CONTINGENCIES PROJECT

AN ANALYSIS OF AUSTRALIAN MORTALITY RATES

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Background

The objective of this report is to recommend a stochastic mortality model which is suitable to model the mortality of Australia's population. We do this by exploring previously proposed models, where our research is primarily based on the works of Cairns et al. (2009), who have compared the models' suitability for different populations.

Our report begins by introducing the relevant notation and assumptions used, followed by a brief analysis of the sample data and a discussion of the strengths and weaknesses of using a longer sample period. Next, we introduce our candidate models and explain their features, whilst fitting the models using the R package, "StMoMo". We then discuss our model selection criteria, and subsequently apply this to recommend the most suitable model. Finally, we use our chosen model to perform forecasts and simulations.

Summary

This report aims to examine the eight models presented by Cairns et al. (2009) with the mortality data in Australia and choose the most suitable one to model the population.

From the exploratory analysis, we note that while Australian mortality generally follows the sense that the death rate decreases with time, there exists special periods such as the year 1970, where the death rates were higher throughout most ages than those in 1960. Additionally, strong cohort effects are found in the cohorts born in 1900, 1922 and 1946. We deduce that a sensible model should incorporate three effects: age, period and cohort. We also discuss how, by re-fitting the model with longer periods of sample, the robustness tests become more accurate, but the inaccuracy of the data during 1920-1950 and the occurrences of some historical events such as warfare may be misleading when forecasting future death rates.

Next, we find that models M1-M3 are nested models of the Lee-Carter model and models M5-M8 are nested models of the CBD model and that M1 and M5 don't incorporate a cohort effect. As a special case, M4 models a smooth function and lacks the ability to generate sample path, and hence is excluded from the candidate models. Then, we observe that although M1 and M2 perform better than M3 for the BIC, they are considered inferior due to the absence of a cohort parameter in M1 and the poor robustness of M2. Even though the standardised residuals of M3 are not as random as M2, it still performs better than the other models. Therefore, M3 is chosen as the most suitable model.

When performing forecasting, we notice a decreasing trend that is tapering off with time, and that the forecasts show the three effects, as intended. The prediction intervals for older ages are also found to be wider and not diverging. Finally, the 10,000 simulated results in the last section show reasonably high survival rates from young to mid-ages.

Based on the observations of past experience, quantitative testing and some implementation to hypothetical cases, the report finalises that M3 is a suitable mortality model for Australian population.

Basis

Notations:

- Calendar year t represents the continuous year from time t to time $t+1$.
- Age x denotes age x last birthday: from exact age x to exact age $x+1$.
- $m(x,t)$ denotes the central rate of mortality at age x in calendar year t : expected number of deaths of lives aged x in calendar year t divided by the exposure at age x in calendar year t.
- $q(x,t)$ denotes the rate of mortality at age x in calendar year t : probability that a life aged x at time t dies in calendar year t.
- $p(x,t) = 1 - q(x,t)$ denotes the survival probability at age x in calendar year t : probability that a life aged x at time t survives to calendar year $t+1$.
- $\mu(x,t)$ denotes the force of mortality at age x in calendar year t : instantaneous rate of mortality of a life aged x at time t.
- $\beta_x^{(i)}$ denotes the i^{th} age effect at age x.
- $\kappa_t^{(i)}$ denotes the i^{th} period effect at calendar year t.
- $\gamma_c^{(i)}$ denotes the i^{th} cohort effect at calendar year of birth c.

Assumptions:

- The cohort index c will cover a range of two years (individuals born in calendar years $t-x-1$ and $t-x$) because of the definitions for calendar year t and age x.
  We assume that the cohort index c takes the value of the second of these two calendar years, so that

$$c = t - x$$

- For simplicity of calculations, we will assume a constant force of mortality between integer ages and over calendar years: for integers x and t and all $0 \leq u, v < 1$, we have that

$$\mu(x + u, t + v) = \mu(x, t)$$

Leading to two relevant implications:

1. $m(x, t) = \mu(x, t)$
2. $q(x, t) = 1 - exp[-m(x, t)]$

Exploratory Analysis of Sample Data

We create some plots that allow us to visualise the trends, features and irregularities of the sample data at the age range 20-89 and period 1960-2016.

First, we want to assess how the mortality rates vary across the period. We create a plot of central death rates across ages, for each decade. The graph starts at age 40 since the rates for ages less than 40 are too small (close to 0.00) and this would increase the scaling of the graph, making it visually inadequate.

