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A Flexible Two-Dimensional Mortality Model for Use in Indirect Estimation

John Wilmoth*, Vladimir Canudas-Romo†, Sarah Zureick*, Mie Inoue**, and Cheryl Sawyer††

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ABSTRACT

Objective. Mortality estimates for many populations must be derived using model life tables, which describe typical age patterns of human mortality. We propose a new system of model life tables as a means of improving both the quality and the transparency of such estimates.

Methods. We describe a flexible two-dimensional model of the age pattern of mortality and fit the model (separately by sex) to a collection of 719 period life tables from the Human Mortality Database (www.mortality.org). The fitted model can be used to estimate full life tables given one or two pieces of information: for example, child mortality only (${}_5q_0$), or child mortality and adult mortality (${}_5q_0$ and ${}_{45}q_{15}$). Using empirical life tables from a variety of sources, we compare the performance of new and old methods by computing standard deviations of estimation errors for three key mortality indicators (e_0, IMR, and ${}_{45}q_{15}$).

Findings. The new model easily outperforms the Coale-Demeny and UN model life tables. Estimation errors are similar to those produced by the modified Brass logit procedure. If desired, the model can be applied in a flexible manner to incorporate non-quantitative information about the age pattern of mortality (similar to the use of regional families in the Coale-Demeny system).

Conclusion. In addition to providing generally smaller estimation errors, the new method offers other advantages over existing techniques. The proposed model is better suited to the practical needs of mortality estimation, because the two input parameters are both continuous yet the second one is optional. Also, since model parameters are closely related to measures of child and adult mortality, the link between data and estimates is more transparent.

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* Department of Demography, University of California, Berkeley
† Bloomberg School of Public Health, Johns Hopkins University, Baltimore
** World Health Organization, Geneva
†† United Nations Population Division, New York
Please send comments to jrw@demog.berkeley.edu.

Introduction

Life expectancy and other summary measures of mortality or longevity are key indicators of the health and wellbeing of a population. The Human Development Index of the United Nations, for example, lists life expectancy at birth as the first of its three components.[1]

By definition, a population's life expectancy at birth is the average age at death that would be observed among a (hypothetical) cohort of individuals if their lifetime mortality experience matched exactly the risks of dying (as reflected in age-specific death rates) observed for the population during a given year or time period. Thus, the starting point for deriving the value of life expectancy at birth is a complete set of age-specific mortality rates; using this information, it is possible to calculate life expectancy at birth and other summary indicators of mortality or longevity. Typically, all of these calculations are made separately by sex.

Currently, three organizations produce regularly-updated estimates of life expectancy at birth by sex for all (or nearly all) national populations: the United Nations Population Division, the World Health Organization, and the U.S. Census Bureau. This task is greatly complicated by the fact that different data sources and estimation methods must be employed for different groups of countries. For wealthy countries with complete and reliable systems for collecting population statistics, age-specific death rates are derived directly from administrative data (by dividing the recorded number of deaths by an appropriate measure of population size).

For most of the world's population, however, the usual administrative data sources (death registration and census information) are inadequate as a means of deriving reliable estimates of age-specific mortality rates and, thus, life expectancy or other synthetic measures. For these populations, mortality estimates are derived using model life tables, which describe typical age patterns of human mortality. Using such models, it is possible to estimate death rates for all ages given limited age-specific data.

For example, in many countries it has been possible to gather empirical evidence about levels of child mortality using survey data and other instruments, even though there is little or no reliable data on adult mortality. For other countries there may also be some means of estimating mortality for young and middle-aged adults, but no reliable information at older ages. In these and other cases, model life tables exploit the strong positive correlations between mortality levels at different ages (as observed in a large body of historical and cross-cultural data) as a means of predicting mortality levels for all ages using the limited information available.

In this paper we propose a new model of age-specific mortality, which we use to develop a new system of model life tables. In addition to producing smaller estimation errors in most cases, this model offers several significant advantages compared to earlier approaches, including its greater flexibility and intuitive appeal. We believe that the new model will be very useful as part of ongoing efforts to improve both the quality and the transparency of global mortality estimates.

We begin the discussion with a brief review of the literature on model life tables, followed by an analysis of the data sources available for deriving and testing such models. We then present the two-dimensional mortality model that we are proposing as the basis for a new system of model

[1] The other two components are education/literacy and personal income. All three components have equal weight in deriving the index, but life expectancy is typically listed first.

life tables. After fitting the model to a vast collection of historical mortality data, we illustrate how it can be used to derive a wide variety of mortality patterns by age.

The model is two-dimensional in the sense that it requires two input parameters in order to produce a complete set of age-specific mortality rates. However, the second input parameter is optional in practice, yielding a flexible one- or two-dimensional model. Thus, the model can be used to estimate mortality at all ages on the basis of child mortality alone (${}_5q_0$), or using information about the mortality of both children and adults (${}_5q_0$ and ${}_{45}q_{15}$). In fact, many combinations of one or two pieces of information can be used as model inputs.

Using empirical life tables from a variety of sources, we compare the performance of new and old methods by computing standard deviations of estimation errors for three key mortality indicators (e_0, *IMR*, and ${}_{45}q_{15}$). The new model easily outperforms the Coale-Demeny and UN model life tables. If desired, it is possible to incorporate non-quantitative information about the age pattern of mortality, and thus to mimic the use of regional families in these earlier model life table systems. Although estimation errors are similar to those produced by the modified Brass logit procedure, we believe that the greater transparency and flexibility of the model proposed here offer significant advantages and will facilitate further improvements in estimation methodology.

Use of model life tables for mortality estimation

Broadly speaking, there are two major categories of models that have been used to depict the age pattern of mortality. On the one hand, there are *functional models*, which are based on fairly simple mathematical functions with a relatively small number of parameters. The most common examples are the models proposed by Gompertz and Makeham in the 19th century (containing two and three parameters, respectively). The two-parameter Weibull model (Weibull, 1951) offers an alternative to the Gompertz.

During the 20th century, different forms of the logistic model (with three or four parameters) were advocated by various authors (Perks, 1932; Beard, 1971; Thatcher *et al.*, 1998). However, functional models with two to four parameters are useful for depicting mortality at adult ages only. For a model that is capable of depicting mortality over the full age range, more parameters are needed: examples include the five-parameter Siler model (Siler, 1979) and the eight-parameter model proposed by Heligman and Pollard (1980).

On the other hand, a variety of *empirical models* have also been used for describing the age pattern of mortality. This category includes model life tables as well as the relational models proposed by Brass (1971) and others. All such models are characterized by having a much larger number of parameters compared to the functional models. However, most of the parameters in an empirical model are determined through an initial analysis of a large collection of historical data and thus become fixed in subsequent applications; after this preliminary analysis, only a small number of parameters (typically, from two to four) remain variable. These remaining parameters are sometimes referred to as the "entry parameters," as they provide the point of entry for all subsequent applications of the empirical model.

Functional models have the virtue of simplicity and are useful for many analytical purposes. However, because empirical models are more flexible and typically provide a closer fit to observed mortality patterns over the full age range, they are better suited for the task of estimating mortality. The model proposed here belongs to the class of empirical models. Others in this class that we have examined closely include the Coale-Demeny regional families of model life tables (Coale and Demeny, 1966, 1983), the United Nations model life tables for developing countries (United Nations, 1982), and a modified version of the Brass logit model proposed by Murray and colleagues (2003). The early model life tables proposed by Ledermann (1969) are seldom used today, but it is worth noting that their underlying structure is similar in certain ways to the model proposed here.

A system of model life tables can be used to predict the relationship between child and adult mortality. However, as shown in Figure 1, the Coale-Demeny tables do not reflect this relationship accurately, especially at low levels of mortality (see also Coale and Guo, 1989). A similar pattern is observed for the UN model life tables, as documented in the supplemental materials for this article (Wilmoth *et al.*, 2009). These results do not suggest a faulty analysis by the creators of earlier systems of model life tables, since the low levels of mortality observed in recent decades were not represented in the datasets used to create those models. The bias is most severe when child mortality drops below about 50-60 per 1000. Due to the rapid decline of mortality in developing countries, a growing number of populations for which mortality estimates are derived using model life tables now have child mortality levels in this range.[2]

Beyond just updating the models used for mortality estimation by incorporating the full body of available data, we have also sought to develop a better underlying model. Although all model life table systems that have found wide use have had two entry parameters, a two-dimensional model may not be adequate for all purposes. At one extreme, it is clear that such a model will not describe accurately the age pattern of male mortality in times of warfare. Nevertheless, as we show by means of historical examples later in the paper, for populations affected by certain epidemics or less severe civil conflicts, a two-dimensional model appears to provide a useful approximation for the true age pattern of mortality.

It is uncertain whether the model proposed here could provide an adequate depiction of mortality in populations heavily affected by the AIDS epidemic. If not, the model life table system proposed here could be used (like earlier systems) as a means of estimating mortality from causes other than AIDS, with estimates of AIDS mortality coming from a simulation model (this is the current practice for all major data providers). This issue requires further investigation but is beyond the scope of this article.

Data from empirical life tables

For fitting the new model and testing it against alternatives, we have used life tables from several sources. Table 1 contains a summary of the four sets of life tables that were used for this study. Data from the Human Mortality Database (HMD, www.mortality.org) are described in Table 1a. This dataset contains 719 period life tables covering (mostly) five-year time intervals and represents over 72 billion person-years of exposure-to-risk, spread across parts of five continents and four centuries. All life tables in this collection were computed directly from observed deaths

[2] For the 2006 round of estimates from the United Nations, more than 20 countries fell into this category, including many small countries but also Indonesia, the Philippines, and Turkey.

and population counts, without adjustment except at the oldest ages.[3] A convenient feature is that all data are available up to an open interval of age 110 and above.

A large collection of life tables was assembled by the World Health Organization a few years ago and was subsequently used for creating a modified form of the Brass logit model of human survival (Murray *et al.*, 2003). This data source is summarized in Table 1b. However, for both this and the following collections of life tables, we have omitted data for countries and time periods that are covered by the HMD. The non-overlapping portion of the WHO life table collection consists mostly of life tables computed directly from data on deaths and population size, which were taken (without adjustment) from the WHO mortality database (the current version of this database is available at http://www.who.int/healthinfo/morttables/en/). Many of these life tables are for countries of Latin America or the Caribbean. A much smaller number of tables were taken from two earlier collections of life tables: those assembled by Preston and his collaborators (Preston *et al.*, 1972), and those used for constructing the UN model life tables for developing countries (United Nations, 1982). Many of the life tables in the UN collection were derived using some form of data adjustment and/or modeling, which were performed with the intent of correcting known or suspected errors. Although most of the life tables in the Preston collection appear to be unadjusted, the accuracy of the underlying data is questionable. All data in the WHO collection are available in standard 5-year age categories, with an open interval for ages 85 and above.

In Table 1c we summarize a collection of 19 life tables from the INDEPTH project, which has brought together data from demographic surveillance sites located in Africa and elsewhere (INDEPTH network, 2002). In these surveillance areas, complete demographic data are collected for relatively small and well-defined populations. All except two of these tables refer to African sites; the other two refer to the Matlab areas (treatment and control) in Bangladesh. The INDEPTH life tables used here are for the time period of 1995-1999 (approximately). These are the only life tables from the INDEPTH project that have been published to date, and in principle they were computed directly from observed data without any form of adjustment.[4]

Data from the Human Life-Table Database (HLD, www.lifetable.de) are summarized in Table 1d (after removing all overlap with the HMD or the WHO collection). These life tables form a disparate collection of data from various countries and time periods. Due to the variety of data sources, the format of the data is not highly standardized. We assembled a uniform set of key mortality indicators (e_0, ${}_1q_0$, ${}_5q_0$, ${}_{45}q_{15}$, and ${}_{20}q_{60}$) for testing the new mortality model, but those are the only data from the HLD that were used for this project. Although we have not checked all sources closely, we suspect that many of these tables were constructed using some form of data adjustment or model fitting (not only at older ages).

[3] HMD data have been corrected for obvious errors in published data sources: for example, an entry of '30,000' that clearly should have been '300' (such corrections are often confirmed by marginal totals). Errors due to misreporting of age have generally not been corrected. A fitted curve following the Kannisto model (Thatcher *et al.*, 1998) assures smoothness (and a more plausible trajectory of old-age mortality in some cases), but only for the oldest ages (above age 95, approximately).

[4] We have heard anecdotally that some estimates in the INDEPTH set of life tables were, in fact, derived using models and thus do not represent direct estimates in all cases. Although we have not obtained more detailed information on this specific point, these few cases appear to be exceptions to a general practice of direct calculation without adjustment or use of models.

Two mortality models

Here, we will consider the following two models:[5]

Log-linear: $\log(m_{xi}) = a_x + b_x h_i + v_x k_i + e_{xi}$

Log-quadratic: $\log(m_{xi}) = a_x + b_x h_i + c_x h_i^2 + v_x k_i + e_{xi}$

These models describe variation in log-mortality over age (x) for a given population (i). For both models, a_x, b_x, c_x, and v_x, are age-specific parameters, which can be combined in various ways to create plausible mortality curves.[6] For a given population, the values of h and k are constant across the life span and thus determine the shape of the mortality curve for a given set of the four age-specific parameters. Lastly, e_{xi} is a random error term.

For the model life table systems derived from these models, we always define $h = \log({}_5q_0)$, where ${}_5q_0$ is the probability of dying before age 5. Thus, h serves as the first (and primary) entry parameter for the system. This formulation reflects the fact that ${}_5q_0$ is the only mortality statistic for which some empirical information is available in recent decades for almost all national populations. The second entry parameter is k, which has a typical value of zero. In fact, most empirical observations of k lie between -2 and +2, and it is rarely outside the range of -4 to +4. Thus, it is often useful for theoretical or practical reasons to set $k = 0$.

The form of the models proposed here is motivated by an empirical finding of approximate linearity in the relationship between mortality levels for various age groups, when mortality rates or probabilities of dying are expressed in a logarithmic scale. Correlation coefficients between $\log({}_nm_x)$ and $\log({}_5q_0)$ are reported in Table 2. Note that these correlations are much higher at younger ages and near zero at the oldest ages.

Building on this empirical relationship, the first portion of the log-linear model, $a_x + b_x h$, describes a linear relationship in a log-log scale.[7] Although this log-linear relationship explains most of the variation in the data, there are two important, non-random deviations from this purely log-linear form that should be reflected in the model. First, as illustrated in Figure 2, many of the empirical relationships show a marked curvature, suggesting that a quadratic term should be added to the model.[8] This curvature is well described by the first portion of the log-quadratic model, $a_x + b_x h + c_x h^2$, which achieves a better overall fit to the data by various measures (as illustrated below). For this reason, the remainder of this discussion will emphasize the log-quadratic model.

