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# Expectation of life at old age predicted from a single death rate: Models and applications

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**Approved by**

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## Contents

## Abstract

This paper introduces empirical relations between the death rate at a given age and the remaining life expectancy at that same age. The relations prove to be of prediction accuracy exceeding that of the common alternative, extrapolation of the death rates into older ages based on data at younger ages. Being close in accuracy to models by Horiuchi, Coale and Mitra, the proposed models may be of use in cases when the latter models may not be applied because of either lack of data on old-age mortality or violation of the underlying assumptions, such as population stability. Combining the proposed models with constrained extrapolations of old-age mortality will be a useful tool in estimating and projecting old-age mortality, completing life tables for young cohorts and extending model and empirical life tables to old age.

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## About the Authors

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# Expectation of life at old age predicted from a single death rate: Models and applications

Dalkhat M. Ediev

## 1. Introduction

Estimating the length of life at old age is a particularly complicated issue for populations with limited and deficient data which include even some developed nations (Duthé et al. 2010; Khlat & Courbage 1996; Kibele et al. 2008; Preston et al. 1996). Some of the problems with data quality at old age may be successfully addressed by pooling the problematic age groups into an extended open age interval and applying indirect methods to estimate the respective remaining life expectancy (Horiuchi & Coale 1982; Mitra 1985; Coale 1985). In many cases, however, the indirect methods are not efficient because of either violations of the underlying assumptions, such as stability of population age composition, or the lack of necessary data. They cannot be applied, for example, to construct life tables for birth cohorts with incomplete life histories. The only conventional method usable in such cases is extrapolation of the death rates from younger to elder ages using a mortality model. Extrapolation is a usual practice in extending empirical data to old age (Mathers & Ho 2014), building model life tables (UN DESA/Population Division 2017) and correcting original data at old age (Wilmoth et al. 2007; Kontis et al. 2017). Accuracy of the extrapolation method, however, appears to be poorer than usually presumed (Ediev 2017).

Here, we consider another method that surpasses in accuracy the current workhorse, the extrapolation of the death rates from younger ages, and is comparable in its accuracy to the indirect methods of Horiuchi-Coale and Mitra. The idea of the method is to make use of the tight empirical association between the death rate at given old age $a$, $M_a$, and the remaining life expectancy at that same age, $e_a$. Figure 1 shows association patterns of cohort remaining life expectancy at various old ages $a$ between ages 55 and 95 years and three life table functions at the same age: The death rate $M_a$ (logarithmic scale), the age $a$ itself, and the surviving probability from the cohort radix to age $a$, $l_a$, for Swedish men and women using the entire data set contained in the Human Mortality Database (HMD 2017) and covering birth cohorts 1751 to 1923 (173 cohort life tables). Associations of the remaining life expectancy with the age or the survival proportion are of weak explanatory power, as expected for such a wide range of mortality profiles. Yet, the pair $(e_a, M_a)$ is tightly correlated, even if with a small drift over time (calendar years are marked by shades in the figure). Our idea is to make practical use of the latter association. The work is organized as follows. In the next section, the data sources and methods are briefly characterized. In Section 3, we discuss model parameterizations and prediction accuracy on HMD data. Examples of the models' applications are presented in Section 4 that is followed by a concluding discussion.

## 2. Data and methods

This research relies on cohort and period data from the Human Mortality Database (HMD 2017). We use the life tables from the HMD that are partly based on smoothing and extrapolating the raw death rates at ages above 80 years. The HMD data are used in fitting the regression models presented in the Section 3 and in some of the discussed applications. To eliminate less reliable historical entries and for a better comparability of period and cohort models, we restrict data to ages a=55 to 85 years and to calendar years 1800 and later (years 1806 and later for birth cohorts). We have also excluded data for Iceland, Luxemburg, New Zealand-Maori, and Northern Ireland for their small population size. Estimating model parameters, we use the standard function *lm*() for linear regression analysis from R package (R Core Team 2016).

## 3. Model specifications and fit

Given the curvilinearity of the association between the death rates and the remaining life expectancy (Figure 1), we use the log-log regression model with additional terms accommodating for finer effects of the death rate, the age-sex effects and (optionally) the period effect[1]. Separately for cohort and period data, we consider two regression models explaining variations in remaining life expectancy at ages $a$=55 to 85 years, data pertaining to years 1800+ for period life tables and 1806+ for birth cohorts (1806 is the first year when an HMD cohort enters age 55 years). In the first, less detailed, model we drop the period effect and only examine effects of the death rate, age and sex:

$$ln(e_a) = C + k_1 ln(M_a) + k_2 M_a + k_3 {M_a}^2 + k_4 a + k_5 a^2 + k_6 Sex + \varepsilon, \quad (1)$$

here, $C, k_1, k_2, \dots, k_6$ are the model parameters (see Table 1 for estimates), 'Sex' is the categorical variable with the reference value 'Total', $\varepsilon$ is the error term. In more detailed models, we also include the period effect:

$$ln(e_a) = C + k_1 ln(M_a) + k_2 M_a + k_3 {M_a}^2 + k_4 a + k_5 a^2 + k_6 Sex + k_7 Period + \varepsilon, \quad (2)$$

here, $C, k_1, k_2, \dots, k_7$ are the model parameters (see Table 2 and Figure 2), 'Sex' and 'Period' are the categorical variables with the reference values 'Total' and the first observation year (1806 for cohorts, 1800 for periods), $\varepsilon$ is the error term. Altogether that makes four models: two cohort models and two period models.

The non-linear terms, except for the log-death rate, are of less importance in all models and are dominated by the corresponding linear terms.

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[1] We have also examined alternative specifications including cohort, survival, country and interaction effects. Those alternatives did not yield substantially lower residual standard errors as compared to the models presented here. It is worthwhile noting that the remaining life expectancy is positively influenced by the survival proportion $l_a$ that may be related to a selection effect. A weaker association of the survival, as compared to the period effect, with the life expectancy and its correlation with the period suggest that the survival effect may channel the period effect when the latter is dropped from the model. This may also suggest that the death rate at single age, our main explanatory variable, may be less strongly associated with the current mortality conditions than when it is supplemented by the survival function. In any case, addition of the survival function only marginally improves the model fit (in the fourth digit of the residual standard error) and we exclude it from analysis, although further studies may reveal interesting selection effects.

Figure 1. Cohort remaining life expectancy $e_a$, vertical scale, years, at various ages $a$ between 55 and 95 years as function of the death rates $M_a$ at age $a$ (upper panels, death rate in the log scale), age $a$ (middle panels) and cohort proportion $l_a$ survived to age $a$ (lower panels). Sweden, men and women, shades mark calendar years to which the data pertain.

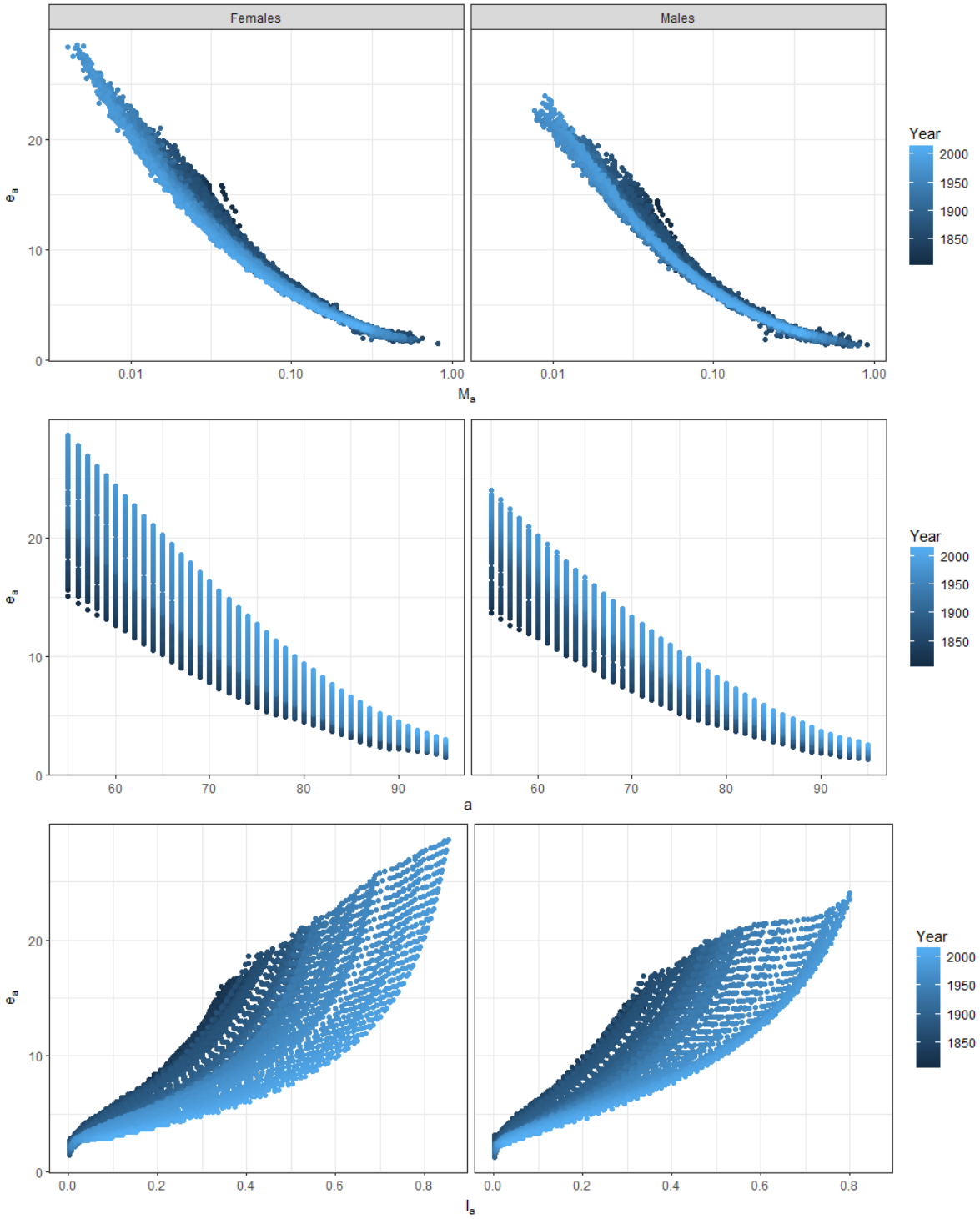


Table 1. Estimates of regression model with no period effect. Reference category for the variable 'Sex': Total.