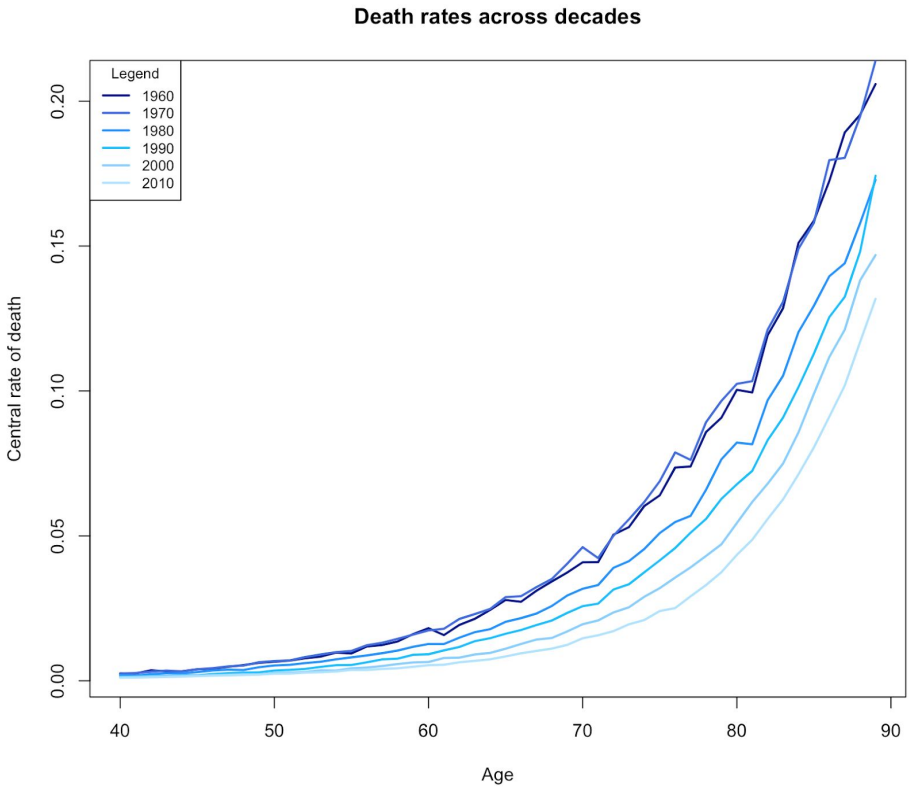

Figure 1.1: Age vs. Central mortality rates, across decades

It is evident that for each period, mortality is increasing with age for the given population. This is generally the case, since the majority of mortality risk factors present themselves, or have an increased risk, as lives age. This effect is referred to as an age effect, and will be incorporated in the models introduced in the following sections.

Mortality seems to be decreasing over time, across all ages. This illustrates how, with time, the increasing presence of life-extending factors such as the advancements made in medicine and

technology tend to result in higher life expectancy. There were also no major catastrophic events during our investigation period. This particular effect is called a period effect, and will also be included in the later models.

We notice that the mortality rates in the year 1970 were higher than those in 1960 for most of the plotted ages. This is contrary to what we would expect given the arguments in the paragraph above. It demonstrates how the mortality for the given population is not necessarily monotone decreasing with time, since the occurrence of particular events may result in fluctuating mortality. This reinforces the need for a period effect when fitting models to the data.

Next, we present a heatmap to illustrate how mortality varies across both age and years, adjacently. A dark region represents high mortality, and a light region represents low mortality.