Second, deviations from exactly linear or quadratic relationships tend to occur simultaneously and in a similar fashion across age groups for the same population. In the models proposed here, such deviations are captured by adding another term, $v_x k$, to the model. When k differs from zero, this term depicts the typical pattern of co-variation across age in deviations from the typical log-linear or log-quadratic form.

[5] The models are modifications of an earlier proposal by Wilmoth, Andreev, and Sawyer (forthcoming).
[6] In theory, the age groups used with these models could have any width. Although x, as written here, refers to single-year age groups, actual calculations involve mostly 5-year age groups (i.e., 0, 1-4, 5-9, …, 105-109, 110+).
[7] A similar log-linear relationship forms the basis of the Lee-Carter mortality model, which has been widely used for mortality forecasting (Lee and Carter, 1992).
[8] Note that the quadratic curves in Figure 2 tend to bend upward at younger ages (except age 0) and downward at older ages.

Fitting the models to observed data

Both models have been fitted separately by sex using various methods applied to a collection of 719 sex-specific life tables from the Human Mortality Database (see Table 1). All of these life tables have the same configuration of age groups (0, 1-4, 5-9, 10-14, …, 105-109, 110+), and almost all of them refer to 5-year time periods. The motivation for using this particular dataset will be discussed in a later section of this article.

The fitting procedure using ordinary least squares (OLS) is quite simple. It consists of fitting a series of linear or quadratic regressions of $\log({}_n m_x)$ as a function of $\log({}_5 q_0)$, in order to obtain the estimated coefficients, $\hat{a}_x$, $\hat{b}_x$, and $\hat{c}_x$. Each of these separate regressions results in a predicted line or curve describing the relationship between $\log({}_5 q_0)$ and $\log({}_n m_x)$ for each age group, as depicted in Figure 2 for broad age groups.[9] In a second step, the last set of estimated coefficients, $\hat{v}_x$, are obtained from the first term of a singular value decomposition computed from the matrix of regression residuals. This term captures the common tendency toward positive co-variation (of unusually high or low mortality rates) for adjacent age groups, especially in the prime adult years.

Both the OLS method and our preferred fitting procedure are described fully in the Appendix of this article. A discussion of alternative means of fitting the model and a justification of our preferred method are available in a supplemental report (Wilmoth *et al.*, 2009). In short, our preferred fitting procedure involves a form of weighted least squares, in which we assign progressively less weight to observations with larger residual values. Compared to ordinary least squares, the difference in fitted values by our preferred method is negligible except for ages 15-59 among males and ages 15-29 among females. The estimated coefficients based on our preferred fitting method are reported here in Table 3 for the log-linear and log-quadratic models.

Mortality estimation using the fitted models

As an estimation tool, the models can be used to derive a full life table given either one or two pieces of information. In the first case, one assumes that the only reliable data that are available refer to child mortality, expressed in the form of ${}_5 q_0$. Lacking independent information about adult mortality, we assume that $k = 0$. In the two-parameter case, one assumes that information is also available about adult mortality, in the form of ${}_{45} q_{15}$.[10] Thus, for a given set of age-specific coefficients and a known value of ${}_5 q_0$, we choose a value of *k* in order to reproduce the observed value of ${}_{45} q_{15}$ exactly.[11]

Using $h = \log({}_5 q_0)$ and *k* derived in this manner, the two models can be used to estimate age-specific mortality rates across the life span by application of the following formulas:

Log-linear: $$\hat{m}_x = e^{\hat{a}_x + \hat{b}_x h + \hat{v}_x k}$$

Log-quadratic: $$\hat{m}_x = e^{\hat{a}_x + \hat{b}_x h + \hat{c}_x h^2 + \hat{v}_x k}$$

These rates can then be transformed into a life table, from which it is easy to derive all of the usual summary measures of mortality, including life expectancy at birth. The errors of

[9] Graphs similar to Figure 2 but with greater age detail are available in a supplemental report (Wilmoth *et al.*, 2009).
[10] Although another summary measure of adult mortality could be used, for this discussion we always use ${}_{45} q_{15}$.
[11] Calculation of *k* in this situation is fairly simple but requires an iterative procedure.

estimation that result directly from this procedure (i.e., assuming the input values are correct) will be discussed in a later section of this article.

Age patterns of mortality implied by the models

Model age patterns of mortality are illustrated in Figure 3, which shows the effect of changes in h and k on the shape of the mortality curve as a function of age for the log-quadratic model.[12] The first parameter, $h = \log({}_5q_0)$, controls the overall level of mortality. Movements up or down in level are accompanied by progressive changes in the tilt and shape of the curve. The second parameter, k, alters the shape of the mortality curve (for a given value of ${}_5q_0$), especially for young and middle adult ages (roughly, from the teens to the 60s). Thus, when k is greater/less than zero, adult mortality is relatively high/low given the associated value of ${}_5q_0$.

The model can be specified using various combinations of one or two pieces of information, from which we derive associated values of h and k by some computational procedure. Our computer programs permit calculation of the full model using various combinations of the following five inputs: ${}_1q_o$, ${}_5q_0$, k, ${}_{45}q_{15}$, and e_0. Any pairing of two out these five quantities is sufficient to specify the model except the pairing of ${}_1q_o$ and ${}_5q_0$, which provides no direct information about adult mortality. Any pairing that involves k can be specified by assuming that $k = 0$; thus, in the absence of convincing evidence about relative levels of child and adult mortality (compared to historical averages), the model can be fully specified given only one of the other four inputs.

Figure 4 illustrates three of these possible pairings, for females on the left and males on the right.[13] In each case, these graphs show changes in the age pattern of mortality as we hold one of the two quantities constant while varying the other one. For this figure only, the age patterns have been smoothed by fitting spline functions to the predicted values of death rates in 5-year age intervals; the smoothing helps to clarify the underlying shape. This exercise demonstrates that the model is capable of reproducing a wide variety of mortality curves, but also that these curves have entirely plausible shapes so long as k stays roughly within +/- 4. In particular, the following three features of these curves are consistent with a large body of cross-cultural and historical evidence:

1. A minimum occurs regularly around ages 10-11;
2. Above age 30 each curve is fairly straight (in a log scale) but with a slight S-shape; and
3. Holding k constant (see middle row panels), the "accident hump" at young adult ages is more prominent at lower levels of mortality and for men. For women, it is possible to observe a gradual transition from a "maternal mortality hump" (roughly, ages 15-45) at the highest levels of mortality, to an attenuated male-type accident hump (roughly, ages 15-25) at lower levels.

For larger values of k (beyond +/- 4, approximately), the mortality curves tend to become distorted (see examples in Wilmoth *et al.*, 2009). For k around +/- 4, these distortion are fairly minor: they may have aesthetic but no practical importance, in the sense that they would have no noticeable effect on calculated values of major summary indicators (such as life expectancy at birth). For more extreme values of k (say, +/- 8), the curves become more severely distorted. For example, with very large negative values, the accident hump tends to disappear, and the

[12] Age patterns produced by the log-linear model are very similar.
[13] Similar graphs with all possible pairings are provided in a supplemental report (Wilmoth *et al.*, 2009).

minimum value can move to much higher ages (around age 30). Because historical values of *k* lie in a fairly narrow range, this parameter can serve as an important plausibility check (for example, by helping to identify unlikely combinations of ${}_5q_0$ and ${}_{45}q_{15}$).

<u>Relationship of the models to historical evidence</u>

Figure 5 illustrates the relationship between the two entry parameters of the log-quadratic model, ${}_5q_0$ and *k*, and the level of adult mortality as measured by ${}_{45}q_{15}$. Five curves trace the predicted relationship between ${}_5q_0$ and ${}_{45}q_{15}$ corresponding to *k* equal to -2, -1, 0, 1, or 2. These curves overlie a scatter plot of the observed values of ${}_5q_0$ and ${}_{45}q_{15}$ from the dataset that was used for estimating the model.

In order to use the fitted model as a tool for estimating a complete age pattern of mortality, we propose choosing *k* to match exactly the value of ${}_{45}q_{15}$ if the latter is available. Following this approach, the model is capable of reproducing any combination of ${}_5q_0$ and ${}_{45}q_{15}$ through an appropriate choice of *k*. Likewise, any combination of ${}_5q_0$ and ${}_{45}q_{15}$ implies a unique value of *k*. It is notable in this regard that the values of *k* implied by this diverse dataset (see Table 1) lie within a fairly narrow range, only rarely departing from the interval of -2 to +2. However, there are three important exceptions.

First, in the left-hand portion of each graph, there is a cluster of points lying above the curve representing $k = 2$. These points correspond to certain countries of the former Soviet Union and Eastern Europe, which have experienced usually high adult mortality in recent decades, especially among men, in the wake of massive social and political changes. Second, a sole data point lies well above the same curve on the right-hand side of the graph for men only. This point corresponds to Finland during 1940-44 and reflects excess mortality among young men fighting in wars against the Soviet Union.[14]

Third, on the right-hand side of the graph there are a few points lying below the curve representing $k = -2$, especially for women. The data points in this area of the graph (both slightly above and below $k = -2$) correspond to countries of Southern Europe during the 1950s and early 1960s,[15] and reflect a situation of unusually low adult mortality relative to child mortality (or, put differently, unusually high child mortality relative to adult mortality). As illustrated in Figure 1, the South family of the Coale-Demeny model life table system depicted accurately the mortality experience of this region during those decades; but afterward, it has deviated from the historical record as mortality fell to lower levels in these countries.

Figure 6 shows results very similar to those in Figure 5 but broken down by smaller age groups. These graphs demonstrate that the relative impact of the *k* parameter on predicted levels of mortality differs for the various age groups and by sex. For both men and women, this parameter helps to distinguish between high or low levels of adult mortality (relative to child levels) throughout the age range from 15 to 59. However, in the age group of 60-79, the importance of the *k* parameter remains for men but diminishes substantially for women. For women at ages

[14] In the dataset used here for estimating the models, the Finnish case of 1940-44 is the only example of a male mortality pattern that is substantially affected by war mortality. It was left in the dataset in order to emphasize this important point: for other countries with substantial war losses during the period covered by the dataset, the series that we have used here reflect exclusively or primarily the mortality experience of the civilian population in times of war. The age pattern of male mortality in these situations is clearly atypical and requires a special treatment.
[15] Portugal and Bulgaria are the most extreme cases.

60-79 and for both sexes at ages 80-99, the variability in the data vastly exceeds the variability implied by choices of k within a plausible range.

These results reflect the fact that the positive co-variation in levels of adult mortality relative to child mortality is limited to a particular age range. The variability in relative levels of mortality at older ages is not highly correlated with the variability observed at younger adult ages and is thus random variation from the perspective of the model. Moreover, the age range where the k parameter has a substantial impact on mortality estimates is somewhat narrower for women than for men. In times of social and political instability, when adults of both sexes are exposed to elevated risks of dying, this excess vulnerability tends to affect men both more intensely and over a broader age range compared to women.

Figure 7 presents six historical examples for the purpose of demonstrating the capabilities of the log-quadratic model as well as its limitations. These examples are not typical of the vast majority of historical observations; rather, each is exceptional in one manner or another. Thus, this illustration is intended to explore the limits of the model as a means of depicting historically well-documented age patterns of mortality. Each graph in Figure 7 shows observed data in comparison to estimates derived from the log-quadratic model. There are two sets of estimates, obtained by inserting observed values of either ${}_5q_0$ alone, or ${}_5q_0$ and ${}_{45}q_{15}$ together, as inputs to the model. The implied values of k are reported in the graph for each set of estimates (in the one-parameter case, $k = 0$ by definition).

The top row of Figure 7 compares the age pattern of mortality for two groups of men in England and Wales during 1940-44. On the left, the total population (including active military personnel) has an age pattern that is severely distorted compared to typical mortality curves. In this case the model is clearly incapable of mimicking the underlying pattern even with two input parameters. On the right, however, the civilian population (excluding the military population) has a highly typical age profile, with a very small implicit value of k in the two-parameter case.

Although the model may do poorly in representing the age pattern of war mortality, the other four examples in Figure 7 depict relatively extreme cases where the model performs reasonably well when both inputs are correctly supplied. The graphs in the middle row document the excess adult mortality due to the Spanish flu (for women in Denmark) and to the Spanish civil war (for men in Spain). The graphs in the bottom row illustrate extreme cases of relatively low or high adult mortality in peacetime (for, respectively, Portuguese women in the 1960s and Russian men in recent years). In all four cases, the two-parameter version of the log-quadratic model provides an imperfect yet, for most purposes, adequate depiction of the age pattern of mortality. By contrast, the one-parameter version of the model yields rather large errors both in the shape of the age pattern and in the resulting value of life expectancy at birth.

<u>Choice of dataset used for fitting the models</u>

The estimated coefficients for the log-linear and log-quadratic models shown in Table 3 were derived using data drawn exclusively from the Human Mortality Database (HMD). After weighing various options, we chose to fit the models using only these data, but to test it using data from all available sources. The first choice is somewhat controversial, since the HMD dataset includes life tables for only two developing countries (Taiwan and Chile), whose mortality experience is not typical of most developing countries, and because there is only one large country (Japan) with a majority population of non-European origin. This feature of our analysis raises the question of the whether the fitted model is appropriate for use in estimating the mortality patterns of developing countries.

We begin our argument by noting that the choice of a dataset in this context is inherently difficult and may have no perfect solution. On the one hand, it seems very important to derive the model using accurate information about the age pattern of mortality. On the other hand, it seems equally important to derive the model using data that are representative of the full range of true mortality patterns occurring throughout the world. Since the quality of available information tends to be much lower in developing countries (in terms of the completeness and reliability of data collected through vital registration and periodic censuses), a tradeoff between the accuracy and representativeness of the data used for fitting the model is unavoidable.

The choice to fit the new model using only the HMD dataset was made for several reasons. Three of these reasons are properties of the HMD dataset itself. First, the dataset is well documented, which helps to assure that the empirical basis of the model will be, if not fully transparent, at least readily accessible. Second, to minimize transcription errors, HMD life tables are derived using data obtained directly from national statistical offices or their regular publications (not through an intermediary like the WHO); data preparation includes procedures designed to detect gross errors and other anomalies. Third, age-specific mortality rates are computed directly from official data, without major adjustment or use of fitted models except for the oldest ages. One consequence of this approach is that countries and time periods included in the HMD have in principle been filtered according to the quality of the available statistical information.

