

A Multifactor Generalisation of the Olivier-Smith Model for Stochastic Mortality

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Abstract

Recent years have seen the development of a number of models for the future development of aggregate mortality rates. Amongst these the Olivier and Smith model (Olivier and Jeffery, 2004, and Smith, 2005) was developed within the forward-rate framework discussed by Cairns et al. (2006) and Miltersen and Persson (2005). This model has a number of useful properties that make it a very good model for use in the valuation of life insurance contracts that incorporate embedded options.

We discuss here a generalisation of the Olivier and Smith model. Dynamics of the model in its published form are driven by a sequence of *univariate* gamma random variables. We demonstrate that the model in this form does not adequately match historical data. We discuss a generalisation of the model that uses multivariate Gamma random variables as drivers. This approach potentially gives us much greater control over the term structure of volatility of spot survival probabilities and over the correlation term structure. We introduce a possible approach for simulation of multivariate gamma random variables that facilitates

1 Introduction

1.1 Stochastic mortality

It is well-understood that aggregate mortality has improving over time in most countries and that the rates of improvement in different years and at different ages is unpredictable. (See, for example, CMI (2005), Currie, Durban and Eilers (2004), Richards, Kirkby and Currie (2006), and Richards et al. (2007).) This has led to the development of a number of stochastic mortality models. Cairns, Blake and Dowd (2006a) review the different approaches that can be taken by considering parallels with interest-rate modelling. A variety of models have been developed with statistical goodness of fit high on the list of criteria for a good model. Examples include Lee and Carter (1992), Brouhns et al. (2002), Renshaw and Haberman (2003, 2006), and Cairns, Blake and Dowd (2006b). Other approaches modelling in continuous time have focused more on the mathematical aspects of modelling with less emphasis on statistical validation. Examples include Dahl (2004), Biffis (2005) and Miltersen and Persson (2005).

1.2 Two types of stochastic mortality model

The first group of models listed above can be described in interest-rate terminology (Cairns et al, 2006b) as discrete-time *short-rate* models. Thus they provide a model that moves the “ q_x ” mortality curve forward one year at a time. The mortality curve in a given year is normally modelled as some function of a state variable $X(t)$ (with one or more factors). The dynamics of mortality rates, therefore, depend on the dynamics of $X(t)$.

As an alternative, *forward-rate* approaches to modelling have been proposed by Miltersen and Persson (2005), Olivier and Jeffery (2004) and Smith (2005). The latter two describe the Olivier and Smith discrete-time forward-rate model. Instead of modelling the one-dimensional mortality curve, this models the dynamics of the two-dimensional sheet of *forward survival probabilities*. In a forward-rate framework we model a hypothetical market in zero-coupon survivor bonds – often also known as pure endowment contracts. These life insurance contracts pay a defined amount of money on a future date T if the policyholder is still alive at time T . We have one such contract for each current age x and for each future payment date T . The prices of these contracts form a two-dimensional array and constitute a key part of the model input at time 0. Forward-rate models directly model the dynamics of the prices of all of these contracts through time.

1.3 Short-rate versus forward-rate models

The advantages and disadvantages of taking one approach over the other are as follows:

- Short-rate models are, in general, more straightforward to fit to historical data,

and get a good fit.

- Short-rate models are, in general, easier to simulate.¹
- Short-rate models make it straightforward to calculate zero-coupon survivor-bond prices at time 0. In contrast, forward-rate models require these prices as part of the input.
- For more complex life-insurance contracts (e.g. annuity guarantees) the value of the contract at some future date T depends on the mortality table in use at time T , including forward survival probabilities at T . With short-rate models this table is typically not available as a simple function of the state variable $X(T)$. Instead, each simulation of $X(T)$ requires a further bundle of simulations from time T to evaluate forward survival probabilities. In contrast, forward survival probabilities are a standard part of the output at time T . Forward-rate models are therefore ideal for pricing contracts with embedded options.

In this paper we will take a close look at the one-factor forward-rate model proposed by Olivier and Smith (see Olivier and Jeffery, 2004, and Smith, 2005). We will describe their original version in detail, but then demonstrate informally that the model does not fit historical data particularly well. Instead, we observe that more than one source of randomness is required in both the age and maturity dimensions, and that there is a non-trivial volatility and correlation term structure.

We discuss how the original Olivier and Smith model can, in theory, be generalised to address these statistical issues. Practical implementation of the generalised model requires simulation of dependent (but not identical) Gamma random variables. The challenge is that pairs of Gamma random variables need to satisfy a constraint that looks simple on paper, but which is difficult to implement.

2 Basic notation and the forward-mortality framework

In this section we will briefly review the basic notation used in the review of Cairns, Blake and Dowd (2006a).

We begin by defining two fundamental quantities

- the cash account, $C(t)$ = the accumulated value of an investment in the short-term money markets, and
- the survivor index $S(t, x) = \exp \left[\int_0^t -\mu(u, x + u) du \right]$,

where $\mu(u, y)$ is the force of mortality at time u for individuals aged y at that time.

¹The Olivier and Smith model is an exception to this, as we shall see later.

In our probabilistic world we let \mathcal{M}_t represent the filtration generated by the evolution of the force of mortality up to and including time t , and we let \mathcal{H}_t represent the augmented filtration that includes both mortality and interest rates up to time t . It follows that, given \mathcal{M}_t , $S(t, x)$ represents the probability that an individual aged x at time 0 survived to age $x + t$.

