

Chapter 4

Stochastic Mortality Models and Pandemic Shocks



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Abstract After decades of worldwide steady improvements in life expectancy, the COVID-19 pandemic produced a shock that had an extraordinary immediate impact on mortality rates globally. This shock had largely heterogeneous effects across cohorts, socio-economic groups, and nations. It represents a remarkable departure from the secular trends that most of the mortality models have been constructed to capture. Thus, this chapter aims to review the existing literature on stochastic mortality, discussing the features that these models should have in order to be able to incorporate the behaviour of mortality rates following shocks such as the one produced by the COVID-19 pandemic. Multi-population models are needed to describe the heterogeneous impact of pandemic shocks across cohorts of individuals. However, very few of them so far have included jumps. We contribute to the literature by describing a general framework for multi-population models with jumps in continuous-time, using affine jump-diffusive processes.

4.1 Stochastic Mortality Models and the COVID-19 Shock

The life expectancy of human individuals worldwide has been steadily increasing since World War II. The Organisation for Economic Co-operation and Development (OECD) estimates that life expectancy worldwide increased by more than 25 years in the last 70 years, moving from 45.7 years in 1950 to 72.6 in 2019. Mortality rates have constantly been declining at all ages, spanning from infants to the elderly. This phenomenon relies mainly on the economic progress of nations, which improved people's well-being, habits, nutrition, and healthcare consumption.

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Advances in medicine have allowed us to prevent and cure common and less common diseases. This progress, with different intensities, was shared by all regions and countries in the world. Importantly, improvements in life expectancy and mortality rates constantly exceeded the expectations. While being good news for humanity, higher-than-expected mortality improvements generated unexpected increases in the value of the liabilities of life insurance companies engaged in the annuity business, of pension funds and public pension schemes. This fact led actuaries to focus on the so-called longevity risk in the last thirty years, i.e., the risk of unexpected improvements in the mortality of individuals. Modelling aims at capturing the uncertainty in the changes of future mortality rates. Modelling longevity risk became crucial for two reasons in particular: first, to assess the likelihood and impact of deviations from expectations; second, to price and hedge longevity risk via risk mitigation techniques such as the use of derivative contracts.

The seminal contribution by Lee and Carter (1992), who first described mortality rates via stochastic processes, paved the way for extensive literature which tried to capture the essential features observed in the mortality dynamics and project them in future. Progressively, the literature moved from the modelling of mortality rates of single populations to the joint modelling of the mortality of multiple socio-economic groups and populations, which display interconnected and specific features at the same time. Because the mortality improvements in the last 100 years in the vast majority of countries (with some notable exceptions due to the effects of wars, as for Italy and Germany during World War II) were following a substantially stable trend, only a few of the proposed models considered adding jumps in the mortality dynamics, and the application of such models has been limited. Nonetheless, the COVID-19 pandemics in 2020 reminded us that sudden shocks to mortality rates might occur, although with (hopefully) relatively low frequency. COVID-19 showed us how epidemics in a highly interconnected world could spread rapidly across continents, affecting people's lives and health conditions. This chapter reviews the literature on stochastic mortality models with jumps whose interest will likely surge in the coming years. To ground our analysis, we first describe briefly in Sect. 4.2 the immediate impact that COVID-19 had on the mortality rates in 2020. This effort helps us highlight that the 2020 shock had largely different effects:

- across countries, as some were better able to contain the spread of the virus than others and/or because their health system was better prepared to respond to the emergency;
- across ages and sexes, because the observed lethality of COVID-19 was higher for males and older people;
- across socio-economic groups, especially in countries with mostly private health systems, due to unequal wealth levels and health-care quality and consumption.

We also point out that it is, at present, unclear whether the shock to mortality rates will have persistent effects or transitory effects only. Direct and lasting effects of “long-COVID” and the impact that the strict lock-down measures adopted in many countries are having on people's habits, health, and economic situation will become apparent in the future. Also, there were indirect effects due to the stress placed by COVID-19 on the health systems, which had to limit to some extent non-COVID-

related treatments of other diseases and screenings. Individuals who reduced health-related consumption may have consequences that will become apparent after some time.