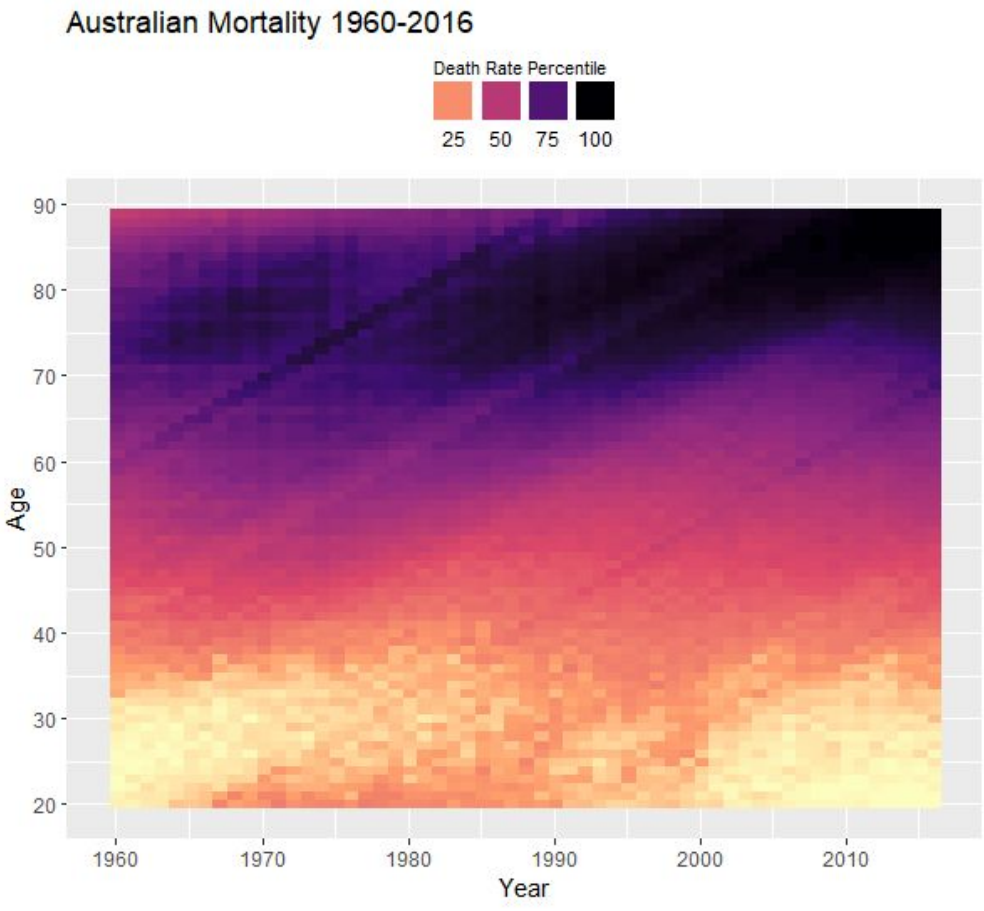

Figure 1.2: Heatmap of death rates across ages and years

Once more, we notice that mortality increases (region gets darker) with increasing age. This supports the presence of an age effect in the data.

Some diagonal lines are noticeable in Figure 1.2 since they are darker (experience higher mortality) compared to their adjacent lighter regions (experience lower mortality). We can make out some apparent cohort effects along the diagonals, notably with those born in 1946. This cohort remained at a higher risk of death for the age range 20-65. That can be explained by the fact that they were born at the end of World War II and may have been raised in unfavourable conditions during the post-war, such as having lost their parents, shelter, or living in a relatively "depressive" society. We can make the same comment about the cohorts born in 1900 and in 1922. Hence we would assume that a desirable model would incorporate a cohort-related parameter.

As a result of the exploratory analysis, we believe that our candidate models should incorporate age, period and cohort effects.

Pros and Cons of using a Longer Sample Period

By extending our sample period to begin earlier, for example at 1920, we have a larger dataset to perform tests for parameter robustness in each model. In particular, there is more data to take subsets from, in which we can refit our models, where we hope to see similar parameter estimates across each subset (indicating robustness). Also, there are more data points, which can be used to give a more accurate depiction of how different effects work over time, for the given population. These can help to create robust models which are closer to reflecting the true underlying mortality of the population, and thus, extending our sample period seem favourable.

However, some practical issues may arise. For example, the data for earlier years may contain inaccuracies due to a lack of technology, resulting in poorer data collection methods. As a result, we are less likely to accurately model the true underlying mortality rate for the population. By including older periods in our sample, certain irrelevant information may be captured. For example, we would observe fluctuations in mortality in the period 1920-1945 due to World Wars and the Great Depression. If creating a stochastic model is to be used for forecasting purposes, we should not incorporate the effects of these events, since we do not expect them to happen again. Ultimately, these are the potential consequences that need to be considered with regards to extending the sample period.

Description of Candidate Models

The data covers the ages 20, 21, … , 89 and calendar years 1960, 1961, … , 2016. We will describe 8 models, named M1, M2, … , M8. We assume that for models M1-M4, deaths follow a Poisson distribution and for models M5-M8, deaths follow a Binomial distribution. Then, we fit them to our data using the StMoMo package in R and produce the plots for each model's parameters , which will be shown when testing for robustness.

Model M1:

This model is the original Lee-Carter (or LC) model (Lee and Carter, 1992). It incorporates two age effects, one period effect and no cohort effect. The model is described as

$$log\ m(x,t) = \beta_x^{(1)} + \beta_x^{(2)}\kappa_t^{(2)}$$

Here, we come across an identifiability problem when estimating the parameters. To overcome this, we use some subjective parameter constraints, as introduced by Cairns et al. (2009):

$$\sum_x \beta_x^{(2)} = 1 \quad \text{and} \quad \sum_t \kappa_t^{(2)} = 0$$

The constraint applied to the period effect results in $\beta_x^{(1)}$ being the average of the $log\ m(x,t)$ values over time.

