Stochastic Modelling of the Hybrid Survival Curve

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Abstract

In this paper, building upon the idea of cross-sectional survival probabilities developed by Brouard (1986), we propose using stochastic models to study the evolution of a new type of survival curves called hybrid survival curve. We find that the three-factor survival model provides a better model fitting than the two-factor survival model. Furthermore, the three time-varying parameters are highly interpretable and their respective trends can be used as an indicator for the rectangularisation of survival curve. On top of that, we demonstrate how the time-varying parameters can be extrapolated into the future to obtain projected hybrid survival curves.

Keywords: period survival curves; cohort survival curves; rectangularisation; stochastic models; time-varying parameters.

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1. Introduction

Human life expectancy has been increasing steadily since 1840 and there is no evident sign of slowing down in the near future. In particular, Oeppen and Vaupel (2002) reported that the maximum female life expectancy across a range of countries has risen at an average pace of about three months per year. The rising trend in life expectancy is caused by the mortality improvements across different ages, which have resulted in the so-called rectangularisation of survival curve. This concept was coined by Fries (1980), who hypothesised that a decreasing variability of age at death would make a survival curve become more rectangular over time.

We can rely on the two existing types of survival curves in studying the rectangularisation phenomenon. A period survival curve is based on the survival probabilities in a given period, which ensures that the complete period mortality data can be taken into account. However, the underlying cohort of a period survival curve is a 'hypothetical cohort', so it may not be realistic for certain demographic applications. In contrast, a cohort survival curve is derived from a single cohort over time, which implies that the actual survivorship experience of a real cohort can be reflected by the corresponding cohort survival curve. However, cohort survival curve is subject to the problem of data incompleteness due to the lack of timeliness in the cohort mortality data.[1]

The first objective of this paper is to demonstrate how to construct a new type of survival curves called hybrid survival curve, which possesses the strengths of both period and cohort survival curves. A hybrid survival curve is made up of the actual cohort survival probabilities (the advantage of cohort survival curve) of multiple old-age cohorts and is free from the problem of data incompleteness (the advantage of period survival curve). With these advantages, the hybrid survival curve provides an alternative to be used in studying the rectangularisation pattern of survival curves. Note that these survival probabilities are also defined as the cross-sectional survival probabilities, which are needed in the calculation of cross-sectional average length of life, first proposed by Brouard (1986) and later studied by Guillot (2003) and Guillot and Kim (2011). However, the construction of hybrid survival curve requires much more historical data and the curve is not strictly decreasing.

The stochastic modelling of mortality rates that takes into account mortality improvements over time has been analysed extensively (see, e.g., Cairns et al., 2009, 2011) since the pioneering work by Lee and Carter (1992). A number of stochastic mortality models were developed to model certain transformed functions of death probabilities or central death rates. For instance, the Lee-Carter model was the first extrapolative model to study the future time trends of logarithmic central death rates in a stochastic setting. However, the modelling of survival probabilities remains largely unexplored, probably because survival probabilities can be expressed in terms of multiplicative

[1] The construction of a complete cohort survival curve requires the complete cohort mortality data, which would only be available after the death of the last cohort member.

products of one minus death probabilities. In this paper, we utilise a different approach and perform the direct modelling of the survival probabilities on a hybrid survival curve.

The second objective of this paper is to build a new class of stochastic models for a suitably transformed function of the hybrid survival curve. Following the general structural form of mortality models in Hunt and Blake (2014), we develop two models for the hybrid survival curve. Our proposed models are similar to that of De Jong and Marshall (2007) who performed mortality projection using the Wang transform (see Wang, 2000). The main difference is that we use logit-transformed annualised survival probability as the model response variable instead of probit-transformed period survival probability. Our models also resemble the Cairns-Blake-Dowd model by Cairns et al. (2006) except for the different underlying response variables.

In more detail, our first proposed model is referred to as two-factor survival model because it consists of two factors that correspond to the intercept and the slope of the transformed hybrid survival curve. We also consider a simple extension by including a curvature parameter and refer to it as three-factor survival model. Using the Bayesian Information Criterion (BIC) as our model selection criterion, we find that the three-factor survival model gives lower BIC values for the gender-specific data sets of Sweden and Bulgaria, which are developed and developing countries, respectively. Besides that, the three time-varying parameters are highly interpretable. In particular, the trend of each parameter can serve as an indicator for the pattern of rectangularisation. By extrapolating the time-varying parameters with a trivariate random walk with drift, we can readily obtain projected hybrid survival curves.

The remainder of this paper is structured as follows. Section 2 illustrates the construction of a hybrid survival curve. Section 3 presents the detailed specifications of the two survival models. Section 4 describes the interpretations of the time-varying parameters in the three-factor survival model with regards to the rectangularisation phenomenon. Section 5 demonstrates the extrapolation procedure for the three time-varying parameters in projecting hybrid survival curves. Section 6 concludes the paper.

2. Survival Curves

2.1. Rectangularisation of Survival Curve

The term 'rectangularisation' of survival curve was coined by Fries (1980), who hypothesised that the survival curve would become rectangular under declining mortality trends and the fact that human life expectancy at that point in time was believed to have an upper limit of 85 years. This concept is graphically represented in Figure 1, where the survival curve tends to shift to the top right corner over time. Fries (1980) also conjectured that the distribution of lifetime illness should be narrowly centered at age 85 due to morbidity compression if the exogeneous causes of death were

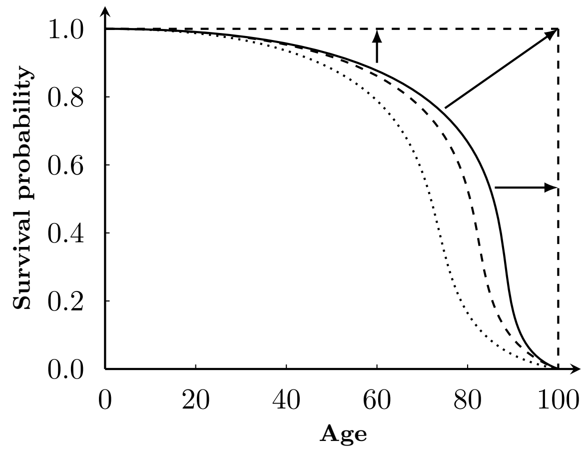


Figure 1 Rectangularisation of survival curve.

eliminated. As a result, the variability of age at death would decrease over time — a phenomenon known as mortality compression. Strictly speaking, the compression of mortality is different from the compression of morbidity, although Fries (1980) predicted that they would occur simultaneously because the latter is naturally assumed to be having a causal impact on the former.

A number of indicators (for a review, see Cheung et al., 2005) were suggested to study the rectangularisation of survival curve and the mortality compression. For example, Wilmoth and Horiuchi (1999) compared 10 highly correlated measures and recommended using the interquartile range (IQR) of the distribution of age at death as the sole indicator of mortality compression. Kannisto (2000) proposed a family of indicators C_α — defined as the shortest age interval covering α% of the total deaths — and documented the evidences of mortality compression for 22 populations in terms of the declining shortest age intervals. By definition, the value of C_{50} is at most equal to the value of IQR, so the former measure is more effective in detecting the concentration of deaths and can be perceived as an improved measure of IQR. On the other hand, Cheung et al. (2005) distinguished the rectangularisation of a survival curve into three dimensions: horizontalisation, verticalisation and longevity extension.

2.2. Existing Types of Survival Curves

Here we discuss the strengths and weaknesses of the existing types of survival curves. The conventions below are used throughout the discussion:

- $D_{x,t}$ is observed number of deaths at age x in year t;
- $E_{x,t}$ is the matching exposures at age x in year t;
- $m_{x,t}$ is the central death rate at age x in year t;
- $q_{x,t}$ is the death probability that a person aged x at the beginning of year t will die within a

year, which can be written as $q_{x,t} = 1 - e^{-m_{x,t}}$ using the assumption of a constant force of mortality between integer ages;

- $1 - q_{x,t}$ is the survival probability that a person aged x at the beginning of t will survive until the end of year t;
- ${}_n s^p_{x,t}$ is the period survival probability that a person aged x at the beginning of year t will survive for n years, based on the one-year death probabilities of multiple cohorts in year t;

$$
{}_n s^p_{x,t} = \begin{cases} 1, & n = 0, \\ \prod_{i=0}^{n-1}(1 - q_{x+i,t}), & n \geq 1. \end{cases} \tag{1}
$$

- ${}_n s^c_{x,t}$ is the cohort survival probability that a person aged x at the beginning of year t will survive for n years, based on the one-year death probabilities of the specific cohort over time;

$$
{}_n s^c_{x,t} = \begin{cases} 1, & n = 0, \\ \prod_{i=0}^{n-1}(1 - q_{x+i,t+i}), & n \geq 1. \end{cases} \tag{2}
$$

A common approach to obtain these probabilities is by using a period life table or a cohort life table. We refer interested readers to Wilmoth and Horiuchi (1999), who analysed the survival curves of Swedish populations constructed from the life tables on both period and cohort bases. On the other hand, Yue (2012) studied the survival curves of Japan, Sweden and the United States constructed from the raw data in order to avoid the influence of graduation methods on the values in life tables. Since our aim is to study the evolution of the hybrid survival curves over the years across the sample period, in this paper we calculate the one-year death probabilities and also the resulting survival probabilities from the central death rates defined as $m_{x,t} = \frac{D_{x,t}}{E_{x,t}}$.

