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

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In this supplemental report, we offer additional information not presented in the main paper on the development, implementation, and testing of the log-quadratic model. First, we present possible alternative methods for fitting the log-quadratic model and defend our choice of both the data set and the bi-weight method utilized for fitting the model. In the second section, we offer additional evidence of the flexibility of the log-quadratic model by discussing how to utilize the model to estimate mortality rates given a variety of input parameters. The third section includes a description of the methods used to fit the modified logit model to the HMD data set. Finally, this supplemental report includes a number of figures that provide additional support for arguments presented in the main article and/or more detailed descriptions of data patterns by age and sex.

Alternative fitting methods

In this section, we discuss alternative statistical methods and additional data that could be utilized to fit the log-quadratic model. The main paper discusses the justification for using the log-quadratic rather than the log-linear form of the model. Estimated coefficients of the log-linear model are presented here in Table 1.

In the main paper, we provide justification for only using the HMD data in the subsection "Choice of dataset used for fitting the models". Below, we compare the log-quadratic model fitted to the HMD data to the log-quadratic model fit to both 719 life tables from the HMD as well as the 134 life tables from the WHO collection of 1,802 life tables that do not overlap with life tables in the HMD. (For another set of estimates, the 19 INDEPTH life tables were included in addition to those from the HMD and WHO collections; the results were very similar to those presented here.) The life tables from the WHO life tables of the same format as the HMD life tables, we fitted the Kannisto model (i.e. a logistic curve with an asymptote equal to one) to the death rates for ages 65-69 to 80-84 and then extrapolated to higher ages in order to extend the age range of life tables in the WHO collection up to age 110+.

We consider three possible fitting methods: ordinary least squares (OLS) and two versions of weighted least squares (WLS). With ordinary least squares, each data point is given equal weight. In the first version of weighted least squares, each observation is weighted by the total population size (more precisely, the total exposure to risk; thus, for each country-period the weight is equal for all ages and both sexes). Finally, the bi-weight approach is a type of weighted least squares, where weights are a function of residual size only (not population size). Thus, compared to the OLS fit, observations associated with large residuals receive little or even zero weight. A detailed description of how to fit the log-quadratic model using the OLS and bi-weight fitting methods is included in the Appendix of the main paper.

Consider the following four combinations of a dataset and a fitting method:

- 1. OLS, HMD-719
- 2. WLS, HMD-719
- 3. Bi-weight, HMD-719
- 4. OLS, HMD-719 + WHO-134

Figure S-1 illustrates the two datasets and the four fitted models (i.e., predicted levels of m_x given ${}_5q_0$ assuming k = 0, according to fitted models derived using a given dataset and method), separately by sex and for broad age groups. Comparing results for the four fitted models, we observe the following key differences:

- The WLS fit is the most distinctive among the four cases examined here. The predicted curves for ages above 30 exhibit much sharper downward concavity compared to the other methods. For ages 30-59, even the direction of the curvature is reversed.
- The bi-weight fit is almost the same as the OLS for all age groups and both sexes except for both females and males aged 15-29 and for males aged 30-59. Giving less weight to extreme observations (e.g. Russia) results in slightly lower values of adult mortality (for a given value of *k*). Additional details on the differences between the OLS and bi-weight fits are included in the Appendix of the main paper.
- The fit that includes the WHO-134 life tables is only slightly different than the OLS fit to only the HMD data except at older ages, especially 80-99. However, note that "observed data" above age 85 in this dataset are extrapolations based on data for age groups 65-69 to 80-84 (using the Kannisto model). By comparison, HMD "observed data" above age 95 (approximately; this age varies by population size) are extrapolations (using the Kannisto model) based on single-year data for all ages 80 and above. Thus, there is no strong reason for including these other life tables and a good reason for excluding them (to avoid possible bias in the predicted model at older ages).

Across all age groups, there is very little difference between cases 1, 3, and 4. Thus, the most important choice is whether to assign weights based on population size (case 2) or to treat each observation (country-period) as equal.

Theoretically, the method of weighted least squares is usually justified as a means of equalizing the variance of the different observations. For a dependent variable in the form of $\log(m_x)$, the natural choice for a weight according to the classical theory is D_x , the number of deaths for that country-period-age-sex combination (i.e., use of weights equal to D_x follows from the fact that variance of $\log(m_x)$ equals $1/D_x$ approximately). In this exercise, we have used the total exposure-to-risk rather than the number of deaths by age and sex. This simplification has little importance for the current discussion, because of the fact that within each age group D_x is highly correlated with total exposure-to-risk for the population.