By these criteria, the additional life tables from the other large collections considered here (WHO and HLD; see Tables 1b and 1d) would be less desirable than the HMD data but not necessarily without value. Thus, our choice not to include the other life table collections when fitting the model was also motivated by certain features of those datasets that we considered less desirable. As a practical matter, the differing age formats of the various life tables presented a minor or a serious obstacle, depending on the case. In order to combine the various life table collections to enable a joint analysis, a common age format was needed. However, to avoid sacrificing the age detail available in the HMD, it was necessary to extend the age groupings of other tables so that they, too, would end with an age category of 110+. For the HLD tables, the variety of age formats would have necessitated a considerable effort in order to create tables with uniform age categories.

By contrast, the life tables of the WHO and INDEPTH collections have uniform age groupings up to age 85, and thus we were able to extend the age range to 110+ with only a modest amount of work.[16] These life tables were combined with the HMD data to produce an alternative fitting of the log-quadratic model. This exercise revealed that adding the life tables from these two collections to the HMD dataset has almost no impact on the fitted model (Wilmoth *et al.*, 2009). Moreover, the only noticeable change induced by adding the WHO and INDEPTH life tables when fitting the model was that predicted values of old-age mortality (especially above age 80) moved slightly downward. However, this change seems undesirable for two reasons. First, the impact of the additional life tables on the estimated model occurs mostly above age 80, yet the

[16] We have extended the age range of life tables in the WHO collection by fitting the Kannisto model to the available data and then extrapolating to higher ages. The Kannisto model implies that death rates at older ages follow a simple logistic curve with an upper asymptote of one.

additional data points above age 85 are not observed values but rather the product of an extrapolative procedure. Second, the slight reduction in fitted values may reflect nothing more than common flaws affecting unadjusted mortality data at older ages, especially in countries with less reliable statistical systems.

Age misreporting is a well-known problem in mortality estimation, especially at older ages, where the resulting bias is always downward (Coale & Kisker, 1990; Preston *et al.*, 1999). Figure 8 is informative in this regard, as it illustrates the relationship between our preferred estimates of the log-quadratic model and data from the WHO and INDEPTH collections for ages 15-59 and 60-79. In the younger age group, the observations from the two latter datasets lie within a plausible range and demonstrate no obvious bias. In the older age groups, however, there is a clear downward bias in the observations from the WHO and INDEPTH datasets relative to the model derived using the HMD data alone. We believe that the first result is a strong confirmation of the general applicability of the model for a wide variety of human populations. At the same time, we believe that the second result is more likely due to imperfections in mortality data at older ages than to some limitation of the estimated model.

For these reasons we conclude that it is better to estimate the new model using a more restricted dataset, but to test the resulting model life table system using data from a wide variety of populations. In all cases we must bear in mind that a failed test may indicate problems with the data or with the model.

Accuracy of estimation

We evaluate the performance of the log-linear and log-quadratic models along two dimensions. First, we examine the performance of the models in comparison to methods used currently by international agencies and national statistical offices for creating official mortality estimates. Second, we examine the performance of the log-quadratic model when applied to populations that were not included in the dataset used for deriving the model.

Model performance was assessed in comparison to three existing methods: Coale-Demeny model life tables, UN model life tables for developing countries, and the modified logit model. We used four datasets to make these comparisons: the HMD dataset, the INDEPTH life tables for 1995-1999, and both the WHO and HLD collections (after excluding life tables that overlap with the HMD). For the new models, tests using the HMD dataset provide information about internal validity, since these same data were used for estimating the models. Since life tables included in the HMD are excluded from the other collections listed in Table 1, we have used the other datasets to examine the external validity of the log-quadratic model.

In order to focus attention on the models themselves (rather than the datasets used for estimating the models), we have re-estimated the modified logit model using the same HMD dataset used for fitting the log-linear and log-quadratic models. When assessing the performance of the modified logit model, we make separate tests using the re-estimated model and the original version proposed by Murray *et al.* (2003). For comparing the performance of the new models and the modified logit model, we assess the accuracy of life table estimates derived using ${}_5q_0$ alone, or using ${}_5q_0$ and ${}_{45}q_{15}$ together.

Comparisons of the log-quadratic model with the Coale-Demeny and UN model life tables are somewhat more complicated, since the latter have discrete regional families rather than a continuous second parameter. Therefore, we created five "families" of the log-quadratic model corresponding to specific values of the *k* parameter (for $k = -2$, -1, 0, 1, and 2). Given just one piece of information about the mortality level of a population, such as ${}_5q_0$, we determine the overall level and age pattern of mortality associated with each region or family of the various model systems. Then, within each model system, we choose the best region or family in order to reproduce as closely as possible some other indicator of mortality, such as ${}_{45}q_{15}$. Following this procedure with the Coale-Demeny model life tables often results in substantial underestimates of ${}_{45}q_{15}$, especially for low values of ${}_5q_0$ (see Figure 1).

When child mortality is at least moderately low, e_0 is less affected by child mortality and is more sensitive to variations in adult mortality. Therefore, we also examine estimation accuracy following the reverse of the procedure described above. That is, for each family or region, we choose the level based on ${}_{45}q_{15}$ and derive a complete life table. Then, within each model system, we choose the best region or family based on the closeness of observed and predicted values ${}_5q_0$.

We have assessed the accuracy of an estimation procedure in terms of the standard deviation of estimation errors for three key mortality indicators: e_0, q_0, and ${}_{45}q_{15}$. The results of all tests using the HMD dataset are given in Table 4. The performance of the log-quadratic model and the re-estimated modified logit model is quite similar in these tests. Not surprisingly, the log-quadratic model performs better than the log-linear model, and the re-estimated modified logit model has an advantage over the original version in this set of tests.

Table 4 also illustrates that the log-quadratic model with 5 discrete families produces much better estimates of e_0 than do the Coale-Demeny model life tables, the UN model life tables, or a combination of the two, whether ${}_5q_0$ or ${}_{45}q_{15}$ is used as the primary input parameter (in the procedures described above). As expected, for the Coale-Demeny and UN model life tables, using ${}_{45}q_{15}$ to choose the mortality level within families and then ${}_5q_0$ to choose the best family produces more accurate estimates than the reverse procedure.

As illustrated in Table 5, the results of the external tests using the HLD, INDEPTH, and WHO collections of life tables are similar to the results of tests using the HMD dataset. Again, the accuracy of estimates is similar when using the log-quadratic model or the modified logit model (in either its original or re-estimated form). Tests based on the WHO dataset indicate a slight advantage for the original modified logit, reflecting the fact that the model was derived using this same dataset. Similarly, performance tests using the HLD and INDEPTH datasets indicate a slight advantage for the original modified logit for estimating female e_0; estimation accuracy for males using these datasets is quite similar for all methods. The results of the INDEPTH tests are unusual in that estimation errors for female e_0 are higher than for male e_0 when estimation is based on ${}_5q_0$ alone. We will return to this issue below when discussing the external applicability of the log-quadratic model.

Having established that the log-quadratic model performs at least as well and often better than the other methods currently in use, we now examine the accuracy of estimates derived from this model in more detail. Estimation errors for e_0 based on the HMD dataset are plotted in Figure 9. The second and third panels of each column show error bands, corresponding to either one or two times the standard deviation of the corresponding set of errors. Note that the bands are rather narrow when two data inputs are used: given both ${}_5q_0$ and ${}_{45}q_{15}$, most of the estimates of e_0 are within about a year of the actual value of e_0. However, when ${}_5q_0$ is the only input, the error bands are much wider, especially for males: in this case, most of the estimated values of e_0 for females fall within about three years of the actual values whereas for men most of the estimates lie within about five years of the actual values.

The results of external tests using the HLD and WHO collections indicate that the log-quadratic model may be applicable in a wide variety of contexts. Using either of these datasets, estimation errors for males using a one-parameter log-quadratic model (i.e., based on ${}_5q_0$ alone) are similar to estimation errors obtained when using the HMD data. For example, the standard deviation of estimation errors for e_0 (in years) is 2.52 using the HMD data, 2.63 using the HLD data, and 2.68 using the WHO collection. Similarly, for males given both ${}_5q_0$ and ${}_{45}q_{15}$ and for females given either one or two inputs, the external tests using HLD and WHO indicate only slightly higher estimation errors in comparison to the internal test.

In comparison to the tests based on other datasets, estimation errors using the INDEPTH data are much higher. The disparity is largest for females in the case where the age pattern of mortality is derived using ${}_5q_0$ alone. Given that the INDEPTH data include several life tables from African countries with high HIV prevalence, these results may suggest that the log-quadratic model fitted to the HMD data does not fully capture the age-pattern of mortality in populations whose mortality experience is heavily affected AIDS. Alternatively, these results may merely reflect a greater influence of random variation in the mortality of these small populations, as well as age reporting errors among the older population. Even if the log-quadratic model does not succeed in capturing the age pattern of AIDS mortality in such populations, it might still be used for estimating mortality from other causes, which could be combined with estimates of AIDS mortality derived separately using simulation models.

Discussion

In addition to showing much promise as an estimation tool, the models proposed here can help to sharpen our understanding of the history of mortality change. Figure 10 illustrates the trajectory of ${}_5q_0$ versus ${}_{45}q_{15}$ for various collections of countries.

As illustrated in Figure 10, most of the countries have followed a fairly regular path over time, in the sense that child and adult mortality did not deviate much from the typical relationship, which is approximately linear in the chosen scale. This group includes the Nordic countries, Western Europe, and all HMD populations from outside Europe (Chile, New Zealand, Australia, Taiwan, Japan, Canada, USA).[17]

The bottom panels of Figure 10 show the more unusual historical trajectories of Southern and Eastern Europe, plus the countries of the former Soviet Union. Southern Europe had a somewhat peculiar pattern back in the 1950s or 1960s, especially among women. Bulgarian men (at the southern end of Eastern Europe) also showed a pronounced “South” pattern, as defined by Coale and Demeny (i.e., relatively low adult mortality or, put differently, relatively high child mortality).

[17] Clearly, this remark pertains only to the period covered for each country by the HMD dataset, which is quite short in some cases. For example, the series for Chile begins in the early 1990s.

However, the dramatic historical pattern traced in recent decades by the former Soviet countries has no close comparison (of the East European countries, the trend for Hungary is most similar). Russia is the most extreme case, with levels of adult mortality (for both men and women) that far exceed those that would be predicted on the basis of child mortality.

It is clear that the log-quadratic model does not fit all known age patterns of human mortality. It may be possible to improve its precision by adding third-order adjustments (i.e., highly tailored v_x profiles for special cases, such as war or major epidemics). However, those are beyond the scope of this paper. As illustrated here, both the log-linear and the log-quadratic models provide useful first- or second- order approximations in a wide variety of situations.

Conclusion

In addition to providing generally smaller estimation errors, the new method offers other advantages over existing techniques. The proposed model is better suited to the practical needs of mortality estimation, because the two input parameters are both continuous yet the second one is optional. Also, since model parameters are closely related to measures of child and adult mortality, the link between data and estimates is more transparent.

Appendix

In order to describe the procedure used for estimating the log-linear and log-quadratic models, it is useful to write the two models as follows:

$$\log(m_{xi}) = a_x + b_x h_i + v_x k_i + \varepsilon_{xi} \tag{A.1}$$

$$\log(m_{xi}) = a_x + b_x h_i + c_x h_i^2 + v_x k_i + \varepsilon_{xi} \tag{A.2}$$

In this notation, *i* is an index for a population or an individual life table. In general $i = 1, \ldots, n$, and here $n = 719$ (see Table 1). Thus, a_x, b_x, c_x, and v_x are age-specific parameters that are fixed across populations. Only the values of h_i and k_i vary across time and space, and in all cases $h_i = \log(Q_5)_i$. Given h_i and k_i, the model predicts the value of the log death rate with an error of ε_{xi}. Fitting the model to some collection of historical data will result in parameter estimates, $\hat{a}_x$, $\hat{b}_x$, $\hat{c}_x$, and $\hat{v}_x$.

We have estimated these models using a variety of techniques, which are described fully in a supplemental report (Wilmoth *et al.*, 2009). Here, we document only two methods. The first one, ordinary least squares, is the simplest and serves as a useful starting point. Our preferred method however, consists of weighted least squares using the bi-square function, which was suggested by Tukey as a means of minimizing or eliminating the influence of extreme observations. We refer here to the preferred procedure as the bi-weight method. As noted in the main text, differences in the fitted models resulting from these two procedures are rather small in magnitude and are concentrated in the young-to-middle adult ages (roughly, ages 15-29 for women and ages 15-59 for men).

Both methods of estimating the models involve a two-step procedure. The two methods differ only on the first step, in which the linear or quadratic portion of the model is fitted separately to each age group. For example, when fitting the linear portion of the log-linear model by the method of ordinary least squares, we obtain estimates of parameters a_x and b_x by minimizing the following sum of squared residuals:

$$\sum_i \left[\ln(m_{xi}) - a_x - b_x \cdot h_i\right]^2 \ . \tag{A.3}$$

When fitting this portion of the model by the bi-weight method, estimates are obtained by minimizing a *weighted* sum of squared residuals,

$$\sum_i w_{xi} \cdot \left[\ln(m_{xi}) - a_x - b_x \cdot h_i\right]^2 \ , \tag{A.4}$$

where the weights, w_{xi}, are a function of the residuals of the fitted model:

$$r_{xi} = \ln(m_{xi}) - \hat{a}_x - \hat{b}_x \cdot h_i \ . \tag{A.5}$$

Since the weights are a function of the residuals, an iterative procedure is required (convergence is rapid in our experience, usually involving no more than 25 iterations).

The bi-square weight function is defined as follows:

$$w_{xi} = \begin{cases} (1 - u_{xi}^2)^2 & \text{if } |u_{xi}| < 1 \\ 0 & \text{if } |u_{xi}| \geq 1 \end{cases} \tag{A.6}$$

where $u_{xi} = \dfrac{r_{xi}}{cS_x}$; in addition, r_{xi} is the residual for a particular observation, S_x is the median absolute value of the residuals for that particular age group, and c is a tuning constant. For this application, we have used $c = 4$ for all age groups because that choice results in a weight of zero for relatively extreme examples in the HMD dataset (for example, adult mortality rates for Russian males in recent years and Portuguese females during the 1950s/1960s receive zero weight when estimating the model by this procedure with $c = 4$).

