) found Asotin and Pacific Counties to be among the 10 low SES counties in Washington State. Neither county has a large "special" population (university, prison, military base, or other large group quarters facility) and both are relatively isolated. In 2010, the population of Asotin County was 21,623 of which 24 percent were aged 65 or over and 89.9 percent were White, non-Hispanic; the 2010 population of Pacific County was 20,920, of which 32 percent were aged 65 and over and 81.7 percent were White, non-Hispanic (U.S. Census Bureau, 2022). The U.S. Internal Revenue Service (2022) reports that of 9,775 federal tax returns filed in 2011 for Asotin County, 142 (1.5%) reported incomes of $200,000 or more. This group of 142 filers had 14.3 percent ($64.89 million) of the $454.6 million in adjusted gross income (AGI) reported for Asotin County in 2011, giving each of these 142 filers an average AGI of $456,951, which is 11.3 times higher than the average AGI of $40,452 for the remaining 9,633 filers. Because of the positive correlation between income and life expectancy noted by Swanson and Sanford (2012) among many others, the high-income group in Asotin is likely to have an average level of life expectancy higher than that in the low income group. Thus, given the homogeneity in its racial/ethnic make-up, this concentration of income among a small proportion of the population may be a reason that Asotin County's variance in age at death (356.48) was the 2nd highest among Washington State's 10 low SES counties in 2010.

Table 3. Estimated Variance in Age at Death for counties in Washington by Year and SES Level					
LOW SES COUNTIES					
County	1990 e0	estimated variance in age at death	County	2010 e0	estimated variance in age at death
Asotin	69.67	416.96	Asotin	74.54	356.48
Columbia	66.49	464.68	Ferry	75.7	343.94
Grant	72.16	384.35	Grays Harbor	74.34	358.71
Grays Harbor	69.75	415.86	Kittitas	77.5	325.70
Kittitas	73.82	364.60	Lewis	75.24	348.84
Klickitat	71.77	389.21	Okanogan	76.18	338.94
Okanogan	70.74	402.48	Pacific	76.21	338.63
Pacific	70.5	405.67	Pend Oreille	75.85	342.37
Pend Oreille	72.18	384.10	Whitman	78.95	311.99
Whitman	74.13	361.07	Yakima	75.74	343.52
MEAN	71.12	398.90	MEAN	76.03	340.91
HIGH SES COUNTIES					
County	1990 e0	estimated variance in age at death	County	2010 e0	estimated variance in age at death
Benton	72.37	381.77	Benton	77.04	330.22
Clark	71.82	388.58	Clark	75.99	340.90
Island	73.74	365.52	Island	79.2	309.71
King	71.85	388.21	King	76.4	336.68
Kitsap	72.59	379.09	Kitsap	76.09	339.87
Pierce	71.55	391.99	Pierce	75.44	346.70
San Juan	75.41	347.02	San Juan	81.67	288.42
Skamania	72.36	381.89	Skagit	76.45	336.17
Snohomish	72.7	377.76	Snohomish	76.86	332.02
Thurston	73.45	368.87	Thurston	77.22	328.44
MEAN	72.78	377.07	MEAN	77.24	328.91

In looking at Pacific County, which has a population composition similar to that of Asotin, we find that 114 (1.2%) of its 9,275 filers had 11.7 percent ($45.71 million) of the total 2011 AGI ($389.46 million), giving each of these 114 filers an average AGI of $400,982 (U.S. Internal Revenue Service, 2022), which is 10.7 times higher than the average $37,523 AGI of the other 9,161 filers in Pacific County. Thus, for Pacific County, where the average income among fewer wealthy people is not as high as in Asotin County, there are likely both fewer and less wealthy people in its high average life expectancy group relative to the low-income group than is the case for Asotin County, which would tend to lower the average life expectancy of the high-income group. This may be a reason why Pacific County has a lower variance in age at death (338.63) in 2010 than found in Asotin County (356.48). As this quick sketch suggests, the combination of

income data, racial/ethnic composition information, life expectancy estimates, and estimates of variance in age at death (along with other variables), may provide a path to more rigorous analyses that could potentially reveal more about life expectancy differentials.

We conclude by stating that our empirical examples show there is a need for a model that can produce reasonably accurate estimates of variance in age at death in a life table and our demonstration model suggests that this can be done using the TL Method. As Tuljapurkar and Edwards observe (2011: 516), "…variance in length of life is costly, whether viewed at the population level as aggregate health inequality or at the individual level as a mean-preserving spread in how long we live." Put another way, this variance represents the final inequality (Tuljapurkar 2010).

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