There are two existing types of survival curves. Period survival curves are based on the age-specific death probabilities in a given year, whereas cohort survival curves are derived from the death probabilities of a specific cohort over time. Each period survival curve takes into consideration the complete period mortality data involving multiple birth cohorts. This can be seen from Equation (1), where the age-specific death probabilities $q_{x+i,t}$'s for $i = 0, \ldots, n-1$ are used to compute the period survival probabilities for $n \geq 1$. However, notice that Equation (1) involves the multiplication of the one-year survival probabilities for a group of successive cohorts at a fixed period t. Therefore, except for the case of $n = 1$, each period survival probability is effectively a mix of different cohorts' experience and does not correspond precisely to the actual survival probabilities of any real cohorts. Instead, the underlying cohort of a period survival curve is a hypothetical cohort that is subject to these one-year survival probabilities obtained in a specific period, hence the period survival curve may not be realistic in practice such as in the projection of

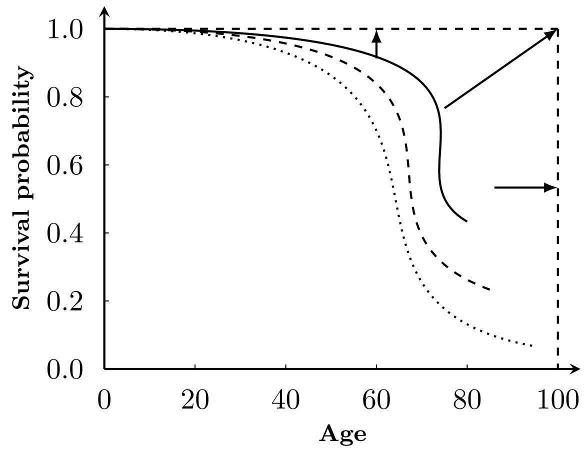


Figure 2 The problem of data incompleteness for cohort survival curves.

life expectancy for real cohorts.

In contrast, each cohort survival curve corresponds to a single real cohort by reflecting its actual survivorship experience over time. The reason is that as expressed in Equation (2), the death probabilities $q_{x+i,t+i}$'s for $i = 0, \ldots, n-1$ used to calculate the cohort survival probabilities correspond to the same cohort over time. However, each cohort survival curve would suffer from the problem of data incompleteness due to the lack of complete cohort mortality data before the death of the last cohort member, as illustrated in Figure 2. This limitation also implies that complete cohort survival curve can only be constructed for extinct cohorts after a long period of time.

From the discussions above, it is clear that each type of survival curves has its own strengths and weaknesses. In particular, cohort survival curves are realistic, while period survival curves are not subject to the problem of data incompleteness. Nonetheless, it should be noted that the rectangularisation pattern can generally be found in both types of survival curves, where period survival curves would exhibit the pattern of rectangularisation over successive time periods and cohort survival curves would move towards a rectangular shape across successive birth cohorts. For further discussions on the relationship between period and cohort measures determined from the respective survival curves, we refer interested readers to Goldstein and Wachter (2006), Wachter (2005) and Wilmoth (2005).

2.3. The Hybrid Survival Curve

In this subsection, building upon the idea of cross-sectional survival probabilities developed by Brouard (1986), we demonstrate how to construct the hybrid survival curve that possesses the advantages of both period and cohort survival curves. Our proposed survival curve in each year comprises of the actual cohort survival probabilities of a number of old-age cohorts and is not subject to the problem of data incompleteness. This new type of survival curves is called hybrid survival curve because it builds upon the strengths of the existing types of survival curves.

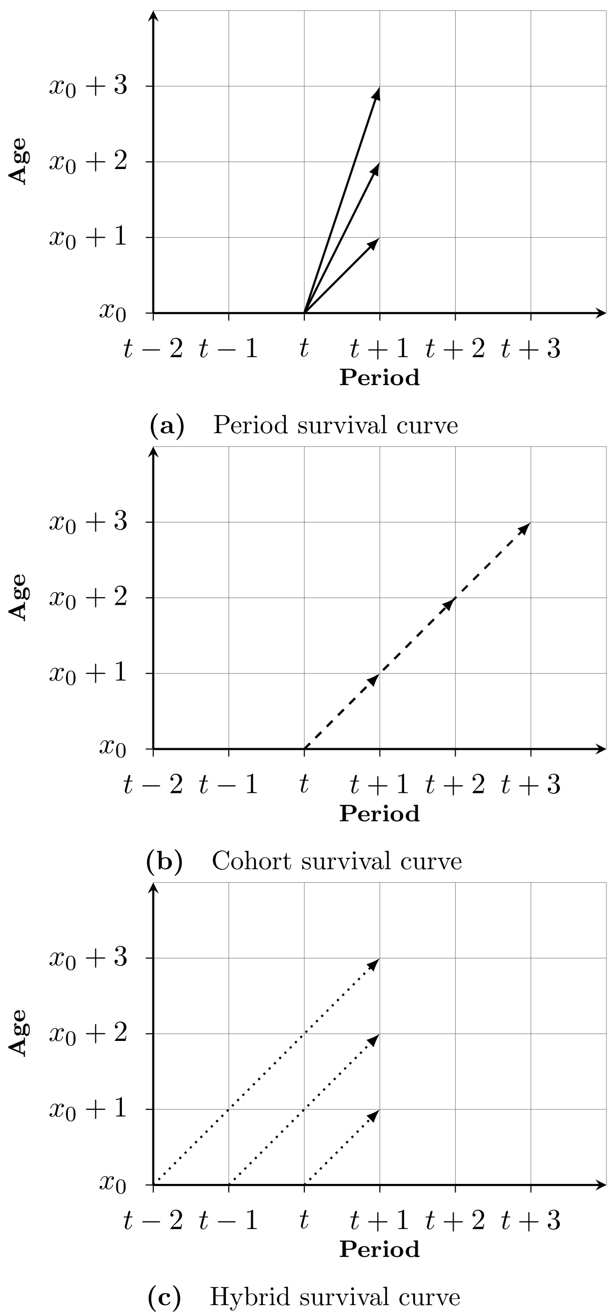
Specifically, a hybrid survival curve in year t comprises of a collection of ${}_{n}s^{h}_{x_0,t}$, for $n = 0, 1, 2, \ldots, N$, where each of them is defined as the cohort survival probability for a person with a fixed starting age of x_0 at the beginning of year $t-n+1$ to survive for n years until the end of year t, expressed in terms of the one-year death probabilities of the corresponding cohort as follows:

$$
{}_{n}s^{h}_{x_0,t} = \begin{cases} 1, & n = 0, \\ \prod_{i=0}^{n-1}(1 - q_{x_0+i,t-n+1+i}), & n = 1, 2, \ldots, N. \end{cases} \tag{3}
$$

The specifications of the death probabilities used to calculate the survival probabilities in Equations (1) – (3) are depicted in the age-period cells in Figure 3. Each arrowed line represents a specific point on survival curve, where the coordinate components (x, t) along the way for integer ages x refer to the death probabilities $q_{x,\lfloor t \rfloor}$'s used in obtaining the survival probabilities. In Figure 3(a), we observe that a period survival curve is only based on the one-year death probabilities in a single period. In contrast, cohort and hybrid survival curves are dependent on the one-year death probabilities of the corresponding cohorts over time, as shown by the 45° diagonal lines in Figure 3(b) and 3(c). The main difference between cohort and hybrid survival curves is that the mortality experience up to year t of multiple cohorts (correspond to $n = 1, 2, \cdots, N$ in Equation (3)) are considered in constructing the hybrid survival curves of year t, whereas the cohort survival curve is only based on a single cohort over time.

In this paper, we assume that the starting age x_0 is age 60 because the significant mortality improvements in premature ages (i.e., before aging-related deaths become substantial at older ages) — referred to as the horizontalisation of survival curve by Cheung et al. (2005) — make the death probabilities below age 60 relatively unimportant. As a result, the survival probabilities from birth until ages below age 60 are moving closer to 1 over time and do not exhibit an obvious varying pattern. One limitation about picking age 60 as the starting age is that this choice may not be appropriate for developing countries in which the mortality rates below age 60 may be comparatively more significant. In such a situation, we may still use the proposed modelling approach by setting a lower starting age. Besides that, the raw mortality data obtained from the Human Mortality Database beyond age 90 may not be sufficiently reliable because the corresponding population counts are estimated by using the extinct cohort method. Hence, we assume that length of survival n years from age 60 is at most 31 years such that the mortality data beyond age 90 are not required in building a hybrid survival curve.

By definition, we have ${}_{0}s^{h}_{60,t}$ equals to 1. Also, the survival probabilities with a starting age of 60 can be expressed in terms of the corresponding survival probabilities with a starting age of 0 as



(a) Period survival curve

(b) Cohort survival curve

(c) Hybrid survival curve

Figure 3 The specification of age-period cells in obtaining the survival probabilities under the three types of survival curves follows:

$$ {}_n s^h_{60,t} = {}_n s^c_{60,t-n+1} = \frac{{}_{60+n} s^c_{0,t-n-59}}{{}_{60} s^c_{0,t-n-59}} \quad n = 1, 2, \ldots, 31. \tag{4} $$

Therefore, the value of ${}_n s^h_{60,t}$ can serve as a good approximation to ${}_{60+n} s^c_{0,t-n-59}$ if the value of ${}_{60} s^c_{0,t-n-59}$ in the denominator of Equation (4) is approaching 1 due to consistent mortality improvements for the ages below 60. As shown in Equation (3), in calculating the n-year cohort survival probabilities, the historical mortality data of the underlying cohort over the period of $[t-n+1, t]$ are needed. With a chosen maximum value of $N = 31$, the corresponding data sample period of $[t-n+1, t]$ for 31 distinct cohorts ($n = 1, 2, \ldots, 31$) are required to construct the hybrid survival curve in year t. This data requirement is a constraint of the hybrid survival curve in comparison to both period and cohort survival curves.

Furthermore, since the hybrid survival curve is made up of the actual survival probabilities of multiple different cohorts, it may not necessarily be strictly decreasing, as opposed to the cases of period and cohort survival curves that monotonically decline. Nonetheless, the monotonically decreasing property of survival curves is not essential in our study given that our aim is to model the evolution of the hybrid survival curves over time.[2]

The hybrid survival curve, which possesses the strengths of both existing types of survival curves, provides an alternative to study the rectangularisation pattern of survival curves. This is because we can search for its empirical evidence by examining the trends of the survival probabilities shown by a multitude of real (not hypothetical) cohorts on a collection of hybrid survival curves over time. Despite the limitation that the construction of the hybrid survival curve of year t requires the historical data of 30 years prior to year t (unlike the period survival curve that is only based on the period mortality data in year t), this approach is able to avoid the problem faced by cohort survival curve that can only be constructed for a specific extinct cohort.

