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Formal Relationship 25

The Gompertz force of mortality in terms of the modal age at death

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Abstract

BACKGROUND
The Gompertz force of mortality (hazard function) is usually expressed in terms of a, the initial level of mortality, and b, the rate at which mortality increases with age.

OBJECTIVE
We express the Gompertz force of mortality in terms of b and the old-age modal age at death M, and present similar relationships for other widely-used mortality models. Our objective is to explain the advantages of using the parameterization in terms of M.

METHODS
Using relationships among life table functions at the modal age at death, we express the Gompertz force of mortality as a function of the old-age mode. We estimate the correlation between the estimators of old (a and b) and new (M and b) parameters from simulated data.

RESULTS
When the Gompertz parameters are statistically estimated from simulated data, the correlation between estimated values of b and M is much less than the correlation between estimated values of a and b. For the populations in the Human Mortality Database, there is a negative association between a and b and a positive association between M and b.

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CONCLUSIONS

Using M, the old-age mode, instead of a, the level of mortality at the starting age, has two major advantages. First, statistical estimation is facilitated by the lower correlation between the estimators of model parameters. Second, estimated values of M are more easily comprehended and interpreted than estimated values of a.

1. Relationship

The Gompertz *force of mortality* (or *hazard*) at age x, $\mu(x)$, has been expressed, at least since Greenwood (1928), as

$$\mu(x) = \mu(x; a, b) = ae^{bx} \,, \tag{1}$$

where a denotes the level of mortality at the initial age, i.e., at $x = 0$, and b is the rate of mortality increase over age. Note that $x = 0$ refers to the starting age of analysis and might not correspond to biological age 0. If x is to denote actual age, while x_0 is the starting age of analysis, then x should be replaced by $x - x_0$ in (1) and all subsequent equivalent formulas.

Gompertz (1825) used the equivalent to (1) notation

$$\mu(x) = \mu(x; a, c) = ac^x \,, \tag{2}$$

with b being the natural logarithm of c. Alternatively, following Gumbel (1958), the Gompertz force of mortality can be represented as a function of M and b as

$$\mu(x) = \mu(x; M, b) = be^{b(x-M)} \,, \tag{3}$$

where M is the old-age modal age at death, or for short, *modal age at death*. In other words, assuming constant age groups for populations with senescent mortality, M is the age at which the highest number of deaths occurs beyond the high number of deaths in the first years of life. This article provides a short proof for (3) and discusses advantages of using a Gompertz parameterization via M (3) instead of a (1).

2. Proof of the relationship

For any hazard $\mu(x)$, the probability density function (p.d.f.) of deaths $d(x) = \mu(x)\ell(x)$, where $\ell(x)$ denotes the survival function, reaches a maximum at the modal age at death. Hence,

$$\frac{d}{dx}\, d(x) = 0 \qquad \Leftrightarrow \qquad \frac{\frac{d}{dx}\, d(x)}{d(x)} = 0 \qquad \Leftrightarrow \qquad \frac{\frac{d}{dx}\, \mu(x)}{\mu(x)} - \mu(x) = 0 \,. \tag{4}$$

Rearranging terms, at $x = M$ the force of mortality equals its relative derivative with respect to age

$$\mu(x) = \frac{d\mu(x)/dx}{\mu(x)} \tag{5}$$

Using (5), one can derive M for various mortality models. In the case of the Gompertz force of mortality given in (1), the relationship in (5) implies that the mode is

$$M = \frac{1}{b} \ln \frac{b}{a} \,. \tag{6}$$

From (6) the parameter a can be expressed in terms of M and b as

$$a = be^{-bM} \,. \tag{7}$$

Substituting (7) in (1), yields (3).

An alternative proof could be based on the fact that in the Gompertz framework M maximizes the p.d.f.

$$d(x) = d(x; a, b) = a \, \exp\left\{bx - \frac{a}{b}(e^{bx} - 1)\right\} \,.$$

Solving

$$M = \arg\max_x \left\{a \, \exp\left\{bx - \frac{a}{b}(e^{bx} - 1)\right\}\right\} \tag{8}$$

yields (6), and a can be expressed in terms of M and b by (7). Substituting (7) in (1), results in (3).

q.e.d.