| Explanatory variable | Coefficient | Std.Error |
|---|---|---|
| **Cohort model** | | |
| Intercept | 2.79E+00 | 1.50E-02 |
| $ln(M_a)$ | -3.07E-01 | 8.96E-04 |
| $M_a$ | -4.56E+00 | 2.95E-02 |
| ${M_a}^2$ | 7.12E+00 | 8.54E-02 |
| $a$ | -2.56E-02 | 3.60E-04 |
| $a^2$ | 1.24E-04 | 2.61E-06 |
| Sex: Females | -1.52E-02 | 3.30E-04 |
| Sex: Males | -6.80E-03 | 3.30E-04 |
| **Period model** | | |
| Intercept | 2.88e+00 | 6.86e-03 |
| $ln(M_a)$ | -2.77e-01 | 3.29e-04 |
| $M_a$ | -4.32e+00 | 1.21e-02 |
| ${M_a}^2$ | 6.65e+00 | 3.59e-02 |
| $a$ | -2.39e-02 | 1.76e-04 |
| $a^2$ | 9.47e-05 | 1.28e-06 |
| Sex: Females | -1.79e-02 | 1.70e-04 |
| Sex: Males | -4.19e-03 | 1.70e-04 |

Note: All coefficients are significant at p-value <2e-16. *Cohort model summary*: Residual standard error: 0.03782 on 83684 degrees of freedom. Multiple R-squared: 0.9939, Adjusted R-squared: 0.9939. F-statistic: 1.954e+06 on 7 and 83684 DF, p-value: < 2.2e-16. *Period model summary:* Residual standard error: 0.04002 on 358528 degrees of freedom. Multiple R-squared: 0.9938, Adjusted R-squared: 0.9938. F-statistic: 8.176e+06 on 7 and 358528 DF, p-value: < 2.2e-16.

The age effect is negative and may be related to the mortality compression (Kannisto 2000; Wilmoth and Horiuchi 1999). When examining the effect of age as a categorical variable (Figure 3), it largely remains linear in terms of age supporting the parametric form of the effect used in our models. One may also note in Figure 3 small regularities around ages 60, 70 and 80 that seem to be pointing to some age heaping problems in the HMD.

The period effect does not add much to the model fit, especially in the period data. Yet, its evolution over time is an interesting reflection of mortality changes. The period effect has increased in the second half of the 20$^{th}$ century when adult and old-age mortality were markedly decreasing (hence, life expectancies were increasing). The stronger increase of the effect in cohort data is a clear reflection of the tempo effect: when mortality declines, period exposures to any given range of the death rate are compressed as compared to the cohort exposures (Ediev 2008b, 2013b). It may also be interpreted as a lag effect, because cohorts remaining lifespans, at any given point in time, cover some future calendar periods. The tempo effect seems to be the major driver here, however, because the period effect of the cohort model has substantially exceeded the maximum values of the period effect of the period model, although the two models started with similar levels of the effect.

Table 2. Estimates of regression model with period effect included (see Figure 2 for the period effect). Reference category for the variable 'Sex': Total.

| Explanatory variable | Coefficient | Std.Error |
|---|---|---|
| **Cohort model** | | |
| Intercept | 2.90E+00 | 1.80E-02 |
| $ln(M_a)$ | -2.37E-01 | 6.87E-04 |
| $M_a$ | -3.66E+00 | 2.12E-02 |
| ${M_a}^2$ | 5.98E+00 | 5.88E-02 |
| $a$ | -1.63E-02 | 2.67E-04 |
| $a^2$ | -1.94E-05 | 2.05E-06 |
| Sex: Females | 2.88E-03 | 2.34E-04 |
| Sex: Males | -2.76E-02 | 2.39E-04 |
| **Period model** | | |
| Intercept | 2.94E+00 | 7.32E-03 |
| $ln(M_a)$ | -2.39E-01 | 3.45E-04 |
| $M_a$ | -3.96E+00 | 1.11E-02 |
| ${M_a}^2$ | 6.13E+00 | 3.27E-02 |
| $a$ | -2.07E-02 | 1.61E-04 |
| $a^2$ | 3.72E-05 | 1.20E-06 |
| Sex: Females | -8.27E-03 | 1.60E-04 |
| Sex: Males | -1.46E-02 | 1.62E-04 |

Note: All coefficients are significant at p-value <2e-16. *Cohort model summary*: Residual standard error: 0.02526 on 83481 degrees of freedom. Multiple R-squared: 0.9973, Adjusted R-squared: 0.9973. F-statistic: 1.466e+05 on 210 and 83481 DF, p-value: < 2.2e-16. *Period model summary:* Residual standard error: 0.03681 on 358313 degrees of freedom. Multiple R-squared: 0.9947, Adjusted R-squared: 0.9947. F-statistic: 3.049e+05 on 222 and 358313 DF, p-value: < 2.2e-16.

The gap between the period effects in cohort and period models is also indicative of the mortality inertia – a prospect of further mortality decline in a process when young cohorts with lower initial death rates replace the older cohorts of higher mortality and contribute to future mortality declines at older ages (Ediev 2011). These compositional dynamics – of younger cohorts of lower mortality replacing older cohorts with higher mortality – will only stop when the gap between the cohort and period remaining life expectancies diminish.

We examine estimation errors of the regression models by comparing the estimated remaining life expectancies $e_a$ to the original HMD estimates. We also assess the estimation errors for the life expectancy at birth as error in the remaining life expectancy at age $a$ multiplied by the survival probability:

$$err(e_0) = ({e_a}^{est} - e_a)l_a, \quad (3)$$

here, ${e_a}^{est}$ and $e_a$ are the model-based and original HMD estimates of the remaining life expectancy, $l_a$ is the survival function of the original HMD life table.

Figure 2. Period effects in the cohort and period models of the remaining life expectancy.

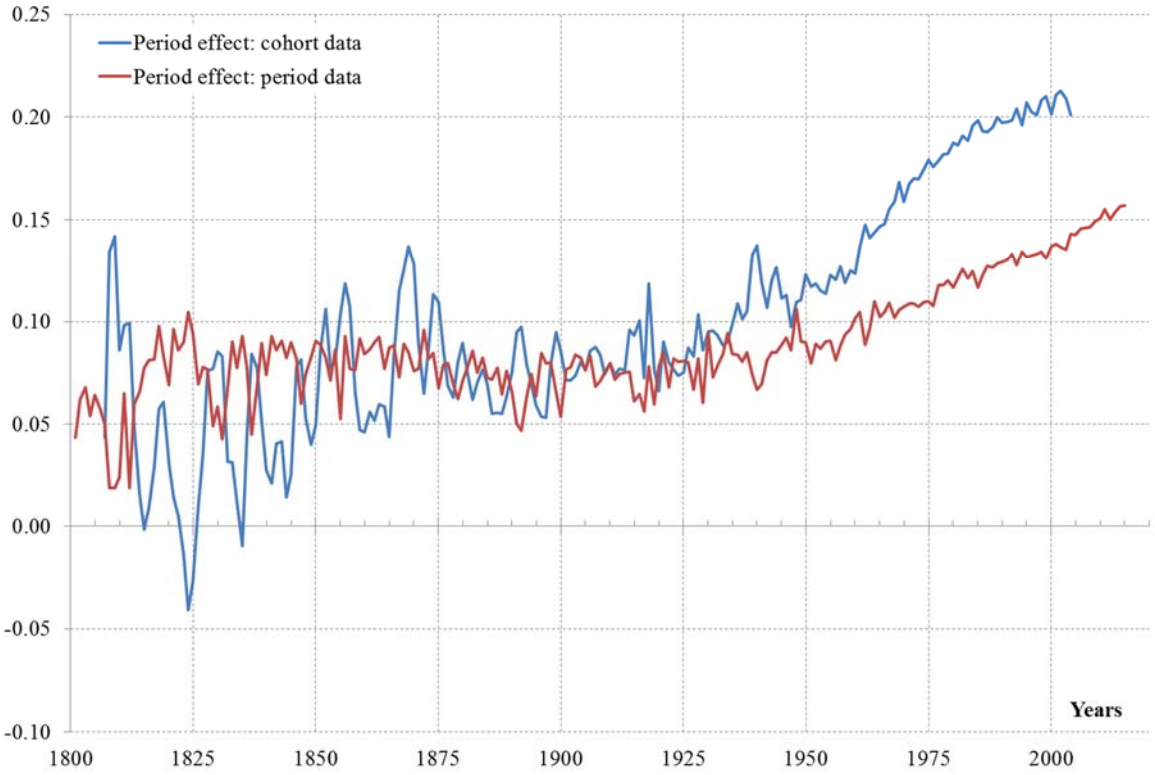
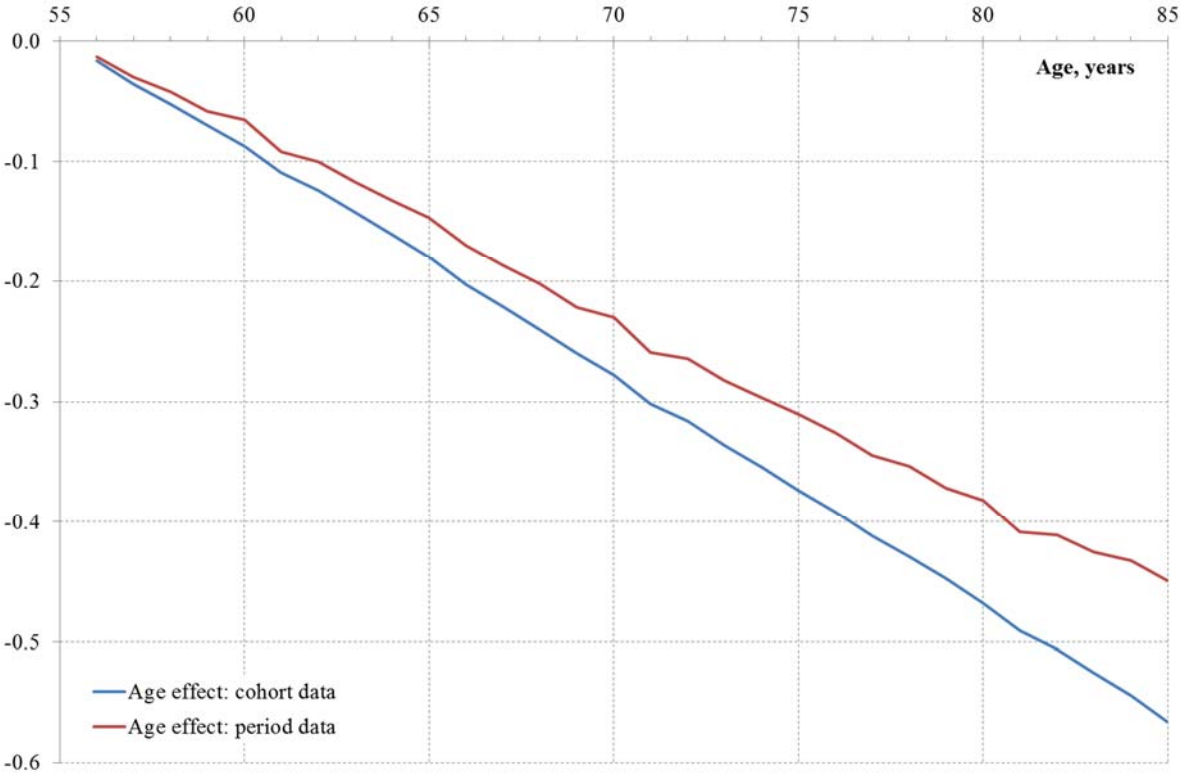



Figure 3. Age effects in the cohort and period models of the remaining life expectancy (age 55 is the reference category).