We now adapt the approaches to forward mortality modelling of Cairns, Blake and Dowd (2006a) and Miltersen and Persson (2005). First, we will work in discrete time rather than continuous time. Second, we consider as our core assets:

- cash, $C(t)$;
- a set of unit-linked, zero-coupon longevity bonds that pay $C(T)S(T, x)$ at time T , for $T = 1, 2, \dots$ and for $x \in \mathbb{Z}$ (we refer to this as the (T, x) bond).²

The price at time t for the (T, x) bond is denoted by $D(t, T, x)$ and we define in addition the discounted asset price processes $\tilde{D}(t, T, x) = D(t, T, x)/C(t)$.

We make the fundamental assumption that this market is arbitrage free and now apply the Fundamental Theorem of Asset Pricing. The assumption of no arbitrage then means that there exists a probability measure Q under which the prices of all assets discounted by the cash account are martingales: that is, the $\tilde{D}(t, T, x)$ are all Q -martingales.

This fundamental result means that³

$$\begin{aligned} D(t, T, x) &= E_Q \left[\frac{C(t)}{C(T)} C(T) S(T, x) \mid \mathcal{H}_t \right] \\ &= C(t) E_Q [S(T, x) | \mathcal{M}_t] \\ &= C(t) S(t, x) p_Q(t, t, T, x). \end{aligned} \tag{1}$$

In this equation we used the notation for market-implied *forward survival probabilities*

$$p_Q(t, T_0, T_1, x) = Pr_Q [\tau_x > T_1 | \tau_x > T_0, \mathcal{M}_t] = \frac{E_Q[S(T_1, x) | \mathcal{M}_t]}{E_Q[S(T_0, x) | \mathcal{M}_t]} \tag{2}$$

where τ_x is the future lifetime of an individual aged x at time 0. That is, $p_Q(t, T_0, T_1, x)$ is the probability, *based on information available at time t* , that, if the individual survives to time T_0 , he will then survive to time T_1 . Here T_0 might be before or after time t . Specifically if $T_0 < t$ and $T_1 > t$ then the forward survival probability is interpreted as the product of two parts: the survival probability from time T_0 to time t , which is measurable at time t , and an estimate of the probability of survival from time t to time T_1 .

²A simpler equivalent is to assume that interest rates are zero.

³In this expression note that the filtration \mathcal{M}_t tells us about the development of $\mu(u, x + u)$ over time. It does not tell us about the future lifetimes of specific individuals. The formula for the implied forward survival probabilities in (2) assumes that $Pr_Q[\tau_x > T_1 | \tau_x > T_0, \mathcal{M}_{T_1}] = S(T_1, x)/S(T_0, x)$: that is, there is no market price of risk for individual-specific mortality risk.

Now in general $E_Q[S(T, x)|\mathcal{M}_u]$ is a martingale under Q . We might decompose it in the following way:

$$E_Q[S(T, x)|\mathcal{M}_{t+1}] = p_Q(t, 0, t, x) \times p_Q(t+1, t, t+1, x) \times p_Q(t+1, t+1, T, x). \quad (3)$$

In this equation $p_Q(u, 0, t, x)$ is known by time $u = t$ and will not change after time t : that is, $p_Q(u, 0, t, x) = p_Q(t, 0, t, x)$ for all $u > t$. Second, $p_Q(u, t, t+1, x)$ will change between $u = t$ and $u = t+1$ but will remain fixed thereafter ($u > t+1$). After time $u = t+1$, $p_Q(u, t, t+1, x)$ is the observed value of $S(t+1, x)/S(t, x)$. The third component of (3) will still vary after time $t+1$.

Since $p_Q(u, 0, t, x)$ remains fixed from t to $t+1$, the martingale property under Q means that for all t we have

$$p_Q(t, t, T, x) = E_Q[p_Q(t+1, t, T, x)|\mathcal{M}_t]. \quad (4)$$

This equation gives us the fundamental requirement for dynamics under Q in a discrete-time arbitrage-free model.

3 The Olivier-Smith model

The presentation by Olivier and Jeffery (2004) describes a model developed by Olivier and Smith (O-S) in which, for all x and for all $T = t, t+1, \dots$,

$$p_Q(t+1, T, T+1, x) = p_Q(t, T, T+1, x)^{b(t+1, T, T+1, x)G(t+1)} \quad (5)$$

where $G(1), G(2), \dots$ is a sequence of independent and identically distributed Gamma random variables with both shape and scaling parameters equal to some constant α . Hence $E_Q[G(t)] = 1$ and $Var_Q[G(t)] = 1/\alpha$. The $b(t+1, T, T+1, x)$ are \mathcal{M}_t -measurable bias-correction factors that are defined below.

In the O-S model, for $t < T+1$, $p_Q(t, T, T+1, x)$ is still an estimate of the survival probability $p_Q(T+1, T, T+1, x)$ that is not observed until time $T+1$. This survival probability can be written in terms of the survivor index, $S(u, x)$, or using the observed force of mortality process, $\mu(u, y)$: that is, $S(T+1, x)/S(T, s) = \exp[-\int_T^{T+1} \mu(u, x+u)du]$. It follows that, for $t \geq T+1$, $p_Q(t, T, T+1, x)$ is constant and equal to the observed value of $S(T+1, x)/S(T, s)$. Thus, we stress that the updating equation (5) applies only when $t \leq T$. Once $t > T$, the updating ceases.