Mathematically, we may deduce that the age and period effects already give the full explanation for mortality since the cohort effect is determined by the cohort index ($c = t - x$), which is dependent on time t and age x. But the model doesn't have a cohort-related parameter itself.

Model M2:

We call this the Renshaw-Haberman (or RH) model (Renshaw and Haberman, 2006), which is an extension of the original LC model as described above, including a cohort effect:

$$log\ m(x,t) = \beta_x^{(1)} + \beta_x^{(2)}\kappa_t^{(2)} + \beta_x^{(3)}\gamma_c^{(3)}$$

Again, we face the same identifiability problems as in M1 which can be overcome by intuitively restricting some parameters (Cairns et al., 2009):

$$\sum_x \beta_x^{(2)} = 1\,, \quad \sum_t \kappa_t^{(2)} = 0\,, \quad \sum_x \beta_x^{(3)} = 1 \quad \text{and} \quad \sum_c \gamma_c^{(3)} = 0$$

Similar to M1, the restrictions on the period-related and cohort-related parameters means that the estimate for $\beta_x^{(1)}$ will be the average of the $log\ m(x,t)$ values over time.

This model considers the correlation between the age effect and cohort effect.

Model M3:

This is a special case of the RH model where we take $\beta_x^{(2)} = 1$ and $\beta_x^{(3)} = 1$, and is called the Age-Period-Cohort (or APC) model. It consists of three individual effects: age, period and cohort and is in the form

$$log\ m(x,t) = \beta_x^{(1)} + \kappa_t^{(2)} + \gamma_c^{(3)}$$

To ensure identifiability, we follow Cairns et al. (2009), and impose the restrictions

$$\sum_c \gamma_c^{(3)} = 0 \quad \text{and} \quad \sum_c c.\gamma_c^{(3)} = 0$$

We also need to impose a tilting parameter δ such that

$$\delta = -\frac{\sum_x (x-\bar{x})(\beta_x^{(1)}-\bar{\beta}_x^{(1)})}{\sum_x (x-\bar{x})^2}$$

Where $\bar{\beta}_x^{(1)} = \frac{\sum_t log\ m(x,t)}{n}$ and $n = 57$ is the number of periods (years) in the sample data.

The model has that the three effects are uncorrelated to each other.

Model M4:

M4 suggests the use of B-splines and P-splines to fit mortality with smoothing of some coefficients θ_{ij} in the age and cohort directions $B_{ij}^{ay}(x,t)$ (Currie, Durban & Eilers, 2004). Its form is

$$log\ m(x,t) = \sum_{i,j} \theta_{ij}\ B_{ij}^{ay}(x,t)$$

M4 assumes that there is smoothness in the underlying mortality surface for all the effects. It is not practical to make these assumptions for our investigation, hence fitting model M4 won't be useful. Also, M4 is unable to generate sample paths (Cairns et al., 2009), which is a further complication as we aim to not only fit the observed mortality, but also forecast future mortality rates. Therefore, we proceed without fitting M4.

Model M5:

This model is the original Cairns-Blake-Dowd (or CBD) model. It consists of two age effects and two period effects.

We assume simple age parameters for ease of computation: $\beta_x^{(1)} = 1$ and $\beta_x^{(2)} = (x - \bar{x})$, where $\bar{x}$ is the average age in the age-range (in our analysis, $\bar{x} = 54.5$). So we get

$$\begin{aligned} log\ \tfrac{q(x,t)}{1-q(x,t)} &= \beta_x^{(1)}\kappa_t^{(1)} + \beta_x^{(2)}\kappa_t^{(2)} \\ &= \kappa_t^{(1)} + \kappa_t^{(2)}(x - \bar{x}) \end{aligned}$$

This model has no identifiability issues.

Note that M5 addresses the correlation between the age and period in the second term.

Model M6:

M6 is an extension of the original CBD model described above, with the addition of a cohort effect.

For simplicity, we assume that the age-related parameter associated with the cohort effect takes the value one ($\beta_x^{(3)} = 1$). The other age parameters are equal to those in M5. Therefore,

$$\begin{aligned} log\ \tfrac{q\,(x,t)}{1-q\,(x,t)} &= \beta_x^{(1)}\,\kappa_t^{(1)} + \beta_x^{(2)}\kappa_t^{(2)} + \beta_x^{(3)}\gamma_c^{(3)} \\ &= \kappa_t^{(1)} + \kappa_t^{(2)}\,(x-\bar{x}) \;+\; \gamma_c^{(3)} \end{aligned}$$

The introduction of the cohort effect leads to an identifiability problem. This is overcome by applying the following parameters constraints (Cairns et al., 2009):

$$\sum_c \gamma_c^{(3)} = 0 \text{ and } \sum_c c.\gamma_c^{(3)} = 0$$

This ensures that the cohort effect fluctuates around zero and has no perceptible linear trend (Cairns et al., 2009).