With these aspects in mind, Sects. 4.3 and 4.4 review the stochastic mortality models that account for jumps in the dynamics of mortality rates, developed either in discrete-time or in continuous-time set-ups. Section 4.3 focuses on single-population models, while Sect. 4.4 considers multi-population ones. We believe this last stream of literature is particularly relevant in light of the heterogeneous effects of the COVID-19 pandemic shock on mortality rates because it can account for common sudden shocks, which may have different impacts across countries and/or socio-economic groups. Recognizing a gap in the literature because, to our knowledge, none of the continuous-time multi-population models proposed so far have considered the presence of jumps, in Sect. 4.5 we generalise the continuous-time multi-population framework in Jevtić and Regis (2019) to the case of jump-diffusive affine processes. Section 4.6 provides some concluding remarks.

4.2 The Impact of COVID-19 on Mortality Rates

Up to 2020 almost uninterrupted improvements in mortality rates were observed in all countries since the end of World War II. Figure 4.1 supports this statement, by

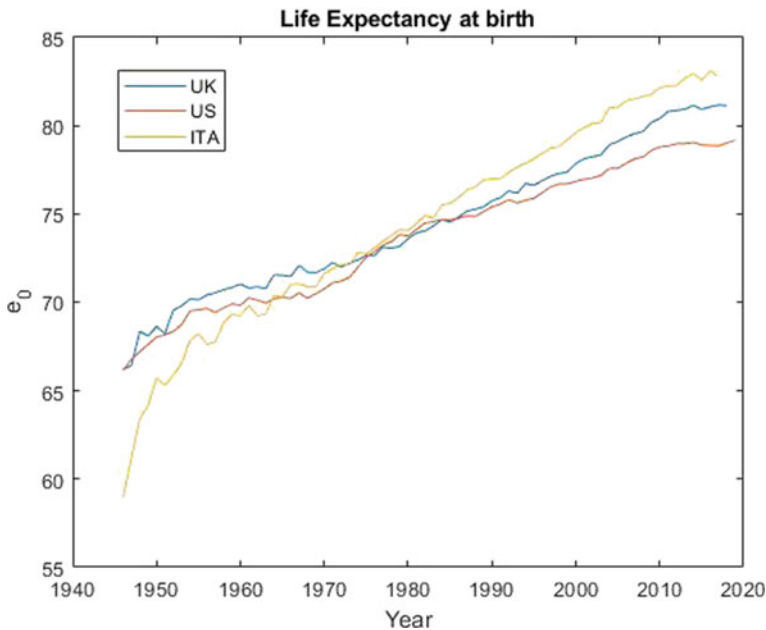


Fig. 4.1 Life expectancy at birth in UK, US and Italy from 1946 to 2019. *Source* Human Mortality Database

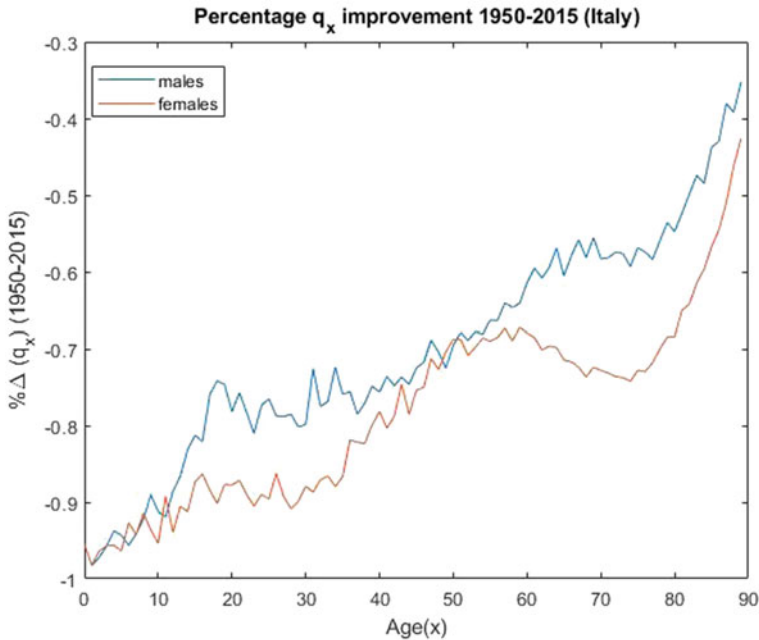


Fig. 4.2 Improvements in annual death probabilities at ages 0–90 in Italy between 2015 and 1950. *Source* Human Mortality Database

portraying the time-evolution of life expectancy at birth for Italy, the United Kingdom and the United States from 1946 to 2019. Nonetheless, the figure shows that the extent of such improvements varied temporally and by country. Mortality decline has been heterogeneous across ages and sexes as well, as testified by Fig. 4.2, which displays the change in conditional yearly death probabilities by age and sex for Italy between 1950 and 2015.