3. History and related results

The Gompertz force of mortality as a function of the mode M (and b) appears first in a short section of Emil J. Gumbel's *Statistics of Extremes* (Gumbel 1958, p. 247) and later, in a demographic context, in two working papers by John H. Pollard (Pollard 1998a,b). More recently, Horiuchi et al. (2013) derived expressions for the hazard in terms of the modal age at death (from senescent causes) in six mortality models: the Gompertz, the Weibull, and the logistic model in the presence (Horiuchi et al. 2013, p. 54) or absence (Horiuchi et al. 2013, p. 52) of a Makeham term. From the general equation (5), one can derive M for other mortality models (see examples in Canudas-Romo 2008; Horiuchi et al. 2013). In Table 1 we present the modal age at death and the associated re-parameterized hazards for three distributions – the Gompertz, the gamma-Gompertz (Beard 1959; Vaupel, Manton, and Stallard 1979), and the Weibull – which represent three different aging patterns: the ones of exponential, logistic, and power-function hazard. Note that the re-parameterization of the gamma-Gompertz hazard via the old-age mode M results in the elimination of the scale parameter λ of the gamma distribution. This is not surprising, as the gamma-Gompertz can be viewed as three-parameter model of a/λ, b, and k

$$\mu(x; a, b, k, \lambda) = \frac{kae^{bx}}{\lambda + \frac{a}{b}\left(e^{bx} - 1\right)} = \frac{k(a/\lambda)e^{bx}}{1 + \frac{a/\lambda}{b}\left(e^{bx} - 1\right)} = \mu(x; a/\lambda, b, k)\,,$$

where a/λ can be interpreted as a scale parameter.

To each one of the models presented in Table 1, a Makeham term c, capturing extrinsic mortality (Makeham 1860), can be easily added. In this case the re-parameterized hazards are augmented by c, and M designates the modal age at death of the senescent mortality component (see Horiuchi et al. 2013, p. 20 for a broader discussion). Easy re-parameterization of the Gompertz hazard from $\mu(x; a, b)$ to $\mu(x; M, b)$ (or vice versa) is not possible in the presence of a Makeham term. Indeed, the mode of the Gompertz-Makeham model

$$M_{GM} = \frac{1}{b}\,\ln\frac{b - 2c + \sqrt{b^2 - 4bc}}{2a}$$

does not offer a convenient expression to exchange M_{GM} and a.

Table 1: Modes of the Gompertz, gamma-Gompertz, and Weibull distributions and the associated re-parameterized hazards: k and λ are the shape and scale parameter of the gamma distribution, and α and β are the shape and scale parameter of the Weibull distribution

Distribution	**Parameters**	$\mu(x)$	M	$\mu(x)$ **with** M
Gompertz	a, b	ae^{bx}	$\frac{1}{b}\,\ln\frac{b}{a}$	$be^{b(x-M)}$
gamma-Gompertz	a, b, k, λ	$\frac{kae^{bx}}{\lambda+\frac{a}{b}\left(e^{bx}-1\right)}$	$\frac{1}{b}\,\ln\frac{\lambda b-a}{ka}$	$\frac{kbe^{bx}}{ke^{bM}+e^{bx}}$
Weibull	α, β	$\frac{\alpha}{\beta^\alpha}\,x^{\alpha-1}$	$\beta\left(1-\frac{1}{\alpha}\right)^{\frac{1}{\alpha}}$	$\frac{\alpha^2\,M^\alpha}{(\alpha-1)}\,x^{\alpha-1}$

The modal age of the life-table distribution of deaths has been suggested as an alternative to life expectancy in studying longevity (Kannisto 2001; Cheung et al. 2005; Cheung and Robine 2007; Canudas-Romo 2008, 2010; Ouellette and Bourbeau 2011; Horiuchi et al. 2013). Life expectancy for Japanese females was estimated to be 86.4 years in 2012 (HMD 2014); most of the deaths in this population, however, will occur 6 years later around the modal age at death at about age 92 (HMD 2014). The burden in hospitals, nursing homes and public health is intensified at ages around the modal age at death. While life expectancy, the mean of the distribution of deaths, is highly dependent on the left tail of mortality at young ages, the modal age at death only depends on mortality at old ages (Kannisto 2001; Canudas-Romo 2010).