As an illustration, we consider the gender-specific mortality data of Swedish and Bulgarian populations with a sample period of years 1947 to 2009 obtained from the Human Mortality Database (2013).[3] With this sample period, the earliest hybrid survival curve for each population is of year 1977. The hybrid survival curves of these gender-specific populations in years 1990 and 2000 are plotted in Figure 4.

We observe that the respective hybrid survival curves of Swedish males and females shift towards the top right corner over time, providing empirical evidence for the rectangularisation phenomenon. Particularly, the hybrid survival curves of Swedish females exhibit a more obvious rectangularisation pattern than that of Swedish males. Also, the increment in survival probabilities

[2]In other words, we are interested in the evolution of the probabilities ${}_n s^h_{60,t}$ over time, instead of studying the survival probabilities across different values of n on a given hybrid survival curve.

[3]Most of the national populations in Human Mortality Database are developed countries. Bulgaria is the developing country with the earliest available mortality data which starts from year 1947.

of Swedish males appear to be more comparable across different ages and symmetrical around age 75 such that the corresponding hybrid survival curves become slightly more vertical over time. On the other hand, the increment in survival probabilities of Swedish females from age 60 to earlier ages are considerably smaller than that of older ages, making the steepness of the hybrid survival curves to remain relatively constant over time.

On the other hand, the hybrid survival curves of Bulgarian males and females exhibit differrent results. Firstly, they are not strictly decreasing, partly due to the mortality experience of Bulgarian populations as a developing country. Also, for Bulgarian females, the hybrid survival probabilities in year 2000 are slightly higher than those of year 1990 especially beyond age 82. The hybrid survival probabilities in year 2000 are lower (higher) than those of year 1990 for most of the ages below (above) age 82 for Bulgarian males. These results suggest that there are no clear evidences of rectangularisation pattern for Bulgarian populations.

For graphical comparison purpose, the survival probabilities of the three types of survival curves for Swedish males and females from age 60 up until age 91 are shown in Figure 5. The illustrated period and hybrid survival curves are of years $t = 1990, 2000$, whereas the cohort that were born in year $t - 60 = 1930, 1940$ are chosen for the cohort survival curves such that these two cohorts would have attained age 60 at the beginning of year t. For the subsequent parts of these curves, the cohort survival curves depend on the cohort mortality rates after year t, the period survival curves use the period mortality rates in year t, while the hybrid survival curves are constructed based on the historical mortality rates of up to year t.

As expected, due to the consistent mortality improvements, the survival probabilities from age 60 to ages 62–91 under the period survival curves are higher than that of under the hybrid survival curves in the same year. This finding suggests that using the period survival curves may overestimate the survival probabilities of the real cohorts under consideration because these multiple cohorts are subject to the mortality experience of up to year t and not solely dependent on the period mortality data in year t as derived from period survival curves. On the other hand, the cohort survival curves yield the highest survival probabilities from age 60 to ages 62–91, because the mortality experience that improve over time are taken into account in building the cohort survival curves. Nevertheless, the cohort survival curves are subject to the problem of data incompleteness (the mortality data is only available up until year 2009) and thus may not be appropriate in demographic applications. Finally, it is evident that all three types of survival curves exhibit the pattern of rectangularisation when we study the evolution of survival curves from year 1990 to year 2000.

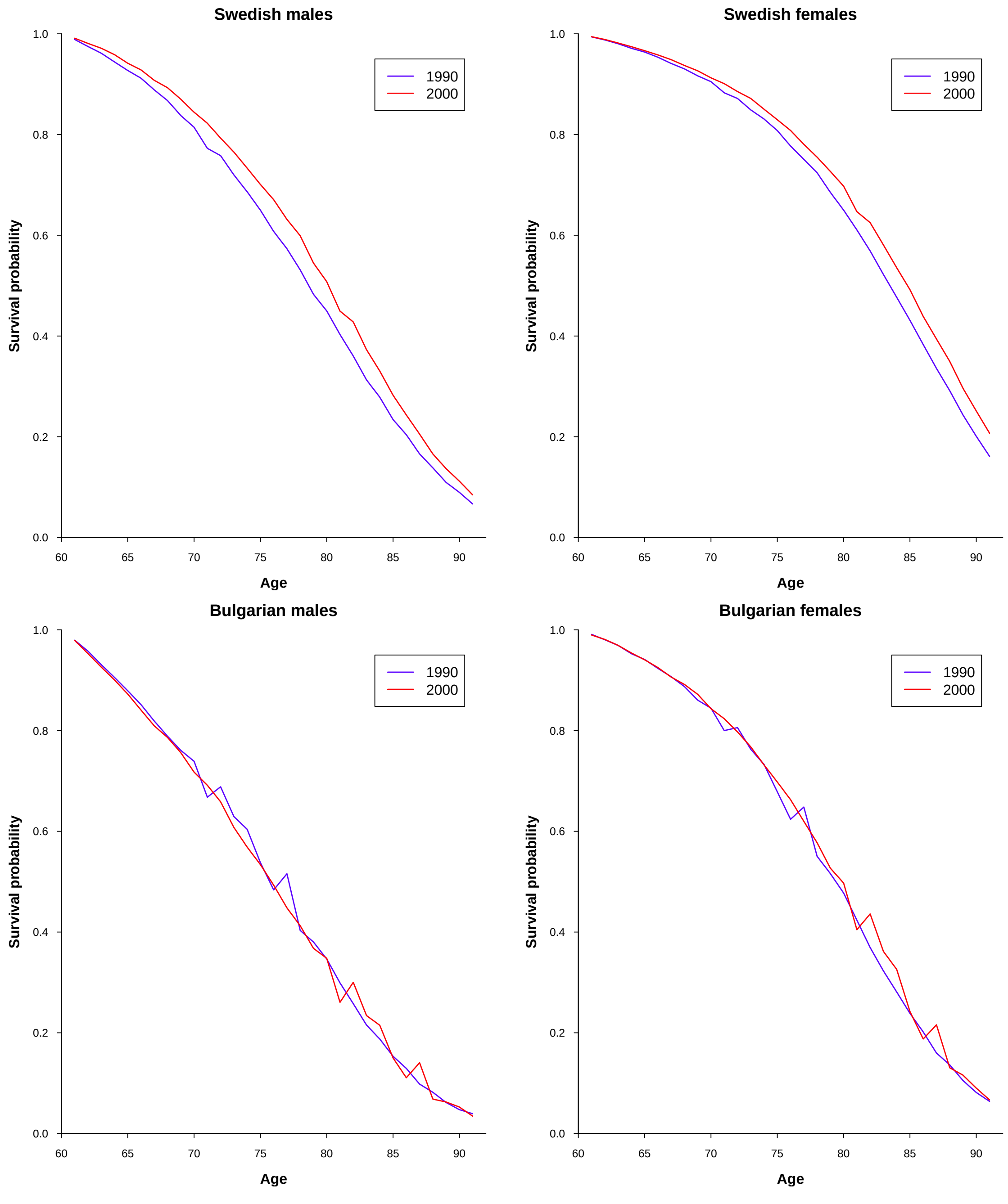


Figure 4 The hybrid survival curves of the gender-specific populations in years 1990 and 2000.

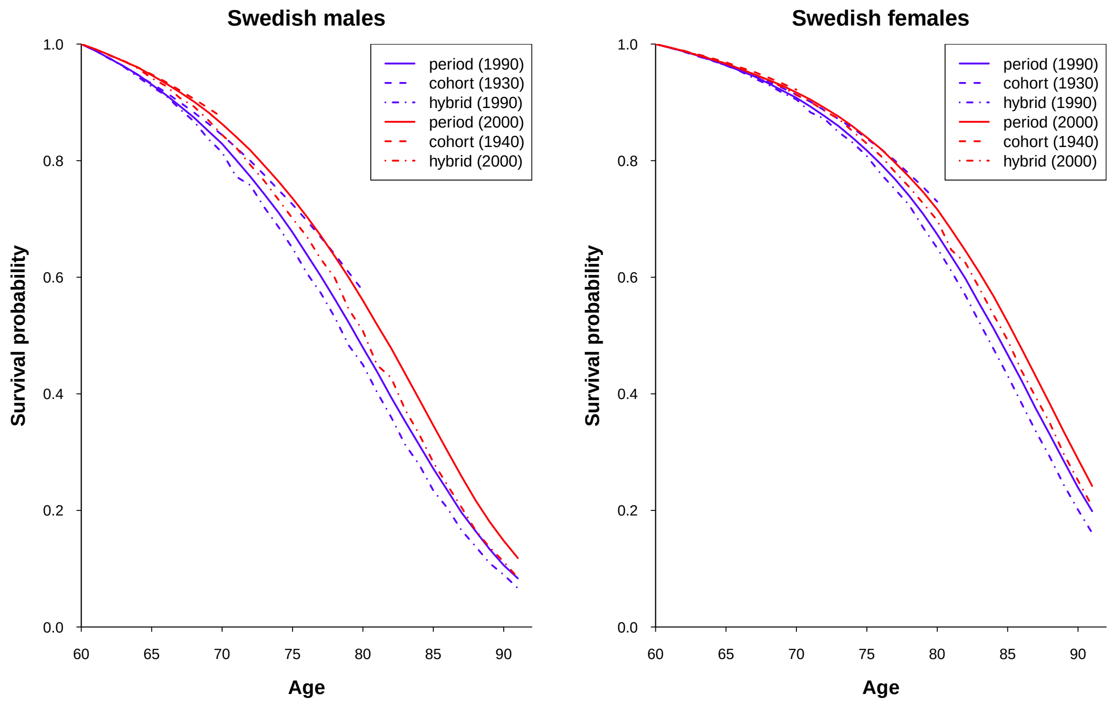


Figure 5 The period, cohort and hybrid survival curves of Swedish males and females.