The year 2020, however, brought a worldwide-shared setback to mortality rates' decrease. In the absence of yearly official 2020 data, to describe the impact of the COVID-19 pandemic on mortality rates of several countries, we use weekly data from the STMF (Short-Term Mortality Fluctuations) dataset provided by the Human Mortality Database. First we consider the changes in the total death rates. Figure 4.3 shows their 2020 weekly series for 6 OECD countries (Spain, Italy, France, Germany, the United Kingdom and the United States) and compares their value with the average of the previous 5 years. The figure displays remarkable deviations from the average for all the countries, starting from the spread of the COVID-19 diseases in March. It highlights also that the pandemic shock affected the mortality rates in different countries differently, both in terms of timing and severity. As for timing, with the exception of Germany, we see total death rates spike in coincidence with the first wave of contagions in March. While during the summer death rates were in line with the average of the previous 5 years in all countries, with the exception of the United

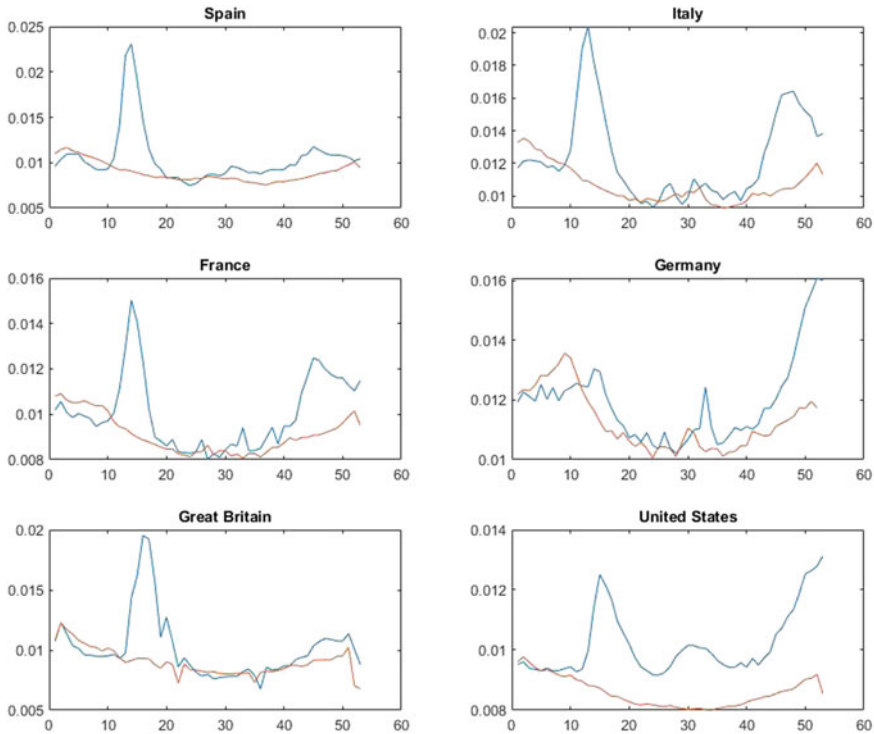


Fig. 4.3 Weekly measured total death rate for 6 countries in 2020. *Source* SMTF Dataset

States, we see the effects of the second wave of contagions in the fall after week 40. As for severity, total death rates, which have been steadily decreasing overtime in the last decades,¹ increased in 2020 by 18.6% in US, 18% in Spain, 15.9% in Italy, 12.2% in Great Britain, 9.89% in France, and 5.3% in Germany compared to their 2015–2019 averages. In Table 4.1 we report the percentage increase in the death rate for the six countries considered for the three age groups—65–74, 75–84 and 85+—which displayed the highest lethality level to the disease. We also distinguish between males and females. The table highlights that, with few exceptions, males death rates for all age groups deteriorated more than females’. The evidence collected in this section is material to our discussion on stochastic mortality models. Indeed, it allows us to stress that the pandemic shock due to the spread of the COVID-19 disease had heterogeneous severity on different countries and age groups. Andrasfay and Goldman (2021) document the disproportionate impact of the shock on the hispanic America and African America sub-populations in the US, for whom the estimated drop in life expectancy in 2020 is far more severe than for the general population. A very important aspect which cannot be ascertained from the data as of yet is to

¹ The average annual change in death rates ranges between -1% and -2% for all age classes and countries in the sample.