For the market to be arbitrage free we require for all $T > t, x$

$$p_Q(t, t, T, x) = E_Q[p_Q(t+1, t, T, x)|\mathcal{M}_t]. \quad (6)$$

Using standard properties of the Gamma distribution, (e.g. Olivier and Jeffery,

2004, Smith, 2005)

$$\begin{aligned}
\prod_{u=t}^{T-1} p_Q(t, u, u+1, x) &= E_Q \left[\prod_{u=t}^{T-1} p_Q(t+1, u, u+1, x) \mid \mathcal{M}_t \right] \\
&= E_Q \left[\prod_{u=t}^{T-1} p_Q(t, u, u+1, x)^{b(t+1, u, u+1, x)G(t+1)} \mid \mathcal{M}_t \right] \\
&= E_Q \left[\exp \left(G(t+1) \sum_{u=t}^{T-1} b(t+1, u, u+1, x) \log p_Q(t, u, u+1, x) \right) \mid \mathcal{M}_t \right] \\
&= \frac{\alpha^\alpha}{\left(\alpha - \sum_{u=t}^{T-1} b(t+1, u, u+1, x) \log p_Q(t, u, u+1, x) \right)^\alpha}. \tag{7}
\end{aligned}$$

To evaluate at time t the bias correction factors $b(t+1, u, u+1, x)$ we proceed in a recursive fashion. Thus we start by solving equation (7) for $u = t$ and then solve recursively for $u = t+1, t+2, \dots$. To this effect we have, first,

$$b(t+1, t, t+1, x) = -\frac{\alpha(p_Q(t, t, t+1, x)^{-1/\alpha} - 1)}{\log p_Q(t, t, t+1, x)}.$$

For $T > t$ solving equation (7) gives us

$$\sum_{u=t}^{T-1} b(t+1, u, u+1, x) \log p_Q(t, u, u+1, x) = -\alpha (p_Q(t, t, T, x)^{-1/\alpha} - 1). \tag{8}$$

However, since in our recursive scheme we already know that

$$\sum_{u=t}^{T-2} b(t+1, u, u+1, x) \log p_Q(t, u, u+1, x) = -\alpha (p_Q(t, t, T-1, x)^{-1/\alpha} - 1)$$

we find that (Olivier and Jeffery, 2004, Smith, 2005)

$$\begin{aligned}
&b(t+1, T-1, T, x) \log p_Q(t, T-1, T, x) \\
&\quad = -\alpha (p_Q(t, t, T, x)^{-1/\alpha} - p_Q(t, t, T-1, x)^{-1/\alpha}) \\
\Rightarrow b(t+1, T-1, T, x) &= -\frac{\alpha p_Q(t, t, T-1, x)^{-1/\alpha} (p_Q(t, T-1, T, x)^{-1/\alpha} - 1)}{\log p_Q(t, T-1, T, x)}.
\end{aligned}$$

We can see, of course, that this last equation can be applied directly without reference to a recursive scheme, and that it applies to the case $T = t+1$ since then $p_Q(t, t, T-1, x)^{-1/\alpha} = 1$.

Simulation of this model can be implemented accurately in discrete time without approximation.⁴ For each timestep t to $t+1$ we start with the full term-structure of forward survival probabilities $p_Q(t, T, T+1, x)$. These allow us to calculate the bias-correction terms, the $b(t+1, T, T+1, x)$. We then simulate the single Gamma(α, α) random variable $G(t+1)$ and update the forward survival probabilities to time $t+1$.

⁴This assumes that an accurate method of simulating Gamma random variables is used. For example, in the statistics package R, the function `rgamma` can be used to simulate gamma random variables with an arbitrary shape parameter.

4 Discussion of the O-S model

The O-S model provides us with an elegant approach to simulating stochastic mortality which exploits well-known properties of the Gamma distribution function. No approximations are required: that is, we can simulate exactly in discrete time.

There are, however, two potential drawbacks to the model. First, the model only accommodates a single source of randomness through the simulated $G(t + 1)$. In contrast, historical data suggests that more than one factor may be appropriate (see, for example, Cairns, Blake and Dowd, 2006b): specifically, changes in mortality rates at different ages are not perfectly correlated. Second, there is no flexibility in how we specify the volatility term structure once α has been set. For example,

$$\begin{aligned} \text{Var}[p_Q(t + 1, u, u + 1, x) | \mathcal{M}_t] &= (b(t + 1, u, u + 1, x) \log p_Q(t, u, u + 1, x))^2 / \alpha \\ &\approx (\log p_Q(t, u, u + 1, x))^2 / \alpha \end{aligned}$$

since $b(t, u, u + 1, x)$ is usually quite close to 1.

4.1 Empirical statistical analysis

We will now present evidence that will argue that the one-factor Olivier and Smith model with a fixed value of α for all ages and maturity dates is inadequate from a statistical perspective.

We have an immediate problem with data: specifically there is no liquid market in zero-coupon survivor bonds that we can use to extract forward survival probabilities from. We, therefore, propose a compromise that looks one year ahead only (which is sufficient to demonstrate that the model needs generalising).