Research on the modal age at death has also considered measures of the dispersion of deaths around it. Instead of studying the standard deviation around the mean, i.e., around life expectancy, one can consider the standard deviation around the mode (Canudas-Romo 2008) or the standard deviation beyond the modal age (Kannisto 2001; Cheung et al. 2005; Cheung and Robine 2007; Thatcher et al. 2010; Horiuchi et al. 2013) as a measure to calculate the dispersion of the distribution of deaths. As suggested by Kannisto (2001), the standard deviation above the mode pertains to senescent mortality without much distortion from non-senescent mortality beyond the modal age. In Kannisto's study, confirmed by Thatcher et al. (2010), the standard deviation above the mode has declined at a slower pace or stagnated in recent decades and the modal age at death has increased with life expectancy, suggesting that mortality is declining at roughly the same rate at all older ages, leading to a shift in the force of mortality to higher and higher ages (Vaupel 1986; Bongaarts 2005; Canudas-Romo 2008).

In sum, the modal age of death is a useful measure. It is more informative in many applications than the value of the force of mortality at age zero. Hence, expressing the Gompertz force of mortality in terms of b and M, as in equation (3), provides deeper understanding than expressing the Gompertz force of mortality in terms of a and b. As explained below, the weaker relation between M and b compared with the one between a and b is a second strong argument for using M rather than a.

4. Application to statistical estimation

Expressing the Gompertz force of mortality in terms of the mode M can be advantageous when fitting the Gompertz model to data. In its specification in (1), the Gompertz model is characterized by a pair of parameters a and b, whose maximum likelihood estimators are highly (negatively) correlated. This correlation originates in the basic structure of the Gompertz distribution, with a density of deaths

$$d(x) = a \exp\left\{bx - \frac{a}{b}(e^{bx} - 1)\right\}, \tag{9}$$

which can be viewed as a truncated version of the Gumbel distribution. If the density of the Gumbel distribution

$$f(x;\nu,\beta) = \frac{1}{\beta}\,\exp\left\{-\frac{x-\nu}{\beta} - \exp\left\{\frac{x-\nu}{\beta}\right\}\right\}, \quad x \in \mathbb{R}, \quad \nu \in \mathbb{R}, \beta > 0 \tag{10}$$

is re-expressed with $x = -x$ and is truncated at 0 (see Figure 1) with

$$b = \frac{1}{\beta} \tag{11}$$

and

$$a = be^{-b\nu}, \tag{12}$$

then (9) is the result (see, for example, Lenart and Missov 2015).

Figure 1: Truncation of the Gumbel distribution: redistribution of the probability mass on the negative half-axis to the positive half-axis to obtain a Gompertz density