It is not clear that the usual theoretical considerations are of major importance in this case. Although it is true that the natural variability of death rates is affected by population size, for most of the observations here (except at very old ages and ages 10-14, and for a few very small countries like Iceland), the number of deaths is so large that random variation is not a major issue. Thus, rather than correcting for differential variability (heteroscedasticity) across observations, the main impact of using weights in the current example is to assign extra influence to the mortality patterns experienced by the largest populations. For this reason, it is helpful to recall the relative population sizes of the various countries/areas represented in the HMD dataset. Japan, Russia, and the United States are by far the most populous countries included in the data set. For each of the three largest populations, there are features of their historical mortality patterns that must be considered extreme: very high mortality among young and middle-aged adults in Russia (especially for males), and very low old-age mortality in Japan and the USA (in all cases, relative to levels of ${}_5q_0$). Figure S-1 shows the observed data for these three countries separately (denoted by "J', "R", and "U"). It seems clear that the data points for Japan and the USA are pulling the fitted model downward at very low mortality levels (especially for older ages), whereas the data points for Russia are pulling the fitted model upward at medium-low levels of ${}_5q_0$ (across a broad adult age range). Given the substantial differences in population size, it seems plausible that the combined effect of these two forces may account for the substantially greater curvature in the predicted trends from the WLS model.

Theoretically, from a demographic rather than a statistical perspective, it is not clear that larger populations should receive more weight in the process of determining the fitted model. It is a question of whether the unit of observation is an individual or a population. Arguably, each country/area in the HMD is the relevant unit of observation – whether a country is large or small, it exists within a common political system and a shared epidemiologic environment. And since large populations in this dataset tend to be extreme (each in its own manner), it seems that there is a strong argument *against* the use of weights based on population size.

In conclusion, there are important arguments against the use of population weights or the additional life tables from the WHO-1802 collection. There is no argument against use of a bi-weight procedure and a modest argument in its favor (slight change in estimate of $_n m_x$ for ages 15-59 for males, up to 10 or 15% difference). Therefore, we conclude that the bi-weight fit using the HMD dataset is the preferred method for fitting the log-quadratic model.

Input parameters

In the main paper, we mainly discuss utilizing the log-quadratic model to estimate mortality given either ${}_5q_0$ or both ${}_5q_0$ and ${}_{45}q_{15}$ as input parameters; however, as noted in the section, "Age patterns of mortality implied by the models", it is possible to specify the model by pairing any two of the following five inputs except for ${}_1q_0$ and ${}_5q_0$: ${}_1q_0$, ${}_5q_0$, k, ${}_{45}q_{15}$, and e_0 . Consider the following possible pairings:

Case 1: ${}_{5}q_{0} \& k$	Case 4: $_{1}q_{0}$ & k	Case 7: $k \& e_0$
Case 2: ${}_{5}q_{0}$ & e_{0}	Case 5: $_{1}q_{0}$ & e_{0}	Case 8: $k \& _{45}q_{15}$
Case 3: ${}_{5}q_{0}$ & ${}_{45}q_{15}$	Case 6: $_{1}q_{0}$ & $_{45}q_{15}$	Case 9: $e_0 \& {}_{45}q_{15}$

We have written a function in R that fits the log-linear or log-quadratic models for all nine cases (available from the authors upon request). The function works well except in extreme cases (some pairings of values for these 5 indicators may be impossible). In general, we have tried to choose input values that lie within the range of documented historical experience, or not too far outside that range.

Figures S-2 and S-3 include graphs resulting from calculations for six cases only: 1, 2, 3, 7, 8, and 9 (cases 4, 5, and 6 are conceptually identical to 1, 2, and 3). For each case, there are (a) and

(b) versions of these graphs. In the (a) version, the first value of the pair (as listed above) is held constant while the second value is varied; in the (b) version, these roles are reversed.

Determining an appropriate range of values for the variable parameter, which sometimes depends also on the value of the constant parameter, was somewhat challenging. The final results, as presented here, were achieved partly by trial and error.