Table 4.1 Percentage increase in the 2020 death rate versus 2015–2019 average. *Source* Authors' elaboration from the SFTM Dataset

Country	Males			Females		
	65–74 (%)	75–84 (%)	85+ (%)	65–74 (%)	75–84 (%)	85+ (%)
Spain	12.29	9.72	13.00	15.38	8.3	11.73
Italy	14.29	14.20	9.99	8.33	10.48	11.71
France	8.12	4.94	8.12	7.40	3.29	7.75
Germany	0.53	4.32	2.13	−0.83	3.42	0.5
Great Britain	10.9	9.24	9.49	7.16	6.05	6.91
United States	16.49	12.61	11.06	12.59	10.09	11.45

what extent the shock to mortality rates we observed in 2020 will cause long-lasting effects, possibly producing a change in the observed mortality trend. Some countries, including Germany and the United Kingdom, experienced the peak of contagions in the first months of 2021, and hence the 2021 mortality figures are expected to be affected by the pandemic shock as well as the 2020 one. How much of the shock will affect mortality rates in future years is at present hard to predict. All in all, the stylised facts and considerations presented in this section make the case for a multi-population analysis and modelling of mortality when pandemic shocks are specifically considered.

4.3 Stochastic Mortality Models and Pandemics: Single-Population Models

The previous section describes the characteristics of the sudden worldwide shock to mortality rates that occurred in 2020. This section reviews the stochastic mortality models proposed in the literature to account for such features. We consider single-population models, distinguishing between contributions in which mortality rates are modelled in discrete-time and continuous-time.

4.3.1 Discrete-Time Single Population Models

The Lee-Carter (1992) model was among the first stochastic models proposed for mortality, and today it is probably the most well-known. Mathematically can be represented as follows:

$$\ln(m_{x,t}) = \alpha_x + \beta_x k_t + e_{x,t}. \quad (4.1)$$

In the equation above, the central death rate for age x in year t , $m_{x,t}$, is a function of a time-varying factor k_t , called the mortality index, which is common across ages but impacts them differently through the coefficients $\beta_x \in \mathbb{R}$. α_x is a constant age-dependent term which represents the baseline level of mortality for age x . Model estimation, which is traditionally achieved by applying a two-stage procedure, captures sudden jumps in mortality through the changes in the k_t values. However, at least two considerations are in order. First, mortality changes captured through k_t affect the different ages through β_x independently of the magnitude of the change. This prevents the model from capturing the age-specificities of pandemic or war-related shocks, as pointed out by Liu and Li (2015). Second, when forecasting, it is necessary to select a model for the k_t series. The modelling choice will obviously impact how past observations shape the distributional properties of future mortality rates. The standard solution is to employ a random walk with drift to model k_t :

$$k_t = \mu + k_{t-1} + \sigma Z_t, \quad (4.2)$$

where μ is the drift term and Z_t is a standard normal. This choice rules out the presence of jumps and their occurrence in projections. Usually, in line with this reasoning, outliers, such as the 1918 Spanish flu-related spike, are either excluded by the estimation process or they are dealt with using ad-hoc interventions (see Li and Chan 2005). Some works have generalised the Lee-Carter model and its most notable extensions (such as the one proposed by Renshaw and Haberman (2006) accounting for cohort effects) to specifically account for jumps in annual mortality rates. Milidonis et al. (2011) introduced a regime switching model, which can capture both jumps and changes in the mortality volatility pattern via the different regime states. Wang et al. (2013) extended the Renshaw and Haberman (2006) model, considering jump processes for the error term. Chen and Cox (2009), building on the continuous-time model proposed by Cox et al. (2006), modified the process k_t in Eq. (4.2) to include a jump component. They proposed two specifications, both based on the inclusion of a jump occurring with probability p and producing a shock $Y_t \sim N(m, s^2)$. One assumes that jumps generate permanent shifts to the mortality index, which is thus modelled as:

$$k_t = k_{t-1} + \mu - pm + \sigma Z_t + Y_t N_t, \quad (4.3)$$

where N_t is a Bernoulli distribution which takes value 1 with probability p and 0 otherwise. An alternative specification assumes that jumps have transitory effects, lasting one period only:

$$k_t = k_{t-1} + \mu + \sigma Z_t + Y_t N_t - Y_{t-1} N_{t-1}, \quad (4.4)$$

The authors claimed that this second choice is more appropriate, because the most severe shocks observed over the last century, such as the pandemic flu of 1918 and the tsunami of 2004 had negligible permanent effects. Whether this will remain

true for the COVID-19 pandemic shock is an open question. While epidemiological similarities with the Spanish flu may suggest that development, the severe downturn experienced by the economies worldwide may produce long-term consequences jeopardising the steady decrease in the mortality index that we have observed so far over previous decades. From the modelling point of view, this may imply changes in the mortality trends, as discussed by Sweeting (2011). The models proposed by Chen and Cox (2009) can be estimated via Conditional Maximum Likelihood. If applied to the US data from 1900 to 2003, the models estimate the probability of observing a jump in k_t to be around 4% under both specifications. When a jump occurs, in the transitory-effect model, the sudden increase in k_t it produces is 4 times greater (in absolute value) than its annual negative drift. The importance of accounting for jumps in the mortality index is confirmed by Özen and Şahin (2020), who improved the model fit by allowing for a non-constant mean time between jump arrivals using renewal processes. In the works we have reviewed so far, jumps affected the mortality index. Thus, jump-driven shocks do not have age-specific effects different from the Brownian shock captured by the no-jump equivalent mortality index. To overcome this issue, Liu and Li (2015) specify the model as follows:

$$\ln m_{x,t} = \alpha_x + \beta_x k_t + N_t J_{x,t} + e_{x,t}, \quad (4.5)$$

where $J_{x,t}$ is a time-dependent response to the presence of a jump. $J_{x,t}$ can then be specified as being an age-dependent response to a common shock or as being fully age-specific. The authors provide evidence that accounting for age-specific jump responses is important to improve the model fit. Given the evidence of Sect. 4.2, such a feature appears crucial when including the COVID-19 shock in the data.

4.3.2 Continuous-Time Single-Population Models

Before the Lee-Carter model was extended to account for jumps, jumps had already been introduced in continuous-time mortality models. Indeed, although introduced by Milevsky and Promislow (2001) almost 10 years later than Lee and Carter (1992), continuous-time stochastic mortality models with jumps were proposed just few years later by Biffis (2005) and by Luciano and Vigna (2008). In the continuous-time framework, the time to death of individuals is modelled as the first jump time of a time-inhomogeneous Poisson process with stochastic intensity. The main advantage of such a framework is that, if the mortality intensity process is chosen within the class of affine processes—as in Biffis (2005) and Luciano and Vigna (2008)—survival probabilities are available in closed form. Moreover, the mortality model can be coupled with standard financial risk models to obtain prices of fairly evaluated life insurance policies and their hedges (see Luciano et al. 2012). More formally, a mortality intensity μ_t^x for an individual aged x at time 0 is affine if it is assumed to be an affine function of a jump-diffusive affine process X_t such that:

$$dX_t = \delta(t, X_t)dt + \sigma(t, X_t)dW_t^x + dJ_t^x, \quad (4.6)$$

where W_t^x is a standard Brownian motion, J_t^x is a pure-jump process, and $\delta(\cdot)$, $\sigma(\cdot)\sigma^T(\cdot)$, and the jump-arrival intensity have an affine dependence on X_t . The symbol T denotes matrix transposition. Within this set-up, the survival probability up to time T , $S_x(t, T)$, under some technical conditions, can be obtained as:

$$S_x(t, T) = \mathbb{E} \left[e^{-\int_t^T \mu_s^x ds} \right] = e^{\alpha(t, T) + \beta(t, T) \cdot X_t}, \quad (4.7)$$

where $\alpha(\cdot)$ and $\beta(\cdot)$ solve a system of Ordinary Differential Equations (ODEs) which depend on the model specification. These processes are very flexible and easy to calibrate. They have been extensively applied in the pricing (Wills and Sherris 2010), hedging (Luciano et al. 2012) and portfolio choice (Menoncin and Regis 2020) contexts. Luciano and Vigna (2008) showed that for several generations, in the Italian population, accounting for jumps improves the model fit, in particular when the intensity follows a Gaussian process. However apart from the analysis in Luciano and Vigna (2008), most of the literature restricts the application of the affine framework to purely diffusive processes (Schrager 2006; Jevtić et al. 2013, for instance). An exception is Luciano et al. (2008), where the dependent lives of couples are considered. Hainaut and Devolder (2008) took instead a different approach, based on the use of pure-jump Lévy processes.