Model M7:

This model extends M6 by adding a quadratic term to the age effect.

$\beta_x^{(3)} = (x - \bar{x})^2 - \hat{\sigma}_x^2$, where $\hat{\sigma}_x$ is the average value of $(x - \bar{x})^2$ (in our analysis, $\hat{\sigma}_x = 20.2052$). The values for the other age parameters are kept the same. We get

$$\begin{aligned} log\,\tfrac{q\,(x,t)}{1-q\,(x,t)} &= \beta_x^{(1)}\kappa_t^{(1)} + \beta_x^{(2)}\kappa_t^{(2)} + \beta_x^{(3)}\kappa_t^{(3)} + \beta_x^{(4)}\gamma_c^{(4)} \\ &= \kappa_t^{(1)} + \kappa_t^{(2)}(x-\bar{x}) \;+\; \kappa_t^{(3)}[(x-\bar{x})^2 - \hat{\sigma}_x^{\,2}] + \gamma_c^{(4)} \end{aligned}$$

Again, we have an identifiability problem which we address by implementing three parameter restrictions (Cairns et al., 2009):

$$\sum_c \gamma_c^{(4)} = 0\,, \quad \sum_c c.\gamma_c^{(4)} = 0\,, \text{ and } \sum_c c^2.\gamma_c^{(4)} = 0$$

These constraints guarantees that the fitted $\gamma_c^{(4)}$ fluctuates around zero and will have no linear trend or quadratic curvature (Cairns et al., 2009).

Model M8:

The final candidate model is another extension of the original CBD model M5, with a cohort effect correlated to a linear age effect.

M8 differs from M6 such that the associated age-related parameter is in a linear decreasing ($\beta_x^{(3)} = x_c - x$), where x_c is a constant value to be estimated or chosen arbitrarily. $\beta_x^{(1)} = 1$ and $\beta_x^{(2)} = x - \bar{x}$ as in the previous CBD extensions. The model is in the form

$$\begin{aligned} log\ \frac{q(x,t)}{1-q(x,t)} &= \beta_x^{(1)}\kappa_t^{(1)} + \beta_x^{(2)}\kappa_t^{(2)} + \beta_x^{(3)}\gamma_c^{(3)} \\ &= \kappa_t^{(1)} + \kappa_t^{(2)}(x - \bar{x}) + \gamma_c^{(3)}(x_c - x) \end{aligned}$$

Here we only need to introduce one parameter constraint to avoid identifiability problems (Cairns et al., 2009):

$$\sum_c \gamma_c^{(3)} = 0$$

Prior to fitting M8, we need to estimate the constant x_c. We do this by considering how varying x_c impacts our log likelihood and parameter robustness, as these will affect how well M8 performs compared to different models. After testing for different values of x_c, we estimate that $x_c = 89$ provides an optimal balance between log likelihood and parameter robustness.

Some notable key differences between the models:

- M1-M3 are nested models of the Lee-Carter model whereas M5-M8 are nested models of the Cairns-Blake-Dowd model.
- M1-M4 model mortality using the logarithmic function of the central rate of mortality ($log\ m(x,t)$), whereas M5-M8 use the logit function of rate of mortality ($log\ \frac{q(x,t)}{1-q(x,t)}$).
- M1 and M5 only use age-related parameters ($\beta_x^{(i)}$) and period-related parameters ($\kappa_t^{(i)}$) whereas M2-M3 and M6-M8 also incorporate a cohort-related parameter ($\gamma_c^{(i)}$).
- M1-M3 and M5-M8 are step functions whereas M4 is a smooth function.
- M1-M3 and M5-M8 are able to generate sample paths whereas M4 can't.

Model Selection Criteria

Bayesian Information Criterion (BIC):

The BIC for a model is defined as

$$BIC = l(\Phi) - \frac{1}{2} v \times log(n)$$

Where:
$l(\Phi)$: maximum log-likelihood
v : number of parameters being estimated
n : number of observations

It is obvious that models with more parameters will generate higher log-likelihoods, at the expense of overfitting, so we compare the BIC for each model as this penalises over-parameterised models. The BIC values of the models are listed below.

Model	Maximum log-likelihood	Number of effective parameters	BIC	n	Rank
M1	-23758.56	195	-24567	3990	2
M2	-19850.39	388	-21459	3990	1
M3	-23572.24	250	-24608	3990	3
M5	-83612.67	114	-84085	3990	7
M6	-30301.54	238	-31288	3990	6
M7	-28008.93	294	-29227	3990	4
M8	-28988.14	238	-29974	3990	5

Table 5.1: BIC table

For the BIC criterion, M2 comes out on top since it has the highest BIC and M5 came out last. The Lee-Carter family of models (M1, M2, M3) perform better than the CBD family (M5, M6, M7, M8) under this test.