For both methods, the second step involves estimating the $v_x k_i$ term by computing a singular-value decomposition (SVD) of the resulting residual matrix:

$$\mathrm{SVD}\left[r_{xi}\right] = \mathbf{PDQ^T} = d_1 \mathbf{p_1 q_1^T} + \ldots \tag{A.7}$$

where $\mathbf{P} = \left[\mathbf{p_1}, \mathbf{p_2}, \ldots\right]$ and $\mathbf{Q} = \left[\mathbf{q_1}, \mathbf{q_2}, \ldots\right]$ are matrices of left- and right-singular vectors, respectively, and $\mathbf{D}$ is a diagonal matrix with elements d_1, d_2, …. Only the first term of the SVD, $d_1 \mathbf{p_1 q_1^T}$, is used for obtaining parameter estimates. Specifically, the typical age pattern of deviations from an exact log-linear or log-quadratic model is depicted by the first left-singular vector; thus, the values of $\hat{v}_x$ are set equal to the elements of $\mathbf{p_1}$.[18]

For some purposes the best estimate of k_i for the populations used for fitting the model (i.e., the 719 life tables of the HMD collection) would be derived by multiplying d_1 times the appropriate element of the first right-singular vector, $\mathbf{q_1}$. However, as a practical tool for estimating the full

[18] After fitting, $\hat{v}_x$ was set to zero for certain age groups (0, 1-4, and above 90) and for a few cases (only at older ages) where it was (slightly) negative. See Table 3.

age pattern of mortality in situations with more limited data, we propose choosing a value of k_i in order to match ${}_{45}q_{15}$ exactly for a given population (if that quantity is known; otherwise, we propose setting $k = 0$ or else making an arbitrary choice based on expert knowledge of the health and circumstances of the population).

Fitting the models using the bi-weight method rather than ordinary least squares tends to pull the $k = 0$ line or curve toward the center of the main cloud of historical data points, either by down-weighting or by completely ignoring extreme observations. By varying the value of *c*, we have tuned the procedure so that the weights in the age range of 15-59 taper off to zero at a *k* value of around ± 2. This choice is arbitrary but seems sensible.

The choice between the two estimation procedures matters more for the log-quadratic than for the log-linear model. For the log-quadratic model, the results can be summarized as follows:

- Except for very old ages (where random fluctuations play an important role), differences in predicted mortality levels are negligible except for ages 15-29 among both men and women, and ages 30-59 for men only.
- For these broad age groups, differences in estimated mortality rates (for a given value of *k*) reach a maximum of 9-11% (over the typical range of ${}_5q_0$).
- For some 5-year age groups among males aged 25-44, these differences reach a maximum of 14-16%.
- Differences in predicted levels of life expectancy at birth are less than 0.1 years for women but as high as 0.6 years for men.

In our opinion the model predictions resulting from the bi-weight estimation procedure are preferable. It is clear that some extreme observations (in particular, the recent experience of some Eastern European and former Soviet countries) are pulling the OLS curves upward, in particular for certain adult age groups. Thus, OLS predictions of some mortality levels for the default case (when $k = 0$) appear to be slightly overestimated.

By some measures the bi-weight method yields a less optimal fit. As shown in Table 4 of the main text, standard deviations of estimation errors are slightly bigger for the bi-weight method compared to the OLS procedure. However, these differences in the overall goodness-of-fit are slight and seem acceptable as a means of reducing the apparent bias in certain age groups that results from the OLS fitting method.

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Table 1
Life tables from various sources used for this analysis
a) Human Mortality Database

Country or Area	Year	Number of tables	Exposure-to-risk (millions of person-years)
Australia	1921-2004	17	971
Austria	1947-2004	12	433
Belarus	1960-2007	10	459
Belgium	1841-1913, 1920-2006	33	1,200
Bulgaria	1947-2004	12	478
Canada	1921-2004	17	1,599
Chile	1992-2004	3	188
Czech Republic	1950-2006	12	567
Denmark	1835-2007	35	568
England and Wales	1841-2006	34	6,044
Estonia	1960-2007	10	68
Finland	1878-2007	27	491
France	1816-2006	39	7,909
Germany, East	1956-2006	11	841
Germany, West	1956-2006	11	3,154
Hungary	1950-2004	11	563
Iceland	1838-2007	35	22
Ireland	1950-2006	12	189
Italy	1872-2004	27	5,737
Japan	1947-2006	13	6,496
Latvia	1960-2007	10	116
Lithuania	1960-2007	10	162
Luxembourg	1960-2006	10	18
Netherlands	1850-2006	32	1,339
New Zealand	1876-2003	26	239
Norway	1846-2006	33	458
Poland	1958-2006	11	1,724
Portugal	1940-2007	14	630
Russia	1960-2006	10	6,503
Scotland	1855-2006	31	695
Slovakia	1950-2006	12	270
Slovenia	1983-2006	6	48
Spain	1908-2006	21	3,023
Sweden	1751-2007	52	1,227
Switzerland	1876-2007	27	633
Taiwan	1970-2007	8	741
Ukraine	1960-2006	10	2,288
United States	1933-2004	15	14,424
Total		719	72,517

Notes:
(1) Life tables by sex are counted only once. Throughout Table 1, we count a maximum of one life table per country-period.
(2) If the death counts used to construct the life table come from more than one year, we count exposure-to-risk over the full period.
(3) Data for New Zealand refer to the non-Maori population prior to 1950 and to the full national population after 1950.

b) WHO life table collection

Country or Area	Year(s)	Number of tables	Exposure-to-risk (millions of person-years)
Argentina	1966-1970, 1977-1979, 1982-1997	24	715
Australia	1911	1	5
Chile	1909, 1920, 1930, 1940, 1950, 1955-1982, 1984-1991	41	378
Colombia	1960, 1964	2	23
Costa Rica	1956-1983, 1985-1998	42	92
Croatia	1982-1998	17	79
Cuba	1970-1998	29	290
Czechoslovakia	1934	1	15
El Salvador	1950, 1971	2	13
Georgia	1981-1992, 1994-1996	15	77
Greece	1928, 1956-1998	44	404
Guatemala	1961, 1964	2	8
Honduras	1961, 1974	2	15
India	1971	1	1,685
Iran (Islamic Republic of)	1974	1	131
Israel	1975-1998	24	108
Matlab (Bangladesh)	1975	1	1
Mauritius	1990-1998	9	10
Mexico	1958-1959, 1969-1973, 1981-1983, 1985-1998	24	1,763
Moldova	1981-1998	18	76
Panama	1960	1	1
Peru	1970	1	40
Philippines	1964, 1970	2	141
Portugal	1920, 1930	2	13
Republic of Korea	1973	1	170
Romania	1963, 1969-1978, 1980-1998	30	660
Singapore	1955-1998	44	100
Slovenia	1982	1	2
South Africa (colored pop.)	1941, 1951, 1960	3	3
Sri Lanka	1946, 1953	2	45
Taiwan, Province of China	1920, 1930, 1936	3	29
Thailand	1970	1	112
The former Yugoslav Republic of Macedonia	1982-1997	16	32
Trinidad and Tobago	1990-1995, 1997	7	9
Tunisia	1968	1	10
United States of America	1900-1916, 1920-1932	30	2,039
Yugoslavia	1982-1997	16	166
Sub-total WHO 1802 only	--	461	9,460
Overlap with HMD	--	1,341	43,075
Total	--	1,802	52,535

Notes:

(1) Life tables in this collection that overlap with the HMD (Table 1a) are not listed here individually.

(2) This collection of life tables was used by Murray *et al.* (2003) in creating the modified logit model and life table system.

c) INDEPTH life tables

Population aggregate	Year(s)	Number of tables	Exposure-to-risk (millions of person-years)
Africa, low HIV	1995-1999	8	1.7
Africa, high HIV	1995-1999	9	2.3
Bangladesh (Matlab)	1995-1999	2	0.2
Total	--	19	4.2

Source: INDEPTH network (2002)

d) Human Life-Table Database

Country or Area	Year(s)	Number of tables	Exposure-to-risk (millions of person-years)
Austria	1865-1882,1889-1892,1899-1912,1930-1933	10	221.7
Bahrain	1998	1	0.6
Bangladesh	1974, 1976-1989,1991-1994,1996	22	2,014.2
Brazil	1998-2004	7	1,236.9
Bulgaria	1900-1905	1	23.3
China	1981	29	1,012.0
Czech Republic	1920-1933, 1935-1949	29	391.0
Egypt	1944-1946	1	54.9
Estonia	1897,1922-1923,1932-1934,1958-1959	4	8.9
Gaza Strip	1998	1	1.1
Germany	1871-1911,1924-1926,1932-1934	8	2,481.2
Germany, former Dem. Rep.	1952-1955	3	72.2
Germany, former Fed. Rep.	1949-1951	1	208.0
Greece	1926-1930,1940	2	38.4
Greenland	1971-2003	9	1.8
India	1901-1999	46	45,646.4
Iraq	1998	1	23.7
Ireland	1925-1927,1935-1937,1940-1942,1945-1947	4	35.6
Israel	1997-2005	20	55.8
Jordan	1998	1	4.6
Kuwait	1998	1	2.0
Lebanon	1998	1	3.7
Luxembourg	1901-1959	59	16.5
Malta	2001,2003-2005	4	1.6
Mexico	1980	1	69.3
Oman	1998	1	2.3
Poland	1922,1927,1948,1952-1953	4	134.1
Qatar	1998	1	0.6
Republic of Korea	1970,1978-1979,1983,1985-1987,1989,1991	8	355.8
Russia	1956-1959	4	463.1
Saudi Arabia	1998	1	19.7
Slovenia	1930-1933,1948-1954,1960-1962,1970-1972, 1980-1982	6	30.2
South Africa	1925-1927,1969-1971	3	90.7
Spain	1900	1	18.6
Sri Lanka	1963,1971,1980-1982	3	68.6

Country or Area	Year(s)	Number of tables	Exposure-to-risk (millions of person-years)
Syria	1998	1	15.7
Taiwan	1926-1930,1936-1940,1956-1958,1966-1967	4	104.8
USSR	1926,1927,1938,1939,1958,1959	3	1,047.1
United Arab Emirates	1998	1	2.9
United Kingdom, N. Ireland	1980-2003	22	38.8
United States of America	1917-1919	3	309.3
Uruguay	2005	1	3.3
Venezuela	1941-1942,1950-1951	2	18.1
West Bank	1998	1	1.6
Yemen	1998	1	17.1
Total	--	337	56,367.8

Notes:

(1) Person-year estimates are based on historical population data for each area. If the death counts used to construct the life table come from more than one year, we count exposure-to-risk over the full period.

(2) For some areas, life tables represent subpopulations.

(3) Life tables from the HLD that overlap with those in the HMD or the WHO collection (see Tables 1a and 1b) are not listed here.

Source: Human Life-Table Database, http://www.lifetable.de.

Table 2

Correlation coefficients, age-specific death rates vs. probability of dying under age 5 (both in logarithmic scale), Human Mortality Database life tables (n = 719)

Age group	Female	Male
0	0.983	0.984
1-4	0.969	0.963
5-9	0.944	0.935
10-14	0.944	0.940
15-19	0.936	0.900
20-24	0.939	0.768
25-29	0.949	0.829
30-34	0.958	0.871
35-39	0.961	0.883
40-44	0.962	0.874
45-49	0.947	0.845
50-54	0.942	0.814
55-59	0.930	0.774
60-64	0.942	0.775
65-69	0.928	0.772
70-74	0.912	0.798
75-79	0.873	0.779
80-84	0.812	0.747
85-89	0.713	0.658
90-94	0.565	0.473
95-99	0.378	0.363
100-104	0.155	0.218
105-109	-0.045	0.093
110+	-0.174	0.004

Note: Table shows correlations between $\log\left({}_n m_x\right)$ and $\log\left({}_5 q_0\right)$.

Table 3

Coefficients for two mortality models, estimated using HMD life tables (n = 719)

a) Log-linear model

Age	Female a_x	Female b_x	Female v_x	Male a_x	Male b_x	Male v_x
0	-0.3329	0.9684	0.0000	-0.2383	0.9873	0.0000
1-4	--	--	--	--	--	--
5-9	-3.4361	1.1034	-0.3250	-3.6541	1.0265	0.1950
10-14	-4.1152	0.9705	-0.3617	-4.4284	0.8470	0.1861
15-19	-4.0162	0.8438	-0.4113	-4.4827	0.5845	0.2291
20-24	-3.7625	0.8612	-0.4014	-4.1096	0.5862	0.3163
25-29	-3.6613	0.8515	-0.3665	-4.1028	0.5877	0.3686
30-34	-3.6205	0.7922	-0.3302	-4.0417	0.5743	0.3858
35-39	-3.6407	0.7041	-0.2781	-3.9224	0.5413	0.3786
40-44	-3.6847	0.5975	-0.2260	-3.8047	0.4805	0.3515
45-49	-3.7326	0.4858	-0.1658	-3.6920	0.3991	0.2989
50-54	-3.5757	0.4240	-0.1293	-3.5188	0.3238	0.2429
55-59	-3.3363	0.3835	-0.0987	-3.3122	0.2602	0.1824
60-64	-2.9276	0.3720	-0.0604	-2.9746	0.2277	0.1420
65-69	-2.5609	0.3411	-0.0247	-2.6561	0.1896	0.0991
70-74	-2.1192	0.3161	0.0071	-2.2485	0.1754	0.0671
75-79	-1.7692	0.2640	0.0293	-1.8662	0.1549	0.0352
80-84	-1.4554	0.2089	0.0341	-1.4828	0.1389	0.0168
85-89	-1.1650	0.1567	0.0290	-1.1390	0.1178	0.0000
90-94	-0.9061	0.1120	0.0000	-0.8464	0.0921	0.0000
95-99	-0.6531	0.0766	0.0000	-0.5730	0.0761	0.0000
100-104	-0.4635	0.0448	0.0000	-0.3866	0.0546	0.0000
105-109	-0.3236	0.0211	0.0000	-0.2526	0.0365	0.0000
110+	-0.2297	0.0084	0.0000	-0.1682	0.0250	0.0000

Note: There are no estimated coefficients for ages 1-4 by design. Since ${}_5q_0$ is an input to the model, ages 1-4 are excluded. After using the model to estimate mortality for age 0, we derive mortality for ages 1-4 as a residual component of ${}_5q_0$. This procedure assures that the input and output values of ${}_5q_0$ are identical.