For the cohort data, we also compare errors of the regression models to those of the common extrapolation method (errors of the latter method on period data are available elsewhere (Ediev 2016)). To this end, for any given age $a$, we fit the Kannisto mortality model at ages $x \in [a-19, a]$ (20 years-long base) and use it to extrapolate the death rates to ages $x > a$ until age 110, with no jump at age $a$. Extrapolated rates are used to build the life table and estimate the remaining life expectancy $e_a$ in the usual way (Preston et al. 2001). For the extrapolation, we use the Kannisto model (Doray 2008; Thatcher et al. 1998) with the background mortality term:

$$M_x = m + \frac{Ce^{bx}}{1+Ce^{bx}}, \quad (4)$$

where $m$ is the background mortality, $C$ and $b$ are the model parameters.

In Figures 4 and 5, we present estimation errors of the life expectancy at birth for the cohort and period models (2) at selected ages $a$ for which the remaining life expectancy was found from the model. Estimation errors of the extrapolation method are presented in Figure 6. Root mean square errors (RMSE) are summarized in Tables 3 and 4 for selected ranges of the life expectancy at birth and modeled ages $a$.

Naturally for a log-linear model, estimation errors increased as life expectancy increased. Estimation errors of $e_0$ increase with life expectancy but decrease with model age $a$, because of the modulation by the survival function in Equation (3). For the remaining life expectancy, RMSEs are highest at lower and higher ends for the cut age $a$ and reach a minimum at around age $a = 65$.

On cohort data, model (1) without the period effect has considerably higher errors than model (2) with the period effect. The difference is especially large for female cohorts. For female cohorts with life expectancy 70-80 years, for example, at $a = 85$, RMSE of model (1) was 0.13 years against RMSE 0.07 years for model (2).

For cohort data, for males and for the total population, choosing the model age at least $a = 75$ years guarantees RMSE of life expectancy at birth about 0.1 years or less in model (1). For female cohorts with life expectancy 60 years or larger, one should increase the model age to $a = 85$ years to produce RMSE 0.1 years or less (apparently, the same may apply to male cohorts, missing in our dataset, with $e_0$ above 70 years or both sexes combined with $e_0$ above 80 years).

For the period model, inclusion of the period effect was not important, perhaps because the effect was already indirectly absorbed by grouping data into calendar years. This comes in strong support to our model showing that the effects of age and death rate on the remaining life expectancy do not change much over time. The period effect was more significant for the cohort data simply because it has captured year-to-year variations in mortality conditions along the lifespan of a birth cohort.

The patterns of the errors of our method (increasing along with increasing life expectancy) are similar and of the same order of magnitude as the errors of the Horiuchi-Coale and Mitra methods (Ediev 2016) and much lower as compared to the life table and extrapolation methods. In Table 3 we reprint selected root mean square errors from Ediev (2016) for the Mitra and extrapolation models and compare them to our results for the regression model (2) with the period effect, all applied to period female data of the HMD to obtain the remaining life expectancy at age 75. Although the Mitra (and, similarly, Horiuchi-Coale) methods produces more accurate estimates than our models, the

difference is small when compared to the extrapolation method. The extrapolation method seems to produce even larger errors on cohort data than it was reported to produce on period data. On both the cohort and period data, errors of the extrapolation method are several times larger as compared to the errors of either of the regression models proposed here.

Before proceeding to the models' applications, it is worthwhile discussing the parameter space where the models may safely be applied. As noted above, the age effect seems to be rather close to linear even when the age is treated as categorical variable (Figure 3) which suggests the regression models (1) and (2) may be extended somewhat beyond the age range 55 to 85 years that we examined. Nonetheless, it would be risky to extend the models to old ages where the terms quadratic in age start contributing substantially to the result. The models should also be used with caution at ages considerably younger than 55 years where the mortality curve may be substantially different. As a simplified rule of thumb, we would not recommend using the models beyond range 50 to 90 years. Extending the models beyond the ranges of the death rates in our data (1st and 99th percentiles of $M_x$ were about 0.007 to 0.21 for the birth cohorts and 0.005 to 0.22 for the period life tables) should also be discouraged, because the death rate is the primary predictor in our models and the mortality curves' behavior outside the observed ranges may differ from what our models predict.

Table 3. Selected RMSEs for three model for the expectation of life at ages 75+.

| | | | **RMSE in $e_0$ by model (years)** | | | |
|---|---|---|---|---|---|---|
| **Sex** | **$e_0$ range, years** | **a** | **Regr. (1)** | **Regr. (2)** | **Mitra (regr.)** | **Extrapol.** |
| **Females** | **40...50** | **75** | 0.06 | 0.05 | 0.05 | 0.16 |
| **Females** | **50...60** | **75** | 0.12 | 0.12 | 0.08 | 0.25 |
| **Females** | **60...70** | **75** | 0.14 | 0.15 | 0.09 | 0.29 |
| **Females** | **70...80** | **75** | 0.23 | 0.25 | 0.13 | 0.56 |
| **Females** | **80...90** | **75** | 0.34 | 0.30 | 0.27 | 2.11 |

Note: $e_0$= life expectancy at birth; a= age at which the remaining life expectancy is estimated from the model; "Regr. (1)/(2)"=regression model (1) or (2) without/with the period effect; "Mitra (regr.)"=Mitra model with the mean population age indirectly estimated as in (Ediev 2016); "Extrap."=extrapolation of the death rates using the Gompertz model; "RMSE" = root-mean squared estimation errors.

Source: results for the regression model (2): own calculations; results for the Mitra and extrapolation models: (Ediev 2016).

Figure 4. Estimation errors of the life expectancy at birth based on remaining life expectancy at selected ages $a$ (shown to the right-hand side from the panels) obtained from model (2) with period effect on cohort data. Horizontal axis: Original HMD estimates of the life expectancy at birth.

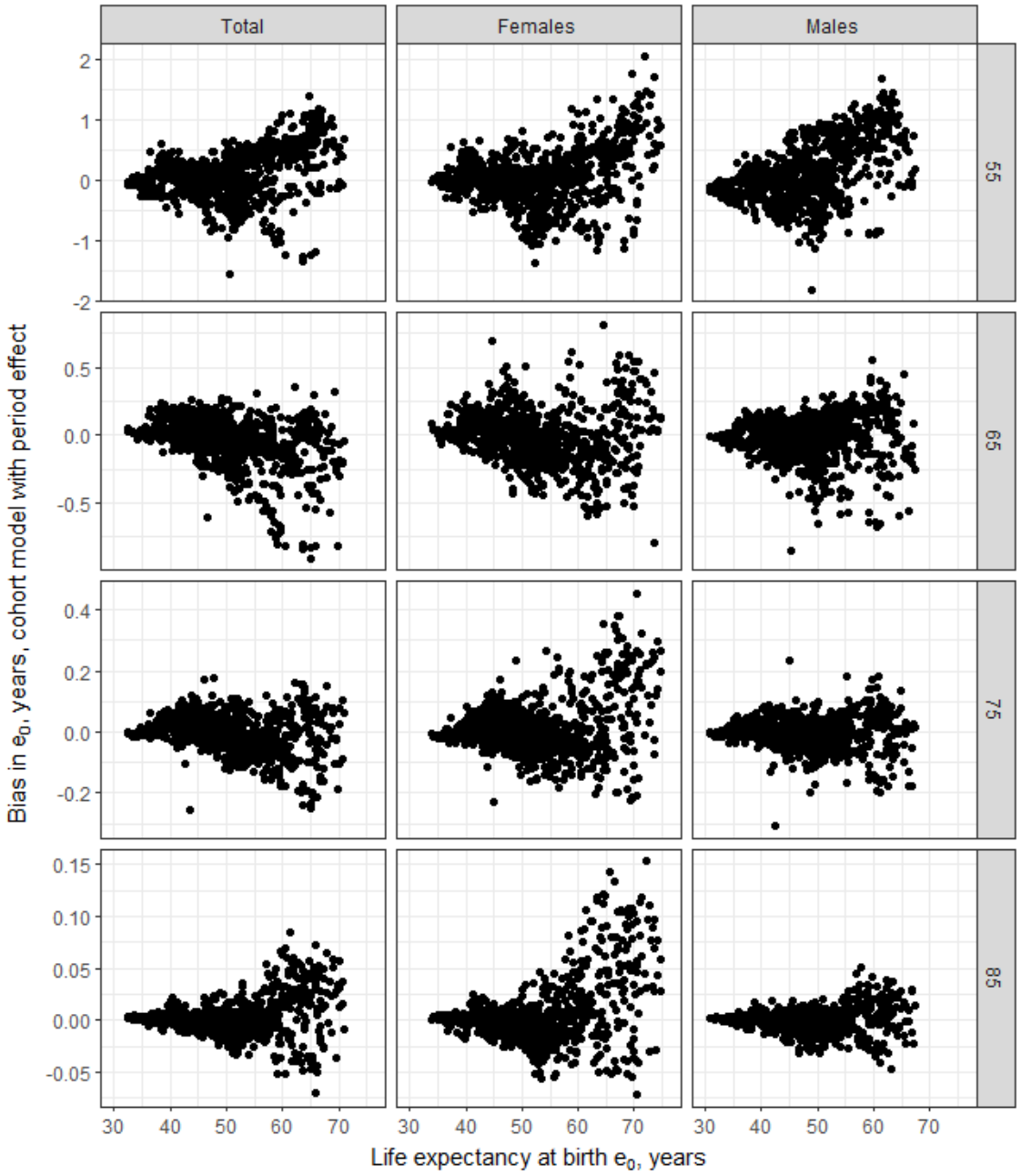


Figure 5. Estimation errors of the life expectancy at birth based on remaining life expectancy at selected ages $a$ (shown to the right-hand side from the panels) obtained from model (2) with period effect on period data. Horizontal axis: Original HMD estimates of the life expectancy at birth.