Likelihood Ratio Test (LRT):

We conduct the LRT to compare our nested candidate models.

We are testing H_0 : The restricted model is better than the general model vs H_1 : The general model is better than the restricted model. The likelihood ratio test statistic is believed to follow a chi-squared distribution.

$$2\,[\,l_G(\Phi) - l_R(\Phi)\,] \sim \chi^2_{n-m}$$

Where n and m are the degrees of freedom of the general and restricted models respectively.

Restricted model	General Model	Test Statistic	DF	P-value
M1	M2	7816.3	193	<0.000001
M3	M2	7443.7	138	<0.000001
M5	M6	106622	124	<0.000001
M5	M7	111207	180	<0.000001
M6	M7	4585.22	56	<0.000001
M5	M8	109249	124	<0.000001

Table 5.2: LRT table

It is obvious that the p-value of each test is small enough so that restricted model is better than the general model. Also the rejection of M1 and M5 proves the existence of cohort effects.

Standardised Residuals:

The standard residuals is calculated for each model by the following equation

$$Z(x,t) = \frac{\textit{Observed number of deaths} - \textit{Expected number of deaths}}{\textit{Standard deviation of number of deaths}}$$

Note that the formulas for M1-M3 are different to those for M5-M8 since they respectively follow Poisson and Binomial distributions.

Theoretically, $Z(x,t)$ is independent and normally distributed and the plot of residuals should be randomly distributed with a mean of 0 and variance of 1. Here, the positive and negative patterns of standardised residuals are shown in Figure 5.1, where the grey boxes represent the positive standardised residuals given the year and age, and the black boxes represent the negative ones.