3. Stochastic Models

3.1. Existing Stochastic Mortality Models

The existing stochastic mortality models can be categorised into two broad classes based on the underlying response variable. One of them features the modelling of logarithmic central death rates denoted as $\ln(m_{x,t})$. The original Lee-Carter (LC) model (Lee and Carter, 1992) was the first extrapolative model developed for the logarithmic central death rates, estimated through the method of singular value decomposition (SVD). Since then, this model has been extended to account for certain important features of mortality rates, to jointly model the mortality rates of multiple populations and to improve the model fitting.

For instance, Renshaw and Haberman (2006) incorporated the cohort effect parameters in the Renshaw-Haberman (RH) model, which can be seen as a general case for the Age-Period-Cohort (APC) model studied by Osmond (1985). Li and Lee (2005) suggested the common factor model and its augmented version to cater for the joint mortality modelling of both sexes. Other extensions included the use of higher order SVD terms (Booth et al., 2002) and additional parameters (Renshaw and Haberman, 2003) to enhance the goodness-of-fit. More recently, Li (2013) proposed the Poisson common factor model as an extension of the augmented common factor model to allow for additional gender-specific factors.

The logit-transformed death probabilities denoted as $\ln(\frac{q_{x,t}}{1-q_{x,t}})$ is the response variable in another class of mortality models. This type of modelling was first featured in the Cairns-Blake-Dowd

(CBD) model by Cairns et al. (2006). The original CBD model is a two-factor model, in which its two factors correspond to the intercept and the slope of the logit-transformed $q_{x,t}$ for higher ages above age 60. This model is subsequently extended to incorporate cohort effect and quadratic age effect by Cairns et al. (2009).

The variables of interest in these two classes of mortality models are $m_{x,t}$ and $q_{x,t}$. This may explain why the modelling of period survival probabilities was not considered in previous research, possibly because the modelling of $m_{x,t}$ and $q_{x,t}$ provides a one-to-one correspondence to the modelling of period survival probabilities, which can be expressed in terms of multiplicative products of one minus death probabilities $(1 - q_{x,t})$'s for a fixed period t as shown in Equation (1). The modelling of cohort survival probabilities was not addressed mainly because it only keeps track of the survival probabilities of a single cohort over time, which implies that the estimated parameters would only offer little practical use for forecasting purposes.

3.2. A New Class of Stochastic Models

With the newly developed hybrid survival curve, we are essentially analysing a collection of cohort survival probabilities from age 60 to survive to year t. In this subsection, we aim to develop a new class of stochastic models based on the hybrid survival curve, which can be used to complement the existing mortality models in summarising the different elements of longevity trends. In building new stochastic models, a useful reference is Hunt and Blake (2014), who generalised all of the models discussed in Section 3.1 except the RH model into a general structural form. Note that although Hunt and Blake (2014) focused on mortality models, the structural form is still relevant and useful for developing survival models, because both types of models are driven by mortality data. In more detail, a link function is needed to transform the observed data into an appropriate form for modelling purpose, and a series of age/period/cohort terms — which could be parametric or non-parametric — are utilised to fit the transformed response variable.

In what follows, we demonstrate that by using a suitably chosen transformation, a hybrid survival curve can be transformed into a form suitable for modelling, in which a series of age functions and time-varying parameters can be utilised to model the transformed hybrid survival curve between ages 61–91 in each year. Empirically, we find that the appropriate combination of transformations for the survival probabilities are as follows:

- we first annualise the survival probabilities, that is, calculate the $1/n$-th power of the n-year survival probabilities, for $n = 1, 2, \cdots, 31$;
- we then apply the logit transformation onto the annualised survival probabilities,

whereby the resulting transformed survival probabilities appear to be a simple function of age x and can be fitted accordingly. The use of logit transformation ensures that both the annualised

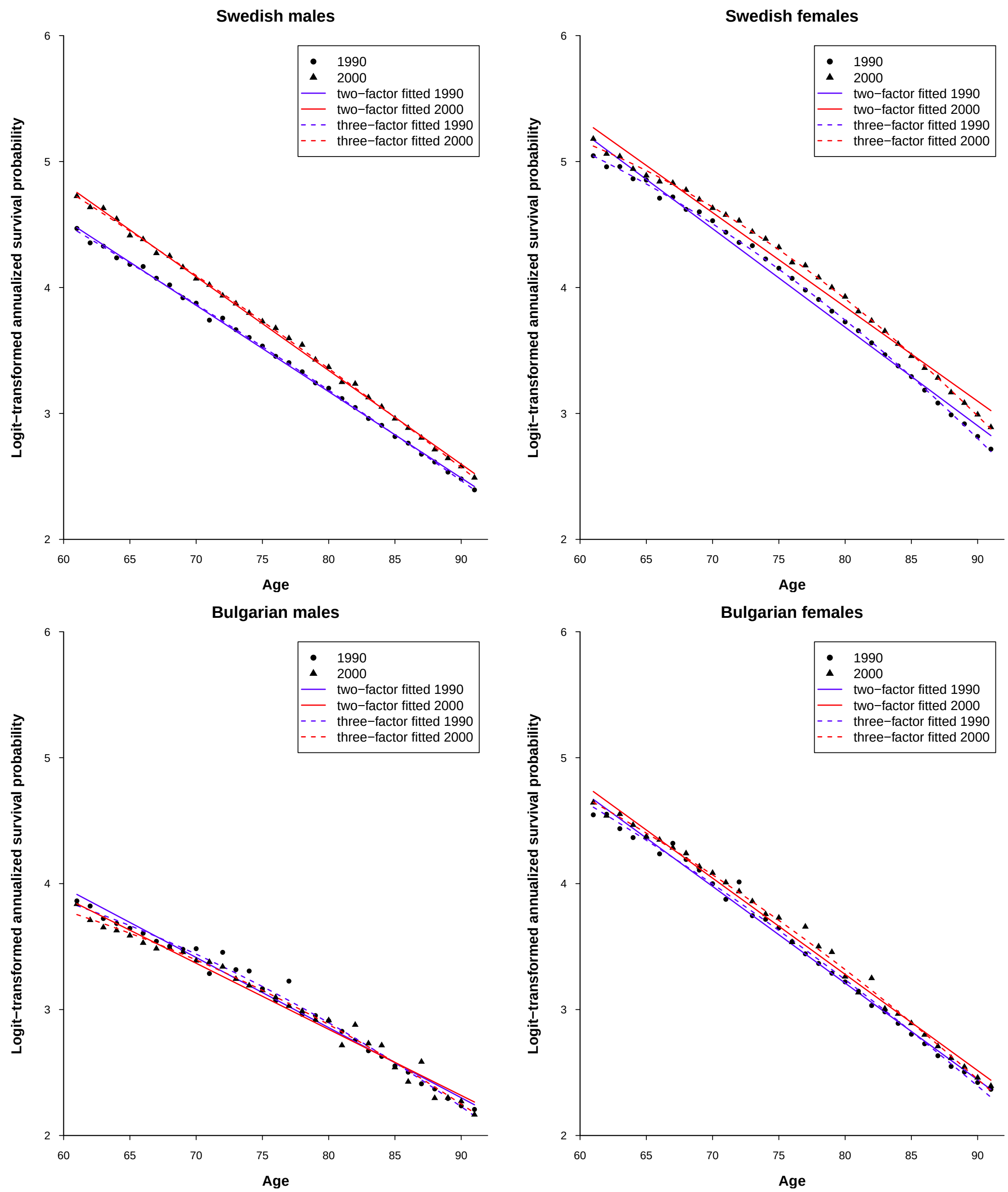


Figure 6 The logit-transformed annualised survival probabilities and the corresponding fitted curves using the two-factor and three-factor survival models.

and original survival probabilities are bounded between 0 and 1 when they are transformed back from the fitted model response variables. In addition, the data point of ${}_0s^h_{60,t} = 1$ is not included in the model parameter estimation because it is undefined under the chosen logit transformation.

To illustrate, the transformed hybrid survival curves for Swedish males and females as shown in Figure 6 suggest that linear and quadratic functions of age x can be used to fit the curves. Accordingly, we propose to model them by using linear and quadratic functions of $(x - \bar{x})$ because the fitted curves by using functions of x and $(x-\bar{x})$ are the same although the estimated parameters are different.

3.3. *The Stochastic Survival Models*

The two survival models are written as follows:

$$\begin{aligned}
\ln\left(\frac{{}_n s_{60,t}^{h\ \ 1/n}}{1-{}_n s_{60,t}^{h\ \ 1/n}}\right) &= \sigma_t^{(1)} + \sigma_t^{(2)}(x-\bar{x}) \\
&= \sigma_t^{(1)} + \sigma_t^{(2)}(n-\bar{n}), \qquad (5) \\
\ln\left(\frac{{}_n s_{60,t}^{h\ \ 1/n}}{1-{}_n s_{60,t}^{h\ \ 1/n}}\right) &= \sigma_t^{(1)} + \sigma_t^{(2)}(x-\bar{x}) + \sigma_t^{(3)}\left((x-\bar{x})^2 - s^2\right) \\
&= \sigma_t^{(1)} + \sigma_t^{(2)}(n-\bar{n}) + \sigma_t^{(3)}\left((n-\bar{n})^2 - s^2\right), \qquad (6)
\end{aligned}$$

where $x = 60+n$ is the attained age at the end of year t if the person survives, for $n = 1, 2, \ldots, 31$ and thus the second model expressions in Equations (5) and (6) follow; $\sigma_t^{(i)}, i = 1, 2, 3$ are the time-varying parameters; $\bar{x} = 76$ and $s^2 = 80$ are the arithmetic averages of x and $(x-\bar{x})^2$ over the sample age range respectively, or equivalently, $\bar{n} = 16$ and $s^2 = 80$ are the arithmetic averages of n and $(n-\bar{n})^2$.