When k is the variable parameter in the given pair, we have tried to use values from -4 to +4. In other cases, we tried to confine the range of values for this parameter within +/-4 approximately. The shape of the mortality curve often becomes unrealistic when k lies outside this range, as can be seen in Figure S-4.

Results were derived first for 5-year age groups. Death rates for 1-year age groups were found by means of spline interpolation of the 5-year data. Figure S-2 shows results for 1-year age groups alone while Figure S-3 shows the same curves overlying the values for 5-year age groups.

There appear to be 3 basic patterns:

Pattern I: Cases 1b, 7a, 8a (*k* is held constant) Mortality goes up and down with no major change of shape, except a gradual tilt in the curve (because the change is greater at younger ages). Note also the increased prominence of the

accident hump at lower mortality levels (for both males and females). No crossovers.

Pattern II: Cases 1a, 2a, $3a({}_{5}q_{0} \text{ is held constant})$

There is no variation in child mortality and only slight variation on old-age mortality. The age curve changes shape in the middle age range as adult mortality moves higher or lower. No crossovers.

Pattern III: All other (e_0 or ${}_{45}q_{15}$ is held constant)

Unlike the previous two patterns, in this one there are lots of crossovers in each set of mortality curves. The crossovers reflect the fact that ${}_5q_0$ and k are changing in opposite directions: in order to maintain a constant e_0 or ${}_{45}q_{15}$, one of them (${}_5q_0$ or k) has to move up as the other moves down.

Additional commentary on the results of this analysis are included in the subsection of the main paper entitled "Age patterns of mortality implied by the model".

Fitting algorithm for modified logit model

In this section, we describe the methods utilized for fitting the modified logit model to the HMD dataset and the methods used to model the relationship between survivorship to age 5, l(5), and survivorship to age 60, l(60). We re-estimated the modified logit model using HMD data in order to compare the log-quadratic and modified logit models on an equal basis. The estimated coefficients for the modified logit model fitted to the HMD data are presented in Table S-2.

In its original form, the modified logit model was fitted to a large collection of empirical life tables by Murray *et al.* (2003). The details of their fitting method are not entirely clear from the published paper, however, and may have been unnecessarily complicated (it is reported that the method involved "repeated sampling of a randomly selected subset" from their collection of life tables). We devised the following simple method for fitting this model. When applied to the same set of life tables used by Murray *et al.*, this method produces nearly identical parameter values for the fitted model.

We start with a set of life tables characterized by survival probabilities, $l_i(x)$, for ages x = 0, 1, 5, 10, ..., and for populations i = 1, 2, ..., I, where $l_i(0) = 1$ for all *i*. The model will be fitted to this collection of life tables.

The modified logit model has the following general form:

$$\operatorname{logit}(l_i(x)) = \alpha_i + \beta_i \operatorname{logit}(l_s(x)) + \left(1 - \frac{\operatorname{logit}(l_i(5))}{\operatorname{logit}(l_s(5))}\right) \gamma(x) + \left(1 - \frac{\operatorname{logit}(l_i(60))}{\operatorname{logit}(l_s(60))}\right) \theta(x)$$

for ages x = 1, 5, 10, ..., where the logit function is defined as follows:

$$\operatorname{logit}(y) = \frac{1}{2} \ln \left(\frac{y}{1 - y} \right) \quad \text{for } 0 < y < 1.$$

In this equation, the parameters α_i and β_i vary across populations or life tables, whereas $l_s(x)$, $\gamma(x)$, and $\theta(x)$, are constant across all populations. Thus, fitting the model consists of determining appropriate values for these three sets of age-specific parameters based on a given collection of data. The first of these three, $l_s(x)$, describes the life table for a *standard* (i.e., typical or average) population. The other two, $\gamma(x)$ and $\theta(x)$, are adjustment factors used (in conjunction with α_i and β_i) to transform the standard life table so that it resembles a wide variety of observed life tables. Following Brass (1971), Murray et al. (2003) defined their model in terms of logit $(1 - \ell(x))$. We prefer the formulation presented here, $logit(\ell(x))$, for its simplicity. However, as noted also by Brass, it makes no difference for outcomes of interest whether the model is based on the logit of l(x) or 1 - l(x).