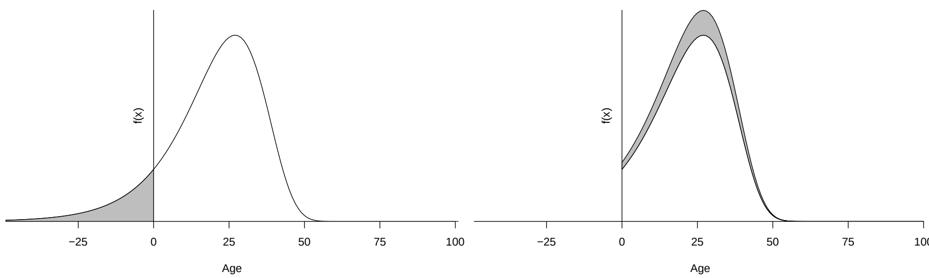
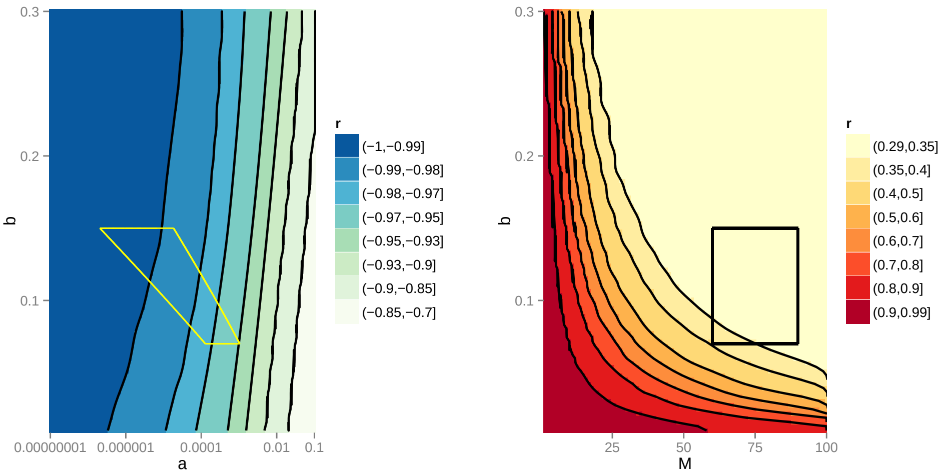


Figure 2: Values of the a-b correlation (left panel) and the M-b correlation (right panel) for a set of values of b (0–0.3), values of a (0–0.1) and values of M (0–100)



Notes: The areas framed by a yellow border on the left panel and a black border on the right panel present the set of maximum-likelihood estimates for a, b and M from fitting a Gompertz model for all Human Mortality Database (HMD 2014) countries, years 1950 to last available, ages 50–90 (year-by-year estimates are presented in Figures 3 and 4). The range of the estimated parameters is 10^{-7}–0.002 for a, 0.06–0.15 for b, and 60–93 for M.

The Gumbel distribution is a location-scale distribution with ν denoting the mode and β being the scale parameter. The maximum likelihood estimators of Gumbel parameters are often independent. In general, location-scale distributions can be re-parameterized so that the maximum likelihood estimators are fully independent (Gupta and Székely 1994). The Gompertz parameters a and b, however, are often highly dependent on one another, as suggested by the expression in (12) and as documented in Table 4. This dependency arises because of the truncation of the Gumbel distribution and because of the use of a instead of M as a parameter. Parameterization (3) partially overcomes this problem because it requires estimation of M instead of a (Lenart and Missov 2015). In mortality research, the "inverse relationship" between a and b is first identified by Strehler and Mildvan (1960, eq. 16, p. 16) who derive an age-independent formula that links $\ln a$ and b from a resulting dual representation of death rates (Strehler and Mildvan 1960, model on p. 15–16). They show empirical evidence for this relationship by fitting a Gompertz model to human mortality data. Figure 2 shows the correlations between the estimators of a and b (left panel), as well as M and b (right panel), for a set of b-values (0–0.3) and a-values (0–0.1). The a-values in the left panel can be transformed into respective M-values by (7). Figure 2 suggests that for typical $\hat{a}$ ($\propto 10^{-5}$) and $\hat{b}$ (≈ 0.1) of human mortality, the absolute correlation between the maximum-likelihood estimators can be reduced from values above 0.95 to values below 0.4 by fitting model (3) instead of (1).

The estimation procedure is based on the assumption that death counts $D(x)$ at age x are Poisson-distributed with parameter $E(x)\mu(x)$, where $E(x)$ denotes exposure to risk (Brillinger 1986). As a result we maximize a Poisson log-likelihood

$$\ln L = \sum_x [D(x) \ln \mu(x) - E(x)\mu(x)] \, .$$

This is equivalent to fitting a Poisson regression with $D(x)$ as the response, age x as a single covariate, and $\ln E(x)$ as an offset.