Table 3 (cont.)

b) Log-quadratic model

Age	Female a_x	Female b_x	Female c_x	Female v_x	Male a_x	Male b_x	Male c_x	Male v_x
0	-0.6619	0.7684	-0.0277	0.0000	-0.5101	0.8164	-0.0245	0.0000
1-4	--	--	--	--	--	--	--	--
5-9	-2.5608	1.7937	0.1082	0.2788	-3.0435	1.5270	0.0817	0.1720
10-14	-3.2435	1.6653	0.1088	0.3423	-3.9554	1.2390	0.0638	0.1683
15-19	-3.1099	1.5797	0.1147	0.4007	-3.9374	1.0425	0.0750	0.2161
20-24	-2.9789	1.5053	0.1011	0.4133	-3.4165	1.1651	0.0945	0.3022
25-29	-3.0185	1.3729	0.0815	0.3884	-3.4237	1.1444	0.0905	0.3624
30-34	-3.0201	1.2879	0.0778	0.3391	-3.4438	1.0682	0.0814	0.3848
35-39	-3.1487	1.1071	0.0637	0.2829	-3.4198	0.9620	0.0714	0.3779
40-44	-3.2690	0.9339	0.0533	0.2246	-3.3829	0.8337	0.0609	0.3530
45-49	-3.5202	0.6642	0.0289	0.1774	-3.4456	0.6039	0.0362	0.3060
50-54	-3.4076	0.5556	0.0208	0.1429	-3.4217	0.4001	0.0138	0.2564
55-59	-3.2587	0.4461	0.0101	0.1190	-3.4144	0.1760	-0.0128	0.2017
60-64	-2.8907	0.3988	0.0042	0.0807	-3.1402	0.0921	-0.0216	0.1616
65-69	-2.6608	0.2591	-0.0135	0.0571	-2.8565	0.0217	-0.0283	0.1216
70-74	-2.2949	0.1759	-0.0229	0.0295	-2.4114	0.0388	-0.0235	0.0864
75-79	-2.0414	0.0481	-0.0354	0.0114	-2.0411	0.0093	-0.0252	0.0537
80-84	-1.7308	-0.0064	-0.0347	0.0033	-1.6456	0.0085	-0.0221	0.0316
85-89	-1.4473	-0.0531	-0.0327	0.0040	-1.3203	-0.0183	-0.0219	0.0061
90-94	-1.1582	-0.0617	-0.0259	0.0000	-1.0368	-0.0314	-0.0184	0.0000
95-99	-0.8655	-0.0598	-0.0198	0.0000	-0.7310	-0.0170	-0.0133	0.0000
100-104	-0.6294	-0.0513	-0.0134	0.0000	-0.5024	-0.0081	-0.0086	0.0000
105-109	-0.4282	-0.0341	-0.0075	0.0000	-0.3275	0.0001	-0.0048	0.0000
110+	-0.2966	-0.0229	-0.0041	0.0000	-0.2212	0.0028	-0.0027	0.0000

Table 4

Standard deviations of estimation errors for e_0, q_0, and ${}_{45}q_{15}$ by sex, various model life table methods, Human Mortality Database life tables (n = 719)

	Female			Male		
	e_0	q_0	${}_{45}q_{15}$	e_0	q_0	${}_{45}q_{15}$
Given ${}_5q_0$ only:						
Log-linear (bi-weight)	1.64	0.011	0.032	2.59	0.012	0.061
Log-linear (OLS)	1.66	0.010	0.033	2.60	0.011	0.062
Log-quadratic (bi-weight)	1.62	0.010	0.032	2.52	0.011	0.060
Log-quadratic (OLS)	1.62	0.010	0.032	2.52	0.011	0.060
Modified logit (re-est.)	1.65	0.010	0.032	2.47	0.011	0.060
Modified logit (orig.)	1.79	0.014	0.033	2.52	0.017	0.067
Given ${}_5q_0$ and ${}_{45}q_{15}$:						
Log-linear (bi-weight)	0.82	0.011	0	0.66	0.012	0
Log-linear (OLS)	0.78	0.010	0	0.62	0.011	0
Log-quadratic (bi-weight)	0.70	0.010	0	0.58	0.011	0
Log-quadratic (OLS)	0.69	0.010	0	0.57	0.011	0
Modified logit (re-est.)	0.67	0.010	0	0.60	0.011	0
Modified logit (orig.)	0.87	0.013	0	0.93	0.018	0
Best family given ${}_5q_0$:						
Log-quadratic (5 families)	0.94	0.010	0.013	1.18	0.011	0.027
Coale-Demeny (4 families)	2.04	0.010	0.021	2.95	0.014	0.061
UN tables (5 families)	2.16	0.013	0.026	2.69	0.011	0.057
C-D or UN (9 families)	1.97	0.011	0.020	2.67	0.013	0.055
Best family given ${}_{45}q_{15}$:						
Log-quadratic (5 families)	0.99	0.013	0	1.61	0.017	0
Coale-Demeny (4 families)	1.24	0.014	0	2.61	0.028	0
UN tables (5 families)	1.28	0.016	0	1.89	0.017	0
C-D or UN (9 families)	1.34	0.013	0	1.72	0.018	0

Note: For these comparisons, the log-quadratic model was estimated using either ordinary least squares (OLS) or weighted least squares using a bi-square weight function of residuals (the bi-weight method). Estimation errors for the log-quadratic model in the two sets of "best family" comparisons were derived using the bi-weight method (see Appendix for more explanation).

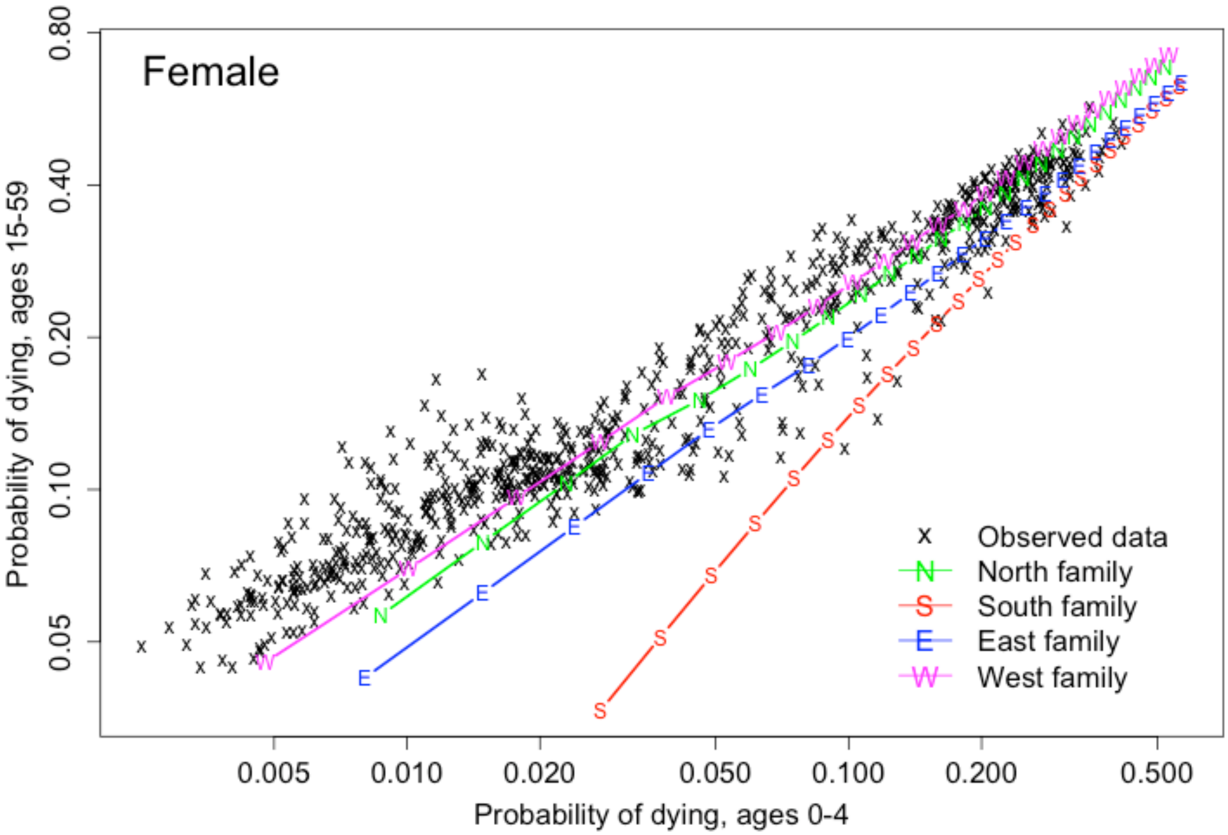
Table 5

Standard deviations of estimation errors for e_0, q_0, and ${}_{45}q_{15}$ by sex, various model life table methods, other (non-HMD) life tables

	Female			Male		
	e_0	q_0	${}_{45}q_{15}$	e_0	q_0	${}_{45}q_{15}$
WHO-1802 life tables						
Given ${}_5q_0$ only:						
Log-quadratic	2.43	0.008	0.041	2.68	0.008	0.054
Modified logit (re-est.)	2.50	0.007	0.041	2.63	0.007	0.055
Modified logit (orig.)	2.34	0.008	0.041	2.62	0.008	0.055
Given ${}_5q_0$ and ${}_{45}q_{15}$:						
Log-quadratic	1.02	0.008	0	0.82	0.008	0
Modified logit (re-est.)	1.05	0.007	0	0.80	0.007	0
Modified logit (orig.)	0.92	0.007	0	0.76	0.008	0
INDEPTH life tables						
Given ${}_5q_0$ only:						
Log-quadratic	4.05	0.023	0.112	3.78	0.021	0.113
Modified logit (re-est.)	3.98	0.023	0.112	3.86	0.022	0.114
Modified logit (orig.)	4.04	0.024	0.113	3.84	0.026	0.114
Given ${}_5q_0$ and ${}_{45}q_{15}$:						
Log-quadratic	1.91	0.023	0	1.41	0.021	0
Modified logit (re-est.)	1.56	0.025	0	1.41	0.023	0
Modified logit (orig.)	1.55	0.025	0	1.45	0.027	0
Human Life-table Database						
Given ${}_5q_0$ only:						
Log-quadratic	2.34	0.012	0.057	2.63	0.012	0.061
Modified logit (re-est.)	2.35	0.011	0.057	2.66	0.011	0.062
Modified logit (orig.)	2.33	0.013	0.058	2.73	0.012	0.065
Given ${}_5q_0$ and ${}_{45}q_{15}$:						
Log-quadratic	0.86	0.012	0	0.78	0.012	0
Modified logit (re-est.)	0.76	0.015	0	0.80	0.011	0
Modified logit (orig.)	0.70	0.014	0	0.85	0.013	0

Figure 1

Relationship between child and adult mortality levels (${}_5q_0$ and ${}_{45}q_{15}$),
observed data (n = 719) and Coale-Demeny model life tables (4 regional families)



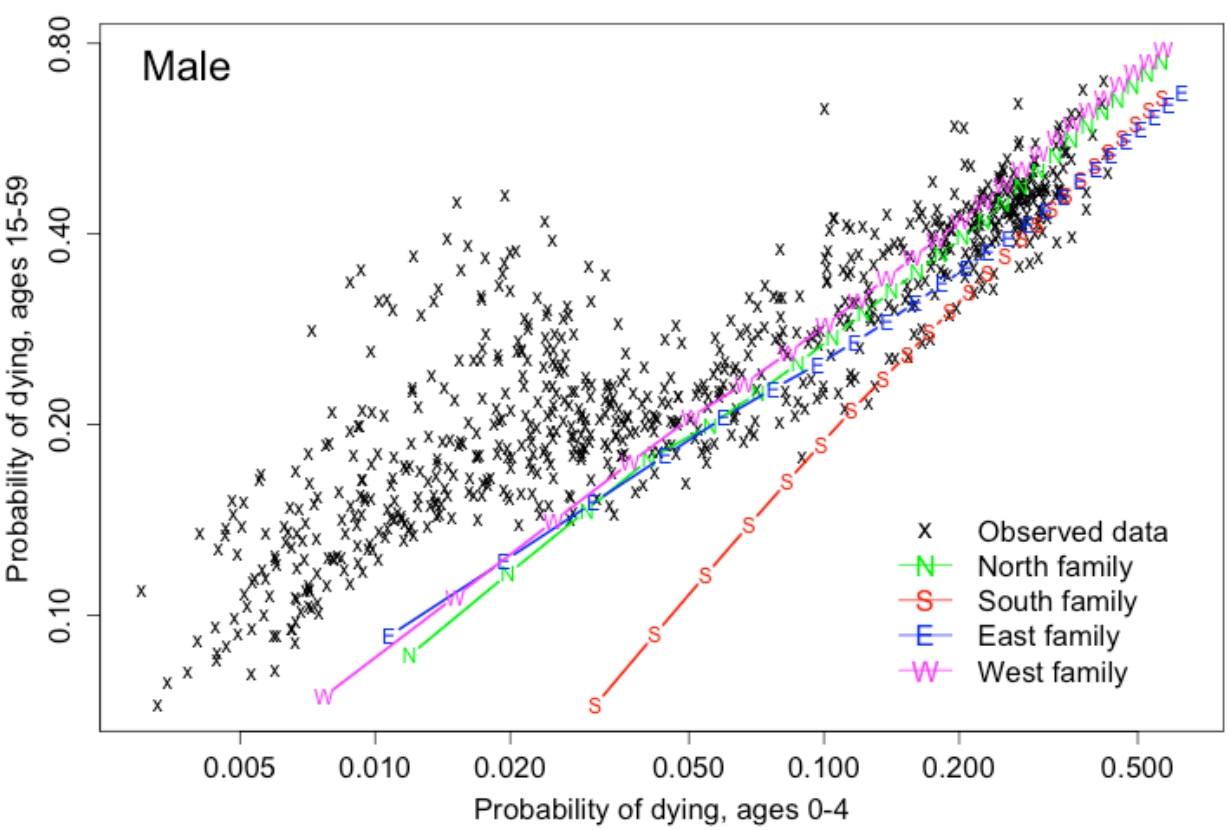


Figure 2
Age-specific death rates ($_nM_x$) vs. child mortality ($_5q_0$),
log-linear vs. log-quadratic models, total population (sexes combined)