The model in Equation (5) is built similarly as the original CBD model except for the different response variables. The original CBD model is used to model the logit-transformed death probabilities, whereas our model in Equation (5) is built to model the logit-transformed annualised cohort survival probabilities for a given year t. For brevity, we refer to this model as two-factor survival model because it involves two estimated parameters. Similarly, the model specified in Equation (6) is referred to as three-factor survival model. Our models are also similar to that of De Jong and Marshall (2007) who proposed the use of probit transformation onto the period survival probabilities and subsequently utilised the Wang transform in the mortality projection.

We perform Gaussian maximum likelihood estimation (MLE) to obtain the time-varying parameters $\sigma_t^{(i)}, i = 1, 2, 3$, which means that Equations (5) and (6) are assumed to be subject to normally distributed error terms. Note that the estimated time-varying parameters from Gaussian MLE are identical to those obtained from the least squares estimation. This approach is chosen because our response variable is dependent on the mortality experience in the previous n years, which implies that it is not possible to perform the commonly used Poisson MLE (see Brouhns et al., 2002) in the form of $D_{x,t} \sim \text{Poisson}(E_{x,t}m_{x,t})$. In more detail, the Poisson MLE is only applicable to response variable linked to the mortality data of a given age-period pair (x,t), that is, when $m_{x,t} = f(RV) = f\big(g(x,t)\big)$, where RV denotes the response variable written as a function g of mortality data of the age-period pair (x,t). For our proposed model, the term $m_{x,t}$ cannot be written in terms of the model response variable on the left hand side of Equations (5) and (6), because $\ln\left(\frac{{}_n s_{60,t}^{h}{}^{1/n}}{1-{}_n s_{60,t}^{h}{}^{1/n}}\right)$ is dependent on the mortality data of multiple age-period cells including the cells of $(60, t-n+1), (61, t-n+2), \cdots, (60+n-1, t)$. Due to the same reason, Poisson MLE was not used in the modelling of mortality improvement rates in Haberman and Renshaw (2012), in which the model response variable is expressed in terms of the mortality rates in two adjacent years.

The fitted curves using both models are also shown in Figure 6. Graphically, it can be seen that the three-factor survival model provides a much better fitting than that of the two-factor survival model for Swedish populations, especially for the survival curves of Swedish females. This finding indicates that the inclusion of the curvature parameter would provide an improved fitting under the presence of significant curvature effect. In contrast, it is not clear graphically that which of the survival models provides a better fit for the Bulgarian males and females.[4]

The maximum likelihood estimates of $\sigma_t^{(i)}$ for $i = 1, 2, 3$ for all gender-specific populations are depicted in Figure 7. The maximum likelihood estimates of $\sigma_t^{(i)}$ for $i = 1, 2$ are identical in both models due to the specification of functions of $(x - \bar{x})$. In particular, we find that the values of $\sigma_t^{(1)}$ for both Swedish populations and Bulgarian females appear to be increasing linearly over time, whereas the values of $\sigma_t^{(1)}$ for Bulgarian males are fairly stable.

Apart from that, the two-factor survival model is a special case of the three-factor survival model with $\sigma_t^{(3)} = 0$, so the log-likelihood value of the latter is guaranteed to be larger. To strike a balance between goodness of fit and model parsimony, we make use of the Bayesian Information Criterion (BIC) defined as $\text{BIC}_r = -2\hat{l}_r + v_r \log n_d$, where $\hat{l}_r$ is the maximised log-likelihood value of model r, v_r is the effective number of free parameters and n_d is the number of observations in the data. For the indicative purpose of selecting between these two models, we prefer a model with a lower BIC value.

As parameter estimation for each of the survival models is carried out for each year separately, the BIC is also calculated for each year (if there are also age-specific or cohort-related parameters, we cannot compute the value of BIC for each year), and the values of BIC are shown in Figure 8. It is evident that the BIC values produced by the three-factor survival model are consistently better over time for all populations since year 1984, indicating that the inclusion of curvature parameter in each year significantly improves the model fitting. The differences in BIC values between both survival models are the largest for Swedish females, consistent with the curvature effect as shown in Figure 6. Besides that, as we shall discuss in Section 4, each of the three parameters is highly interpretable.

[4]Nevertheless, as we shall see later, the three-factor survival model provides a better fitting in terms of the Bayesian Information Criterion (BIC). Also, due to the unclear evidence to support the rectangularisation for Bulgarian populations, the numerical illustrations and discussions in Sections 4 and 5 only focus on the gender-specific Swedish populations.

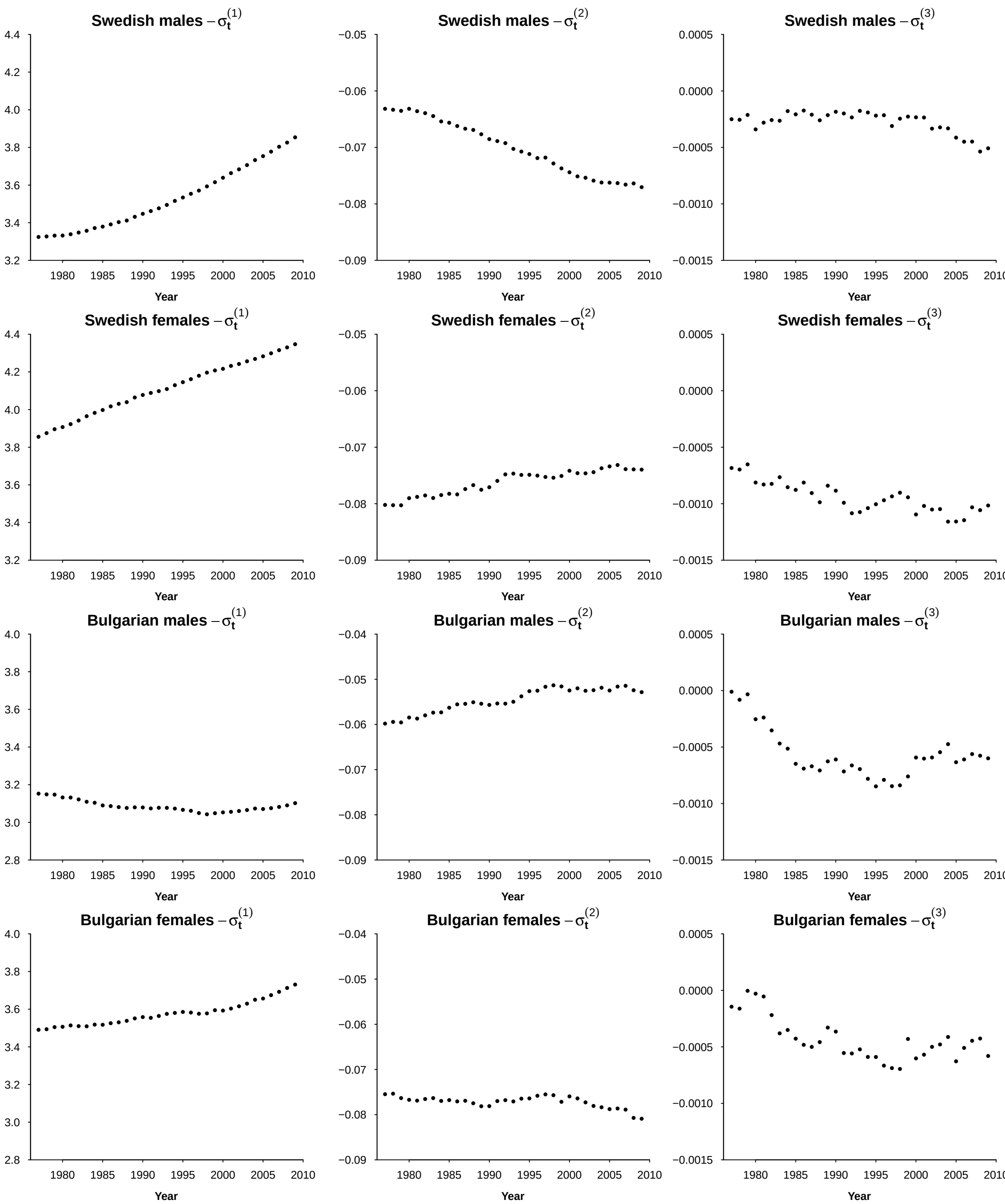


Figure 7 The maximum likelihood estimates (MLE) of $\sigma_t^{(i)}$ for $i = 1, 2, 3$.