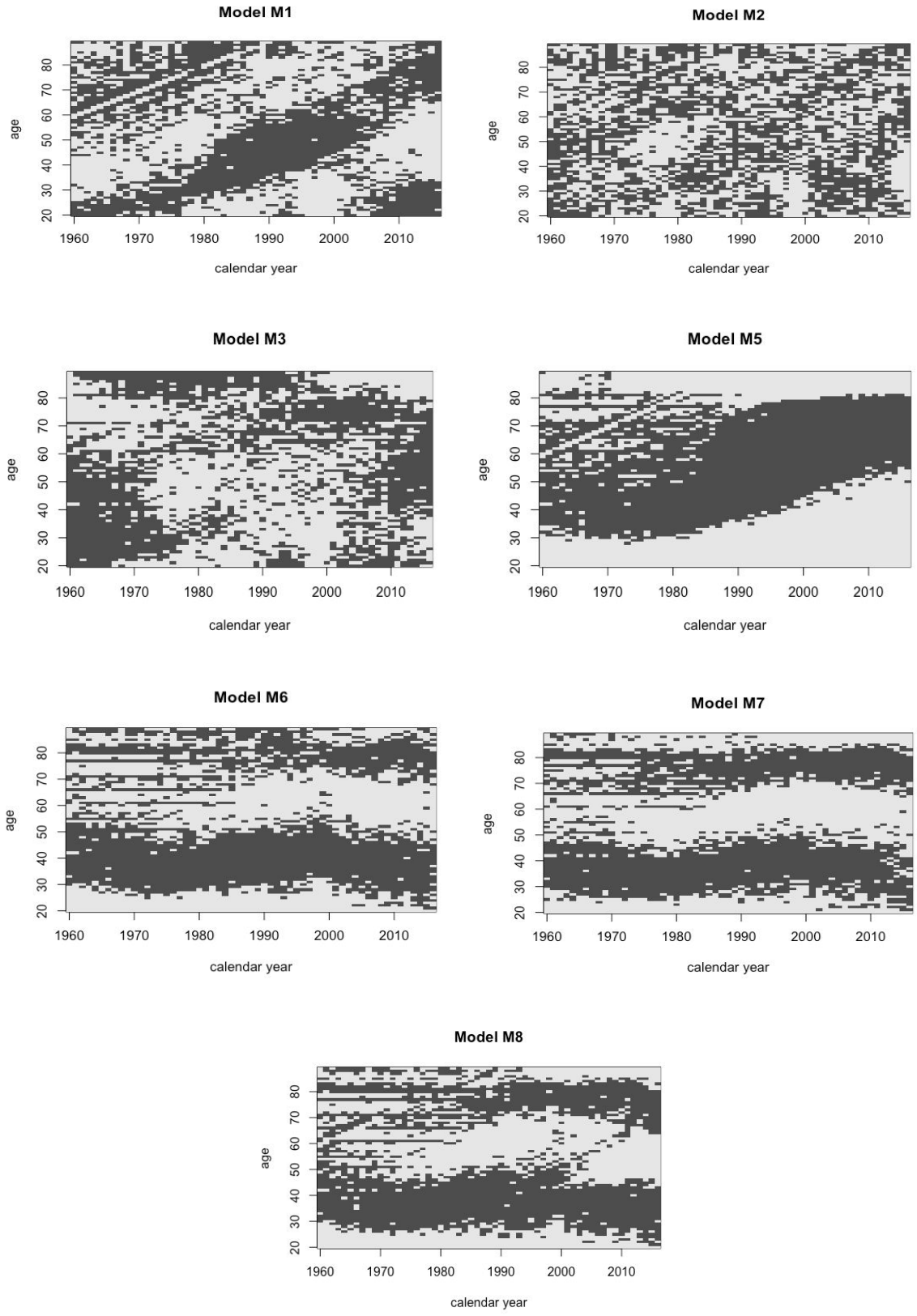

Figure 5.1: Standardise residuals

- The M2 residuals are the most randomly distributed.
- M3 does not perform as good as M2 in terms of residual randomness, as there are some clusters in the plot, but perform better than the other models.
- For M1, there is a diagonal cluster of positive and negative residuals, which is due to the absence of a cohort effect in the model.
- For models M5, M6, M7 and M8, there are horizontal black and grey clusters, which means the age effect may be smoothed too much.

Robustness:

Robustness measures how stable the parameter estimates vary over time. We prefer models with consistent parameter estimates when using different time periods. Here, the models' robustness are examined using the periods 1960-2016 and 1980-2016 and age range 20-89. The dots represent the parameter estimates for 1960-2016 and the solid blue lines represent the parameter estimates for 1980-2016.