- $p_Q(t, t - 1, t, x - t + 1)$ represents the most-recently-observed one-year survival probability for individuals aged x at time $t - 1$ (age $x - t + 1$ at time 0).
- The data were smoothed over age for each calendar year to calculate the $p_Q(t, t - 1, t, y)$ survival probabilities.
- We predict, at time t , the one-year survival probability for an individual aged x based on $p_Q(t, t - 1, t, x - t + 1)$. Specifically, we assume that $p_Q(t, t, t + 1, x - t) = p_Q(t, t - 1, t, x - t + 1)^{\theta(x)}$ for some age-specific improvement factors $\theta(x)$.
- For each age x we can calculate approximate Gamma random variates by assuming first that the bias-correction factors, $b(t + 1, T - 1, T, x)$, are equal to 1. Thus

$$G(t + 1, x) = \frac{\log p_Q(t + 1, t, t + 1, x - t)}{\log p_Q(t, t, t + 1, x - t)}.$$

If the 1-factor Olivier and Smith model is accurate then we should find that the $G(t + 1, x)$ over the observed range of x 's are all perfectly correlated, while over time we should find that the Gamma distributions for different ages are the same: $\text{Gamma}(\alpha, \alpha)$.

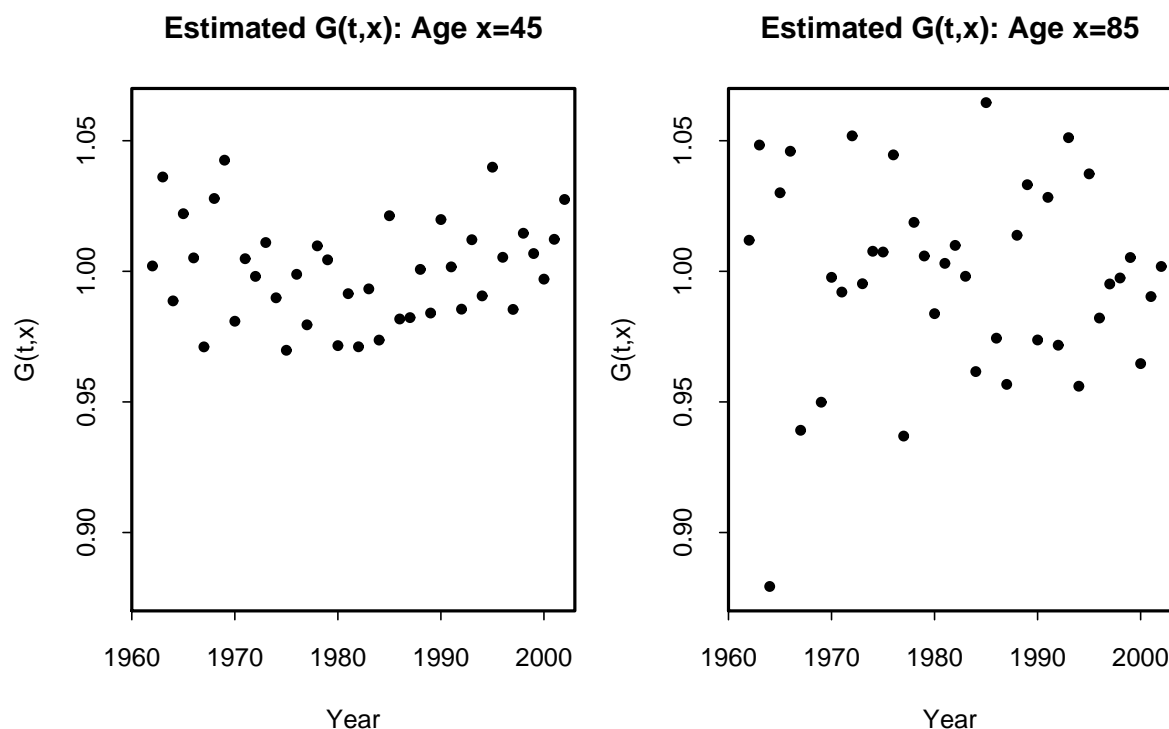


Figure 1: Estimated Gamma random variates, $G(t, x)$, for ages $x = 45$ and $x = 85$, for $t = 1960$ to 2002 .

Various ways of illustrating the output from this exercise are plotted in Figures 1 to 4.

- Figure 1 provides a first indication that at different ages (here 45 and 85) the variances of the Gamma random variables are not equal, and that there is not perfect correlation.
- Figure 2 takes cross sections in the other dimension. The plots look quite different from Figure 1 being, here, rather smooth as a result of having smoothed the survival probabilities in each calendar year. This shows the high degree of correlation between similar ages, but it also reveals that correlation is not perfect and declines as the age gap widens.
- Figure 3 plots the correlation between the Gamma random variables at pairs of ages and presents this in the form of a contour plot. This makes more obvious the point that correlation is high at adjacent ages and falls away as ages diverge.
- In Figure 4 we make the hypothesis that, for a fixed x , the $G(t, x)$ are i.i.d. Gamma random variables with mean 1 and variance $1/\alpha(x)$. Using the method of moments we estimate $\alpha(x)$. It is clear from Figure 4 that the $\alpha(x)$ vary considerably with age, rather than remain constant.

