A calendar year mortality model in continuous time

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Introduction

Actuarial valuation involves to consider the uncertainty arising from the evolution of longevity.

Statistical approaches such as the Lee and Carter (LC) model (1992), became a standard in the insurance industry because they are robust and reliable...

...but survival probabilities do not have a closed form expression. Premium or solvency capital requirement calculations rely then on Monte-Carlo (MC) simulations.

Affine diffusion processes (e.g. Luciano and Vigna (2005)) offer an interesting alternative for modeling the mortality of a cohort. Good trade-off between complexity and computational tractability of pricing...
Introduction

...their calibration requires either to observe the mortality of cohorts till their extinction or to fit them to prospective tables built with a different statistical method.

Another difficulty arises for the joint-modeling of multiple cohorts.

This article proposes a calendar year model in the sense that we associate to each age $x$, a mortality process indexed by the calendar time. Advantages:

- estimation a small and recent time window
- analytical survival probabilities
- joint-modeling of cohorts
Calendar year model

We note $\tau_{t,x}$: the random remaining lifetime of a $x$ years old individual at calendar time $t$.

Mortality rate processes are denoted by $(\mu_{t,x})_{t \geq 0, x \geq 0}$ where $t \geq 0$ is the calendar time and $x \in [0, \omega]$ is the age.

**Warning**

Contrary to existing affine frameworks, we consider a continuum of mortality processes for each age $x$ instead of a single mortality process per cohort.

The set of mortality rates is then a random field indexed by time and age (see next plot)
Calendar year model

The survival probability depends then on a continuum of random variables \((\mu_{t+u,x+u}, u \in [0, s-t])\)

\[
s_p_{t,x} = P(\tau_{t,x} \geq s) = \mathbb{E}_t \left( \exp \left( - \int_0^{s-t} \mu_{t+u,x+u} du \right) \right)
\]
Calendar year model

Our model is a calendar year approach because for each age $x$, there is a mortality process indexed by the calendar time.

In comparison, cohort based models use a single process.
Calendar year model

1) **Mortality processes** are Gaussian with a mean reverting dynamic defined by

\[ d\mu_{t,x} = \kappa (\theta_t \mu(x) - \mu_{t,x}) dt + \Sigma(x)^\top d\mathbf{W}_t^\mu, \]  

(1)

where \( \kappa \in \mathbb{R}^+ \), \((\mathbf{W}_t^\mu)_{t \geq 0} \in \mathbb{R}^d\) are BM and \( \mu(x) \) is a function of age (e.g. Gompertz Makeham).

2) \( \Sigma(x) = (\Sigma_1(x), \ldots, \Sigma_d(x)) \) where, \( \Sigma_k(x) \) are functions of age (t.b.d.)

3) \((\theta_t)_{t \geq 0}\) is a stochastic process driving the evolution of longevity:

\[ d\theta_t = \alpha (\beta(t) - \theta_t) dt + \nu d\mathbf{W}_t^\theta + dL_t, \]  

(2)

where \( \alpha \in \mathbb{R}^+ \) and \((\mathbf{W}_t^\theta)_{t \geq 0}\) is a BM independent of \((\mathbf{W}_t^\mu)_{t \geq 0}\).
4) The function $\beta(t) : \mathbb{R}^+ \to \mathbb{R}^+$ is strictly positive and decreasing. We assume that $\beta(t)$ is equal to

$$\beta(t) = \theta_0 e^{-\gamma t} + \bar{\theta} (1 - e^{-\gamma t}) .$$

where $\theta_0$, $\bar{\theta}$ and $\gamma \in \mathbb{R}^+$. For this choice of $\beta(t)$, $\theta_t$ converges on average to $\bar{\theta}$ that is lower than $\theta_0$.

5) The process $L_t$ is a jump process with positive expo($\rho$) jumps to replicate mortality shocks e.g. caused by a pandemics such as COVID 19

$$L_t = \sum_{k=1}^{N_t} J_k .$$

$N_t$ is a Poisson process of intensity $\lambda$ and the mgf of jumps is

$$\psi(\omega) = \frac{\rho}{\rho - \omega} .$$
Survival probabilities

**Proposition**

The survival probability of a $x$-year old individual at time $t$ up to time $s$ is:

$$s p_{t,x} = \exp \left( - s - t m_{t,x} + \frac{1}{2} s - t v_{t,x} + A(0, s - t) \right)$$

where $\xi m_{t,x}$ is drift of the integral $\int_0^\xi \mu_{t+u,x+u} du$

$$\xi m_{t,x} = \int_0^\xi e^{-\kappa u} \mu_{t,u+u} du + \frac{\kappa \theta_t}{\kappa - \alpha} \int_0^\xi \mu(x + u) \left( e^{-\alpha u} - e^{-\kappa u} \right) du +$$