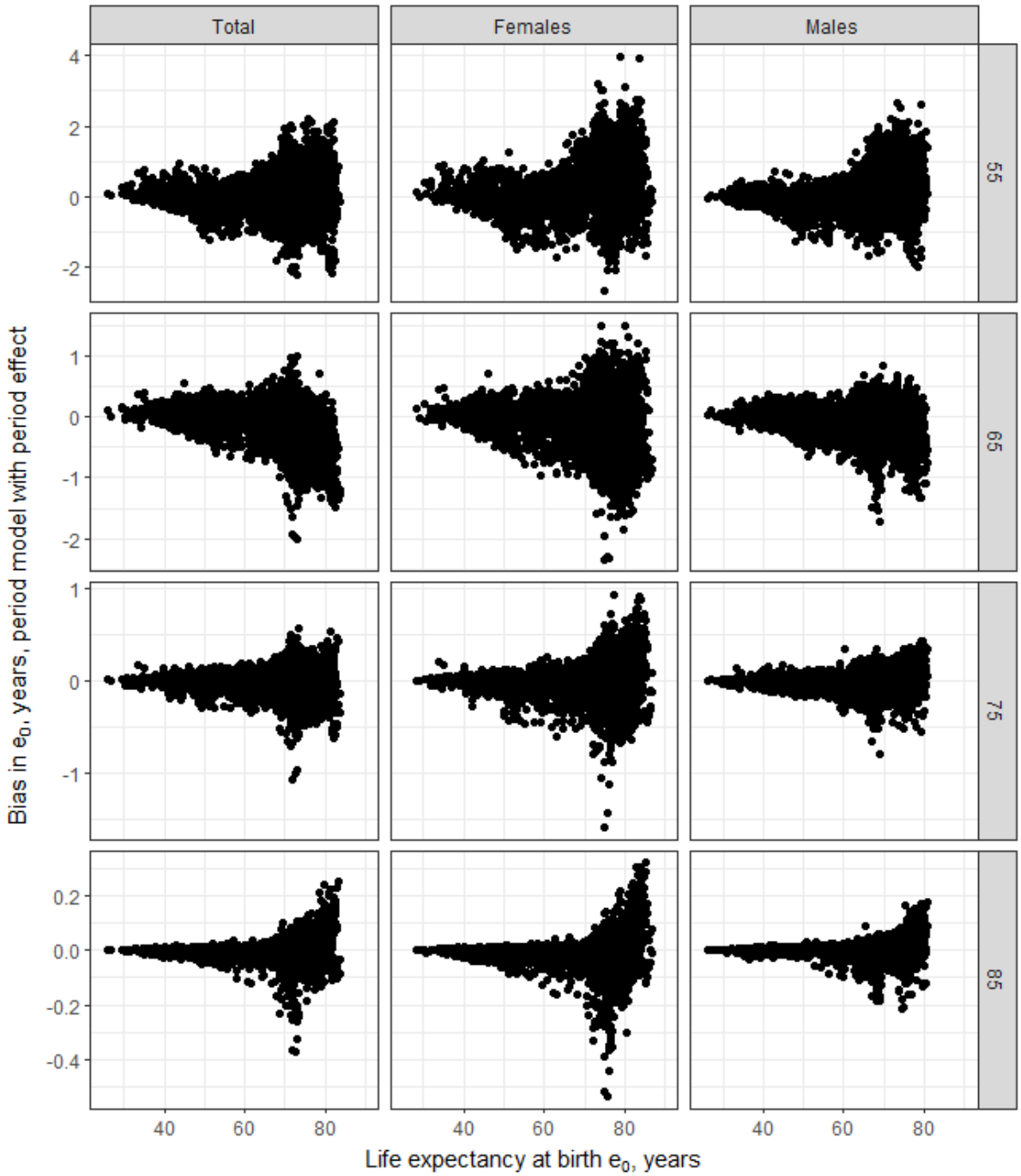


Figure 6. Estimation errors of the life expectancy at birth based on remaining life expectancy at selected ages $a$ (shown to the right-hand side from the panels) obtained from extrapolations of the age-specific death rates using the Kannisto model (4) on cohort data. Horizontal axis: Original HMD estimates of the life expectancy at birth.

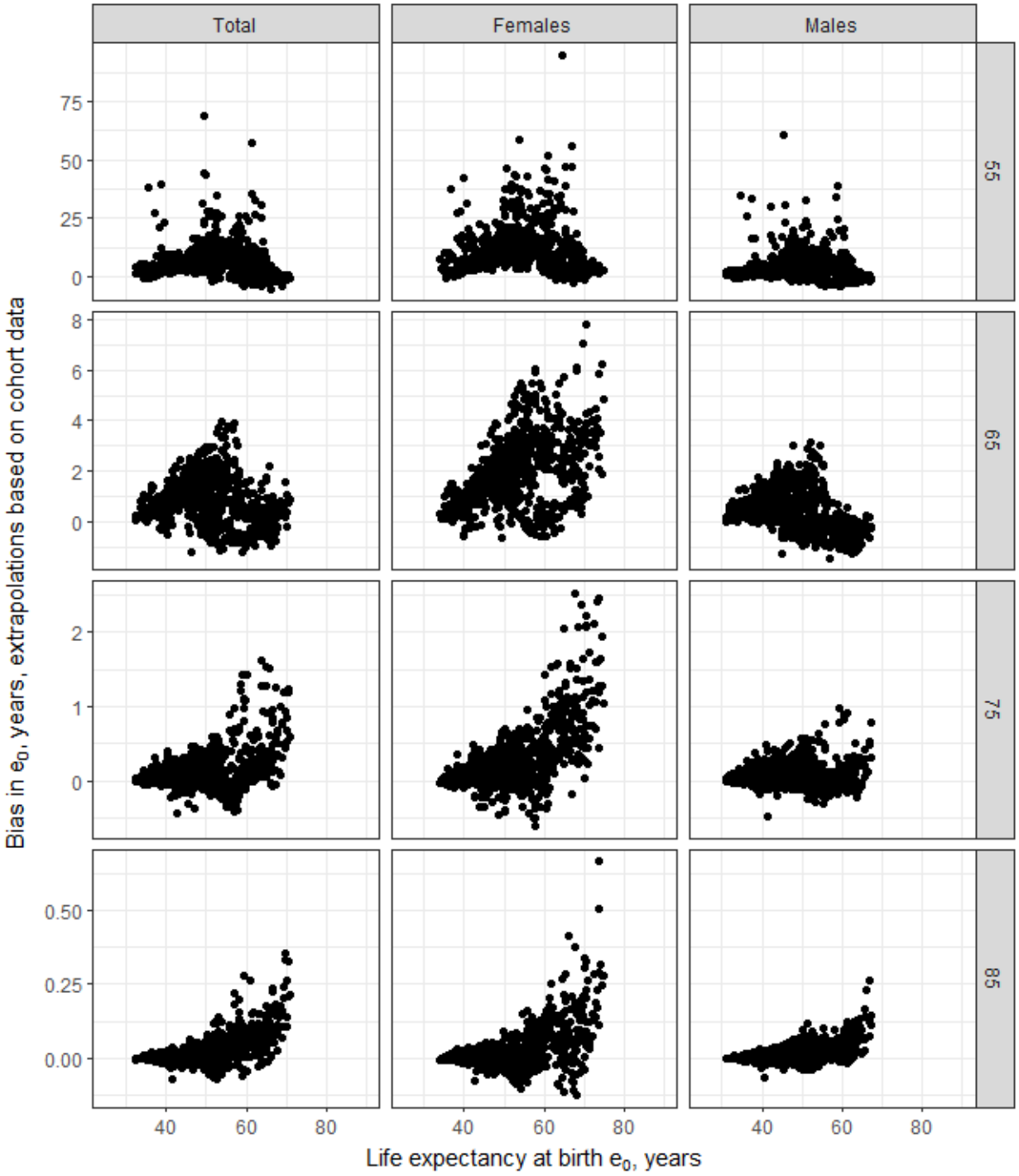


Table 3. Root-mean squared estimation errors (absolute and percentage values) of estimates of the life expectancy at birth and at given age *a*, cohort data