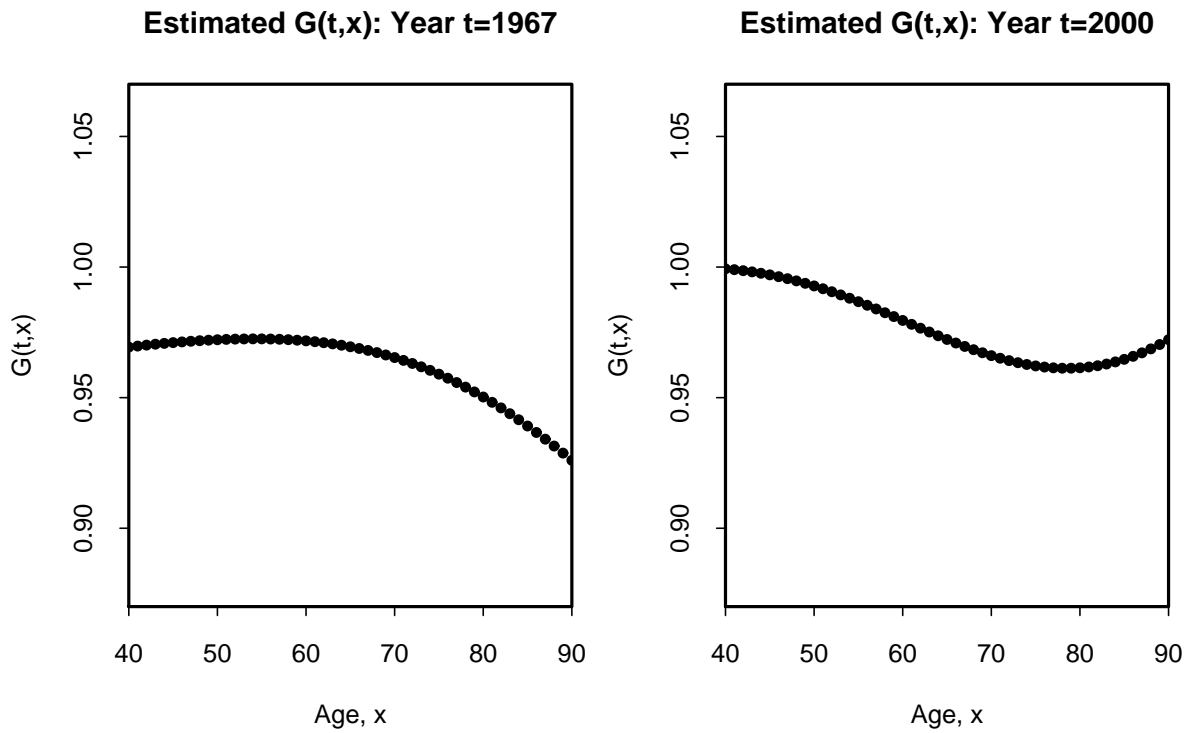


Figure 2: Estimated Gamma random variates, $G(t, x)$, for ages 40 to 90, for $t = 1967$ to $T = 2000$.

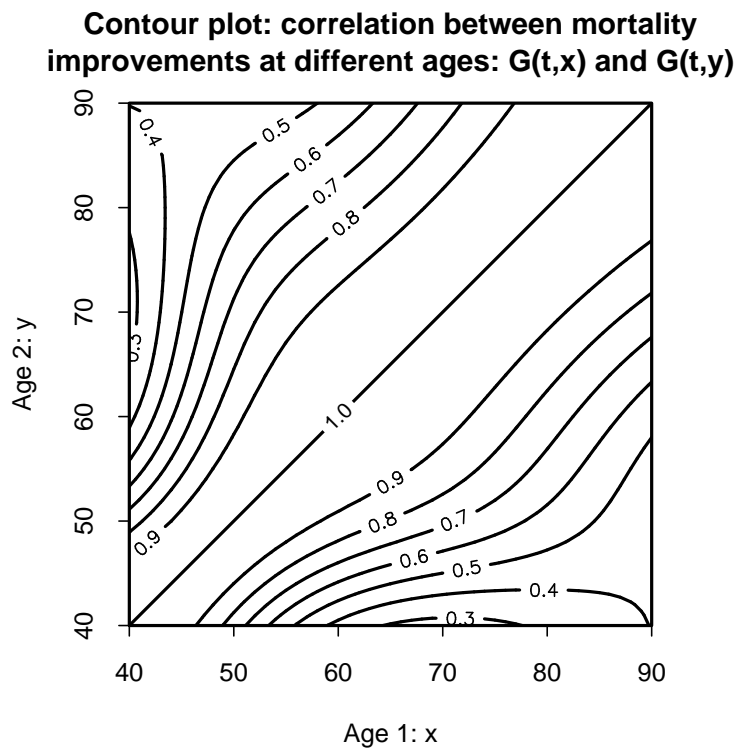


Figure 3: Estimated correlation between $G(t, x)$ and $G(t, y)$ for $x, y = 40, \dots, 90$.