4.4 Stochastic Mortality Models and Pandemics: Multi-population

Pandemic shocks have the crucial characteristic of manifesting themselves globally in a short time frame, affecting the mortality patterns of many populations (countries) and sub-groups within populations. Capturing the heterogeneity and the dependence of such impacts across different groups is a non-trivial task, which requires the use of multi-population models.

Multi-population models have started emerging in the mid-2000s to capture the joint evolution of mortality dynamics across countries and/or socio-economic groups within the general population. In this section, we review the most prominent, highlighting that only two contributions, up to our knowledge, included jumps in a multi-population setting.

4.4.1 Discrete-Time Models

Li and Lee (2005) applied the original Lee-Carter model to describe the mortality rates of multiple countries jointly. The model they proposed assumes a common

mortality index driving the mortality rates of different populations. Several papers extended this set-up to account for issues such as (semi)-coherence (i.e. long-run convergence of the mortality rates of several populations, see Li et al. 2017), Bayesian estimation (see Antonio et al. 2015), cointegration (see Yang and Wang 2013; Jarner and Jallbjørn 2020), factor-based approaches (see Chen et al. 2015). To our knowledge, only Zhou et al. (2013) and Özen and Şahin (2021) considered two-population models with jumps in the discrete-time framework. Zhou et al. (2013) modelled jointly the dynamics of two populations, assuming that:

$$\ln m_{x,t}^j = \alpha_x^j + \beta_x^j k_t^j, \quad j = 1, 2, \quad (4.8)$$

where $m_{x,t}^j$ denotes the central death rate for the individual aged x at time t and belonging to population j . They define

$$k_t^j = \hat{k}_t^j + N_t^j Y_t^j, \quad (4.9)$$

where \hat{k}_t^j is the stochastic effect free of jumps, N_t^j is the counting process for jumps at time t in the mortality of population j , whose range is $\{0, 1\}$ and whose distribution may be dependent across populations, and Y_t^j is the severity of a jump at time t for the j -th population. Jumps have transitory (one-period only) effects. While imposing a stationary $AR(1)$ process on $\hat{k}_t^{(1)} - \hat{k}_t^{(2)}$, the framework allows for different—but possibly dependent—jump times, frequencies and severities. The model, applied to the populations of Sweden and Finland, is shown to fit the data well, better than the corresponding no-jump process, because it is able to better capture the presence of outliers, such as the 1918 spike due to the Spanish flu. Recently, Özen and Şahin (2021) introduced jumps in a two-population model, modelling jumps in one of the two populations through a renewal process and linking the other population using a Common Age effect model.

4.4.2 Continuous-Time Models

In continuous-time, only a few papers have focused on two-population or multi-population models. Recently, building on the seminal contribution by Dahl et al. (2008), three papers have proposed multi-population continuous-time mortality models. De Rosa et al. (2021) proposed a two-population model that describes the dependence structure among populations and cohorts within them. The stochastic mortality intensities there follow a square-root process, which guarantees non-negativity. Similarly, Sherris et al. (2020) introduced a model in which common and idiosyncratic Gaussian factors drive the mortality surface of two populations. Jevtić

and Regis (2019) described a general set-up for multi-population continuous-time stochastic mortality models using affine processes. All these works considered purely diffusive processes. To our knowledge, no multi-population model in continuous-time proposed so far includes jumps. In the next section, to fill this gap, we present an extension of the general framework in Jevtić and Regis (2019) to jump-diffusive affine processes.

4.5 A Continuous-Time Multi-population Model with Jumps

We propose here a continuous-time multi-population model with jumps. Consider the following setting. The mortality intensity of an individual aged $x + t$ at time t belonging to population j , with $j = 1, \dots, M$, is defined as:

$$\mu_{x+t}^j := g_0^j(x + t, t, x) + \mathbf{g}_1^j(x + t, t, x) \mathbf{X}_t^j, \quad (4.10)$$

where \mathbf{X}_t^j is a stochastic process in \mathbb{R}^N , $g_0^j(x + t, t, x)$ is a base-line level of mortality for the individual and $\mathbf{g}_1^j(x + t, t, x)$ is the vector of responses of \mathbf{X}_t^j . Here, \mathbf{X}_t^j is described by the following stochastic differential equation:

