From the Compression of Mortality Scenario to the Shifting Mortality One: The Canadian Experience

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1 Introduction

Over the last century, we have witnessed major changes in the level of mortality in regions all across the globe. This remarkable mortality decrease has also been characterized by important changes in the age-at-death distribution, which inevitably led to substantial modifications in the shape of the survival curve over time. The measurement of transformations in the survival curve quickly became a subject of great interest among researchers, as implications of these changes on every society's health-care system and social programs, among others, are profound.

In fact, demographers have suggested several indicators monitoring changes in the distribution of deaths. Recently, more than 20 existing indicators have been identified by Cheung et al. (2005), some being methodologically and conceptually more advisable than others, as previously discussed by Wilmoth and Horiuchi (1999) and Kannisto (2000, 2001).

Even though the debate regarding which indicator to favour still has to be sorted out, most authors agree that countries usually go thru a compression of mortality regime during the epidemiological transition. That is, deaths tend to concentrate into a shorter age interval over time, as figure 1 shows for Japanese women between the 1950-54 and 1990-94 periods.

Indeed, as time went by, the age-at-death distributions became less and less spread out. Note that they have also progressively moved to higher ages. However, very recent studies
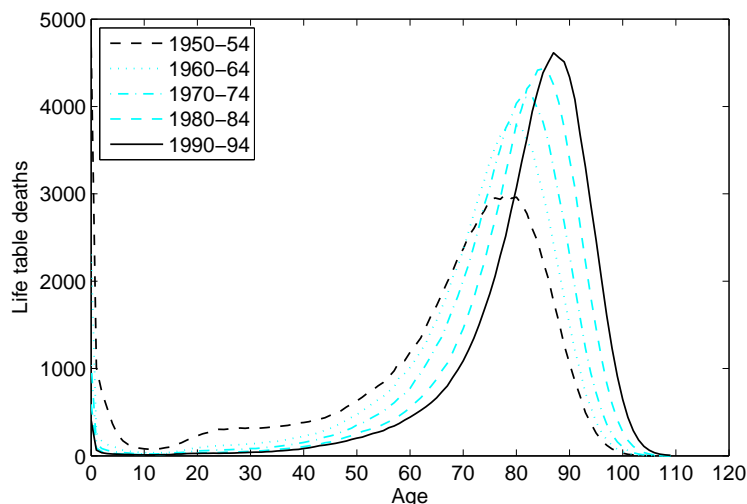

Figure 1: Life table age-at-death distribution, Japanese women,1950-54 to 1990-94
Source: Human Mortality Database

suggest that an increase in the most frequent age at death might not always be accompanied by such compression of mortality occurring above it (Cheung and Robine 2007, Cheung et al. 2008). Instead, after a strong compression episode, the authors suggest that countries may enter a new era where compression has ceased and the whole distribution of adult life durations slides to higher ages.

Figure 2 indicates that Japanese women may have been experiencing this new era since 1995-99 because from that point in time, their age-at-death distribution then moves to higher ages while its shape remains unchanged. Note that this new era would be in accordance with what Kannisto (1996) and Bongaarts (2005) have described as the shifting mortality scenario.

Furthermore, after analysing data from very low mortality countries such as Japan, France, Italy and Switzerland (Cheung and Robine 2007, Cheung et al. 2008), the authors assert that these data failed to demonstrate that human populations were approaching an upper limit in terms of longevity. Nevertheless, this view is clearly not shared by all scientists (Carnes and Olshansky 2007).

Following these recent advancements, the first objective of this paper is to present a flexible nonparametric approach based on regression splines, specifically *B*-splines with penalties
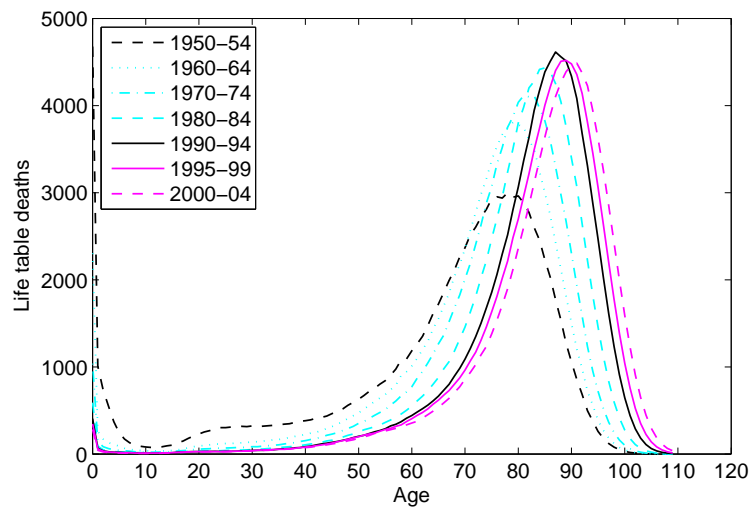
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Figure 2: Life table age-at-death distribution, Japanese women,1950-54 to 1990-94
Source: Human Mortality Database