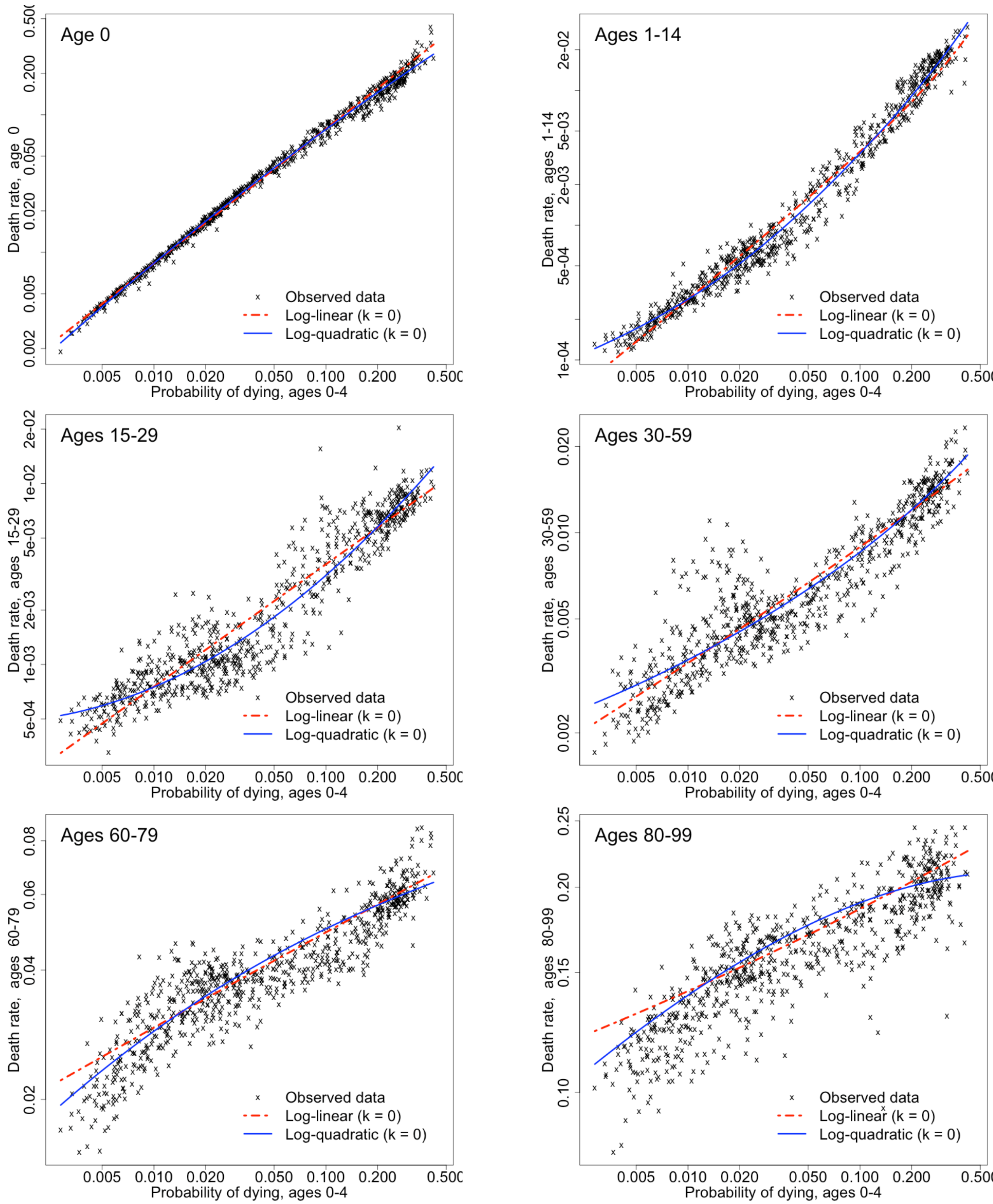
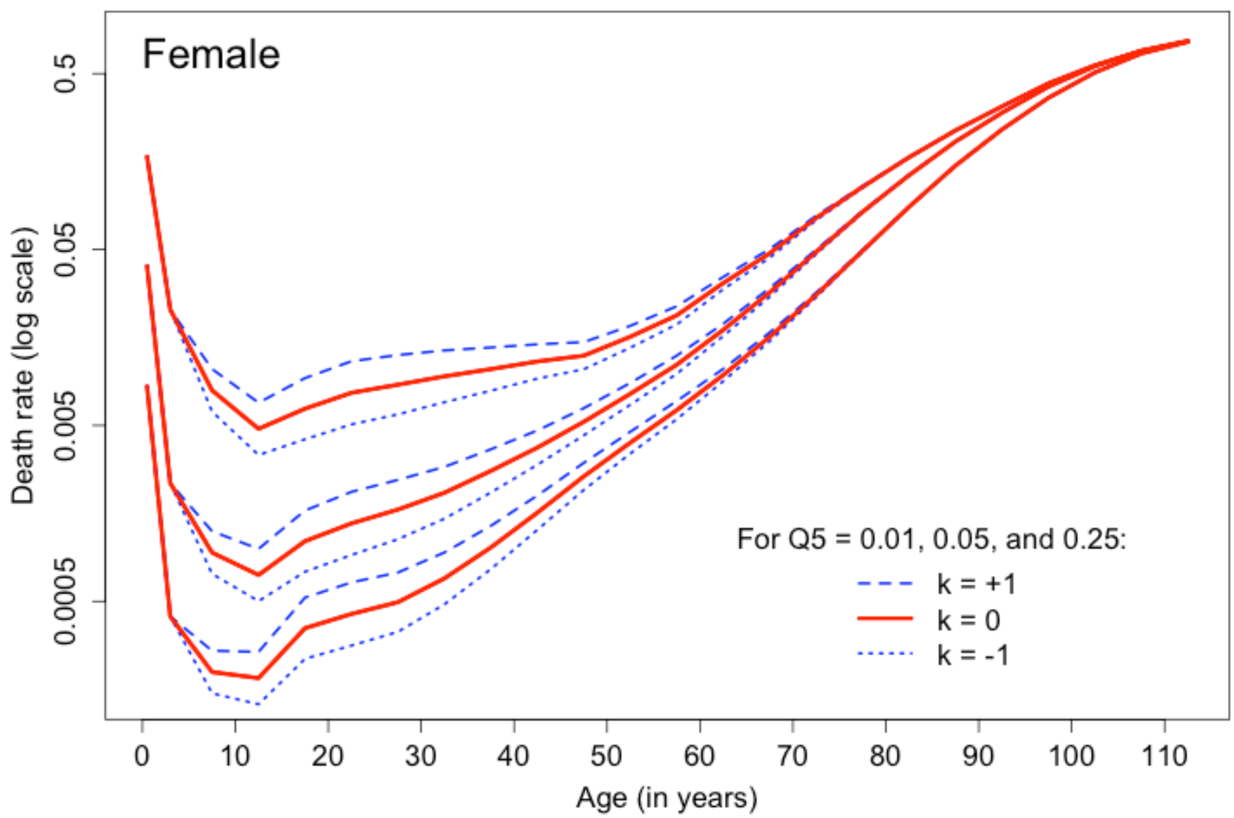


Figure 3
Typical age patterns of mortality implied by the log-quadratic model



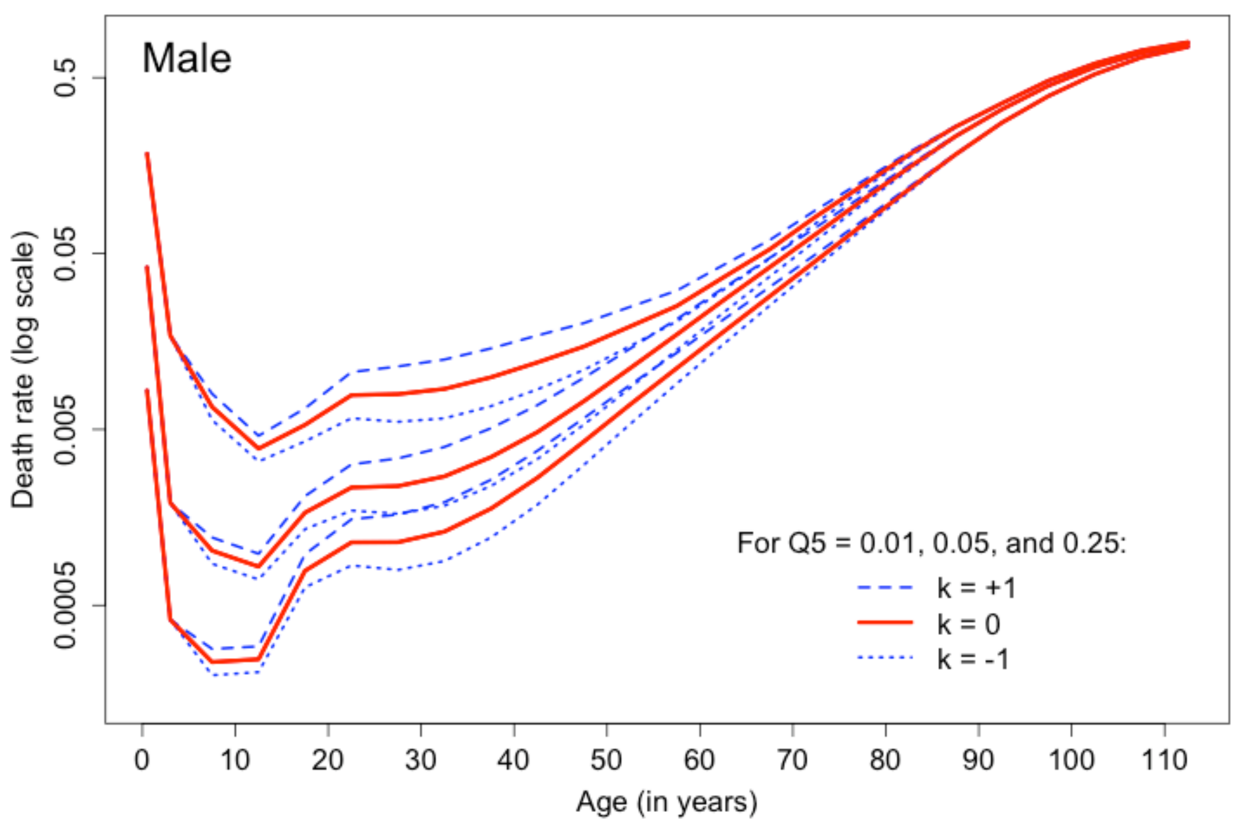


Figure 4
Age patterns of mortality implied by various selections of two input parameters

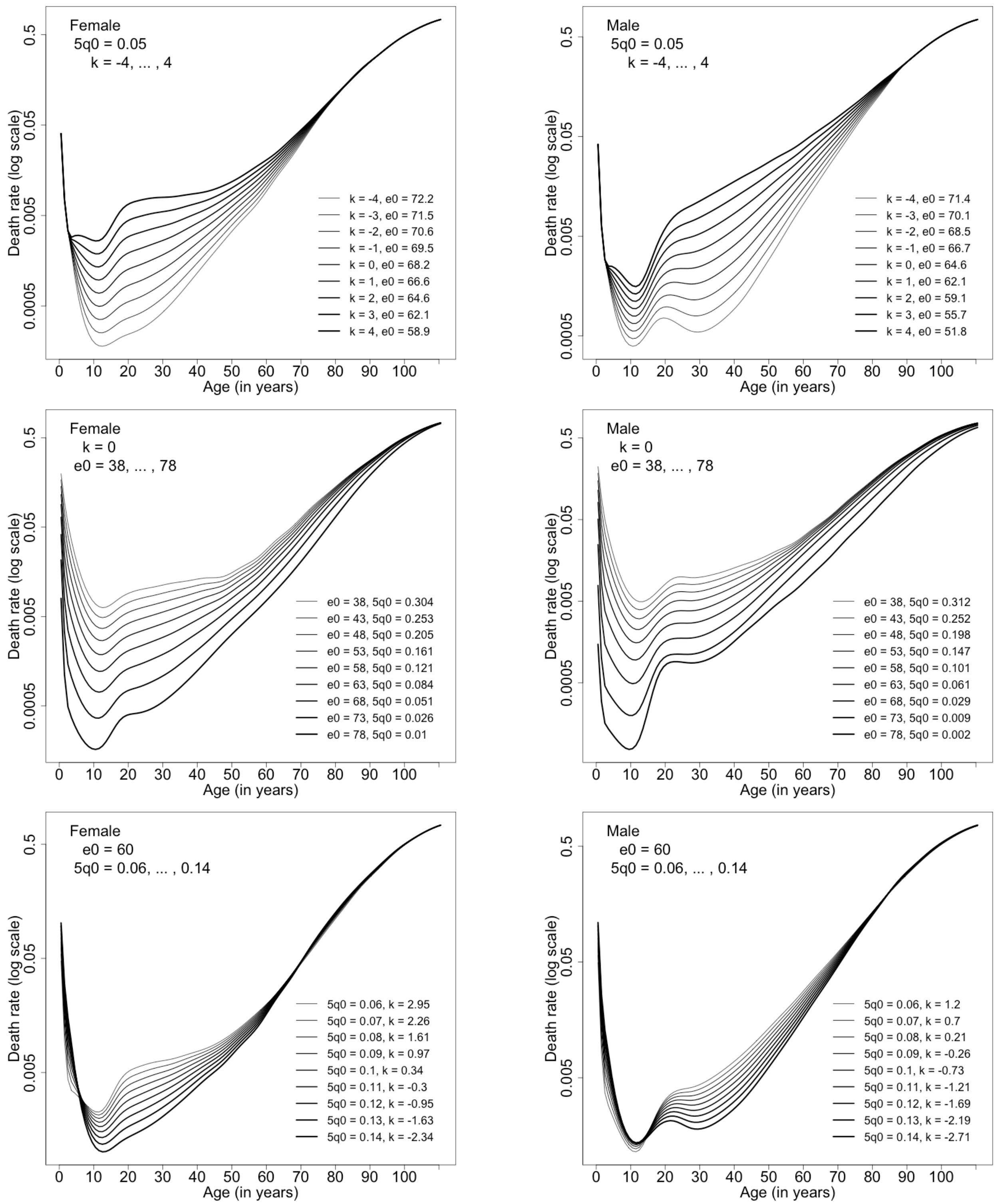
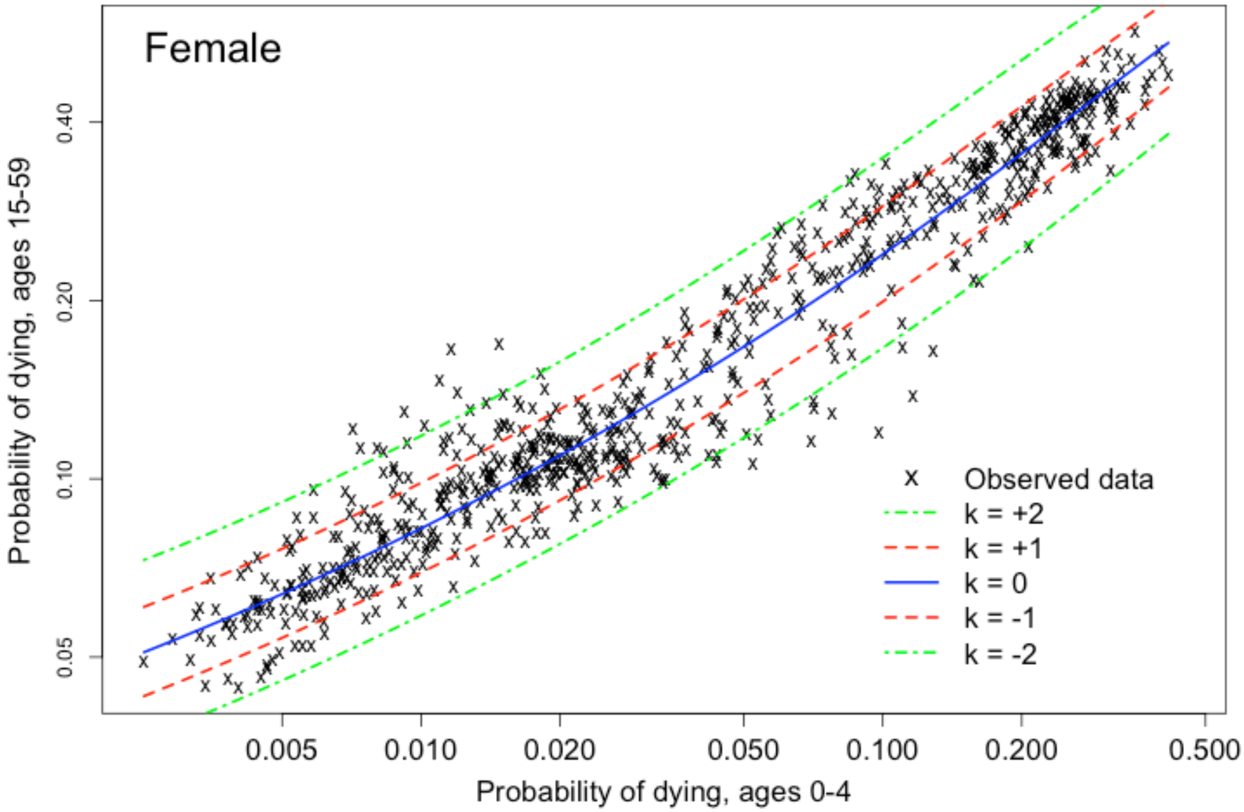