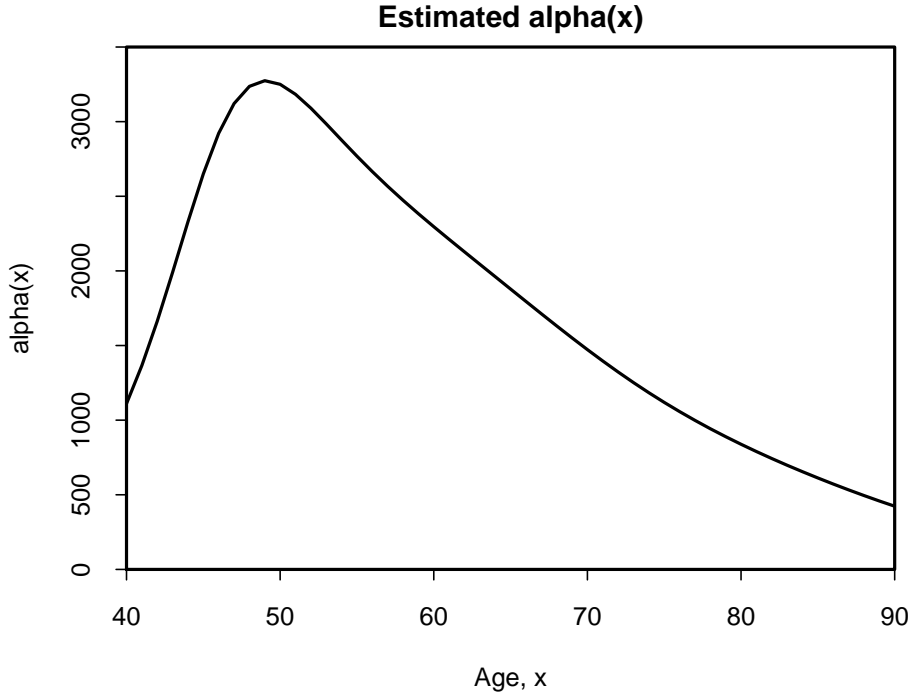


Figure 4: For each age x , estimated values for the Gamma shape parameter $\alpha(x)$ based on observations of the Gamma random variable $g(t, x)$ for $t = 1961$ to 2002.

4.2 Possible generalisations

From our diagnostic analysis in the preceding section it seems that we need to develop a model that exploits the analytical properties of the Gamma but allows for greater richness in the dependency structure.

Where we previously had one Gamma random variable $G(t + 1)$ covering all maturities we now potentially have one Gamma random variable for each age and for each maturity: $G(t + 1, T, x)$. Our problem is how do we simulate a two-dimensional array of dependent Gamma random variables.

This problem would be simple if we had to simulate an array of correlated log-normal random variables. These could be simulated relatively easily using, potentially, a small number of i.i.d. standard normal random variables as input.

5 The generalised model

In the new approach we work with the *spot survival probabilities* rather than the forward survival probabilities. Specifically their dynamics are governed by the relationship

$$p_Q(t + 1, t, T, x) = p_Q(t, t, T, x)^{g(t+1, T, x)G(t+1, T, x)} \quad (9)$$

where for each x and for each $T \geq t + 1$,

$$\begin{aligned} G(t + 1, T, x) &\sim \text{Gamma}\left(\alpha(t + 1, T, x), \alpha(t + 1, T, x)\right) \\ \text{and } g(t + 1, T, x) &= -\frac{\alpha(t + 1, T, x) \left(p_Q(t, t, T, x)^{-1/\alpha(t+1, T, x)} - 1\right)}{\log p_Q(t, t, T, x)}. \end{aligned} \quad (10)$$

The $g(t + 1, T, x)$ are normalising constants for the generalised model in the same way that the $b(t + 1, T - 1, T, x)$ are in the original model (equation 5).

So far we have not indicated what the relationship is between the $G(t + 1, T, x)$ for the different values of T and x . For different values of t these sets of values are assumed to be independent. For a given t the matrix of values for the $G(t + 1, T, x)$ over $T > t$ and x are assumed to be dependent Gamma random variables that might be generated, for example, using a suitable copula.

Remark

It is not obvious from equation (9) that the O-S model (equation 5) is a special case, since (9) is framed in terms of the spot survival probabilities instead of the forward survival probabilities. However, we can note that O-S is indeed a special case provided:

- $G(t + 1, T, x) \equiv G(t + 1) \sim \text{Gamma}(\alpha, \alpha)$ for all $T \geq t + 1$ and x .
- the $g(t + 1, T, x)$ can be shown to satisfy the following relationship. For each $T = t + 1, t + 2, \dots$

$$g(t + 1, T, x) \log p_Q(t, t, T, x) = \sum_{u=t+1}^T b(t + 1, u - 1, u, x) \log p_Q(t + 1, u - 1, u, x).$$

Now from equation (8)

$$\sum_{u=t+1}^T b(t + 1, u - 1, u, x) \log p_Q(t + 1, u - 1, u, x) = -\alpha \left(p_Q(t, t, T, x)^{-1/\alpha} - 1 \right).$$

On the other hand equation (10) gives us

$$g(t + 1, T, x) \log p_Q(t, t, T, x) = -\alpha \left(p_Q(t, t, T, x)^{-1/\alpha} - 1 \right).$$

5.1 Problem

A general simulation procedure might mean that the attainable range of values that a specific Gamma random variable in the matrix might is $(0, \infty)$ regardless of the values taken by the other Gamma random variables in the array. This means that simulation algorithms will not, in general, preserve the monotonicity of $p_Q(t + 1, t, T, x)$. In the normal course of events we would expect that $p_Q(t + 1, t, T, x)$ is decreasing in T . But this is not guaranteed using arbitrary copulas (e.g. the Gaussian copula). Therefore an alternative approach is required to simulate the Gamma random variables.

5.2 Required properties of a simulation model

Any simulation model we propose must satisfy the following properties

- Property A: $p_Q(s, t, T, x)$ is a martingale under the pricing measure Q for $s, t, t + 1$: that is, for all T and x , $E_Q[p_Q(t + 1, t, T, x) | \mathcal{M}_t] = p_Q(t, t, T, x)$.
- Property B: $0 < p_Q(s, t, T, x) < 1$ for all $s = t, t + 1, T$ and x .
- Property C: for $s = t, t + 1$ and for all x , $p_Q(s, t, T, x)$ is a strictly decreasing function of T .

Let us assume that properties B and C are already satisfied at time t . The martingale property A is satisfied by calculating the value of the normalising constant $g(t + 1, T, x)$ at time t . Since $g(t + 1, T, x)$ and $G(t + 1, T, x)$ are both positive it follows that $0 < p_Q(t + 1, t, T, x) < 1$ (property B).