$$d\mathbf{X}_t^j = \mathbf{A}^j(\mathbf{X}_t^j, t)dt + \mathbf{\Sigma}(\mathbf{X}_t^j, t)d\mathbf{W}_t + d\mathbf{Z}_t, \quad (4.11)$$

where \mathbf{W}_t is a vector of standard Brownian Motions and \mathbf{Z}_t is a pure-jump process. Notice that \mathbf{W}_t and \mathbf{Z}_t are in principle the same across populations. In Jevtić and Regis (2019) the different populations j and ages within them are modelled jointly by assuming that they respond differently to a set of common Brownian noises. To that setting, we add a jump component. Notice that the age-specific and population-specific responses \mathbf{g}_1^j allow for a very rich description of the heterogeneous effects of Brownian and jump shocks. If functions $\mathbf{A}^j(\cdot)$, $\mathbf{\Sigma} \mathbf{\Sigma}^T(\cdot)$ and the jump intensity $\lambda(\mathbf{X}_t^j)$ of process \mathbf{Z}_t have an affine dependence on \mathbf{X}_t^j , the survival probabilities $S_x^j(t, T)$ can be computed analytically. Suppressing time-dependence for notational convenience, we assume that:

- $\mathbf{A}^j = K_0 + K_1 \cdot \mathbf{X}^j$;
- $(\mathbf{\Sigma} \mathbf{\Sigma}^T)_{ij} = (H_0)_{ij} + (H_1)_{ij} \cdot \mathbf{X}^j$;
- $\lambda = l_0 + l_1 \cdot \mathbf{X}^j$;
- $\theta(\cdot)$ defines the “jump transform” that determines the jump-size distribution.

Then, following Duffie et al. (2000), the survival probability of an individual aged x at time t can be computed analytically as:

$$S_x^j(t, T) = \mathbb{E} \left[e^{-\int_t^T \mu_{x+t+s}^j ds} \right] = e^{\alpha(t, T) + \beta(t, T) \cdot \mathbf{X}_t^j}, \quad (4.12)$$

where $\alpha(t, T)$ and $\beta(t, T)$ solve the following system of ODEs:

$$\dot{\beta}(t) = \mathbf{g}_1^j(x + t, t, x) - K_1^T \beta(t) - \frac{1}{2} \beta(t)^T H_1 \beta(t) - l_0(\theta(\beta(t)) - 1) \quad (4.13)$$

$$\dot{\alpha}(t) = g_0^j(x + t, t, x) - K_0 \cdot \beta(t) - \frac{1}{2} \beta(t)^T H_0 \beta(t) - l_1(\theta(\beta(t)) - 1). \quad (4.14)$$

The solution to this system of equations depends on the specification taken by Eqs. (4.10) and (4.11). Under particular conditions, the solution is available in closed form. For instance, this applies to multi-cohort extensions of the jump processes proposed in Luciano and Vigna (2008) for the single-cohort case. Indeed, when the continuous part of (4.11) follows a multi-dimensional Ornstein-Uhlenbeck-process or a Feller-process and jumps are compound Poisson with constant intensity l and exponentially distributed size, $\mathbf{g}_0^j = 0$ and $\mathbf{g}_1^j = \mathbf{1}$, the system of equations above has an analytical solution. More generally, such a solution may be approximated analytically. A pure-jump factor through (4.11) may be considered, in particular, to allow for population-specific and age-specific responses to sudden shocks, which may not otherwise be well captured by purely-diffusive model specifications.

4.6 Conclusions

This chapter reviewed the literature on stochastic mortality models featuring multiple populations and jumps, which can better capture the effects of pandemic shocks and their heterogeneous intensity across countries, cohorts, socio-economic groups. On top of that, the chapter proposes a modelling framework based on continuous-time jump-diffusive processes. The framework is flexible and rich enough to describe the observed differential mortality across groups and capture the cohort-specific and population-specific effects of jumps. It has the advantage of providing closed-form expressions for the survival probabilities of ages within sub-populations. Additionally, it can be coupled with standard financial risk models to provide valuation and management tools for insurance and reinsurance products affected by mortality risk. However, the affine framework may be restrictive when it comes to the jump component modeling relative to pure-jump specifications, such as the one proposed by Hainaut and Devolder (2008). Also, model estimation, depending on the model specification, may require particular care. We postpone it to further research and future data availability.

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