

Forecasting vital rates from demographic summary measures

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Abstract

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1 Introduction

Future levels of mortality and fertility can be predicted by modelling and extrapolating rates over age and time, or by forecasting summary measures of each phenomena and then converted in age-specific rates. For example, in developed countries, the linear increase in life expectancy over some periods has made it easier to fit trends over time of this summary indicator than fitting more complex models based on age-specific dynamics of mortality (White 2002). Therefore, several methods have been proposed to forecast life expectancy. For instance, Torri and Vaupel (2012) forecast life expectancy for a given country assuming a tendency towards a predicted best practice life expectancy. Pascariu et al. (2018) proposed incorporating the analysis of the gap between female and male life expectancy to more accurately predict the overall level of mortality in a country. Similarly, Raftery et al. (2013) forecast life expectancy for several countries using a Bayesian hierarchical model for females, and then model the sex gap to estimate male life expectancy (Raftery et al. 2014). Subsequently, the overall level of mortality given by life expectancy is converted to a age-specific profile (Ševčíková et al. 2016). This latter method has been adopted by the United Nations. However, life expectancy, as an average, conceals the variation in the death distribution (van Raalte et al. 2018). Recently, Bohk-Ewald et al. (2017) proposed to incorporate the variation in ages at death as an additional indicator to evaluate mortality forecast. They found that some methods struggle to account for trends in lifespan variation, which results in a mismatch between life expectancy and lifespan variation. In most developed countries, life expectancy and lifespan variation are often negatively correlated (Smits and Monden 2009; Vaupel et al. 2011; Colchero et al. 2016), however in some countries this association is less strong, such as Eastern European which might lead to different levels of lifespan variation given a value of life expectancy when forecasted (Aburto and van Raalte 2018). Therefore, incorporating the dynamics of both life expectancy and lifespan variation to obtain an age-specific mortality profile that matches both is a step forward on more accurately predicting future longevity.

In fertility studies, forecasts usually predict the average number of children that will be born by women over their reproductive lifetime (Bohk-Ewald et al. 2018). Recently,

Bohk-Ewald et al. (2018) compared the performance of 20 major methods, including parametric curve fitting methods, extrapolation, Bayesian approaches and context-specific methods, aimed at completing lifetime fertility of women that have not yet reached their last reproductive age. The authors found that more complex methods do not necessarily outperform simpler methods. As in the case of mortality, some of these methodologies rely on modelling age-specific fertility rates (e.g. Coale and Trussell (1974); Chandola et al. (1999); Schmertmann (2003); Peristera and Kostaki (2007); Hyndman and Booth (2008)). Others, rely on probabilistic projections of the total fertility rate (TFR). For example, Alkema et al. (2011) developed a methodology to forecast TFR for all countries using a Bayesian projection model. From these estimates, the age-specific profile can be derived (Ševčíková et al. 2016). However, important information in other summary measures such as variance of childbearing age is often ignored (Hruschka and Burger 2016).

In this article, we propose a model to obtain future mortality and fertility age-patterns that comply with the projected summary measures. Unlike comparable approaches, we assume only smoothness of future vital rates which is achieved by a two-dimensional P -spline approach as in Currie et al. (2004). Since summary measures are commonly nonlinear functions of the estimated penalized coefficients, Lagrangian multipliers cannot be directly implemented. We hence opted for a Sequential Quadratic Programming (SQP) procedure (Nocedal and Wright 2006) to perform the associated constrained nonlinear optimization. We illustrate our approach with two data sets: mortality of Japanese females, based on future life expectancy predicted by United Nations World Population Prospects (United Nations 2017) and Spanish fertility constrained to total fertility rates, mean and variance of age at childbearing derived by classic time-series analysis.

2 Model on Japanese mortality data

For ease of presentation, we formulate the model on mortality data. We suppose that we have deaths, and exposures to risk, arranged in two matrices, $\mathbf{Y} = (y_{ij})$ and $\mathbf{E} = (e_{ij})$, each $m \times n_1$, whose rows and columns are classified by age at death, \mathbf{a} , $m \times 1$, and year of death, \mathbf{t}_1 , $n_1 \times 1$, respectively. We assume that the number of deaths y_{ij} at age i in year j is Poisson distributed with mean $\mu_{ij} e_{ij}$. Forecasting aims to reconstruct trends in

μ_{ij} for n_2 future years, $\mathbf{y}_2, n_2 \times 1$.

Usually demographers and actuaries summarize mortality age-patterns by computing life expectancies. Time-trends of this summary measure are often regular and well-understood. Forecasting a single time-series is therefore relatively easy. Figure 1 (left panel) presents observed life expectancy at age 1 for Japanese females from 1960 to 2016 along with the medium variant up to 2050 as computed by the UN, which consider available data for all countries in the world. Future mortality patterns, both by age and over time, must adhere to this predicted trend.