$$\frac{\kappa \alpha (\theta_0 - \bar{\theta})}{\kappa - \alpha} e^{-\gamma t} \int_0^\xi \mu(x + u) \left( \frac{e^{-\gamma u} - e^{-\alpha u}}{\alpha - \gamma} - \frac{e^{-\gamma u} - e^{-\kappa u}}{\kappa - \gamma} \right) du +$$

$$+ \frac{\kappa \alpha \bar{\theta}}{\kappa - \alpha} \int_0^\xi \mu(x + u) \left( \frac{1}{\alpha} (1 - e^{-\alpha u}) - \frac{1}{\kappa} (1 - e^{-\kappa u}) \right) du.$$
Survival probabilities

Proposition, cont’d

\( \xi v_{t,x} \) is the variance of the Brownian part of \( \int_0^\xi \mu_{t+u,x+u} \, du \):

\[
\xi v_{t,x} = \left( \frac{\kappa \nu}{\kappa - \alpha} \right)^2 \int_0^\xi \left( \int_z^\xi \mu(x + u) \left( e^{-\alpha(u-z)} - e^{-\kappa(u-z)} \right) \, du \right)^2 \, dz \\
+ \int_0^\xi \left( \int_z^\xi \Sigma(x + u) e^{-\kappa(u-z)} \, du \right)^\top \left( \int_z^\xi \Sigma(x + u) e^{-\kappa(u-z)} \, du \right) \, dz.
\]

\( A(\xi, s - t) \) solves the following ordinary differential equation (ODE) and is null if no jumps:

\[
\partial_\xi A(\xi, s - t) = -\lambda \left( \psi \left( -\frac{\kappa}{\kappa - \alpha} \int_\xi^{s-t} \mu(x + v) \left( e^{-\alpha(v-\xi)} - e^{-\kappa(v-\xi)} \right) \, dv \right) - 1 \right),
\]

For various functions \( \mu(.) \) and \( \Sigma(.) \), integrals admits (long) closed form expressions.
Survival probabilities

For instance if $\mu(.)$ is a Makeham function (to estimate)

$$\mu(x) = a + bc^x,$$

and $\Sigma(.)$ is a bivariate vector

$$\Sigma(x)^\top = (\sigma_0, \sigma_1 e^{\sigma_2 x}),$$

and in absence of jumps, the survival probabilities admit a full (but long) analytical formula (See Corollary 3.4 in the paper).
The quest of a formula for $t p_x$, why?

The survival probability of a $x$ year old individual at time $t$ up to $s$ is

$$s p_{t,x} = \mathbb{E} \left( \exp \left( - \int_0^{s-t} \mu_{t+u,x+u} du \right) \mid \mathcal{F}_t \right).$$

In the context of Solvency II, estimating the solvency capital requirement (SCR) for longevity risk is computationally intensive if no formula (simulations in simulations).

Let us imagine that we generate $n_{\text{sim}}$ primary scenarios of mortality and evaluate survival probabilities, noted $(s p^{(k)}_{t,x})_{k=1,...,n_{\text{sim}}}$ in each simulation.
The quest of a formula for $tp_x$, why?

In absence of analytical formula, we simulate for each primary scenario, mortality paths up to $s$ to approximate $sp^{(k)}_{t,x}$:

$$sp^{(k)}_{t,x} \approx \frac{1}{n_{sec.\;sim.}} \sum_{j=1}^{n_{sec.\;sim.}} \left( \exp \left( - \sum_{u=0}^{s-t-1} \mu^{(k,j)}_{t+u,x+u} \right) \right),$$

Without analytical $sp_{t,x}$

With analytical $sp_{t,x}$
Filtering of $\theta_t$ & estimation

$(\theta_t)_{t \geq 0}$, the longevity process, is hidden $\Rightarrow$ need to filter it from observations. Assumption: no jump for this step.

Data set: mortality rates $\mu_{t,x}$ at $n + 1$ equispaced times $\{0, 1, ..., n\}$ for $p$ ages $(x_j)_{j=1,...,p}$.

Model with $p$ Brownian motions and a step-wise volatility $p$-vector:

$$
\Sigma(x_j) = \left(\sigma_0 e^{\sigma_1 x_j} \times e^{-(j-k)^2/(\sigma_2 x_j)^2}\right)_{k=1,...,p} \quad j = 1, ..., p(3)
$$

The variance of mortality rates increases with age / the covariance between $\mu_{t,x_j}$ and $\mu_{t,x_k}$ is proportional to a normal kernel.