For a fixed b and a list of values of M, a unique list of corresponding values of a can be determined. Table 4 compares – for $b = 0.1$ and a list of values of M and (corresponding) values of a – the M-b correlation (denoted by R) with the (corresponding) a-b correlation (denoted by r). For pertinent values of the adult modal age at death for modern humans, i.e. $M = 60, 80, 100$, the use of (3) instead of (1) pays off in terms of a much smaller correlation (in absolute terms) between the maximum-likelihood estimators of model parameters. Note that a parameterization

$$\mu(x) = \mu(x; a, b, x^*) = a^* e^{b(x-x^*)} \, , \tag{13}$$

where x^* denotes an age (e.g., 70) that centers the distribution of deaths and a^* is the death rate at x^*, can also reduce the correlation between the Gompertz parameters, a^* and b in this case, as (1) is a log-linear GLM on age (see Dowd et al. 2010, model M5).

The lower correlation between the estimators of M and b plays an important role when a Gompertz model is fitted to death rates that do not increase exponentially over the entire range of study, e.g., when background mortality (captured by the Makeham term) is not negligible or when at later ages there is evidence for mortality deceleration (captured by a gamma distribution with a single parameter $\gamma = 1/k = 1/\lambda$). In both cases b is underestimated and a is overestimated, whereas M is overestimated when frailty is neglected and underestimated when the Makeham term is omitted (Nemeth and Missov 2014). However, due to the smaller M-b correlation, the relative absolute bias in M is smaller than the one in a. The relative absolute bias is defined as

$$AB_\theta = \frac{|\hat{\theta} - \theta|}{\theta} \, , \tag{14}$$

where $\hat{\theta}$ is the estimated value of parameter θ (Pletcher 1999). Tables 2 and 3 present the relative absolute bias in estimated b, a and M from simulated data with non-negligible Makeham term c (Table 2) or frailty term γ (Table 3). If a Gompertz model is fitted to data for a population for which there is some age-invariant mortality or some heterogeneity in frailty, then this misspecification tends to lead to errors in estimates of a that are much greater than errors in the estimates of M. As a result, a model misspecification leads to a relatively small bias in estimated M in comparison to the bias in the estimated a. Nevertheless, if the target of inference is the force of mortality at a particular age, the relative absolute bias in the corresponding estimate will be the same, regardless of model parameterization.

Table 2: Relative absolute bias (averaged over 100 simulations) in estimated b (row 2), a (row 3) and M (row 4) if a Gompertz model is fitted to simulated data from a Gompertz-Makeham ($a = 0.00002$, $b = 0.09$) with c-values given in the first row.

c **term**	0.0004	0.002	0.004	0.006	0.008	0.01
bias in b	0.0759	0.2958	0.4563	0.5596	0.6326	0.6877
bias in a	0.9532	10.3378	38.7082	86.5563	151.3701	229.4323
bias in M	0.0082	0.0434	0.0929	0.1514	0.2221	0.3061

Table 3: Relative absolute (averaged over 100 simulations) bias in estimated b (row 2), a (row 3) and M (row 4) if a Gompertz model is fitted to simulated data from a gamma-Gompertz ($a = 0.00002$, $b = 0.09$) with γ-values given in the first row

γ	0.01	0.05	0.1	0.2	0.225	0.25	0.3	0.4
bias in b	0.0070	0.0308	0.0620	0.1222	0.1364	0.1494	0.1782	0.2368
bias in a	0.0985	0.2666	0.5382	1.2324	1.4395	1.6392	2.1556	3.5443
bias in M	0.0015	0.0046	0.0097	0.0186	0.0213	0.0234	0.0288	0.0394

The Gompertz curve is often used to describe human mortality starting from age 30 or 50. In this case, when the Gompertz distribution is left-truncated at an age higher than 0, the modal age at death decreases by the same amount. For example, if the fitting of the Gompertz distribution to a population with a modal age at death of 80 starts not from age 0, but from age 30, the modal age at death of the truncated population will appear as 50. Equivalently, a higher starting age corresponds to a higher Gompertz a. As indicated in Table 4, the Gompertz model formulated in terms of M and b yields fewer correlated parameter estimates than the Gompertz a and b model whenever the modal age at death is not close to zero. Note that the value of R approaches a limit of about 0.31 as M increases.