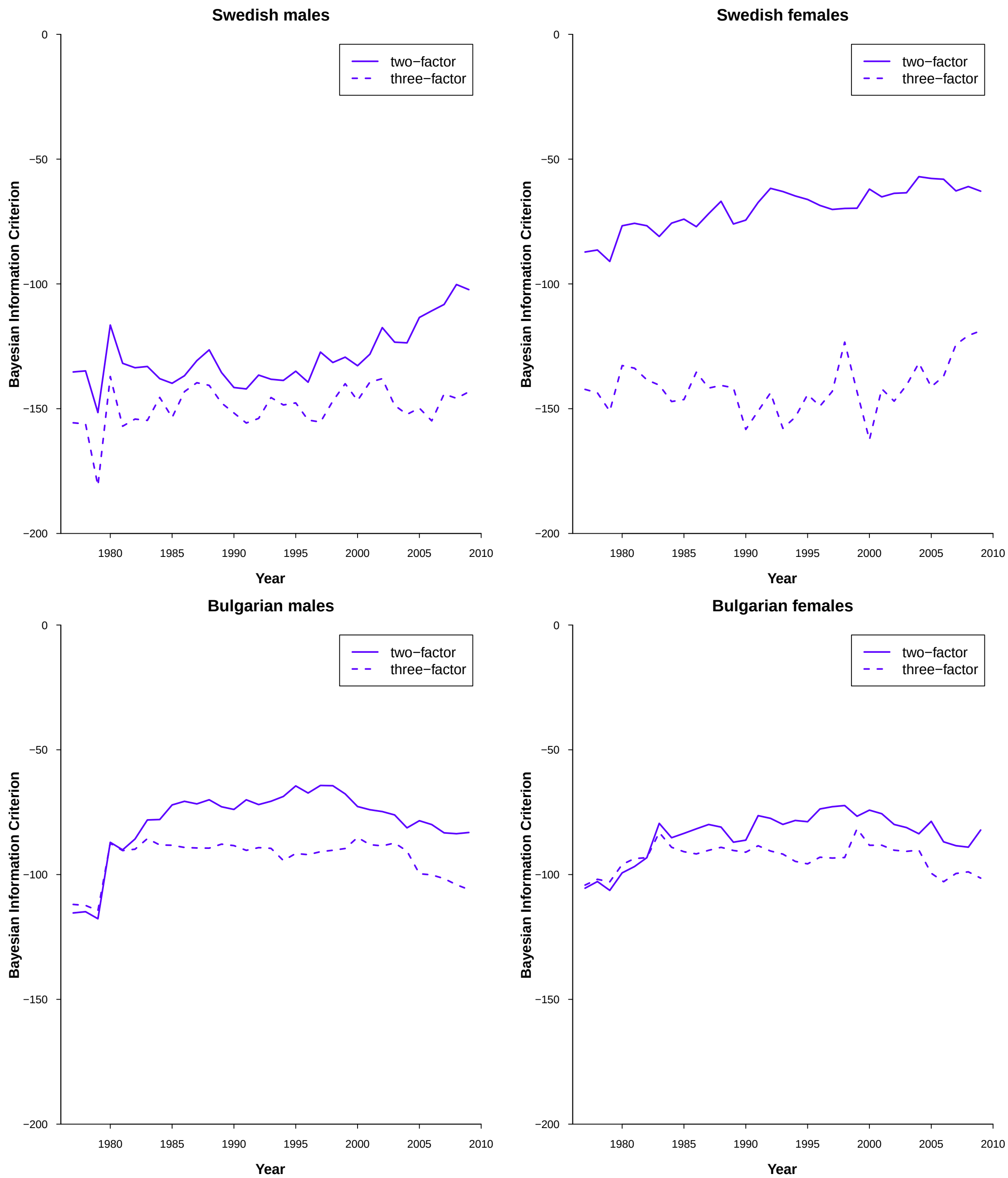


Figure 8 Values of the Bayesian Information Criterion (BIC) for the two-factor and three-factor survival models.

4. Interpreting the Three-Factor Survival Model

The time-varying parameters of the three-factor survival model can be used to summarise the longevity patterns exhibited by a multitude of cohorts in each year. For each year t, the three time-varying parameters represent the estimated intercept, slope and curvature of the transformed hybrid survival curve, respectively. Apart from that, the trends of these time-varying parameters are useful in detecting the rectangularisation and the verticalisation of survival curve. In what follows, we first describe the alternative ways of interpreting these two concepts before we associate them with the trends of the time-varying parameters.

The rectangularisation of survival curve (of any types, including period, cohort and hybrid) means that given the specific age attained $x = 60 + n$, each of the survival probabilities increases over time. This phenomenon can be graphically represented by an upward shift for the survival probabilities over successive time periods. Therefore, we can make use of the positive change of the area under the survival curve over time as an indication of the rectangularisation phenomenon. Note that the area under the hybrid survival curve of year t can be interpreted as a special case of the cross-sectional average length of life (CAL) discussed by Guillot (2003), whereby each of the survival probabilities being considered here has a fixed starting age of 60 instead of 0 (at birth).

The verticalisation of survival curve is associated with an increasing magnitude of the steepness of survival curve. The steepening of survival curve can be attributed to the concentration of death ages for period and cohort survival curves. However, due to the different structure of survival curves, the quantities used by Cheung et al. (2005) in measuring the degree of verticalisation are not applicable for hybrid survival curves.

To overcome this problem, let us suppose, as an illustrative concept, that the degree of verticalisation is approximated by the angle formed between: 1) two specific points on the hybrid survival curve that form an approximated tangential line to the curve and 2) a vertical line. Note that we do not specify how these two points are chosen, the only requirement is that these two points are located around the centre portion of the hybird survival curve such that it offers a good approximation to the tangential line.

The main reason for the verticalisation of hybrid survival curve is that the mortality improvements for the cohorts of younger ages are faster than those of older ages, in such a way that the increment of survival probabilities for younger ages are larger than that for older ages. As shown graphically in Figure 9, these movements of survival probabilities lead to a steeper tangential line formed by the two specific points used in the approximation and result in a smaller angle (i.e., $\theta_{t_2} < \theta_{t_1}$), indicating that the survival curve possesses the verticalisation pattern.

With these descriptions in place, in what follows, we discuss the interpretation of each time-varying parameter (keeping other things being equal) towards the phenomenons of rectangularisa-

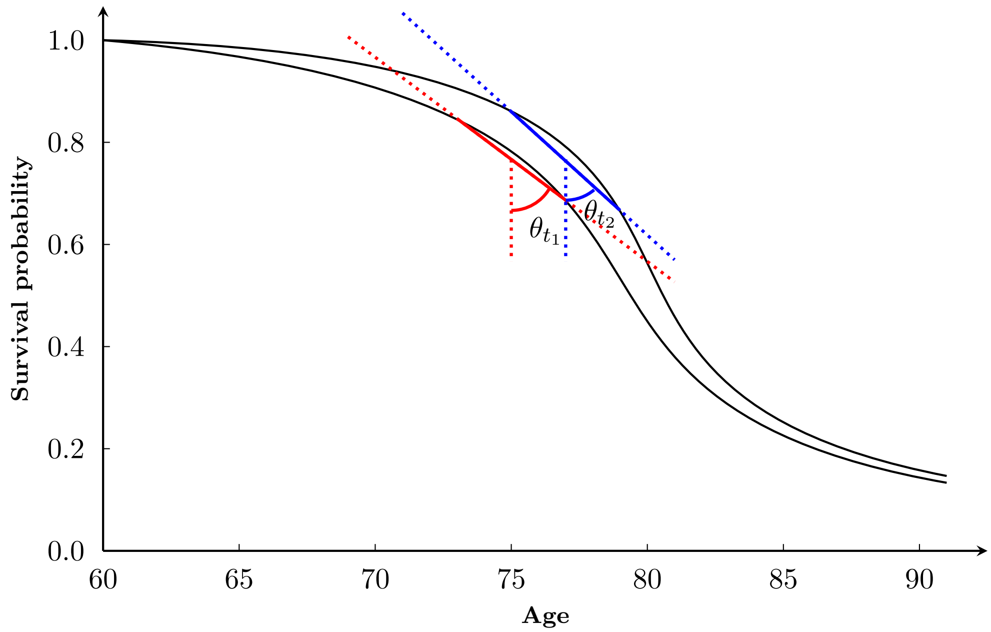


Figure 9 Verticalisation of survival curve.

tion and verticalisation of survival curve, as illustrated graphically in Figure 10.

An upward trend in the value of $\sigma_t^{(1)}$ would result in a higher value of n-year survival probabilities for all n, which can be seen by deriving the following partial derivative:

$$\frac{\partial {}_n s_{60,t}^h}{\partial \sigma_t^{(1)}} = {}_n s_{60,t}^h \cdot \frac{n}{1 + e^{\sigma_t^{(1)} + \sigma_t^{(2)}(n-\bar{n}) + \sigma_t^{(3)}((n-\bar{n})^2 - s^2)}} > 0, \text{ for } 1 \leq n \leq 31. \tag{7}$$

This implies that the hybrid survival curve would shift up for each age x and move towards a rectangular shape, as shown in solid and dashed lines in Figure 10. It is easy to see that the area under the curve will grow over time. While $\sigma_t^{(1)}$ is an indicator for rectangularisation, it does not tell us exactly how the survival curve verticalise, largely because the resulting increments of survival probabilities vary with age and do not yield straightforward inferences about the steepness of survival curve.

A larger magnitude of negative value of $\sigma_t^{(2)}$ (i.e., a steeper slope) leads to a more vertical hybrid survival curve, as displayed in solid and dotted lines in Figure 10. In particular, the verticalisation is due to the change of survival probabilities with respect to the change of $\sigma_t^{(2)}$ in different directions according to the range of n, derived as follows:

$$\frac{\partial {}_n s_{60,t}^h}{\partial \sigma_t^{(2)}} = {}_n s_{60,t}^h \cdot \frac{n(n-\bar{n})}{1 + e^{\sigma_t^{(1)} + \sigma_t^{(2)}(n-\bar{n}) + \sigma_t^{(3)}((n-\bar{n})^2 - s^2)}} \begin{cases} < 0, & \text{for } 1 \leq n < 16, \\ = 0, & \text{for } n = \bar{n} = 16, \\ > 0, & \text{for } 16 < n \leq 31. \end{cases} \tag{8}$$

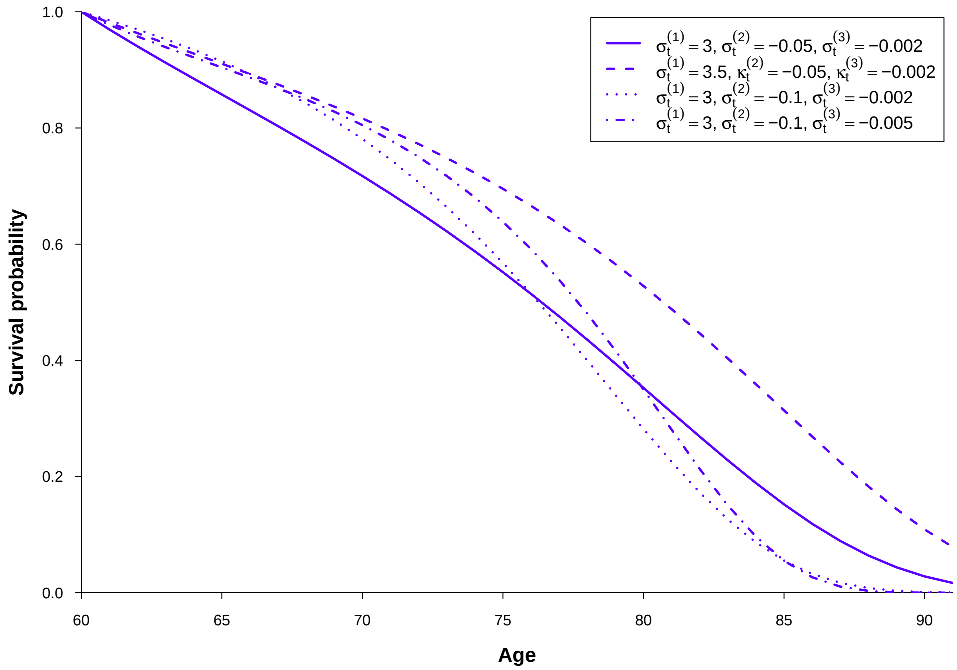


Figure 10 The hybrid survival curves implied by four different combinations of the time-varying parameters.