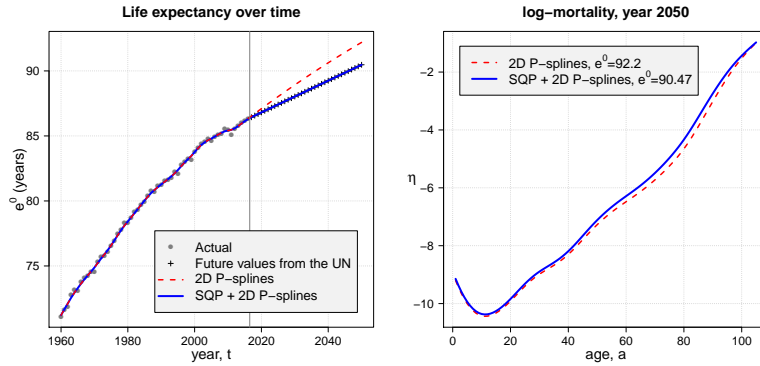


Figure 1: Left panel: Actual, estimated and forecast life expectancy at age 1 by United Nations, 2D P -splines and the SQP+2D P -splines. Right panel: Mortality age-pattern in 2050 by 2D P -splines and the SQP+2D P -splines. Japanese females, ages 1-105, years 1960-2016, forecast up to 2050.

We arrange data as a column vector, that is, $\mathbf{y} = \text{vec}(\mathbf{Y})$ and $\mathbf{e} = \text{vec}(\mathbf{E})$ and we model our Poisson death counts as follows: $\boldsymbol{\eta} = \ln(E(\mathbf{y})) = \ln(\mathbf{e}) + \mathbf{B}\boldsymbol{\alpha}$, where \mathbf{B} is the regression matrix over the two dimensions: $\mathbf{B} = \mathbf{I}_{n_1} \otimes \mathbf{B}_a$, with $\mathbf{B}_a \in \mathbb{R}^{m \times k_a}$. Over time, we employ an identity matrix of dimension n_1 because we will incorporate a constraint for each year. In order to forecast, data and bases are augmented as follows:

$$(1) \quad \check{\mathbf{E}} = [\mathbf{E} : \mathbf{E}_2], \quad \check{\mathbf{Y}} = [\mathbf{Y} : \mathbf{Y}_2], \quad \check{\mathbf{B}} = \mathbf{I}_{n_1+n_2} \otimes \mathbf{B}_a,$$

where \mathbf{E}_2 and \mathbf{Y}_2 are filled with arbitrary future values. If we define a weight matrix $\mathbf{V} = \text{diag}(\text{vec}(\mathbf{1}_{m \times n_1} : \mathbf{0}_{m \times n_2}))$, the coefficients vector $\boldsymbol{\alpha}$ can be estimated by a penalised version of the iteratively reweighted least squares algorithm:

$$(2) \quad (\check{\mathbf{B}}^T \mathbf{V} \check{\mathbf{W}} \check{\mathbf{B}} + \mathbf{P}) \tilde{\boldsymbol{\alpha}} = \check{\mathbf{B}}^T \mathbf{V} \check{\mathbf{W}} \tilde{\mathbf{z}},$$

where a difference penalty \mathbf{P} enforces smoothness behaviour of mortality both over age and time. Outcomes from this approach in terms of life expectancy is depicted with a dashed red line in Figure 1 (left panel), and a departure from the UN projected values is evident.

Life expectancy is a nonlinear function of the coefficients vector $\boldsymbol{\alpha}$:

$$(3) \quad e^0(\boldsymbol{\alpha}) = (\mathbf{1}_{1 \times m} \otimes \mathbf{I}_n) \exp[(\mathbf{I}_n \otimes \mathbf{C})\text{vec}(\exp(\mathbf{B}\boldsymbol{\alpha}))] + 0.5$$

where \mathbf{C} is a $(m \times m)$ lower triangular matrix filled only with -1.