Table 4: **a-b correlation (r, column 3) vs M-b correlation (R, column 4) for a fixed $b = 0.1$, a list of fixed M-values (column 1), and a uniquely determined, using (6), list of corresponding values of a (column 2). The last column contains the respective life expectancies e_0 calculated by eq. (5), p. 30 in Missov and Lenart (2013).**

M	a	r	R	e_0
0	1.0×10^{-1}	-0.82	0.97	6.0
5	6.1×10^{-2}	-0.84	0.93	8.2
10	3.7×10^{-2}	-0.86	0.86	11.0
20	1.4×10^{-2}	-0.90	0.68	17.8
40	1.8×10^{-3}	-0.95	0.41	35.0
60	2.5×10^{-4}	-0.98	0.34	54.4
80	3.4×10^{-5}	-0.99	0.32	74.3
100	4.5×10^{-6}	-0.99	0.31	94.2
600	8.8×10^{-28}	-1.00	0.31	594.2

5. Values of a, b and M for human populations

Figures 3 and 4 show scatter plots of a-b values and M-b values, respectively, estimated for all HMD countries, years 1950 to last available, ages 50–90, by gender. The estimated value of b tends to increase as a declines and as M increases. Note that this result holds when the Gompertz model is fitted to the data. Other, better-fitting mortality models might yield a more or less constant b over time and across populations, as hypothesized by Vaupel (2010) but not yet demonstrated.

Figure 3: The relationship of a and b based on estimated parameters for all HMD countries, years 1950 to last available, ages 50–90, by sex. The yellow curve results from applying a cubic regression spline to the data (we use the 'gam' function from the 'mgcv' R package: Wood 2012).

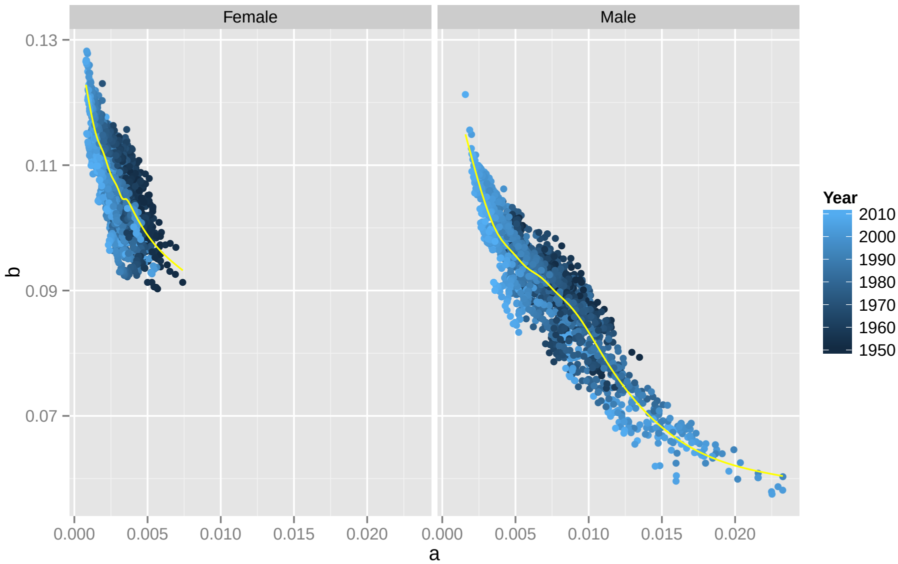


Figure 4: The relationship of M and b based on estimated parameters for all HMD countries, years 1950 to last available, ages 50–90, by sex. The yellow curve results from applying a cubic regression spline to the data (we use the 'gam' function from the 'mgcv' R package: Wood 2012).