known as *P*-splines (Eilers and Marx 1996), that has the potential to improve our monitoring of transformations in the survival curve over time.

Secondly, we wish to focus on the Canadian experience, for which there has been very few studies on the topic. The work of Nagnur (1986) on Canada from 1921 to 1981, and the study by Martel and Bourbeau (2003) on the province of Quebec between 1921 and 1999 essentially form the literature on the subject. Both of these papers assessed the presence of a compression of mortality regime during the epidemiological transition. As a continuation, we verify whether Canadians have reached this new era of shifting mortality demographers have recently been speaking of. Precisely, Canadian provinces are first compared against each other to reveal regional disparities, and the Canadian experience is then analysed in an international perspective.

2 Lexis's normal life durations

The German statistician Wilhelm Lexis is widely known among demographers for the very useful Lexis diagram which allows a systematic location on one plane of the three classical demographic coordinates, namely the age, period and cohort. However, another great contribution following his work on the normal life durations (Lexis 1878) remained largely

3

ignored by the scientific community during the twentieth century (Véron et al. 2003). In 2001, Kannisto, followed by other authors (Cheung et al. 2005, Cheung and Robine 2007, Cheung et al. 2008, Canudas-Romo 2008), demonstrated the utility of Lexis's normal life durations concept to measure the transformation of the survival curve ever since the very first stages of the epidemiological transition.

According to Lexis (see Figure 3), the modal age at death corresponds to the most central and natural characteristic of human longevity. Deaths occurring at this age and above can then be seen as "normal deaths". Furthermore, by symmetry of distribution falling above the modal age at death, the left hand side of the normal life duration distribution can be obtained. This allows disentangling infant and premature deaths from those referred as normal deaths by Lexis.
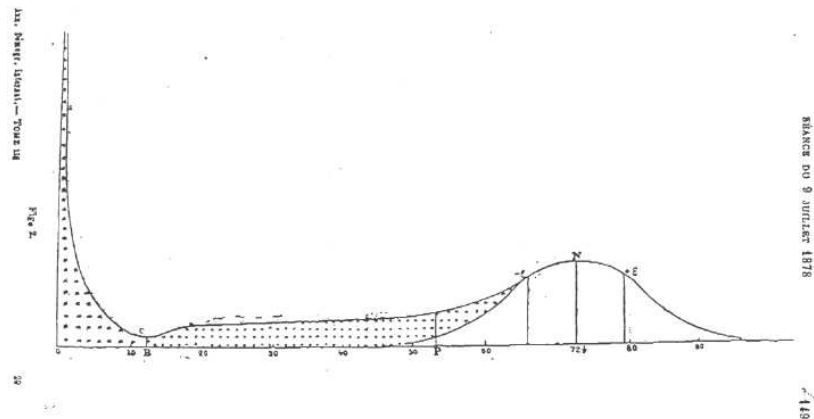

Figure 3: Normal life durations concept introduced by Lexis in 1878
Source: Lexis (1878)

Inspired by the work of Lexis (1878) on normal life durations, Kannisto (2001) suggested the use of the adult modal age at death (M) and the standard deviation of individual life durations occurring above the modal age at death ($SD(M+)$) as indicators of the human life span. The adult modal age at death consists in a central longevity indicator while the standard deviation above it measures the dispersion of ages at death above the mode. In a recent paper, Cheung and Robine (2007) developed an additional indicator in the form of $M + kSD(M+)$ to describe how far the highest normal life durations can go beyond the adult modal age at death M.