This explanation is aligned with the earlier descriptions about the faster mortality improvements for the cohorts of younger ages than those of older ages. Also, it should be noted that empirically the slope of the logit-transformed curve is negative because the mortality rates at older ages are generally higher, so the logit-transformed annualised survival probabilities are lower for larger value of n (surviving to older ages). Nevertheless, the opposed changes of survival probabilities due to $\sigma_t^{(2)}$ based on the range of n does not offer simple interpretations about the change of the area under the curve and hence on the rectangularisation phenomenon.

A smaller value of $\sigma_t^{(3)}$ leads to a larger area under the curve, as depicted in the dotted and dashed dotted lines in Figure 10. The reason for this interpretation is that the directional sensitivity of survival probabilities towards the change of $\sigma_t^{(3)}$ behaves according to the range of n as shown in the following partial derivative:

$$\frac{\partial_n s_{60,t}^h}{\partial \sigma_t^{(3)}} = {}_n s_{60,t}^h \cdot \frac{n\left((n-\bar{n})^2 - s^2\right)}{1 + e^{\sigma_t^{(1)} + \sigma_t^{(2)}(n-\bar{n}) + \sigma_t^{(3)}((n-\bar{n})^2 - s^2)}} \begin{cases} < 0, & \text{for } 17 < n < 25, \\ > 0, & \text{for } 1 \le n \le 7, 25 \le n \le 31, \end{cases} \tag{9}$$

and also because the magnitude of changes are larger in the range of $17 < n < 25$. Moreover, the trend of $\sigma_t^{(3)}$ does not indicate how the survival curve vertilcalise over time. This is possibly because the implied changes of survival probabilities are relatively smaller due to the smaller magnitude change of $\sigma_t^{(3)}$, such that the steepness of the hybrid survival curve remains unaffected.

Hence, we could interpret an upward trend of $\sigma_t^{(1)}$ and a downward trend of $\sigma_t^{(3)}$as the indicators for the rectangularisation pattern, whereas the verticalisation of survival curve can be inferred from the declining value of $\sigma_t^{(2)}$. These interpretations, together with the estimated parameters as shown in Figure 7 and desribed as follows, are aligned with the earlier observations in Figure 4 for both Swedish populations:

- The value of $\sigma_t^{(1)}$ ($\sigma_t^{(3)}$) for Swedish females is increasing (decreasing, though with random oscillating fluctuations over time) at a faster pace than those of Swedish males, suggesting that the hybrid survival curves of Swedish females display a more obvious rectangularisation pattern over time.
- The value of $\sigma_t^{(2)}$ for Swedish males is subject to a downward trend, indicating that the hybrid survival curves of Swedish males tend to verticalise over time.
- For Swedish females, the upward trend in the value of $\sigma_t^{(2)}$ and the offsetting effect from the increment of $\sigma_t^{(1)}$ (which shifts up survival probabilities for all ages at varying extents) can be used to explain why the steepness of the hybrid survival curves for Swedish females remains relatively constant.

5. Forecasting with the Three-Factor Survival Model

Similar to other stochastic mortality models, the three-factor survival model is an extrapolative model, whereby the time-varying parameters can be extrapolated to obtain future forecasted values. In this section, we demonstrate how extrapolation and forecasting can be accomplished.

It is common to model the time-varying parameters in a stochastic mortality model with a univariate or multivariate random walk with drift. For example, this approach was used in the original work of Lee and Carter (1992) and Cairns et al. (2006). Following this approach, we utilise a trivariate random walk with drift for the time-varying parameters in the three-factor survival model. The time-varying parameters $\sigma_t^{(i)}, i = 1, 2, 3$ are jointly written in the form of a trivariate time series process $\boldsymbol{\sigma}_t = (\sigma_t^{(1)}, \sigma_t^{(2)}, \sigma_t^{(3)})'$ as follows:

$$\boldsymbol{\sigma}_t = \boldsymbol{\sigma}_{t-1} + \boldsymbol{\mu} + \boldsymbol{C}\boldsymbol{Z}_t, \tag{10}$$

where $\boldsymbol{\mu}$ is a constant 3×1 vector of drift coefficients, $\boldsymbol{C}$ is a constant 3×3 lower triangular matrix and $\boldsymbol{Z}_t$ is a 3×1 vector of standard normal variables. The innovation terms $\boldsymbol{\epsilon}_t$'s defined as $\boldsymbol{\epsilon}_t = \boldsymbol{\sigma}_t - \boldsymbol{\sigma}_{t-1} - \boldsymbol{\mu}$ are independently and identically distributed trivariate normal vectors with mean zero and constant variance-covariance matrix $\boldsymbol{\Sigma}$, and the matrix $\boldsymbol{C}$ is obtained from the Cholesky decomposition of the matrix $\boldsymbol{\Sigma}$. Note that a trivariate random walk with drift process may not be the best time series process for modelling these time-varying parameters. For instance, as shown by Chan et al. (2014), a random walk with drift process does not capture any serial- or cross-correlations that may exist within the time series parameters, thus they suggested to utilise a general class of Vector Autoregressive Integrated Moving Average (VARIMA) models for modelling purpose.[5] Nevertheless, since the aim of this section is to demonstrate the forecasting procedure for the three time-varying parameters and the projected hybrid survival curves, in our illustration we choose to utilise a trivariate random walk with drift. More importantly, the extrapolation procedure can be easily extended with the only extra complexity being the order identification of VARIMA process.

The extrapolation of the three-factor survival model is performed as follows. The MLE of $\boldsymbol{\sigma}_t$ for $t = 1977, 1978, \ldots, 2009$ in Figure 7 are fitted to the process specified in Equation (10) to estimate the values of $\boldsymbol{\mu}$ and $\boldsymbol{C}$. We then simulate 5000 realisation paths of standard normal $\boldsymbol{Z}_t$ and plug them into Equation (10) with the estimated values of $\boldsymbol{\mu}$ and $\boldsymbol{C}$ to obtain the forecasts of $\boldsymbol{\sigma}_t$ in years $t = 2010, 2011, \ldots, 2030$.

For both Swedish males and females, the mean forecasts and the 95% prediction intervals of the time-varying parameters $\sigma_t^{(i)}, i = 1, 2, 3$ are displayed in Figure A.1. It can be seen that the mean forecasts of the time-varying parameters follow their respective trends in the past due to the specification of random walk in Equation (10). For each parameter, the forecasting uncertainties in the future periods are captured by their 95% prediction intervals that fan out over time around the underlying trend.

With these forecasted parameters, we can project the hybrid survival curve into the future. Specifically, the average projections of the hybrid survival curve in year t is determined by averaging the survival probabilities ${}_n s^h_{60,t}$ for each $n = 1, 2, \ldots, 31$ obtained from the 5000 simulated scenarios. As an illustration, the projected hybrid survival curves of Swedish males and females are shown graphically in Figure 12. We observe that the hybrid survival curves of both populations are expected to rectangularise in the future periods.

Furthermore, it can be seen that the extent of rectangularisation is faster for the hybrid survival curves of Swedish females than those of Swedish males, largely due to the faster rising (declining) trends in the forecasted values of $\sigma_t^{(1)}$ ($\sigma_t^{(3)}$) for Swedish females as depicted in Figure A.1. This finding is consistent with the interpretations presented in Section 4 regarding the trends of $\sigma_t^{(1)}$ and $\sigma_t^{(3)}$ to indicate the rectangularisation pattern. Also, it appears that the verticalisation pattern can be found in the hybrid survival curves for Swedish males. This observation is mainly because of the downward trend shown by the extrapolated value of $\sigma_t^{(2)}$ for Swedish males in Figure A.1, consistent with the discussion in Section 4 that associates the trend of $\sigma_t^{(2)}$ to the verticalisation pattern.

[5] A trivariate random walk with drift is a special case of the general VARIMA (p, d, q) process with an order of $(0, 1, 0)$. For comparison purpose, we illustrate the forecasting of the parameters using a trivariate random walk with drift and the identified general VARIMA process in the Appendix. It is found that these time series processes produce similar forecasted values.