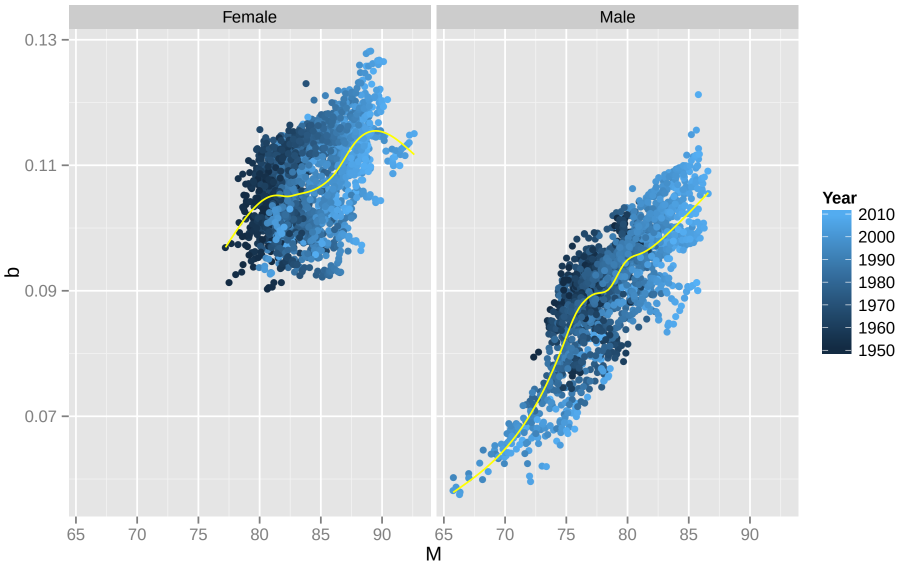


Table 5 summarizes the relationship between a and b and between M and b by presenting estimated values of a, b and M at selected times and for selected populations. Note that the values of M tend to be more informative than the values of a. The fact that a was 0.018 for Swedish females in 1800–1809 as compared to 0.007 in 1900–1909 is more difficult to interpret than is the fact that the modal age at death increased from almost 69 years to more than 78 years. Similarly, knowing that a for U.S. males in recent years was a seventh of the value for Russian males is not as enlightening as knowing that the mode for U.S. males was more than 83 compared with a mode for Russian males of less than 68.

Table 5: Gompertz maximum likelihood estimates of different populations from the Human Mortality Database, ages 50–90

Country	**Year**	**Gender**	$\hat{a}$	$\hat{b}$	$\hat{M}$
Sweden	1800–09	Female	0.018	0.075	68.95
		Male	0.022	0.070	66.06
	1900–09	Female	0.007	0.094	78.46
		Male	0.009	0.088	76.47
	2000–09	Female	0.001	0.116	88.36
		Male	0.002	0.110	84.58
Japan	2000–09	Female	0.001	0.113	91.84
		Male	0.003	0.098	85.43
France	2000–09	Female	0.001	0.112	90.20
		Male	0.004	0.091	84.10
USA	2000–09	Female	0.003	0.098	87.32
		Male	0.005	0.090	83.20
Russia	2000–09	Female	0.005	0.095	81.28
		Male	0.020	0.061	67.94

6. Conclusion

Demographers, actuaries, epidemiologists, population biologists, and reliability engineers should make it standard practice to express the Gompertz curve using (3) rather than (1). The parameter M, the old-age modal age at death, in (3) is more informative and more readily comparable across populations in an understandable way than the parameter a, the force of mortality at the initial age, in (1). Furthermore, when the correct model might be a Gompertz-Makeham or gamma-Gompertz model and the Makeham or gamma term might become significant if the sample size were larger, then (as shown in Tables 2 and 3) it is preferable to estimate M rather than a. The lower correlation between parameter estimators in (3) can also be beneficial in projection models that contain a Gompertz component, as well as in Bayesian estimation procedures which the lower correlation leads to faster convergence of the associated MCMC algorithm. Unless there are compelling reasons to use $\mu(x) = ae^{bx}$, we recommend that demographers and other population scientists should start expressing the Gompertz curve as $\mu(x) = be^{b(x-M)}$.

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