Figure 5
Adult mortality (${}_{45}q_{15}$) vs. child mortality (${}_{5}q_{0}$), by sex,
observed data (n = 719) and log-quadratic model (for 5 values of k)



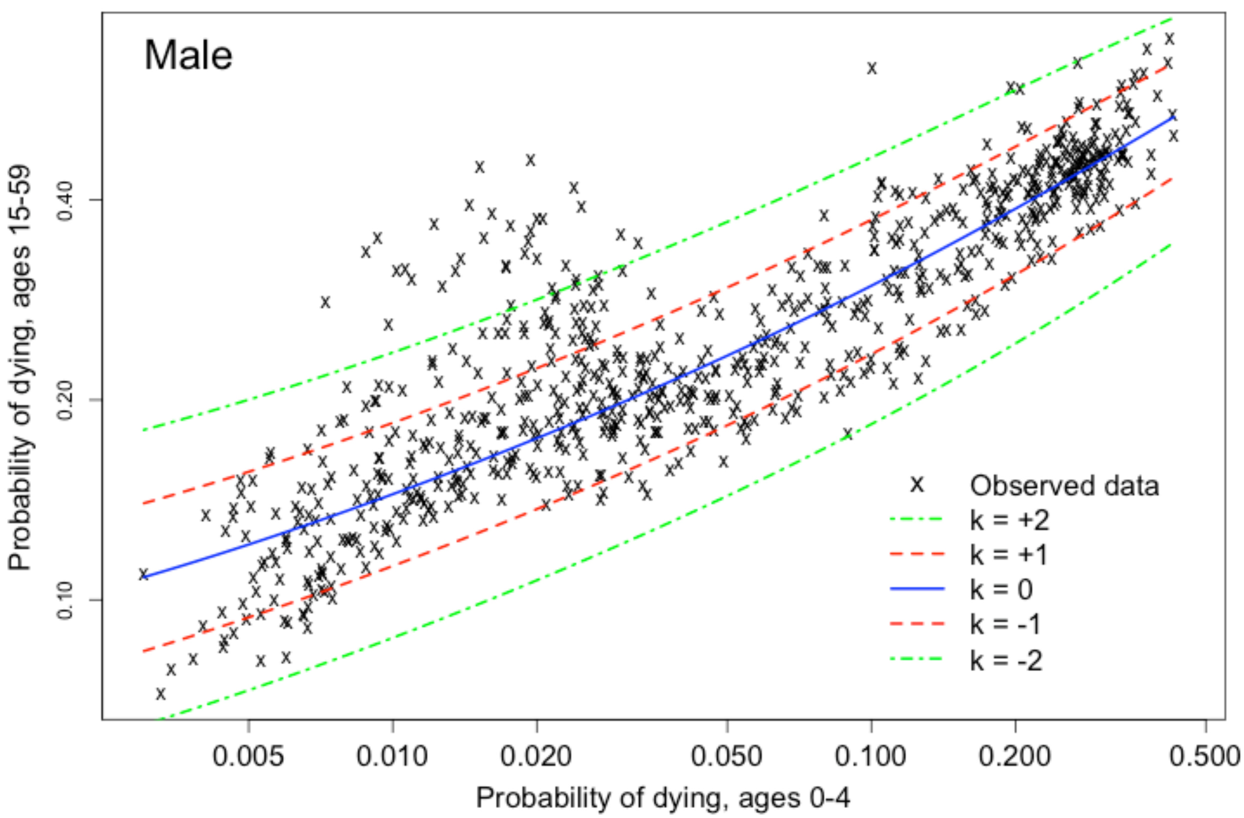


Figure 6

Age-specific death rates ($_nM_x$) vs. child mortality ($_5q_0$) for 6 age groups, observed data (n = 719) and log-quadratic model (for 5 values of k)

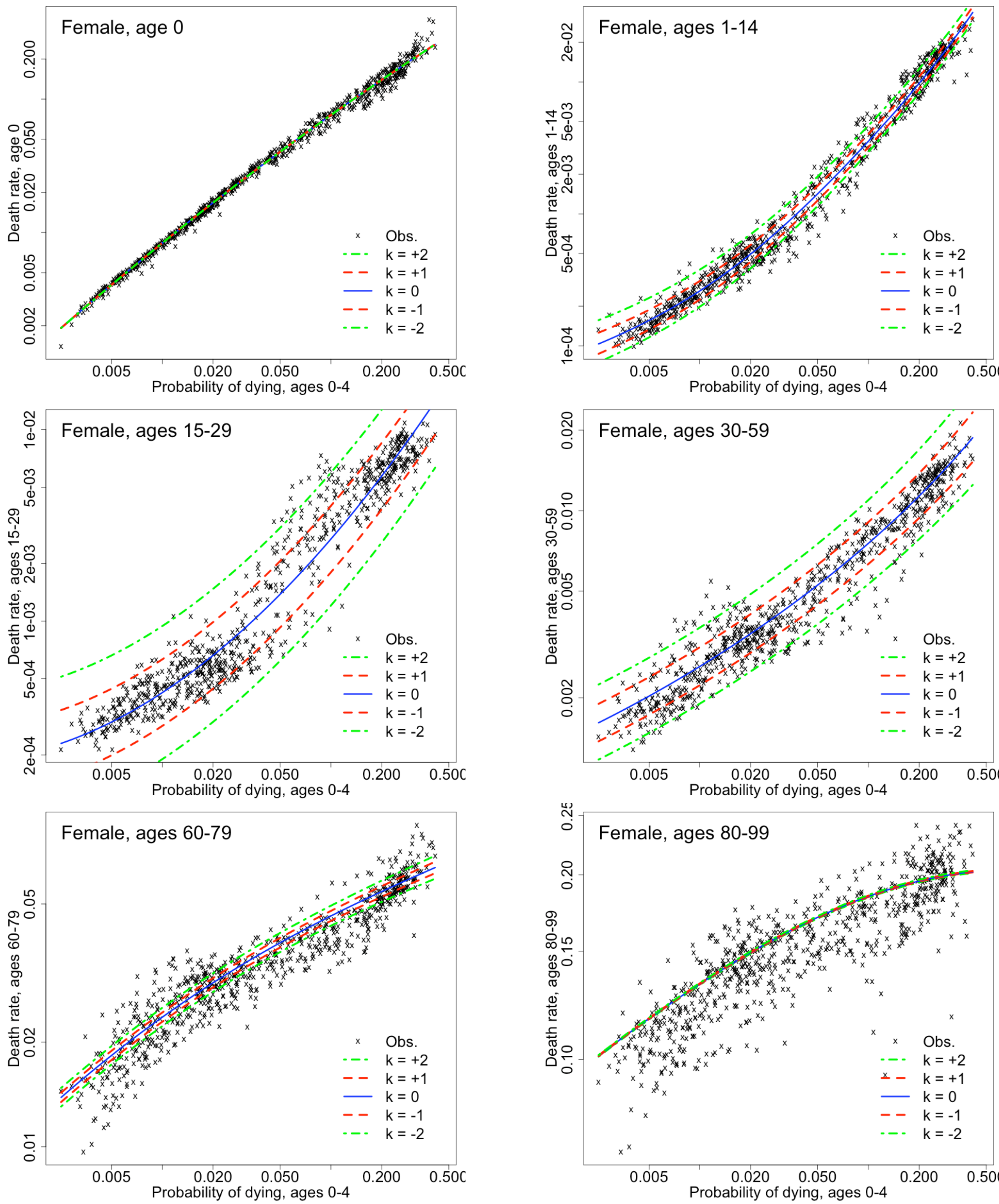


Figure 6 (cont.)

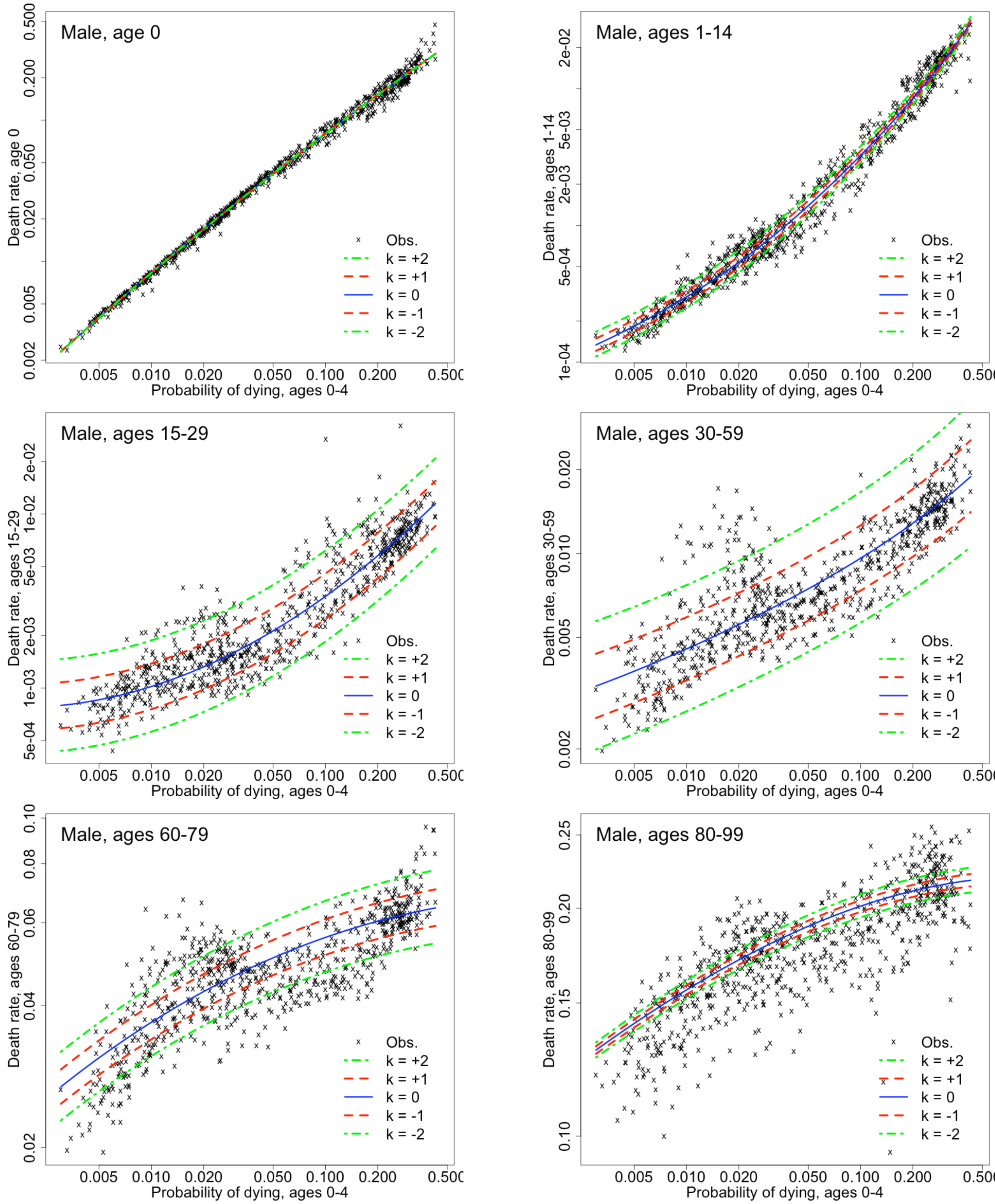


Figure 7

Six examples of mortality curves derived using
the log-quadratic model (given ${}_5q_0$ only, or ${}_5q_0$ and ${}_{45}q_{15}$)