Constrained nonlinear optimization is therefore necessary and a SQP approach is implemented. Let denote with \mathbf{e}_T^0 the n_2 -vector of target life expectancy for future years and with \mathbf{N} the $(k_a n_2 \times n_2)$ matrix with derivatives of (3) with respect to $\boldsymbol{\alpha}$ for each future year. The solution of the associated system of equations at the step $\nu + 1$ is given by

$$(4) \quad \begin{bmatrix} \boldsymbol{\alpha}_{\nu+1} \\ \boldsymbol{\omega}_{\nu+1} \end{bmatrix} = \begin{bmatrix} \mathbf{L}_\nu & \mathbf{H}_\nu \\ \mathbf{H}_\nu^T & \mathbf{0}_{n_2 \times n_2} \end{bmatrix}^{-1} \begin{bmatrix} \mathbf{r}_\nu - \mathbf{L}_\nu \boldsymbol{\alpha}_\nu \\ \mathbf{e}_T^0 - \mathbf{e}^0(\boldsymbol{\alpha}_\nu) \end{bmatrix},$$

where \mathbf{L} and \mathbf{r} are left- and right-hand-side of the system in (2), and matrix $\mathbf{H}^T = [\mathbf{0}_{n_2 \times k_a n_1} : \mathbf{N}^T]$. Vector of $\boldsymbol{\omega}$ denotes the current solution of the associated Lagrangian multipliers.

Forecast e^0 by the proposed method is exactly equal to the UN values (Figure 1, left panel). The right panel of Figure 1 shows the forecast mortality age-pattern in 2050: Shape obtained by the suggest approach is not a simple linear function of the plain P -splines outcome.

3 Spanish Fertility Data

We forecast Spanish fertility using three commonly-used summary measures: Total Fertility Rate, mean and variance of childbearing age, forecast by conventional time-series analysis. We then smooth and constrain future fertility age-patterns to comply these forecast values. Summary measures as well as fertility rates in 2050 are presented in

Figure 2.

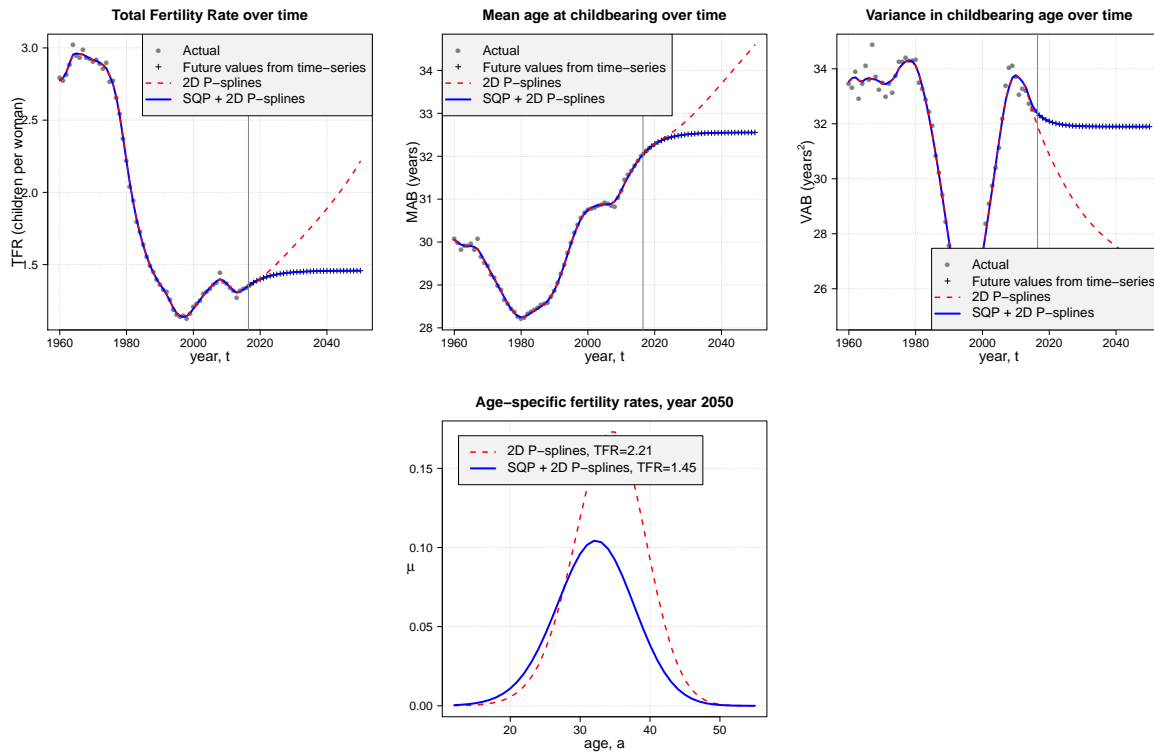


Figure 2: Top and left-bottom panels: Actual, estimated and forecast Total Fertility Rate, Mean and Variance in childbearing age by time-series analysis, 2D P -splines and the SQP+2D P -splines. Right-bottom panel: Age-specific fertility rate in 2050 by 2D P -splines and the SQP+2D P -splines. Spain, ages 12-55, years 1960-2016, forecast up to 2050.

4 Discussion

Appendix A

R code

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