Makeham function for the baseline mortality $\mu(x) = a + bc^x$. 

Filtering of $\theta_t$ & estimation

$\Sigma(x_j)$ for $x_j = 40, 60, 80$ with $\sigma_0 = 1$, $\sigma_1 = 0.01$ and $\sigma_2 = 0.09$. 
Filtering of $\theta_t$ & estimation

**Proposition**

If $\mu_t = (\mu_{t,x})_{x=x_1,\ldots,x_p}$ and no jumps, $(\mu_{t+1}, \theta_{t+1} \mid \mu_t, \theta_t)$ is a multivariate normal:

$$
\left( \begin{array}{c} 
\theta_{t+1} \\
\mu_{t+1}
\end{array} \right) \mid 
\left( \begin{array}{c}
\theta_t \\
\mu_t
\end{array} \right) 
\sim 
N \left( 
\left( \begin{array}{c}
m_\theta(t, \mu_t, \theta_t) \\
m_\mu(t, \mu_t, \theta_t)
\end{array} \right), 
\left( \begin{array}{cc}
\sigma^2_{\theta} & \sigma_{\mu,\theta}^	op \\
\sigma_{\mu,\theta} & \sigma^2_{\mu}
\end{array} \right) \right),
$$

where

$$
m_\theta(t, \mu_t, \theta_t) = e^{-\alpha} \theta_t + \bar{\theta} \left( 1 - e^{-\alpha} \right) + \frac{\alpha (\theta_0 - \bar{\theta})}{\alpha - \gamma} e^{-\gamma t} \left( e^{-\gamma} - e^{-\alpha} \right),
$$

$$
m_\mu(t, \mu_t, x_j, \theta_t) = e^{-\kappa} \mu_{t,x_j} + \frac{\kappa \theta_t \mu(x_j) (e^{-\alpha} - e^{-\kappa})}{\kappa - \alpha} 
+ \mu(x_j) \frac{\kappa \alpha \bar{\theta}}{\kappa - \alpha} \left( \frac{1}{\alpha} \left( 1 - e^{-\alpha} \right) - \frac{1}{\kappa} \left( 1 - e^{-\kappa} \right) \right) 
+ \mu(x_j) \frac{\kappa \alpha (\theta_0 - \bar{\theta}) e^{-\gamma t}}{\kappa - \alpha} \left( \frac{e^{-\gamma} - e^{-\alpha}}{\alpha - \gamma} - \frac{e^{-\gamma} - e^{-\kappa}}{\kappa - \gamma} \right).
$$
Filtering of $\theta_t$ & estimation

**Proposition (cont’d)**

The covariance vector $\sigma_{\mu,\theta} = (\sigma_{\mu,\theta}(x_j))_{j=1,...,p}$ of dimension $p - 1$

$$
\sigma_{\mu,\theta}(x_j) = \nu^2 \frac{\kappa \mu(x_j)}{\kappa - \alpha} \left( \frac{1}{2\alpha} (1 - e^{-2\alpha}) - \frac{1}{\alpha + \kappa} (1 - e^{-(\alpha + \kappa)}) \right).
$$

The $(p - 1) \times (p - 1)$ covariance matrix $\sigma^2_{\mu} = (\sigma^2_{\mu}(x_j, x_k))_{j,k=1,...,p}$ contains the following elements

$$
\sigma^2_{\mu}(x_j, x_k) = \frac{\Sigma(x_j)^\top \Sigma(x_k)}{2\kappa} (1 - e^{-2\kappa}) + \mu(x_j) \mu(x_k) \left( \frac{\kappa \nu}{\kappa - \alpha} \right)^2 \\
\times \left( \frac{1}{2\alpha} (1 - e^{-2\alpha}) + \frac{1}{2\kappa} (1 - e^{-2\kappa}) - \frac{2}{\alpha + \kappa} (1 - e^{-(\alpha + \kappa)}) \right).
$$
Filtering of $\theta_t$ & estimation

$\theta_t$ is not directly visible. Using the properties of conditional expectation for a multivariate, we recursively estimate $\theta_{t+1}$:

$$
\hat{\theta}_{t+1} = \mathbb{E}\left(\theta_{t+1}|\mu_{t+1}, \mu_t, \hat{\theta}_t \right)
$$

$$
= m_\theta(t, \mu_t, \hat{\theta}_t) + \sigma_{\mu,\theta}^\top (\sigma_{\mu}^2)^{-1} \left( \mu_{t+1} - m_\mu(t, \mu_t, \hat{\theta}_t) \right).
$$

(4)