It is worth noting that unlike the life expectancy at birth, the late modal age at death

is strictly influenced by adult mortality and therefore much more sensitive to changes in mortality among the elderly population. It therefore consists in an useful tool to monitor and explain changes in the age-at-death distribution in populations where most deaths occur at older ages (Kannisto 2000, Kannisto 2001, Robine 2001, Cheung et al. 2005, Cheung and Robine 2007, Canudas-Romo 2008).

In order to obtain an accurate estimation of the late modal age at death for a given region and period, parametric models, which imply fairly rigid theoretical assumptions and modeling structure, have been used by Cheung et al. (2007, 2008). We propose to use a flexible nonparametric approach based on regression splines, specifically B-splines with roughness penalties known as P-splines (Eilers and Marx 1996), to obtain a smooth density function describing the distribution of deaths. Quantiles from both sides of the estimated late modal age at death serve as our dispersion indicators and are used to monitor changes in the compression of mortality regime over time.

3   Data and methods

For a given region and period, the observed number of deaths Y_i and person-years E_i at age $i = 1, \ldots, n$ are taken from the *Canadian Human Mortality Database* (CHMD) or the *Human Mortality Database* (HMD). Note that throughout this paper, we will focus on mortality occurring at age 10 and above. Infant and child mortality present unique features that would require the use of a methodology suited for ill-posed data, which goes beyond the scope of this research.

The CHMD gathers detailed data on Canada, its provinces and territories, while the HMD is an international database which currently holds data on 37 countries and regions. Both databases are updated on a regular basis and are respectively available to researchers thru the following Internet sites: `www.bdlc.umontreal.ca` and `www.mortality.org`. The fact that these databases rely on a common methodology is a definite advantage for result comparison. The high level of data quality offered by the CHMD and the HMD also makes these databases very attractive.

Let m_i denote the death rate at age i given by the following ratio

$$m_i = \frac{Y_i}{E_i}.$$

Under the assumption of a true constant instantaneous death rate μ_i within each age and time interval, the number of deaths Y_i is Poisson-distributed with mean $E_i \cdot m_i$, that is

$$Y_i \sim \text{Poisson}(E_i \cdot m_i). \tag{1}$$

The Poisson regression model used in this paper is based on this assumption. Since our response variable $\boldsymbol{y}$ is non-normally distributed, we introduce a linear predictor $\boldsymbol{\eta}$ and the logarithm as the (canonical) link function $g(\cdot)$, such that

$$\begin{aligned}
\boldsymbol{\eta} &= g(\text{E}[\boldsymbol{y}]) \\
&= \ln(\text{E}[\boldsymbol{y}]).
\end{aligned} \tag{2}$$

Alternatively, we have

$$\begin{aligned}
\text{E}[\boldsymbol{y}] &= g^{-1}(\boldsymbol{\eta}) \\
&= e^{\boldsymbol{\eta}}.
\end{aligned}$$

The Poisson regression model assumes that $\boldsymbol{\eta}$ can be modelled by a linear combination of unknown parameters. We suggest the use a flexible nonparametric approach based on regression splines, specifically B-splines with penalties known as P-splines, to estimate those parameters.

B-splines consists of polynomial pieces that are joined at certain abscissa values called "knots". The degree of the polynomial is set by the user, while the number of knots and their position can be chosen according to automatic optimization schemes developed by Friedman and Silverman (1989) and Kooperberg and Stone (1991, 1992). Formulas by de Boor (1977, 1978), Cox (1981) or Dierckx (1993) can then be used to compute the B-splines recursively.

A set of B-splines is called a "B-spline basis" and is well-suited for smoothing observed data points (x_i, z_i), $i = 1, \ldots, n$. Figure 4 shows an example of a B-spline basis, which contains a set of 8 equally-spaced B-splines of degree 3 (cubic B-splines). The basis matrix $\boldsymbol{B}$ associated with this particular B-spline basis is defined as

$$\boldsymbol{B} = \begin{bmatrix} B_1(x_1) & B_2(x_1) & \ldots & B_8(x_1) \\ B_1(x_2) & B_2(x_2) & \ldots & B_8(x_2) \\ \vdots & \vdots & \vdots & \vdots \\ B_1(x_n) & B_2(x_n) & \ldots & B_8(x_n) \end{bmatrix},$$