| Sex | $e_0$ range, years | *a* | RMSE in $e_0$ by model (years) | | | RMSE in $e_a$ by model (years) | | | Percentage RMSE in $e_a$ by model (%) | | |
|---|---|---|---|---|---|---|---|---|---|---|---|
| | | | Extrap. | Regr. (1) | Regr. (2) | Extrap. | Regr. (1) | Regr. (2) | Extrap. | Regr. (1) | Regr. (2) |
| **Females** | **40...50** | **55** | 10.62 | 0.35 | 0.25 | 29.44 | 0.69 | 0.50 | 99.75 | 3.45 | 2.50 |
| **Females** | **40...50** | **65** | 1.65 | 0.21 | 0.15 | 7.95 | 0.49 | 0.36 | 27.98 | 3.69 | 2.72 |
| **Females** | **40...50** | **75** | 0.20 | 0.08 | 0.06 | 6.70 | 0.30 | 0.20 | 9.26 | 3.81 | 2.62 |
| **Females** | **40...50** | **85** | 0.02 | 0.01 | 0.01 | 9.42 | 0.16 | 0.12 | 5.80 | 3.78 | 2.86 |
| **Females** | **50...60** | **55** | 16.94 | 0.48 | 0.42 | 38.69 | 0.78 | 0.69 | 117.59 | 3.32 | 2.96 |
| **Females** | **50...60** | **65** | 2.62 | 0.22 | 0.18 | 10.42 | 0.40 | 0.33 | 30.14 | 2.47 | 2.10 |
| **Females** | **50...60** | **75** | 0.32 | 0.10 | 0.07 | 6.04 | 0.25 | 0.18 | 8.22 | 2.60 | 1.91 |
| **Females** | **50...60** | **85** | 0.04 | 0.03 | 0.02 | 8.63 | 0.17 | 0.13 | 4.24 | 3.21 | 2.47 |
| **Females** | **60...70** | **55** | 17.53 | 0.78 | 0.61 | 35.98 | 1.05 | 0.81 | 92.18 | 3.91 | 3.03 |
| **Females** | **60...70** | **65** | 2.63 | 0.45 | 0.27 | 11.70 | 0.66 | 0.40 | 20.52 | 3.62 | 2.12 |
| **Females** | **60...70** | **75** | 0.80 | 0.20 | 0.14 | 5.90 | 0.35 | 0.25 | 11.62 | 3.08 | 2.15 |
| **Females** | **60...70** | **85** | 0.12 | 0.07 | 0.05 | 7.80 | 0.21 | 0.17 | 6.07 | 3.38 | 2.78 |
| **Females** | **70...80** | **55** | 3.40 | 0.92 | 0.99 | 21.04 | 1.11 | 1.19 | 14.48 | 3.93 | 4.22 |
| **Females** | **70...80** | **65** | 3.86 | 0.33 | 0.29 | 14.17 | 0.42 | 0.37 | 24.61 | 2.17 | 1.85 |
| **Females** | **70...80** | **75** | 1.39 | 0.31 | 0.20 | 6.35 | 0.47 | 0.31 | 16.44 | 3.77 | 2.45 |
| **Females** | **70...80** | **85** | 0.23 | 0.13 | 0.07 | 7.42 | 0.31 | 0.17 | 8.29 | 4.73 | 2.59 |
| **Males** | **40...50** | **55** | 6.63 | 0.42 | 0.39 | 19.92 | 0.82 | 0.76 | 70.15 | 4.29 | 3.93 |
| **Males** | **40...50** | **65** | 1.00 | 0.17 | 0.14 | 6.55 | 0.43 | 0.35 | 20.08 | 3.30 | 2.67 |
| **Males** | **40...50** | **75** | 0.17 | 0.07 | 0.05 | 6.97 | 0.31 | 0.19 | 9.39 | 4.15 | 2.62 |
| **Males** | **40...50** | **85** | 0.02 | 0.01 | 0.01 | 9.55 | 0.13 | 0.10 | 5.28 | 3.25 | 2.41 |
| **Males** | **50...60** | **55** | 8.21 | 0.79 | 0.63 | 21.06 | 1.22 | 0.97 | 61.95 | 5.77 | 4.73 |
| **Males** | **50...60** | **65** | 1.10 | 0.36 | 0.20 | 6.72 | 0.68 | 0.39 | 15.22 | 4.71 | 2.71 |
| **Males** | **50...60** | **75** | 0.21 | 0.11 | 0.05 | 6.55 | 0.33 | 0.15 | 6.71 | 3.89 | 1.79 |
| **Males** | **50...60** | **85** | 0.03 | 0.02 | 0.01 | 8.91 | 0.12 | 0.10 | 5.13 | 2.52 | 2.12 |
| **Males** | **60...70** | **55** | 4.25 | 0.82 | 0.85 | 14.47 | 1.11 | 1.13 | 26.92 | 4.99 | 5.15 |
| **Males** | **60...70** | **65** | 0.58 | 0.46 | 0.26 | 6.35 | 0.73 | 0.41 | 6.14 | 4.67 | 2.65 |
| **Males** | **60...70** | **75** | 0.27 | 0.14 | 0.09 | 6.14 | 0.31 | 0.20 | 5.79 | 3.22 | 2.06 |
| **Males** | **60...70** | **85** | 0.08 | 0.02 | 0.02 | 8.48 | 0.11 | 0.10 | 7.04 | 2.18 | 2.01 |

| Sex | $e_0$ range, years | *a* | RMSE in $e_0$ by model (years) | | | RMSE in $e_a$ by model (years) | | | Percentage RMSE in $e_a$ by model (%) | | |
|---|---|---|---|---|---|---|---|---|---|---|---|
| | | | Extrap. | Regr. (1) | Regr. (2) | Extrap. | Regr. (1) | Regr. (2) | Extrap. | Regr. (1) | Regr. (2) |
| **Total** | **40...50** | **55** | 8.38 | 0.33 | 0.23 | 23.76 | 0.66 | 0.46 | 77.55 | 3.34 | 2.32 |
| **Total** | **40...50** | **65** | 1.28 | 0.18 | 0.12 | 7.23 | 0.45 | 0.29 | 23.80 | 3.38 | 2.19 |
| **Total** | **40...50** | **75** | 0.18 | 0.08 | 0.05 | 6.79 | 0.31 | 0.19 | 9.00 | 4.07 | 2.47 |
| **Total** | **40...50** | **85** | 0.02 | 0.01 | 0.01 | 9.44 | 0.13 | 0.10 | 5.40 | 3.25 | 2.49 |
| **Total** | **50...60** | **55** | 9.96 | 0.61 | 0.45 | 26.24 | 0.96 | 0.71 | 73.45 | 4.13 | 3.16 |
| **Total** | **50...60** | **65** | 1.50 | 0.38 | 0.22 | 8.05 | 0.69 | 0.39 | 19.23 | 4.27 | 2.42 |
| **Total** | **50...60** | **75** | 0.31 | 0.12 | 0.06 | 6.18 | 0.33 | 0.17 | 7.51 | 3.49 | 1.76 |
| **Total** | **50...60** | **85** | 0.05 | 0.02 | 0.02 | 8.58 | 0.13 | 0.09 | 5.08 | 2.55 | 1.81 |
| **Total** | **60...70** | **55** | 9.39 | 0.78 | 0.69 | 21.99 | 1.05 | 0.91 | 54.06 | 4.21 | 3.71 |
| **Total** | **60...70** | **65** | 0.65 | 0.55 | 0.28 | 7.91 | 0.84 | 0.43 | 5.66 | 4.82 | 2.36 |
| **Total** | **60...70** | **75** | 0.52 | 0.15 | 0.10 | 5.81 | 0.30 | 0.20 | 8.46 | 2.83 | 1.78 |
| **Total** | **60...70** | **85** | 0.11 | 0.05 | 0.04 | 7.95 | 0.18 | 0.14 | 6.72 | 2.98 | 2.36 |
| **Total** | **70...80** | **55** | 0.85 | 0.30 | 0.48 | 15.65 | 0.36 | 0.57 | 3.93 | 1.35 | 2.22 |
| **Total** | **70...80** | **65** | 0.79 | 0.47 | 0.19 | 9.39 | 0.63 | 0.25 | 5.80 | 3.44 | 1.38 |
| **Total** | **70...80** | **75** | 0.92 | 0.09 | 0.09 | 5.86 | 0.16 | 0.15 | 13.19 | 1.40 | 1.31 |
| **Total** | **70...80** | **85** | 0.24 | 0.08 | 0.02 | 7.51 | 0.24 | 0.07 | 10.93 | 3.84 | 1.13 |

Note: $e_0$= life expectancy at birth; a= age at which the remaining life expectancy is estimated from the model; “Extrap.”=extrapolation of the death rates using the Kannisto model (3) with background mortality term; “Regr. (1)/(2)”=regression model (1) without the period effect or (2) with the period effect; “RMSE” = root-mean squared estimation errors; “Percentage RMSE” = root-mean squared estimation errors as percent of original HMD values.

**Table 4.** Root-mean squared estimation errors (absolute and percentage values) of estimates of the life expectancy at birth and at given age *a*, period data

| Sex | $e_0$ range, years | a | RMSE in $e_0$ by model (years) | | RMSE in $e_a$ by model (years) | | Percentage RMSE in $e_a$ by model (%) | |
|---|---|---|---|---|---|---|---|---|
| | | | Regr. (1) | Regr. (2) | Regr. (1) | Regr. (2) | Regr. (1) | Regr. (2) |
| **Females** | **40...50** | **55** | 0.34 | 0.29 | 0.67 | 0.58 | 3.80 | 3.28 |
| **Females** | **40...50** | **65** | 0.16 | 0.15 | 0.42 | 0.39 | 3.69 | 3.52 |
| **Females** | **40...50** | **75** | 0.06 | 0.05 | 0.27 | 0.24 | 4.02 | 3.59 |
| **Females** | **40...50** | **85** | 0.01 | 0.01 | 0.24 | 0.24 | 5.77 | 5.84 |
| **Females** | **50...60** | **55** | 0.48 | 0.50 | 0.77 | 0.81 | 3.90 | 4.03 |
| **Females** | **50...60** | **65** | 0.25 | 0.26 | 0.49 | 0.50 | 3.84 | 3.83 |
| **Females** | **50...60** | **75** | 0.12 | 0.12 | 0.37 | 0.36 | 4.96 | 4.80 |
| **Females** | **50...60** | **85** | 0.02 | 0.02 | 0.23 | 0.24 | 5.11 | 5.34 |
| **Females** | **60...70** | **55** | 0.67 | 0.56 | 0.83 | 0.71 | 3.92 | 3.33 |
| **Females** | **60...70** | **65** | 0.33 | 0.34 | 0.49 | 0.51 | 3.57 | 3.64 |
| **Females** | **60...70** | **75** | 0.14 | 0.15 | 0.32 | 0.33 | 3.89 | 4.04 |
| **Females** | **60...70** | **85** | 0.03 | 0.03 | 0.20 | 0.22 | 4.22 | 4.64 |
| **Females** | **70...80** | **55** | 1.10 | 0.93 | 1.20 | 1.02 | 5.00 | 4.24 |
| **Females** | **70...80** | **65** | 0.58 | 0.54 | 0.70 | 0.66 | 4.20 | 3.98 |
| **Females** | **70...80** | **75** | 0.23 | 0.25 | 0.36 | 0.39 | 3.63 | 3.97 |
| **Females** | **70...80** | **85** | 0.07 | 0.07 | 0.23 | 0.24 | 4.19 | 4.38 |
| **Females** | **80...90** | **55** | 1.09 | 1.00 | 1.14 | 1.04 | 3.91 | 3.57 |
| **Females** | **80...90** | **65** | 0.62 | 0.54 | 0.69 | 0.60 | 3.41 | 2.96 |
| **Females** | **80...90** | **75** | 0.34 | 0.30 | 0.42 | 0.37 | 3.35 | 2.99 |
| **Females** | **80...90** | **85** | 0.10 | 0.10 | 0.19 | 0.20 | 2.98 | 3.11 |
| **Males** | **40...50** | **55** | 0.27 | 0.28 | 0.54 | 0.56 | 3.14 | 3.19 |
| **Males** | **40...50** | **65** | 0.14 | 0.13 | 0.38 | 0.35 | 3.54 | 3.19 |
| **Males** | **40...50** | **75** | 0.05 | 0.04 | 0.27 | 0.24 | 4.49 | 3.94 |
| **Males** | **40...50** | **85** | 0.01 | 0.01 | 0.18 | 0.18 | 5.28 | 5.30 |
| **Males** | **50...60** | **55** | 0.42 | 0.42 | 0.66 | 0.67 | 3.69 | 3.53 |
| **Males** | **50...60** | **65** | 0.21 | 0.21 | 0.43 | 0.41 | 3.76 | 3.35 |
| **Males** | **50...60** | **75** | 0.08 | 0.07 | 0.28 | 0.23 | 4.13 | 3.38 |
| **Males** | **50...60** | **85** | 0.01 | 0.02 | 0.20 | 0.19 | 5.40 | 5.09 |