After the filtration of $\hat{\theta}_t$, the log-likelihood of the sample of observations, denoted by $\ln L$, is approached by the following sum

$$
\ln L = \sum_{t=0}^{n-1} \ln \left( f_\mu \left( \mu_{t+1}|m_\mu(t, \mu_t, \hat{\theta}_t), \sigma^2_{\mu} \right) \right)
$$

(5)

where $f_\mu \left( . | m_\mu, \sigma^2_{\mu} \right)$ is the probability density function of a multivariate normal with mean $m_\mu$ and covariance matrix $\sigma^2_{\mu}$. 
Filtering of $\theta_t$ & estimation

Parameters are estimated by log-loglikelihood maximization. The algorithm for computing the log-likelihood is:

**Initialization :**
Set $\hat{\theta}_0$ to $\theta_0$ and $\ln L = 0$

**Main procedure :**
For $t = 0$ to $n - 1$
  1. Filter the longevity process with eq. (4)
  2. Update the log-likelihood with eq. (5)

**End loop** on epochs

The jumps of $\hat{\theta}_t$ are next estimated by a peak-over threshold procedure (Hainaut 2022, Chapter 4, Section 3).
Model validation

Data: Belgian population, ages 20–100 years, period 1950-2010. For identification, $\theta_0 = 1$. 

![Graph showing mu(x) and Theta(t) for female and male populations across age and time periods.](image)
Model validation

Test of the predictive capacity: 1000 scenarios over the period 2011 up to 2020 for ages from 0 up to 105 years. Female population.

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**mu(x), female, year 2015**

- Age (x) vs. Mu(x)
- Comparison between Model and Real data
- 5% and 95% confidence intervals

**mu(x), female, year 2019**

- Age (x) vs. Mu(x)
- Comparison between Model and Real data
- 5% and 95% confidence intervals
Model validation

Same test, male population

mu(x), male, year 2015

mu(x), male, year 2019
Model validation

Comparison with Lee-Carter (LC), the Renshaw Haberman (RH) models:

\[
\ln \mu_x(t) = \alpha_x + \beta_x \kappa_t
\]

\[
\ln \mu_x(t) = \alpha_x + \rho_{t-x} + \beta^1_x \kappa_t
\]

Mean absolute errors:

<table>
<thead>
<tr>
<th></th>
<th>MAE, female</th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td>LC</td>
</tr>
<tr>
<td>2011</td>
<td>3.643e-03</td>
</tr>
<tr>
<td>2013</td>
<td>5.924e-03</td>
</tr>
<tr>
<td>2015</td>
<td>8.477e-03</td>
</tr>
<tr>
<td>2017</td>
<td>5.968e-03</td>
</tr>
<tr>
<td>2019</td>
<td>5.126e-03</td>
</tr>
</tbody>
</table>
Model validation

Comparison with a Gaussian cohort framework in which the mortality rate at time $t$, of a $x + t$ years old individual is

$$\mu_{x+t} = a_x + \lambda_{x+t},$$
$$d\lambda_{x+t} = \kappa_x \lambda_{x+t} dt + \sigma_x dW^x_t,$$

The survival probability in this model, $t p_x = \mathbb{E} \left( e^{-\int_0^t \mu_{x+s} ds} \right)$ is equal to

$$t p_x = \exp \left( - \left( a_x - \frac{\sigma_x^2}{2\kappa_x^2} \right) t - \frac{1}{\kappa_x} \left( e^{\kappa_x t} - 1 \right) \right)$$
$$\times \left( \lambda_x + \frac{\sigma_x^2}{\kappa_x^2} - \frac{\sigma_x^2}{4\kappa_x^2} \left( e^{\kappa_x t} + 1 \right) \right)$$

We fit this model to cohorts of ages 30 to 90 in 2010. Same window of time :1950 to 2010. The 60 sets of parameters $(a_x, \kappa_x, \sigma_x, \lambda_x)$ are estimated by least square minimization between observed and modelled $t p_x$. 
For the female population, the CYM leads to a lower MAE from 2011 to 2020. For the male population, cohort and CYM have a similar predictive power but CYM is more parsimonious (14 par.).