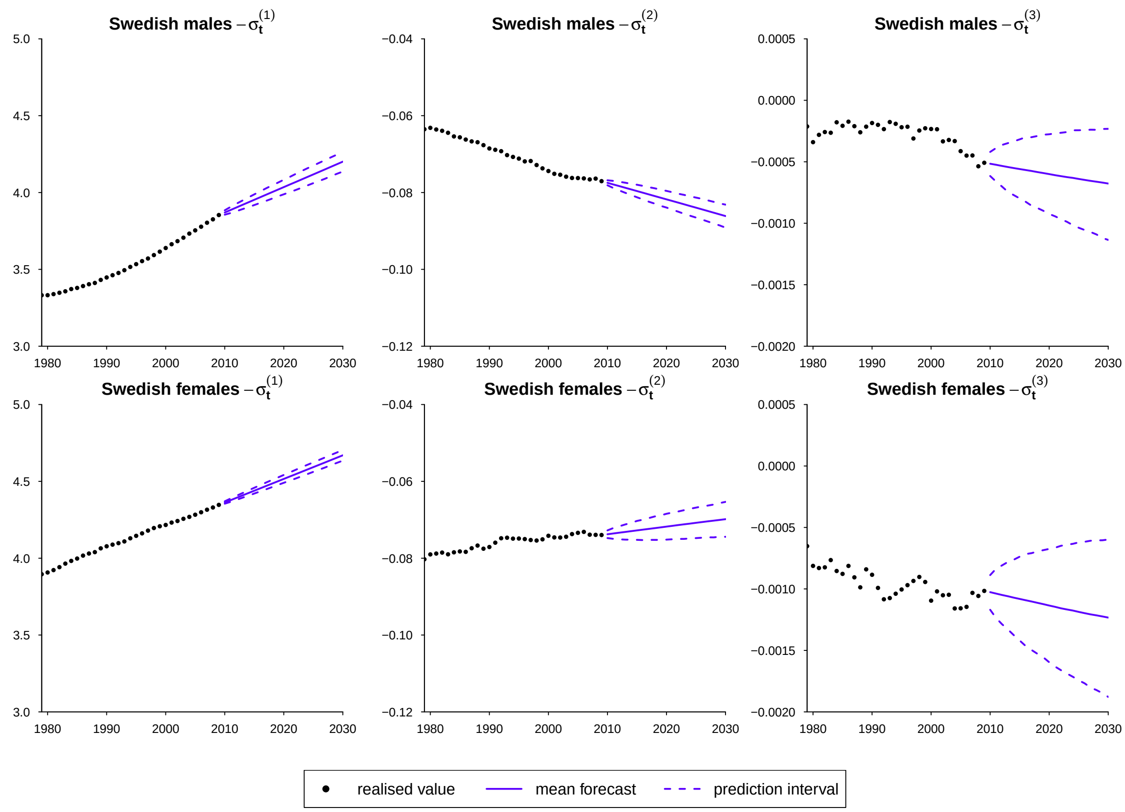


Figure 11 Forecasts of $\sigma_t^{(i)}$ for $i = 1, 2, 3$ in years 2010–2030 for Swedish males and females.

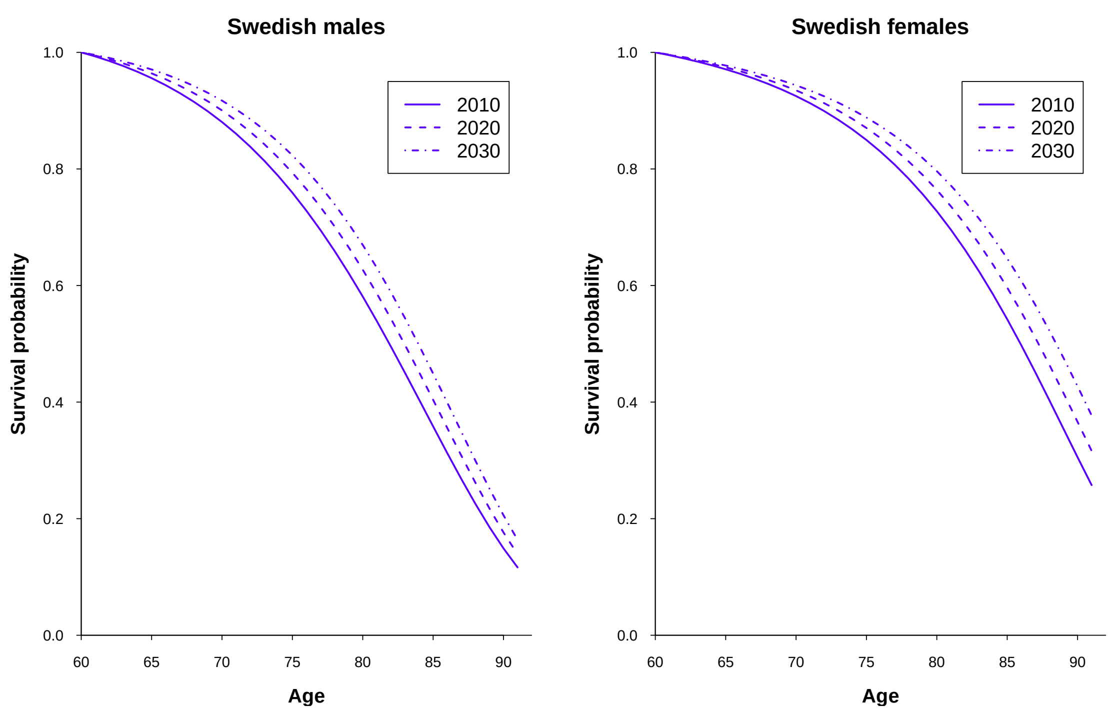


Figure 12 The average projections of the hybrid survival curves in years 2010, 2020 and 2030 for Swedish males and females.

6. Concluding Remarks

In view of the respective weaknesses of the existing types of survival curves, we illustrate the construction of a hybrid survival curve that comprises of the actual cohort survival probabilities and is free from the problem of data incompleteness. Because of these advantages, hybrid survival curve provides an alternative to both period and cohort survival curves in future empirical investigation on the rectangularisation phenomenon. Despite the mentioned advantages, we acknowledge that the idea of hybrid survival curve is subject to two limitations. Firstly, the construction of hybrid survival curve requires much more historical data than both period and cohort survival curves. Secondly, the hybrid survival curve is not guaranteed to be monotonically decreasing.

We develop two stochastic models to fit the hybrid survival curve. The time-varying parameters in the three-factor survival model produce a better fitting to the transformed hybrid survival curve than its two-factor counterpart. Moreover, each of the three parameters is highly interpretable especially with regards to the rectangularisation and the verticalisation patterns of survival curves. On top of that, the time-varying parameters are extrapolated into the future via a trivariate random walk with drift to obtain projected hybrid survival curves.

In this paper, we do not further examine the rectangularisation pattern via the existing indicator measures as reviewed by Cheung et al. (2005). This provides an avenue for future empirical research to examine whether the use of the hybrid survival curve could yield different conclusions regarding the rectangularisation phenomenon on the basis of those indicator measures. Specifically, since the structure of hybrid survival curve is different from that of period and cohort survival curves, modifications or adaptations may be needed in defining certain existing indicator measures. Alternatively, new measures that are specific to hybrid survival curve could be developed. Furthermore, the model expressions in Equations (5) and (6) may also be applicable to period and cohort survival curves. In future research, it is warranted to investigate the practicality and usefulness of extending the proposed survival models to those two types of survival curves.

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Appendix

Applying the modelling procedure described in Chan et al. (2014), both the trivariate time series process $\boldsymbol{\sigma}_t = (\sigma_t^{(1)}, \sigma_t^{(2)}, \sigma_t^{(3)})'$ for Swedish males and females are identified to follow a VARIMA(1,1,0) process. These parameters are then extrapolated to obtain future forecasted values. We find that the mean forecasts and the 95% prediction intervals for Swedish females under a VARIMA process are very close to those from using a trivariate random walk with drift, whereas more notable differences are observed in the forecasted values for Swedish males. Nevertheless, the forecasted values are similar under these two time series processes.

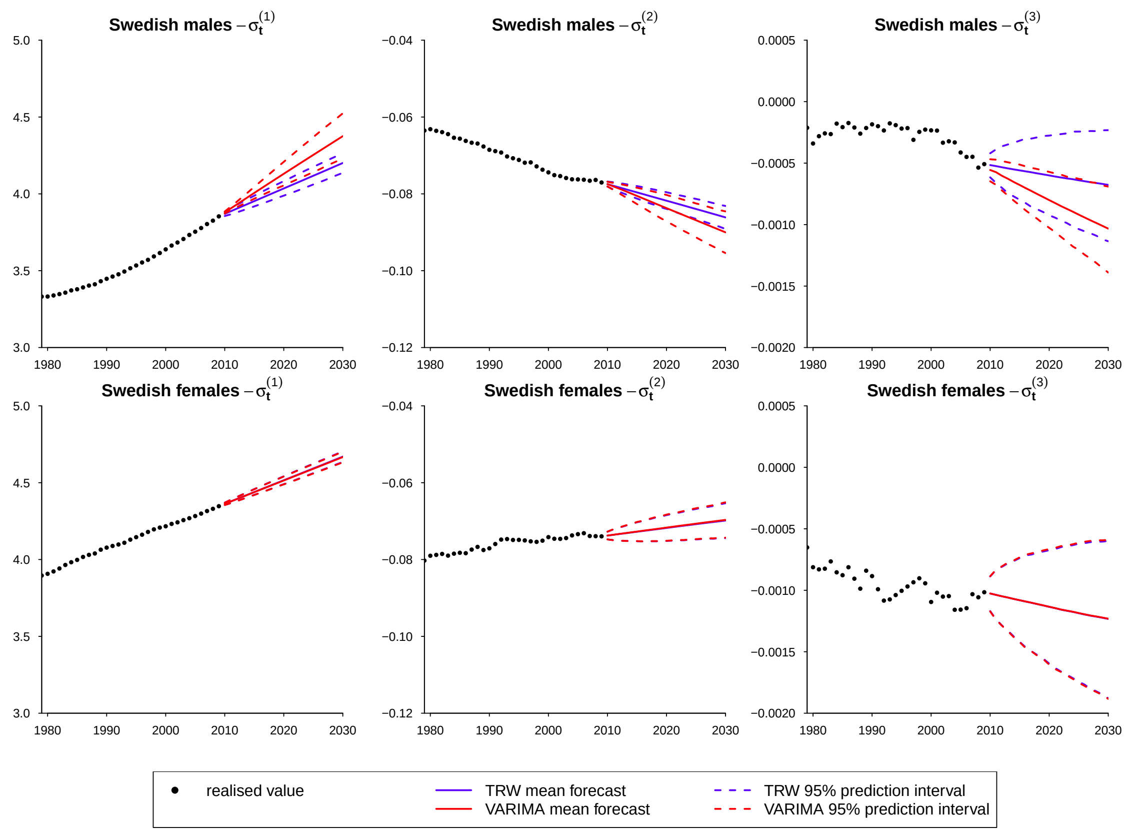

Figure A.1 Forecasts of $\sigma_t^{(i)}$ for $i = 1, 2, 3$ in years 2010–2030 under a trivariate random walk with drift and the identified VARIMA process for Swedish males and females.