| Sex | $e_0$ range, years | a | RMSE in $e_0$ by model (years) | | RMSE in $e_a$ by model (years) | | Percentage RMSE in $e_a$ by model (%) | |
|---|---|---|---|---|---|---|---|---|
| | | | Regr. (1) | Regr. (2) | Regr. (1) | Regr. (2) | Regr. (1) | Regr. (2) |
| **Males** | **60...70** | **55** | 0.76 | 0.62 | 0.95 | 0.76 | 4.96 | 3.93 |
| **Males** | **60...70** | **65** | 0.36 | 0.33 | 0.57 | 0.51 | 4.42 | 3.87 |
| **Males** | **60...70** | **75** | 0.12 | 0.12 | 0.30 | 0.29 | 3.84 | 3.72 |
| **Males** | **60...70** | **85** | 0.03 | 0.03 | 0.19 | 0.20 | 4.21 | 4.49 |
| **Males** | **70...80** | **55** | 0.91 | 0.82 | 1.00 | 0.90 | 4.36 | 3.93 |
| **Males** | **70...80** | **65** | 0.45 | 0.36 | 0.57 | 0.45 | 3.54 | 2.83 |
| **Males** | **70...80** | **75** | 0.14 | 0.13 | 0.24 | 0.23 | 2.57 | 2.38 |
| **Males** | **70...80** | **85** | 0.04 | 0.04 | 0.15 | 0.15 | 2.90 | 2.94 |
| **Males** | **80...90** | **55** | 0.87 | 0.83 | 0.91 | 0.87 | 3.33 | 3.18 |
| **Males** | **80...90** | **65** | 0.68 | 0.61 | 0.78 | 0.69 | 4.04 | 3.61 |
| **Males** | **80...90** | **75** | 0.23 | 0.20 | 0.31 | 0.27 | 2.69 | 2.30 |
| **Males** | **80...90** | **85** | 0.10 | 0.10 | 0.23 | 0.24 | 3.89 | 4.00 |
| **Total** | **40...50** | **55** | 0.28 | 0.25 | 0.56 | 0.50 | 3.18 | 2.85 |
| **Total** | **40...50** | **65** | 0.15 | 0.14 | 0.40 | 0.38 | 3.69 | 3.49 |
| **Total** | **40...50** | **75** | 0.05 | 0.05 | 0.26 | 0.24 | 4.08 | 3.79 |
| **Total** | **40...50** | **85** | 0.01 | 0.01 | 0.18 | 0.19 | 4.77 | 5.03 |
| **Total** | **50...60** | **55** | 0.40 | 0.41 | 0.63 | 0.67 | 3.31 | 3.38 |
| **Total** | **50...60** | **65** | 0.22 | 0.20 | 0.42 | 0.40 | 3.51 | 3.22 |
| **Total** | **50...60** | **75** | 0.09 | 0.08 | 0.30 | 0.27 | 4.24 | 3.78 |
| **Total** | **50...60** | **85** | 0.02 | 0.02 | 0.19 | 0.19 | 4.64 | 4.62 |
| **Total** | **60...70** | **55** | 0.80 | 0.56 | 0.99 | 0.69 | 4.83 | 3.35 |
| **Total** | **60...70** | **65** | 0.35 | 0.31 | 0.53 | 0.45 | 3.84 | 3.31 |
| **Total** | **60...70** | **75** | 0.12 | 0.12 | 0.27 | 0.27 | 3.42 | 3.45 |
| **Total** | **60...70** | **85** | 0.03 | 0.03 | 0.17 | 0.19 | 3.59 | 4.06 |
| **Total** | **70...80** | **55** | 0.88 | 0.72 | 1.00 | 0.80 | 4.32 | 3.47 |
| **Total** | **70...80** | **65** | 0.55 | 0.46 | 0.70 | 0.58 | 4.29 | 3.62 |
| **Total** | **70...80** | **75** | 0.18 | 0.18 | 0.31 | 0.31 | 3.20 | 3.29 |
| **Total** | **70...80** | **85** | 0.05 | 0.05 | 0.18 | 0.20 | 3.27 | 3.66 |
| **Total** | **80...90** | **55** | 0.94 | 0.86 | 0.99 | 0.91 | 3.47 | 3.20 |
| **Total** | **80...90** | **65** | 0.71 | 0.63 | 0.81 | 0.71 | 4.01 | 3.49 |

| Sex | $e_0$ range, years | a | RMSE in $e_0$ by model (years) | | RMSE in $e_a$ by model (years) | | Percentage RMSE in $e_a$ by model (%) | |
|---|---|---|---|---|---|---|---|---|
| | | | Regr. (1) | Regr. (2) | Regr. (1) | Regr. (2) | Regr. (1) | Regr. (2) |
| **Total** | **80...90** | **75** | 0.21 | 0.22 | 0.27 | 0.29 | 2.20 | 2.29 |
| **Total** | **80...90** | **85** | 0.09 | 0.10 | 0.19 | 0.20 | 3.05 | 3.19 |

Note: $e_0$= life expectancy at birth; a= age at which the remaining life expectancy is estimated from the model; "Regr. (1)/(2)"=regression model (1) without the period effect or (2) with the period effect; "RMSE" = root-mean squared estimation errors; "Percentage RMSE" = root-mean squared estimation errors as percent of original HMD values.

## 4. Selected applications

Models linking the remaining life expectancy to the death rate at given age may be used to estimate expectation of life at old age when the Horiuchi-Coale or Mitra methods are not applicable either because of the absence of reliable mortality data or because of violations of the underlying assumptions of those methods such as stability of population age structure. In combination with the constrained extrapolation method (Ediev 2017), the models may be used to extend and complete life tables in the absence of mortality rates at older ages. This is particularly useful in cohort analysis where most of younger cohorts of interest have incomplete life history.

This possibility is illustrated in Figures 7 and 8 where we present results of projecting death rates for HMD cohort populations whose life tables were completed using model (2) (the period effect was fixed constant at the level of the year 2000 for all the following years) and the constrained Kannisto model with the background mortality term. Kannisto model at ages $x > a$ was constrained to the remaining life expectancy $e_a$ estimated from the regression model, where model age $a$, for each cohort, was set to the maximum age with available data (see Ediev 2017 for details of constrained extrapolation). The method was applied only to the cohorts with death rates available until, at least, age 65 years (i.e., for birth cohorts born around 1949 depending on data availability in the HMD). The cut age $a$ did not exceed 90 years, because the HMD provides its own extrapolations for cohorts with data up to age 90. The death rates were only extrapolated when the death rate at the eldest age with available data was in the range 0.002 to 0.2 (see the above discussion of the ranges of applicability of the models).

Figure 7 depicts results for cohort life expectancy at birth and Figure 8 depicts corresponding interquartile ranges (IQR, a measure of mortality compression or rectangularization Kannisto 2000; Wilmoth & Horiuchi 1999). Extrapolations suggest robust continuation of extension of cohort lifespans in developed countries. The life expectancy at birth for cohorts currently in their mid-60s may exceed 80 years for females and 77 years for males. These numbers are not all that unexpected given the already achieved levels of period life expectancy. Our results also indicate near end of the era of mortality compression and come in support to works describing mortality (especially the cohort mortality) as shifting along the age scale with only limited compression (Canudas-Romo 2008; Ediev 2013b; Ediev 2013a; Sasson 2016). Cohort IQRs seem to stabilize around the level of 20 years, i.e., 50 percent of deaths in birth cohorts currently in their 60s or younger, may be concentrated in ages spanning over 20 years only – as compared to 60-70 years in older generations.

Figure 7. Life expectancy at birth (vertical axis, years) for birth cohorts (horizontal axis): HMD estimates (black dots) and extrapolations based on completing cohort life tables for younger cohorts using model (2), selected HMD populations, males (blue crosses) and females (red crosses). Numbers to the left-up and right-down indicate, respectively, female and male life expectancy at birth for the youngest HMD cohorts having data for age 65 (the cohorts are shown next to their life expectancies); in the brackets: Maximum attained period life expectancy at birth for the given HMD population.