<table>
<thead>
<tr>
<th></th>
<th>MAE, female</th>
<th></th>
<th>MAE, male</th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td>Cohort</td>
<td>Calendar</td>
<td>Cohort</td>
</tr>
<tr>
<td>2013</td>
<td>4.630e-03</td>
<td>1.659e-03</td>
<td>3.476e-03</td>
</tr>
<tr>
<td>2015</td>
<td>8.044e-03</td>
<td>3.131e-03</td>
<td>5.443e-03</td>
</tr>
<tr>
<td>2016</td>
<td>7.873e-03</td>
<td>2.831e-03</td>
<td>5.553e-03</td>
</tr>
<tr>
<td>2017</td>
<td>1.059e-02</td>
<td>3.781e-03</td>
<td>8.298e-03</td>
</tr>
<tr>
<td>2018</td>
<td>1.357e-02</td>
<td>5.125e-03</td>
<td>8.944e-03</td>
</tr>
<tr>
<td>2019</td>
<td>1.482e-02</td>
<td>4.892e-03</td>
<td>1.003e-02</td>
</tr>
<tr>
<td>2020</td>
<td>2.865e-02</td>
<td>1.314e-02</td>
<td>2.326e-02</td>
</tr>
</tbody>
</table>
Model estimation 1950-2020

- Data sets: Belgian, UK and Italian, male & female populations,

- Age range: 20 to 105 years. Time window: 1950-2020,

- Parameters: see article,

- Comparison of prospective life expectancies with a LC model.
Example: for UK, a gap appears for life expectancies at older ages. We explain this gap by the trend of the model to overestimate mortality rates between 60 and 85 years (mainly due to the choice of the Makeham-Gompertz).

<table>
<thead>
<tr>
<th>Age</th>
<th>Female, UK</th>
<th>Male, UK</th>
</tr>
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<tbody>
<tr>
<td></td>
<td>$e_x$, 2020</td>
<td>$e_x$, 2020</td>
</tr>
<tr>
<td>0</td>
<td>87.17</td>
<td>83.79</td>
</tr>
<tr>
<td>20</td>
<td>64.99</td>
<td>61.73</td>
</tr>
<tr>
<td>40</td>
<td>43.31</td>
<td>40.33</td>
</tr>
<tr>
<td>60</td>
<td>23.84</td>
<td>21.48</td>
</tr>
<tr>
<td>80</td>
<td>8.57</td>
<td>7.43</td>
</tr>
</tbody>
</table>
We consider annuities with three maturities 10, 15 and 20 years. They are valued for a 60 years old Belgian man.

<table>
<thead>
<tr>
<th>Annuity 10y</th>
<th>0</th>
<th>1</th>
<th>2</th>
<th>3</th>
<th>4</th>
<th>5</th>
</tr>
</thead>
<tbody>
<tr>
<td>1% percentile</td>
<td>8.42</td>
<td>7.56</td>
<td>6.68</td>
<td>5.78</td>
<td>4.85</td>
<td></td>
</tr>
<tr>
<td>Price</td>
<td>9.31</td>
<td>8.50</td>
<td>7.65</td>
<td>6.76</td>
<td>5.84</td>
<td>4.90</td>
</tr>
<tr>
<td>99% percentile</td>
<td>8.58</td>
<td>7.74</td>
<td>6.84</td>
<td>5.91</td>
<td>4.95</td>
<td></td>
</tr>
<tr>
<td>99% relative VaR</td>
<td>0.95%</td>
<td>1.23%</td>
<td>1.28%</td>
<td>1.14%</td>
<td>1.03%</td>
<td></td>
</tr>
</tbody>
</table>

<table>
<thead>
<tr>
<th>Annuity 20y</th>
<th>0</th>
<th>1</th>
<th>2</th>
<th>3</th>
<th>4</th>
<th>5</th>
</tr>
</thead>
<tbody>
<tr>
<td>1% percentile</td>
<td>15.92</td>
<td>15.42</td>
<td>14.89</td>
<td>14.29</td>
<td>13.66</td>
<td></td>
</tr>
<tr>
<td>Price</td>
<td>16.56</td>
<td>16.22</td>
<td>15.77</td>
<td>15.23</td>
<td>14.61</td>
<td>13.92</td>
</tr>
<tr>
<td>99% percentile</td>
<td>16.52</td>
<td>16.13</td>
<td>15.58</td>
<td>14.97</td>
<td>14.22</td>
<td></td>
</tr>
<tr>
<td>99% relative VaR</td>
<td>1.88%</td>
<td>2.32%</td>
<td>2.35%</td>
<td>2.44%</td>
<td>2.16%</td>
<td></td>
</tr>
</tbody>
</table>
Conclusions

We propose calendar year model in which mortality rates revert to a long-term level that is the product of an age specific function and of a mean reverting longevity process.

Interesting features estimation on an adjustable recent time window, correlation between cohorts, closed form expression for survival probabilities.

Our model is capable to explain the evolution of Belgian death rates and that its predictive power competes with Lee-Carter, Renshaw-Haberman and cohort approaches.

Once fitted, we can evaluate the forward longevity VaR’s related to longevity risk.