We derived the standard life table by computing the average value of all survival functions in the dataset after applying the logit transformation. Thus:

$$\operatorname{logit}(l_{S}(x)) = \frac{1}{I} \sum_{i=1}^{I} \operatorname{logit}(l_{i}(x)).$$

Although it would also be possible to use some pre-determined standard life table, the strategy proposed here is likely to produce a closer fit for the given collection of data.

For convenience of notation, also define the following special functions:

$$Y_i(x) = \text{logit}(l_i(x))$$
 and $Y_s(x) = \text{logit}(l_s(x))$.

Using this notation, the modified logit model can also be written as follows:

$$Y_i(x) = \alpha_i + \beta_i Y_S(x) + \left(1 - \frac{Y_i(5)}{Y_S(5)}\right) \gamma(x) + \left(1 - \frac{Y_i(60)}{Y_S(60)}\right) \theta(x) .$$

Following Murray et al. (2003), we constrain four of the model parameters as follows:

$$\gamma(5) = \gamma(60) = \theta(5) = \theta(60) = 0.$$

This constraint assures that the collection of fitted parameter estimates will be unique. Given these constraints the fitted values, $\hat{\alpha}_i$ and $\hat{\beta}_i$ can be computed directly from the original and standard life tables as follows:

$$\hat{\alpha}_i = \frac{Y_i(5)Y_s(60) - Y_i(60)Y_s(5)}{Y_s(60) - Y_s(5)} \text{ and } \hat{\beta}_i = \frac{Y_i(60) - Y_i(5)}{Y_s(60) - Y_s(5)}.$$

This result is obtained by setting x equal to 5 and 60 in the original model and solving those two equations for α_i and β_i .

The remaining two sets of parameters, $\gamma(x)$ and $\theta(x)$, can be found by means of linear regression. Define the dependent variable of this regression as follows:

$$W_i(x) = Y_i(x) - \hat{\alpha}_i - \hat{\beta}_i Y_S(x) ,$$

for ages x = 1, 5, 10, ... Define two independent variables as follows:

$$Z_{i1} = 1 - \frac{Y_i(5)}{Y_s(5)}$$
 and $Z_{i2} = 1 - \frac{Y_i(60)}{Y_s(60)}$

Then fit the linear regression model,

$$W_i(x) = \gamma(x)Z_{i1} + \theta(x)Z_{i2} + \varepsilon_i ,$$

separately for each age x, in order to obtain parameter estimates, $\hat{\gamma}(x)$ and $\hat{\theta}(x)$, for $x = 1, 5, 10, \dots$ (note that this model has no intercept term). In fact, it is not necessary to fit this regression model for ages 5 and 60, since the parameter values for those ages are constrained to equal 0. However, making these calculations can also serve as a confirmation of the internal consistency of the methods, since the regression procedure should return estimates of $\gamma(x)$ and $\theta(x)$ for these two ages that are numerically indistinguishable from 0. This outcome is inevitable, if the calculations are done correctly, since the equations for $\hat{\alpha}_i$ and $\hat{\beta}_i$ given above were derived using the assumption that $\gamma(5) = \gamma(60) = \theta(5) = \theta(60) = 0$.

The fitting method described here can be applied separately by sex (male, female) or for both sexes combined (total). Given estimates for the three sets of fixed parameters, $l_s(x)$, $\gamma(x)$, and $\theta(x)$, the model can be fitted to life tables for populations j = 1, ..., J from outside the original sample simply by computing $\hat{\alpha}_j$ and $\hat{\beta}_j$ according the equations given above. Thus, a full life table for population *j* can be derived using only two input values, $l_i(5)$ and $l_i(60)$.

In some of the tests used to compare the performance of the log-quadratic model with that of the modified logit model, the only input parameter used is the probability of dying below age 5, ${}_5q_0$. Whereas the log-quadratic model can be used directly to estimate a life table given this information, a separate (or side) model is needed in order to derive an estimate of $l_j(60)$ from $l_i(5)$ for use in the modified logit estimation procedure.