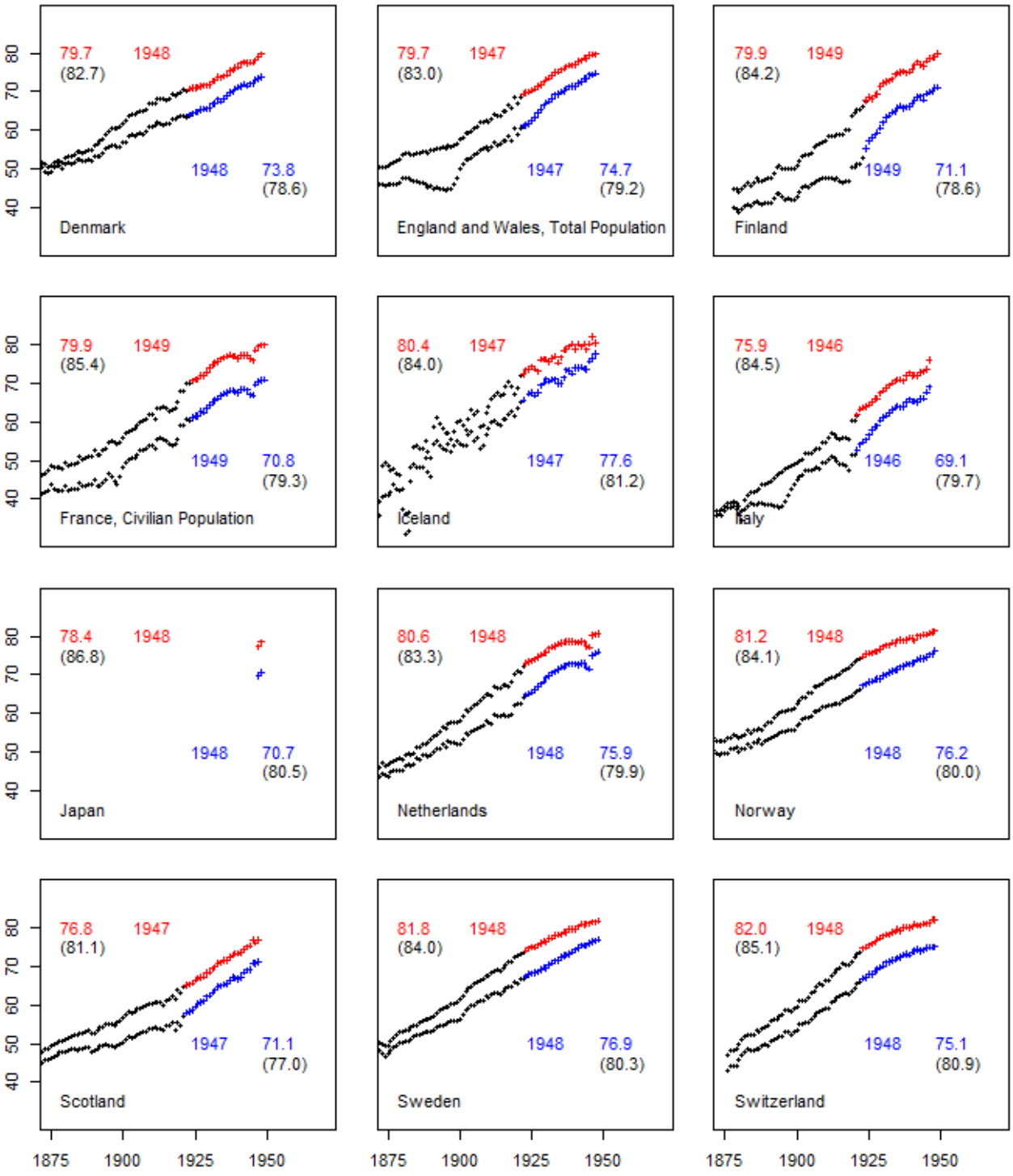
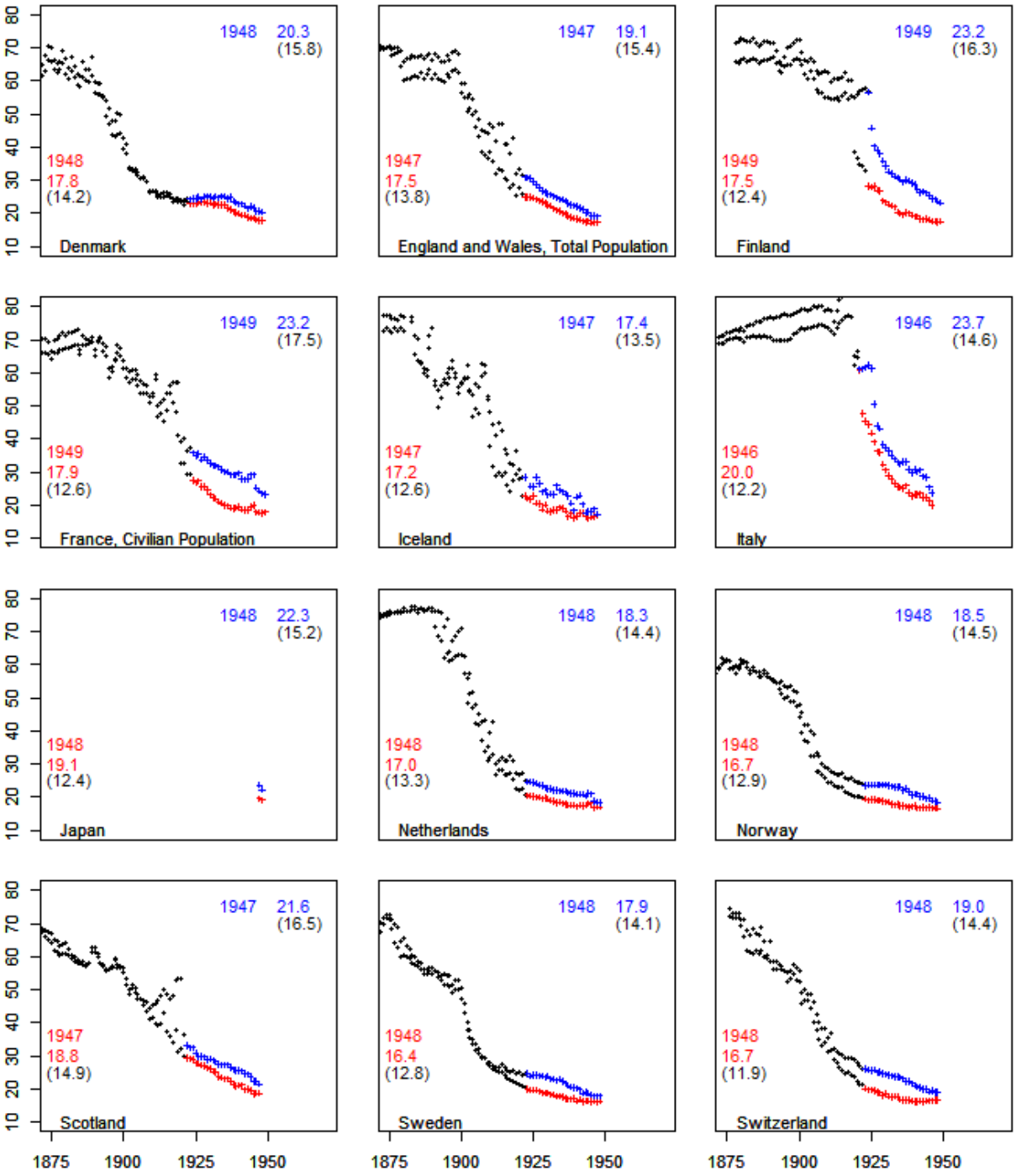


Figure 8. Inter-quartile ranges (IQR, vertical axis, years) of life table deaths distributions for birth cohorts (horizontal axis): HMD estimates (black dots) and extrapolations based on completing cohort life tables for younger cohorts using model (2), selected HMD populations, males (blue crosses) and females (red crosses). Numbers to the left-down and right-up indicate, respectively, female and male IQR for the youngest HMD cohorts having data for age 65 (the cohorts are shown next to IQRs); in the brackets: Minimum attained IQR in period life tables for the given HMD population.



In our next example, we apply our models to improve UN and Coale-Demeney families of model life tables (UN DESA/Population Division 1982; Coale et al. 1983) at advanced old age. We use the version of the model life tables extended by the UN Population Division to cover life expectancy at birth 20 to 100 years and single years of age 0 to 130 (UN DESA/Population Division 2017). The extension to age 130 involved a two-step procedure: Using the Gompertz model at ages 80-99 and then applying the Kannisto model from age 100 onwards. This extrapolation procedure, apparently, might have broken the relation between the death rate and the remaining life expectancy at age 79. To reinstall this relation, we correct the model life tables above age 79 by applying the period data-based model (1) and – in order to retain the diversity of the model life table schedules – by supplementing the model by the effect of the model life table family. To this end, we run linear regression linking the life table family and the log-ratio of the original model life tables' life expectancy $e_a$ to the life expectancy estimated from model (1). In doing so, we restricted the input data from the original model life tables to ages 50 to 70 to limit the influence of originally extrapolated rates on our estimates. We have also restricted the inputs to the range of the life expectancy at birth levels 40 to 80 years to limit the influence of extrapolations used to extend the original dataset to life expectancies beyond the empirically observed ranges. Results of the estimation of life table family effects follow in Table 5.

Table 5. Estimates of effects of model life table families on log-life expectancy.

| **Model life table families** | **Effect** |
|---|---|
| **Coale-Demeny MLT:** | |
| East | -0.0379 |
| North | 0.0071 |
| South | -0.0587 |
| West | -0.0079 |
| **United Nations MLT:** | |
| Chilean | 0.0447 |
| Far_East_Asian | 0.0238 |
| General | 0.0235 |
| Latin | 0.0391 |
| South_Asian | 0.0128 |

Note: Effects are obtained from linear model for the log-ratio of original model life tables' remaining life expectancy at ages 50-70 to life expectancy predicted from model (1): *ln(ex/ex.predicted) ~ 0 + MLT Effect*.

Supplementing model (1) by the life table family effects, we predicted remaining life expectancy at age 79 for each of the model life tables and used constrained extrapolations to fill the death rates at ages 80-130. For the extrapolation, we used the Kannisto model with the background term fit at ages 60-79, with no jump at age 79, whose growth parameter *b* was adjusted to meet the constraint in terms of the remaining life expectancy at age 79. Detailed tables of corrected model life tables are available from the author. Most substantial differences between the original and our corrected model life tables occur at high values of life expectancy at birth. Our corrected model life tables

produce somewhat a higher level of mortality compression at high values of life expectancy at birth, while the original model life tables (more so the UN families for females) produced patterns less compressed even as compared to the recent data on developed countries. This is illustrated in Figures 9 (females) and 10 (males) where we present Inter-Quratile Ranges (IQR) of the original and corrected distributions of deaths in model life tables as functions of life expectancy at birth. Another difference is that our correction suggests mortality compression levelling off, which is consistent with the above results for cohort life tables and with empirical evidence on populations advanced in lifespan extension (Canudas-Romo 2008; Ediev 2013b; Ediev 2013a; Sasson 2016). Meanwhile, the original model life tables, despite lack of compression as compared to the current experience of low-mortality countries, suggest an eventual acceleration of mortality compression. Notably, usual unconstrained extrapolations after age 79 would result in even faster acceleration of mortality compression than the two-step procedure used by the UN (detailed results not shown here). Ours is a one-step extrapolation that enables to produce results more consistent with the current experiences in developed countries and more plausible in the long run. Overall, our corrected life tables seem to evolve more regularly, as compared to the original model life tables, into the area of extended lifespans.

Figure 9. Inter-quartile ranges (IQR, vertical axes) and life expectancy at birth (horizontal axes) in model life tables, females: Original (panel to the left) and corrected using the model (1) supplemented by the life table family effect (panel to the right). Correction applies to ages 80+. Blue triangles: UN life tables; red circles: Coale-Demeny life tables. Grey circles: HMD period life tables, females.