where $B_j(x_i)$, $j = 1, \ldots, 8$ denotes the value at x_i of the jth cubic B-spline. A fitted curve $\hat{z}$ to observed data points (x_i, z_i) is then expressed by

$$\hat{z}(x_i) = \sum_{j=1}^{8} \hat{a}_j B_j(x_i),$$

6

where $\hat{a}_j$ is the estimated regression coefficient of $B_j(x_i)$. More generally, we have

$$\hat{z} = B\hat{a}. \tag{3}$$

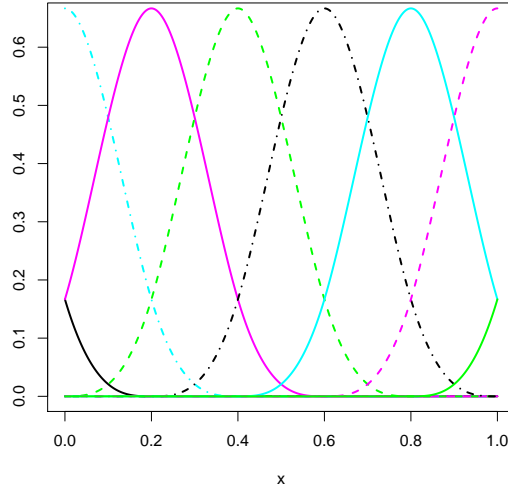Figure 4: B-spline basis containing 8 cubic B-splines with equally-spaced knots

B-splines are certainly attractive for nonparametric modeling, but the task of choosing the optimal number and positions of the knots remains a very complex one. The use of equidistant knots may be seen as a good option, but it often leads to limited control over smoothness and fit. Inspired by the work of O'Sullivan (1988), Eilers and Marx (1996) developed the P-splines approach, which combines B-splines and difference penalties on the estimated coefficients of adjacent B-splines. The idea behind this approach is to use a relatively large number of equally-spaced knots, and to apply a penalty on the regression coefficients to ensure a smooth variation and avoid over-fitting. Recourse to optimization schemes to define knots is therefore no longer required.

From relations (1), (2) and (3), we have

$$\boldsymbol{\eta} = \ln(\mathrm{E}[\mathbf{y}]) = \ln(\boldsymbol{e} \cdot \boldsymbol{m}) = \ln(\boldsymbol{e}) + \ln(\boldsymbol{m}) = \ln(\boldsymbol{e}) + \boldsymbol{Ba},$$

where $\boldsymbol{y}$, $\boldsymbol{e}$, $\boldsymbol{m}$ are repectively deaths, person-years (or exposures) and death rates vectors for a given region and period. The term $\ln(\boldsymbol{e})$ is commonly referred to as the offset in a Poisson regression setting. Furthermore, $\boldsymbol{B}$ is the B-spline basis matrix and $\boldsymbol{a}$ is the vector of respective regression parameters to estimate.

Using the P-spline approach to estimate $\boldsymbol{a}$, we obtain

$$\hat{\boldsymbol{\eta}} = \ln(\boldsymbol{e}) + \boldsymbol{B}\hat{\boldsymbol{a}},$$

and a smoothed trend for the intantaneous death rate, namely the hazard function $h(x)$, can be estimated as well. The corresponding smoothed survival function $\hat{S}(x)$ expressed as

$$\hat{S}(x) = e^{-\int_0^x \hat{h}(t)dt}$$

can then be obtained thru numerical integration techniques. Furthermore, since

$$h(x) = \frac{f(x)}{S(x)},$$

the smoothed density function describing the age-at-death distribution, $\hat{f}(x)$, is given by

$$\hat{f}(x) = \hat{h}(x)\hat{S}(x).$$

The late modal age at death for some region and period in time corresponds to

$$\max_x \hat{f}(x),$$

and quantiles from both sides of this estimated late mode can be easily computed to monitor changes in the compression of mortality over time. Note that as pointed out by Wilmoth (1997), the three curves $h(x)$, $S(x)$ and $f(x)$ are related in such way that changes in one of them will necessarily be reflected in the other two. In this paper, we focus on the smoothed density function describing the age-at-death distribution, but analysis based on $\hat{h}(x)$ or $\hat{S}(x)$ would have led to the same conclusions.

4 Results

To be continued.

5 Acknowledgements

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