The MODMATCH program, written in STATA and available for download on the WHO website (<u>http://www.who.int/healthinfo/global_burden_disease/tools_software/en/</u>), is used by the WHO to estimate the modified logit model given various input parameters such as ${}_5q_0$ alone or in combination with another parameter. Using a similar approach, we propose the following model to describe the relationship between $l_i(5)$ and $l_i(60)$:

For
$$l_j(5) < c$$
, $l_j(60) = \alpha_1 + \beta_1(l_j(5))$.
For $l_j(5) \ge c$, $\operatorname{logit}(l_j(60)) = \alpha_2 + \beta_2 \log(\operatorname{logit}(l_j(5)))$

This model differs only slightly from original methods used by the developers of the modified logit procedure to model the relationship between $l_i(5)$ and $l_i(60)$ in two respects: (1) it does

not include an indicator variable to describe whether a country is a former state of the Soviet Union, and (2) the cutoff point, c, is not fixed at 0.95.

We estimated this new model using both the HMD and WHO collections of life tables for use in testing the re-estimated modified logit model and the original modified logit model, respectively. The model was estimated separately by sex using a constrained linear regression algorithm in STATA so that the two parts of the model produce the same value of $l_j(60)$ at $l_j(5) = c$. The constraint was chosen based on predicted values of $l_j(60)$ at $l_j(5) = c$ using the model $l_j(60) = \alpha_1 + \beta_1(l_j(5))$ fitted to observations where $l_j(5) < c$. The cutoff point, c, was chosen to minimize the sum of squared errors and varies by sex and data set. Our two sets of parameter estimates for the modified logit side model are presented in Table S-3.

Other supplemental figures

The following figures provide additional detail beyond what is presented in the main paper:

- Figure S-5 shows the relationship between child and adult mortality implied by the five families of the UN model life tables for less developed countries (compare to Figure 1 of the main article, which presents similar information for the Coale-Demeny tables).
- Figures S-6, S-7, and S-8 compare the predictions of the log-linear and log-quadratic models. Figure S-6 makes the comparison in terms of age-specific probabilities of dying within six broad age groups. Figure S-7 presents a similar comparison in terms of age-specific death rates (compare to Figure 2 of the main article, which presents such information for the two sexes combined but not separately by sex as shown here). Figure S-8 compares predicted death rates of the log-linear and log-quadratic models within 5-year age groups for females and males separately.
- Figures S-9, S-10, and S-11 illustrate the range of predictions associated with values of the *k* parameter, for k = -2, -1, 0, 1, and 2. Figure S-9 shows the effect of varying *k* on predicted age-specific probabilities of dying for six broad age groups. Figure S-10 presents a similar set of results in terms of age-specific death rates (compare to Figure 6 of the main paper, which presents such information separately by sex but not for sexes combined as shown here). Figure S-11 illustrates the effect of varying *k* on predicted death rates within 5-year age groups for females and males separately.
- Figure S-12 depicts the historical trajectories of child $({}_5q_0)$ versus adult mortality $({}_{45}q_{15})$ for a variety of countries grouped by region. This figure offers more detail on country-specific trends within regions in comparison to Figure 10 in the main paper, which documents these trajectories at the regional level.

Table S-1

Coefficients for log-linear model, estimated using HMD life tables (n = 719)

		Female			Male	
Age	a_x	b_x	v_x	a_x	b_x	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

Notes:

- (1) Estimated coefficients shown here were derived using the bi-weight method (see Appendix of the main paper).
- (2) There are no estimated coefficients for ages 1-4 by design. Since ${}_{5}q_{0}$ is an input to the model, the age group 1-4 is excluded when fitting the model. After using the model to estimate mortality for age 0, we derive the mortality level for ages 1-4 as a residual component of ${}_{5}q_{0}$. This procedure assures that the input and output values of ${}_{5}q_{0}$ are identical.