Property C takes more care.

Define $M(t, T, x) = -\log p_Q(t, t, T, x)$ so that

- $p_Q(t, t, T, x) = \exp[-M(t, T, x)]$;
- $p_Q(t + 1, t, T, x) = \exp[-g(t + 1, T, x)M(t, T, x)G(t + 1, T, x)]$.

For property C to be satisfied at time $t + 1$ we therefore require

$$g(t + 1, T, x)M(t, T, x)G(t + 1, T, x) < g(t + 1, T + 1, x)M(t, T + 1, x)G(t + 1, T + 1, x) \quad (11)$$

$$\Rightarrow G(t + 1, T + 1, x) > \phi(t + 1, T, x)G(t + 1, T, x), \quad (12)$$

where $\phi(t + 1, T, x) = g(t + 1, T, x)M(t, T, x)/g(t + 1, T + 1, x)M(t, T + 1, x)$.

Note that there are no such constraints between the $G(t + 1, T, x)$ for different cohorts.

There remains to us the following open questions:

- Do there exist solutions to the dependent Gamma simulation problem?
- What constraints do we have on the correlation or dependency between the Gamma random variables?

In this paper we can report on partial progress towards answering these questions.

Remark 1

One known solution is to have $G(t + 1, T, x) \equiv \tilde{G}(t + 1)$ for all T, x where $G(t + 1)$ is a $\text{Gamma}(\alpha, \alpha)$ random variable. It is straightforward to see that Properties A and B are satisfied. Property C equates to the requirement that $\alpha G(t + 1)$

$1)(\exp(M_1/\alpha) - 1) < \alpha G(t+1)(\exp(M_2/\alpha) - 1)$ (*) where $M_1 = -\log p_Q(t, t, T_1, x)$, $M_2 = -\log p_Q(t, t, T_2, x)$ and $T_2 > T_1$. It is easy to see that (*) is true since $\exp(M/\alpha)$ is an increasing function of M .

Can we move away from this extreme case?

In the discussions that follow we will focus on a single cohort, x , and two future dates T and $T+1$, which allows us to simplify the notation. Let $M_1 = -\log p_Q(t, t, T, x)$, $\alpha_1 = \alpha(t+1, T, x)$, $G_1 = G(t+1, T, x)$ and $g_1 = g(t+1, T, x)$. Similarly, let $M_2 = -\log p_Q(t, t, T+1, x)$, $\alpha_2 = \alpha(t+1, T+1, x)$, $G_2 = G(t+1, T+1, x)$ and $g_2 = g(t+1, T+1, x)$. Finally define $\phi = \phi(t+1, T, x)$.

Remark 2

G_1 and G_2 cannot be independent, as there would be no guarantee that Property C will be satisfied.

Remark 3

For Property C (12) to be satisfied (that is, $G_2 \geq \phi G_1$) it is necessary that

$$1 \leq \frac{\alpha_2}{\alpha_1} \leq \phi^{-1}. \quad (13)$$

Our proof of this assertion makes no assumption about the form of the dependence between G_1 and G_2 .

Proof

Suppose that there exists dependent random variables $G_1 \sim \text{Gamma}(\alpha_1, \alpha_1)$ and $G_2 \sim \text{Gamma}(\alpha_2, \alpha_2)$ that satisfy $G_2 \geq \phi G_1$.

Suppose that $\alpha_2 < \alpha_1$. From Figure 5 (left) we can see that

$$\begin{aligned} Pr(A) &= Pr(G_2 < \phi u) = Pr(\phi^{-1} G_2 < u) \\ Pr(B) &= Pr(G_1 < u). \end{aligned}$$

We can also observe from Figure 5 that $Pr(B) > Pr(A)$.

However, now compare the densities of $\phi^{-1} G_2$ and G_1 . If $\alpha_2 < \alpha_1$ then we can find some $u > 0$ such that the density of $\phi^{-1} G_2$ is greater than the density of G_1 for all $0 < y < u$ which implies that $Pr(A) > Pr(B)$: that is, a contradiction. Therefore we must have $\alpha_2 \geq \alpha_1$.

A similar proof by contribution applies when $\alpha_2 > \phi \alpha_1$ where we compare the probabilities of regions C and D in Figure 5.

Remark 4

Note that the upper bound in Remark 3 itself depends on α_1 and α_2 . If we combine the definition of $g(t+1, T, x)$ (equation 10) with the definition of ϕ we note that

$$\phi = \frac{\alpha_1(\exp(M_1/\alpha_1) - 1)}{\alpha_2(\exp(M_2/\alpha_2) - 1)}.$$