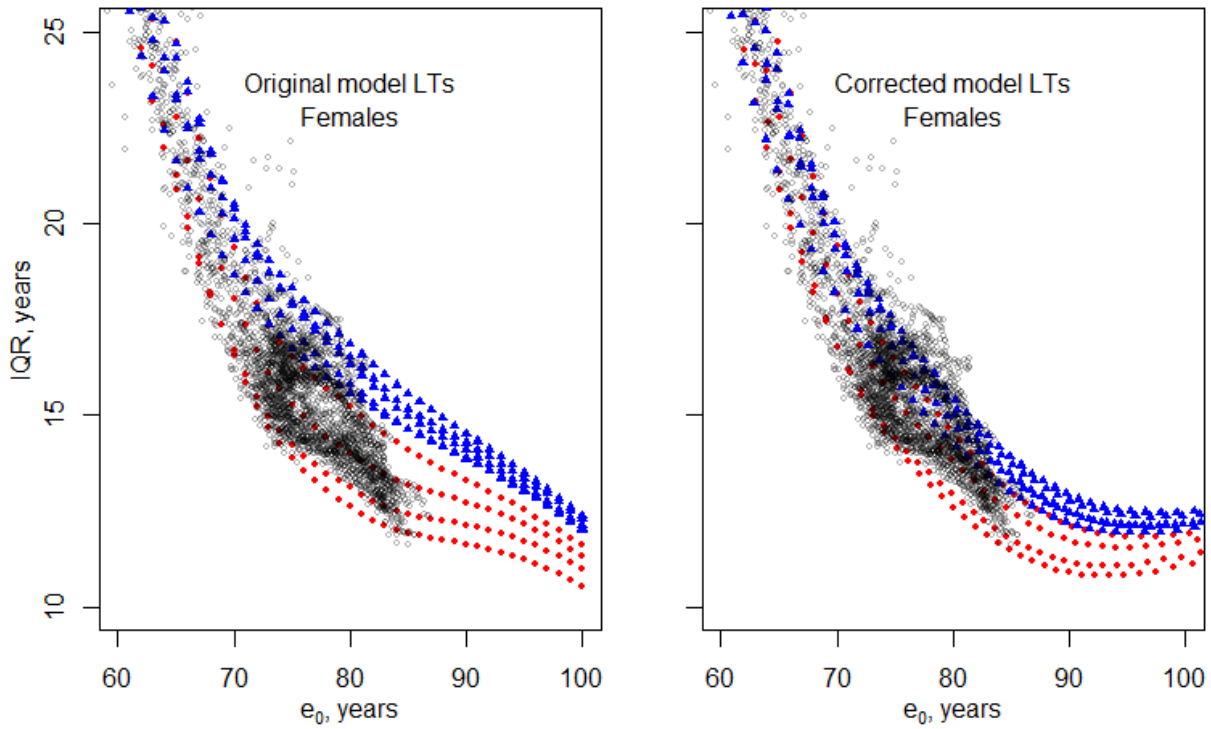
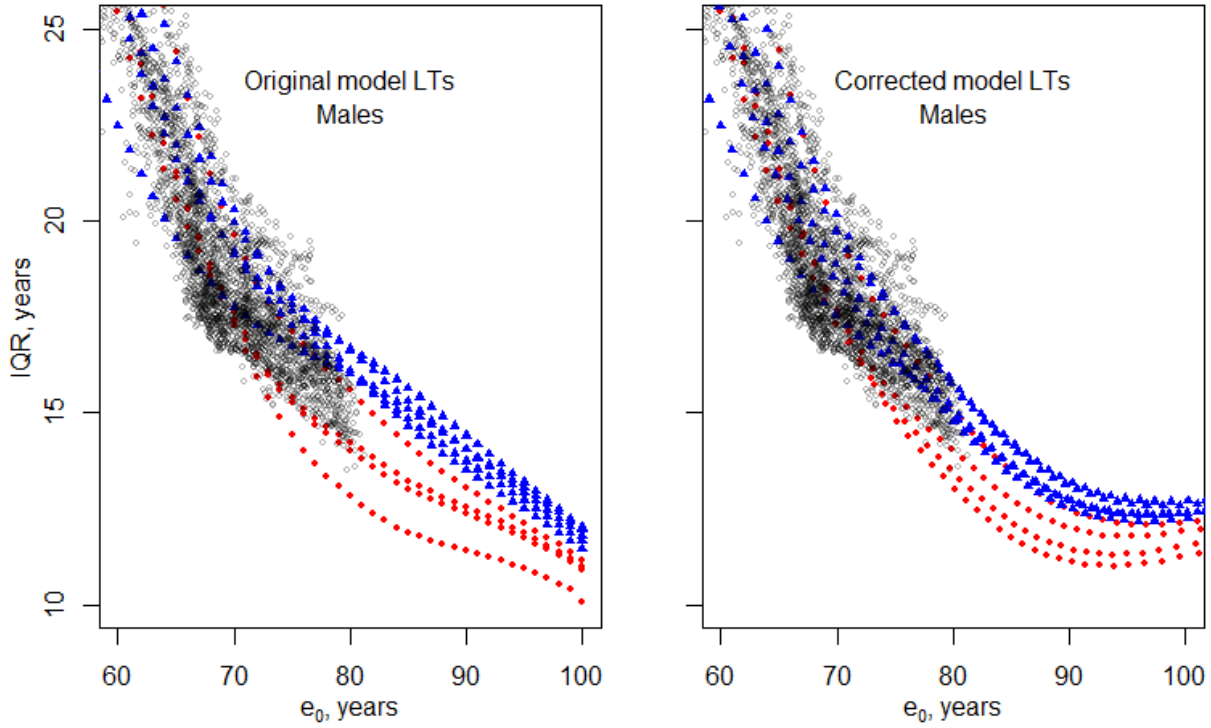


Figure 10. Inter-quartile ranges (IQR, vertical axes) and life expectancy at birth (horizontal axes) in model life tables, males: Original (panel to the left) and corrected using the model (1) supplemented by the life table family effect (panel to the right). Correction applies to ages 80+. Blue triangles: UN life tables; red circles: Coale-Demeny life tables. Grey circles: HMD period life tables, males.




Indeed, the two examples presented above do not exhaust all the applications of the model. It may be applied to mortality projections. The idea is to combine models for the expectation of life and mortality at old age with the conventional extrapolative projection models at younger ages. Most conventional mortality projections assume a continuation of linear trends over time of log-death rates in each age (Carter & Lee 1992; Booth & Tickle 2008; Shang et al. 2011; Stoeldraijer et al. 2013; Ediev 2007; Ediev 2008a; Waldron 2005; Li & Lee 2005). A problem of such methods appears at advanced old age where trends of mortality decline start, typically, with considerable time lag after the mortality decline has advanced at younger ages. In such situations, extrapolative projections being able to capture declining trends at young ages may fail to foresee onsets of mortality declines at older ages. As a result, all extrapolative projections of mortality, if not specially adjusted at old age, tend to produce levelling off improvements in life expectancy contrasting to long-term empirical trends showing no leveling off (White 2002; Oeppen & Vaupel 2002; Stoeldraijer et al. 2013). Although more optimistic alternatives exist that employ lower death rates shifting from young to old age (Bongaarts 2005; Ediev 2011), those alternatives appear to be overly optimistic and less stable at old age because of neglect of mortality compression. Our idea is to construct a middle approach where mortality at young and young adult age is extrapolated continuing the historical time trends, like in the conventional extrapolations, while mortality at older age is projected by combining the models of remaining life expectancy and the constrained

mortality extrapolation by age. Interestingly, such approach implemented cohort-wise is an improvement of the idea of *mortality inertia*. Mortality inertia implies that a birth cohort that reaches a certain age with a mortality level lower than that of elder cohorts in the same age, can keep the mortality advantage through the rest of its lifespan and reach an old age with mortality lower than in the current period life table even assuming constant mortality conditions (Ediev 2011). The method proposed here will do exactly that: Younger cohorts reaching the model age *a* with lower mortality will be predicted to have longer remaining lifespans which, in turn, will imply their lower death rates at older ages.

## 5. Concluding discussion

The association between the age-specific death rate and the remaining life expectancy at the same age appears to be strong enough to be practically useful. The regression models – with or without the period effect – outpace in prediction efficacy the common alternative for reconstructing the missing death rates at old age, the extrapolation method (on both cohort and period data). Our method is comparable in its accuracy to the Horiuchi-Coale and Mitra methods. This is remarkable given that the latter models use empirical data on deaths and population structure in the open age interval, while our method is based on a single death rate.

Although our method only produces the estimate of the remaining life expectancy, not the death rates at old age, the latter may be efficiently reconstructed using the life expectancy estimate to constrain the extrapolation (Ediev 2017) as illustrated by the examples in the previous section.

The ability to extend incomplete life tables and project mortality to old age is important for actuarial analyses, especially for cohorts and subpopulations without full life tables available. For many sub-populations, such as educational and occupational groups, specific populations targeted by businesses, or newly emerging and expanding social groups, there is, usually, no mortality data covering elder ages or elder cohorts – subject top stronger selection in the past – are not informative about expected old-age mortality for younger cohorts. Death rates at younger adult ages, however, are more readily available and of higher quality. In such cases, the models proposed here may be used to reconstruct the entire mortality schedules of the subpopulations of interest.

Inclusion of the country effect did not improve performance of the models presented here. In cohort model (2), for example, inclusion of the categorical country variable reduced the residual standard error (r.s.e.) from 0.0253 to only 0.0248. Including interaction of period and country effects (both categorical) and restricting data to years 1900+ has further reduced the r.s.e. to 0.0185. Nonetheless, considering country effects might be a useful strategy when the focus is on a specific country or a group of countries. When forecasting mortality in a specific country, for example, one may estimate parameters of the models presented here on data for a group of countries/regions with similar mortality dynamics and re-fit the period effect on data for the country of interest. Scenarios for the country-specific period effects may then be a part of more nuanced and accurate mortality forecasts.

Data quality permitting, the models for the remaining life expectancy may be applied to data extending beyond the limiting age 85 used in this paper. Although this is not a simple task as yet (both the HMD and even the Kannisto-Thatcher database rely on

breaking down the open age intervals data using mortality models), increasing survival to old age may provide possibilities for further developing the models at advanced old ages.

By and large, the cohort- and period-type models are consistent with each other and suggest model parameters of a similar magnitude. Yet, the two model types do differ from one another (cohort models suggest longer remaining lifespans and less mortality compression). This reflects the particular historical period, of epidemiological transition, to which the source data pertains. The cohort models suggest IQRs stabilizing for the currently young cohorts at levels around 20 years, while the period models suggest levels of about 12 years. This difference is consistent with the mortality tempo theory (Ryder 1951; Bongaarts & Feeney 2002; Ediev 2008b) that suggests, roughly, that period life table deaths distributions should be compressed by about 1/(1-0.4)=1.67 times as compared to the cohort life tables when lifespan of birth cohorts increases by about 0.4 years (as in Figure 7) from one cohort to the next one. These differences rise an interesting and practically important question about which of the two model types is better to be used in mortality forecasts. If lifespan developments are assumed to continue into the future without cooling off, both models should produce consistent results about future mortality. If one assumes sudden acceleration or, vice versa, slowing down of the pace of lifespan extensions, however, the two models may lead to different predictions about mortality developments. This matter deserves a separate study, in a context of application to the mortality forecasts.

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