Table S-2

Fitted coefficients for WHO relational mortality model fitted to HMD

		Female			Male	
Age	γ_x	θ_{x}	ℓ_x^s	γ_x	θ_{x}	ℓ_x^S
0	0.0000	0.0000	100000	0.0000	0.0000	100000
1-4	0.0984	0.0844	97119	0.2317	-0.0029	96401
5-9	0.0000	0.0000	96025	0.0000	0.0000	95153
10-14	0.0142	-0.0337	95577	-0.0350	-0.0019	94592
15-19	0.0357	-0.0555	95224	-0.0445	-0.0012	94139
20-24	0.0995	-0.0936	94637	-0.0009	-0.0062	93076
25-29	0.1373	-0.1222	93923	0.0675	-0.0286	91574
30-34	0.1568	-0.1420	93112	0.1230	-0.0513	90090
35-39	0.1783	-0.1588	92107	0.1698	-0.0717	88460
40-44	0.2024	-0.1700	90771	0.2067	-0.0877	86444
45-49	0.2203	-0.1688	88945	0.2276	-0.0955	83743
50-54	0.2050	-0.1407	86423	0.2103	-0.0857	80019
55-59	0.1372	-0.0860	82944	0.1385	-0.0550	74871
60-64	0.0000	0.0000	78212	0.0000	0.0000	67966
65-69	-0.2523	0.1318	71495	-0.2064	0.0718	58820
70-74	-0.6273	0.3119	62026	-0.4893	0.1607	47434
75-79	-1.1467	0.5403	48875	-0.8687	0.2643	34075
80-84	-1.8189	0.8158	32790	-1.3830	0.3913	20443
85-89	-2.6447	1.1300	17130	-2.0759	0.5476	9342
90-94	-3.7500	1.5356	6227	-3.0637	0.7697	2884
95-99	-5.1937	2.0530	1408	-4.3913	1.0735	536
100-104	-7.2044	2.8091	170	-6.2513	1.5277	54
105-109	-9.7272	3.8002	10	-8.6069	2.1335	3
110+	-12.6981	5.0068	0	-11.3918	2.8748	0

Note: Estimated coefficients shown here were derived using an OLS fitting procedure (see Appendix of the main paper).

Table S-3	
Fitted coefficients for model of the relationship between $l(5)$ and $l(60)$	

		С	$lpha_{_1}$	$eta_{_1}$	$lpha_2$	eta_2
WHO (<i>n</i> = 1802)	Male	0.98	-0.870	1.682	-0.185	1.222
	Female	0.85	-0.402	1.130	0.266	1.051
HMD (<i>n</i> = 719)	Male	0.98	-0.735	1.527	-0.317	1.345
	Female	0.88	-0.600	1.318	0.208	1.107

Figure S-1

Age-specific death rates $\binom{n}{k}$ vs. child mortality $\binom{5}{5}q_0$, log scale, six age groups, observed data from HMD-719 and WHO-1802 (non-overlap only), with predicted levels (k = 0) according to four methods of fitting the log-quadratic model



Figure S-1 (cont.)

Age-specific death rates $\binom{n}{k}$ vs. child mortality $\binom{5}{5}q_0$, log scale, six age groups, observed data from HMD-719 and WHO-1802 (non-overlap only), with predicted levels (k = 0) according to four methods of fitting the log-quadratic model



Figure S-1 (cont.)

Age-specific death rates $\binom{n}{k}$ vs. child mortality $\binom{5}{5}q_0$, log scale, six age groups, observed data from HMD-719 and WHO-1802 (non-overlap only), with predicted levels (k = 0) according to four methods of fitting the log-quadratic model





Age patterns of mortality implied by various selections of two input parameters (1-year age groups, $Q5=_5q_0$, $QQ=_{45}q_{15}$)























Figure S-3









Figure S-3 (cont.)





















Figure S-5

Relationship between child and adult mortality levels, ${}_{5}q_{0}$ and ${}_{45}q_{15}$ (in logarithmic scale), observed data (n = 719) and UN model life tables for less developed countries (5 regional families)









Figure S-6 (cont.) Age-specific probability of dying $(_nq_x)$ vs. child mortality $(_5q_0)$ log-linear vs. log-quadratic models (logarithmic scales)



Figure S-6 (cont.) Age-specific probability of dying $(_nq_x)$ vs. child mortality $(_5q_0)$ log-linear vs. log-quadratic models (logarithmic scales)

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Figure S-11 (cont.) Log-quadratic model (k = -2, -1, 0, 1, and 2) for detailed age groups, with observed values (n = 719) of $_n M_x$ vs. $_5q_0$ (logarithmic scales)













Figure S-12Adult mortality ($_{45}q_{15}$) vs. child mortality ($_{5}q_{0}$),country patterns plus log-quadratic model (for 5 values of k)



Figure S-12 (cont.) Adult mortality $({}_{45}q_{15})$ vs. child mortality $({}_{5}q_{0})$, ntry patterns plus log-quadratic model (for 5 values c