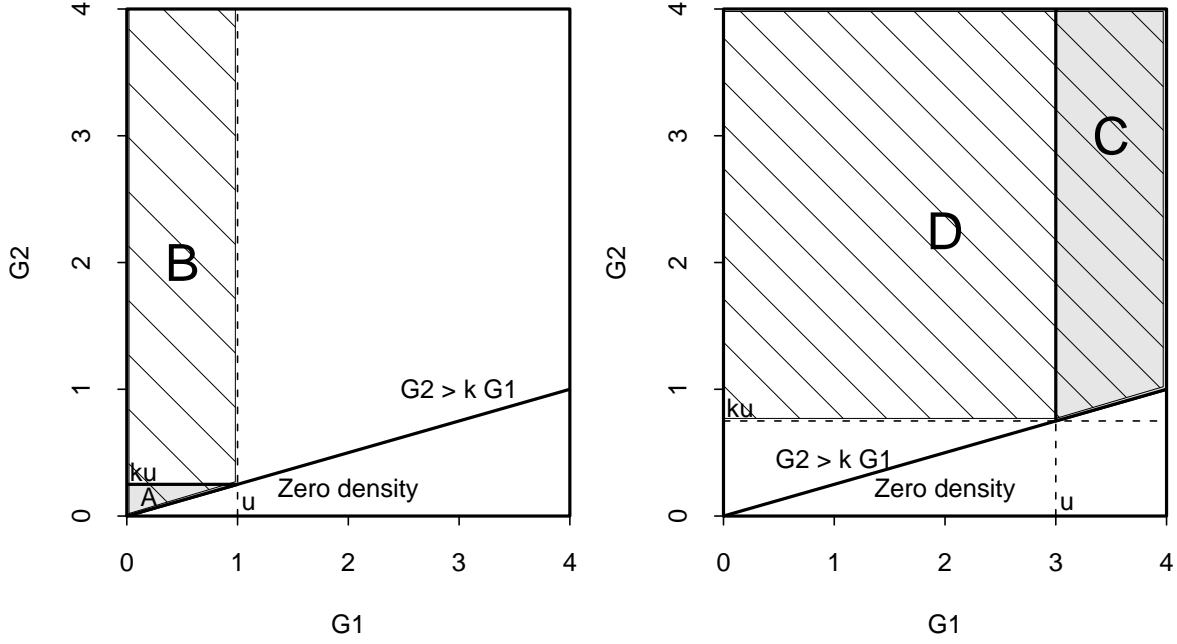


Figure 5: Region A (grey) $\Rightarrow G_1 \leq u, G_2 \leq ku, G_2 \geq kG_1$. Region B (hatched) $\Rightarrow G_1 \leq u, G_2 \geq kG_1$. Region C (grey) $\Rightarrow G_1 \geq u, G_2 \geq ku, G_2 \geq kG_1$. Region D (hatched) $\Rightarrow G_2 \geq ku, G_2 \geq kG_1$.

It follows that $\alpha_2/\alpha_1 = \phi^{-1}$ if and only if $(\exp(M_1/\alpha_1) - 1)/(\exp(M_2/\alpha_2) - 1) = 1$. From this we infer that $M_1/\alpha_1 = M_2/\alpha_2$.

The constraints in (13) are thus equivalent to

$$1 \leq \frac{\alpha_2}{\alpha_1} \leq \frac{M_2}{M_1}.$$

Property C':

Suppose that we relax property C to require that $p_Q(t, t, T, x)$ is a decreasing function of T (that is, not strictly decreasing).

Remark 5

If we allow for the possibility that for some t , $M(t, T, x) = M(t, T + 1, x)$ (which satisfies property C' but not C) then preservation of the relaxed C' implies that $M(s, T, x) = M(s, T + 1, x)$ for all $s > t$.

This then implies that the actual mortality of this cohort will ultimately be exactly zero between T and $T + 1$.

Sketch of proof

First it can be shown that we must have $\alpha(t + 1, T, x) = \alpha(t + 1, T + 1, x)$.

This implies that $g(t + 1, T, x) = g(t + 1, T + 1, x)$.

Preservation of C' implies that we must have $G(t + 1, T, x) = G(t + 1, T + 1, x)$.

Hence $M(t + 1, T, x) = M(t + 1, T + 1, x)$.

5.3 A non-trivial dependency structure

Alfred Müller (2006, personal communication) has proposed the following copula-based approach.

Recall that G_1 and G_2 are our dependent Gamma distributed random variables that are required to satisfy the constraint $G_2 \geq \phi G_1$. Let $F_1(x)$ and $F_2(x)$ be the cumulative distribution functions of G_1 and G_2 respectively. Let $V_1 = F_1(G_1)$ and $V_2 = F_2(G_2)$. The constraint $G_2 \geq \phi G_1$ implies that the minimum permissible value of V_2 is $F_2(\phi F_1^{-1}(V_1)) = g(V_1)$. Our problem is therefore transferred to a copula simulation problem with the requirement that $V_2 \geq g(V_1)$. Müller suggests the following algorithm.

- Let U_1 and U_2 be i.i.d. uniform random variables.
- Define $\bar{U}_2 = \max\{f(U_1), U_2\}$, and let $\bar{F}(u_2)$ be the cumulative distribution function of \bar{U}_2 .
- Define $V_1 = U_1$ and $V_2 = \bar{F}(\bar{U}_2)$. Then V_1 and V_2 are dependent uniform random variables. Furthermore, given V_1 the minimum value taken by V_2 is $V_1 f(V_1)$.
- Define $G_1 = F_1^{-1}(V_1)$ and $G_2 = F_2^{-1}(V_2)$.

We equate $vf(v)$ with $g(v)$ to derive the form for $f(v)$ required to ensure that $G_2 \geq \phi G_1$.

This algorithm establishes that there are non-trivial dependency structures that allow simulation of a pair of Gamma random variables that satisfy the property $G_2 \geq \phi G_1$. In future work we will develop Müller's algorithm to investigate whether or not we can gain better control over the dependency between G_1 and G_2 (at present, none). In addition, we aim to avoid having non-zero probability mass along the ϕG_1 boundary. The reason for this lies in Remark 5, since $G_2 = \phi G_1$ results in $M(t+1, T, x) = M(t+1, T+1, x)$ which in turn implies zero mortality rates between T and $T+1$, which we consider to be biologically unreasonable.

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