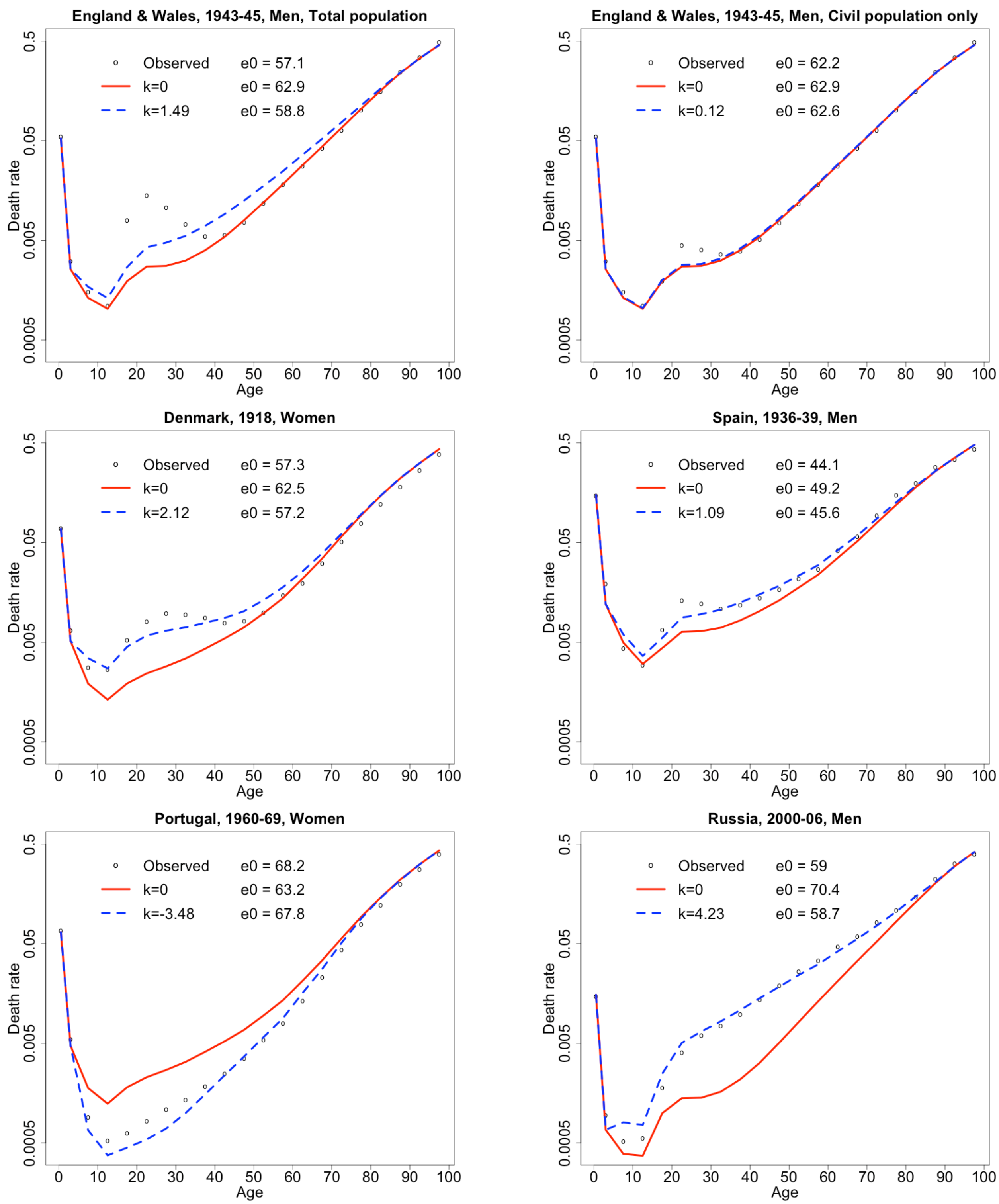
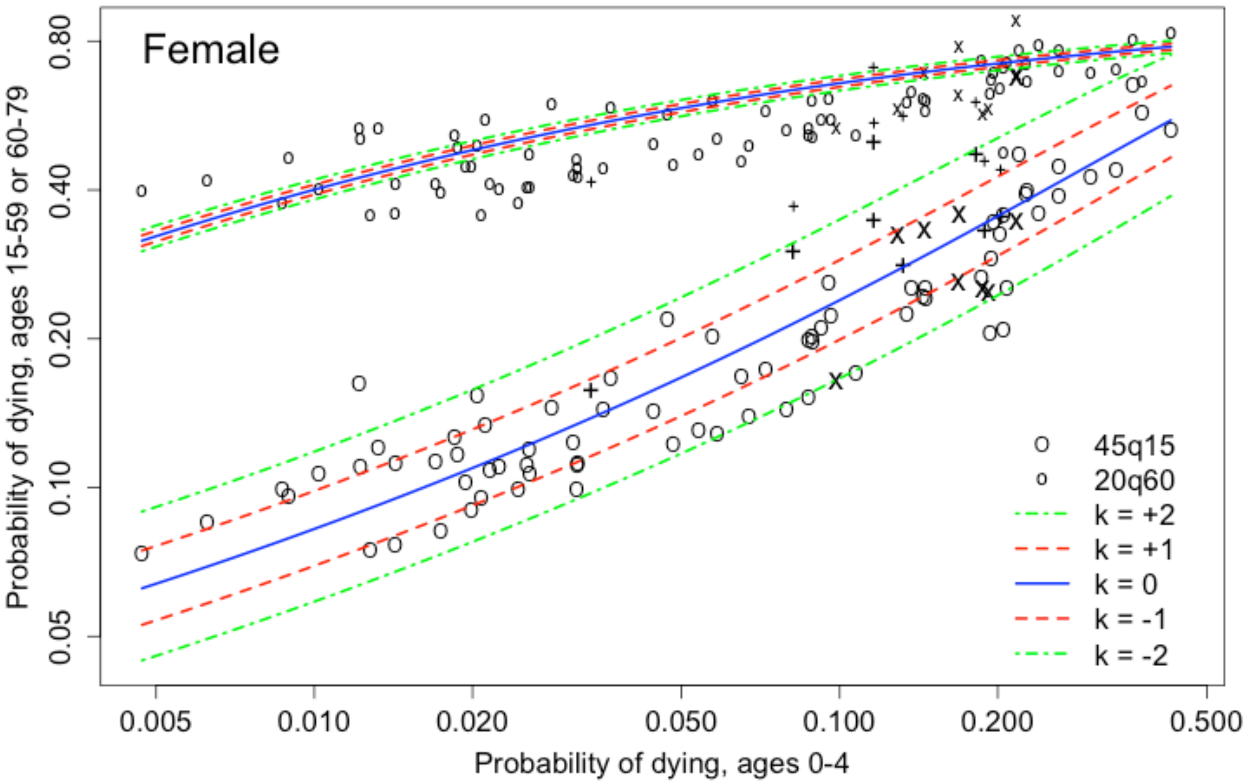
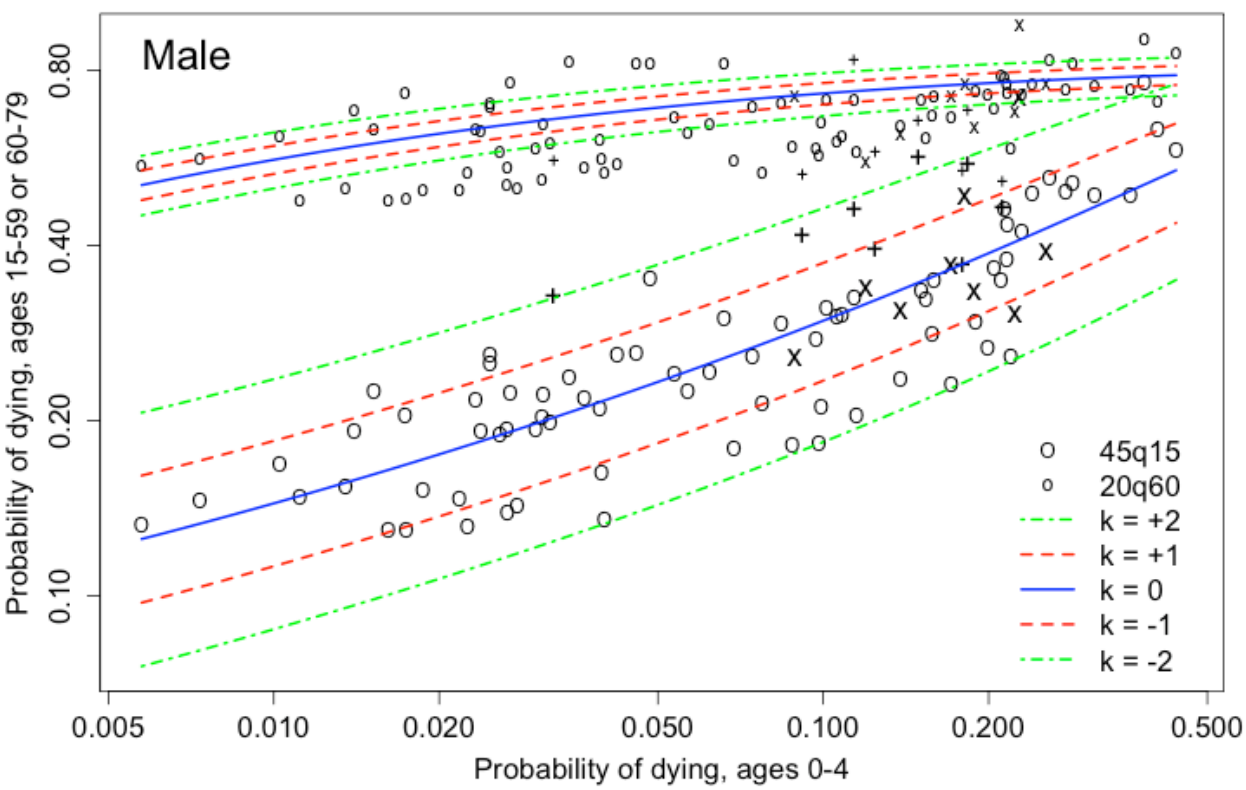


Figure 8
Adult and old-age mortality ($_{45}q_{15}$ and $_{20}q_{60}$) vs. child mortality ($_{5}q_{0}$) for various developing country populations, compared to predictions of the log-quadratic model





o = WHO-1802 developing country only, x = INDEPTH low HIV, + = INDEPTH high HIV

Figure 9
Estimation errors for life expectancy at birth (estimated minus observed),
with error bands (plus/minus 1 or 2 standard deviations),
for 1- and 2-dimensional log-quadratic model

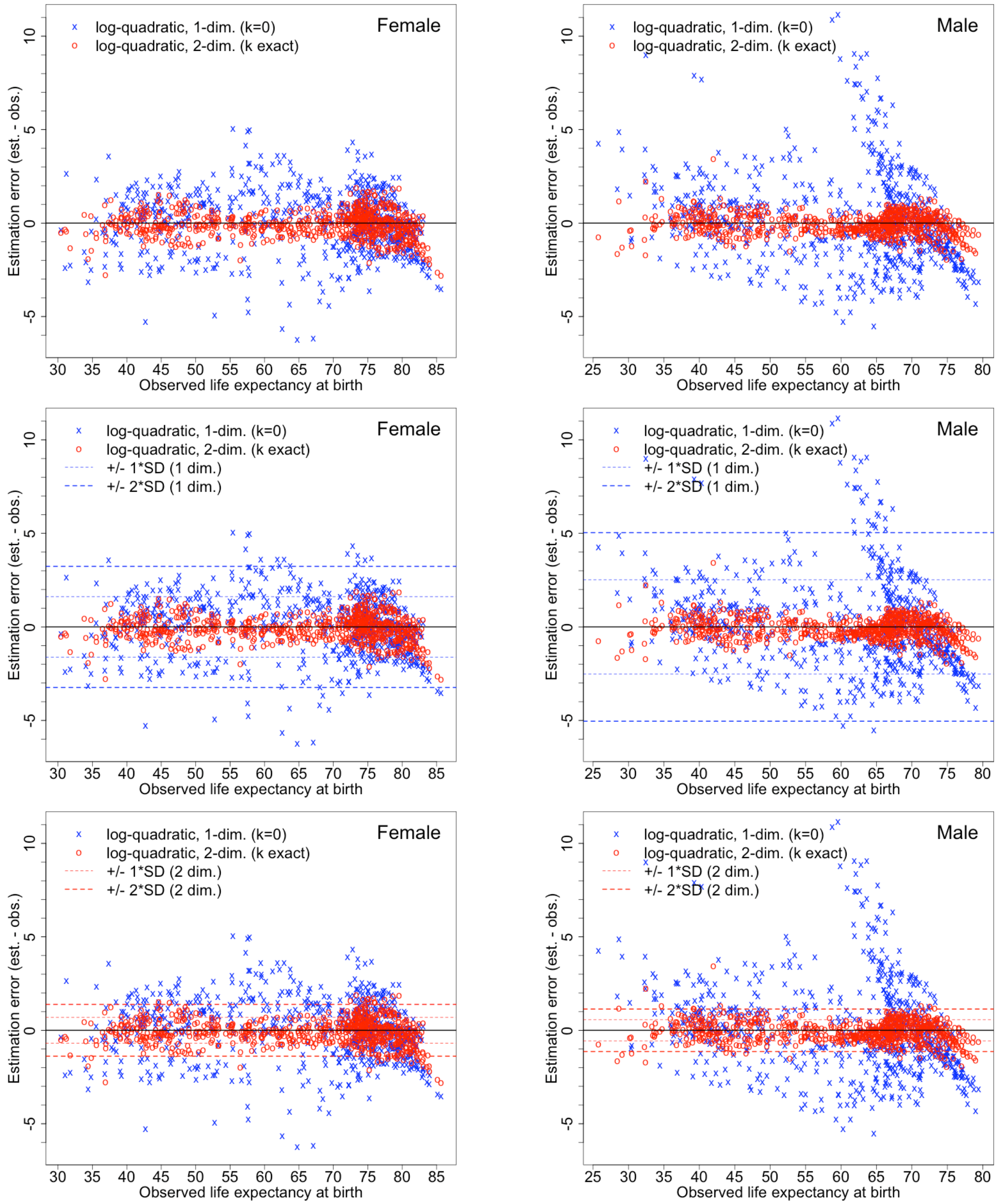


Figure 10
Adult mortality ($_{45}q_{15}$) vs. child mortality ($_{5}q_{0}$),
country patterns plus log-quadratic model (for 5 values of k)