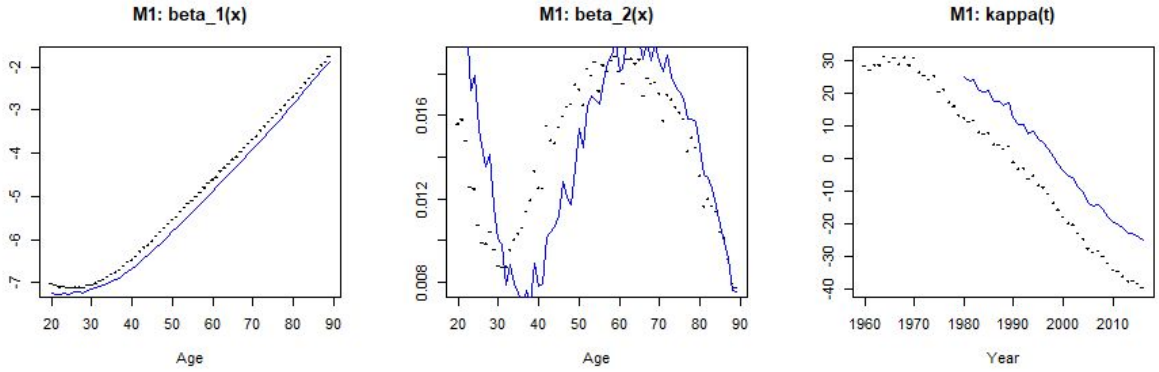

Figure 5.2: Robustness of M1 parameters

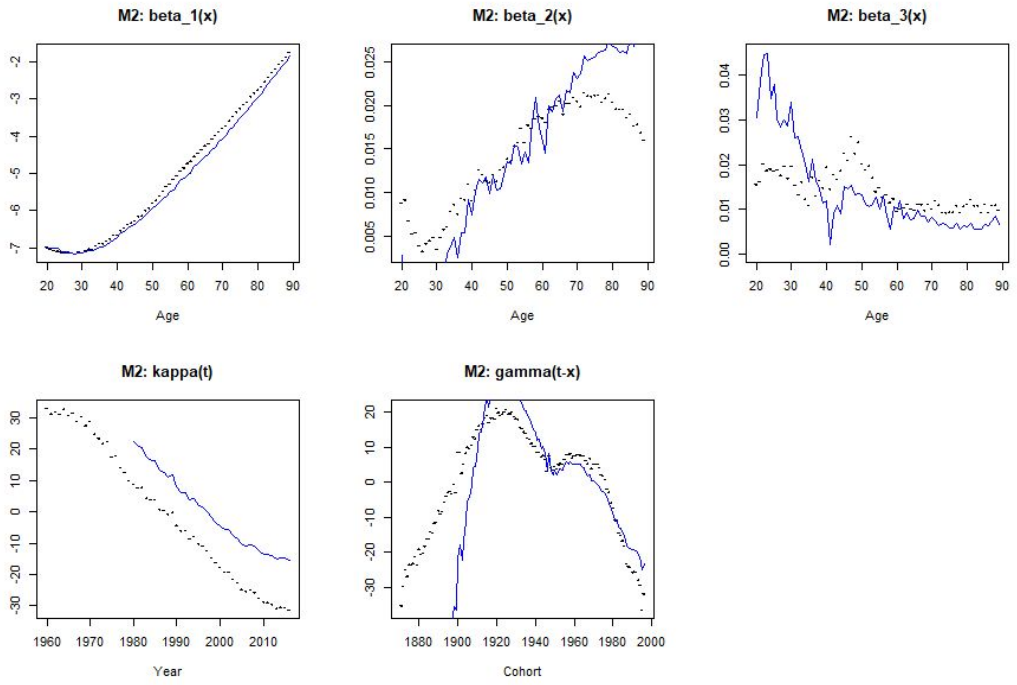

Figure 5.3: Robustness of M2 parameters

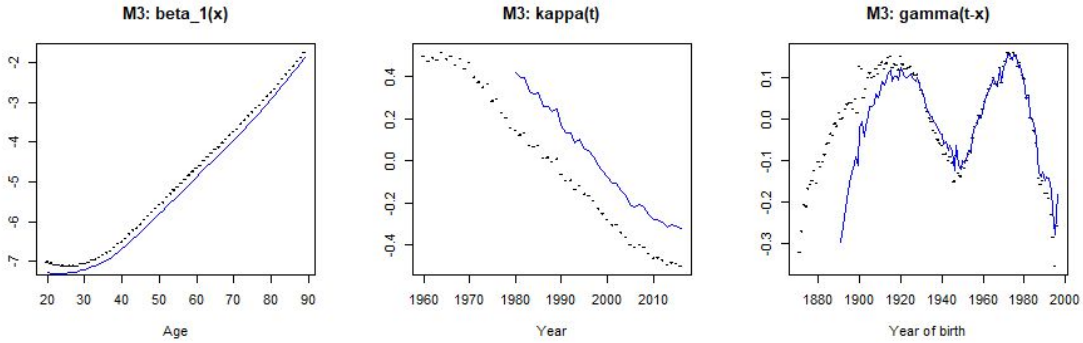

Figure 5.4: Robustness of M3 parameters

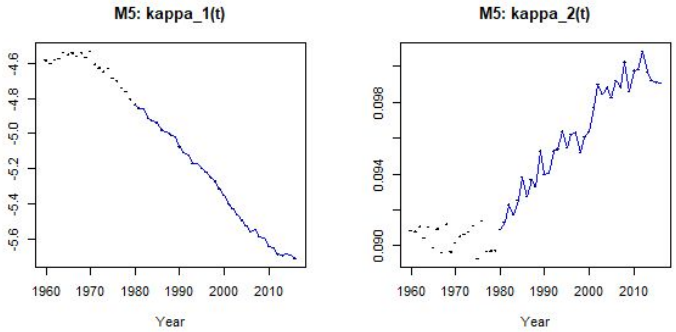

Figure 5.5: Robustness of M5 parameters

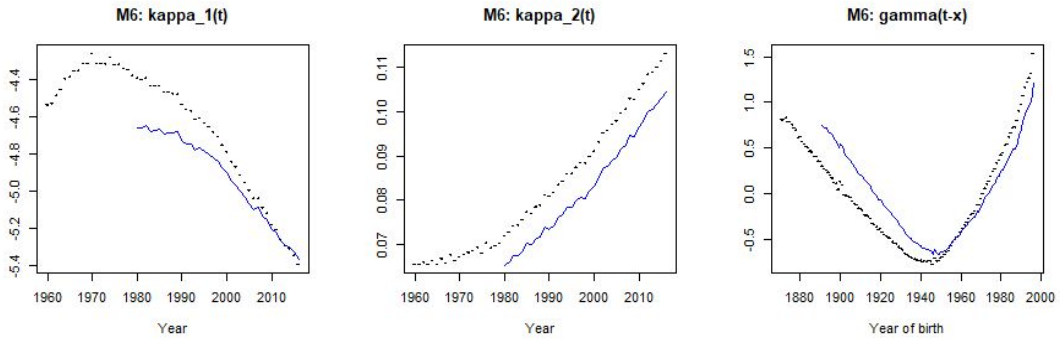

Figure 5.6: Robustness of M6 parameters

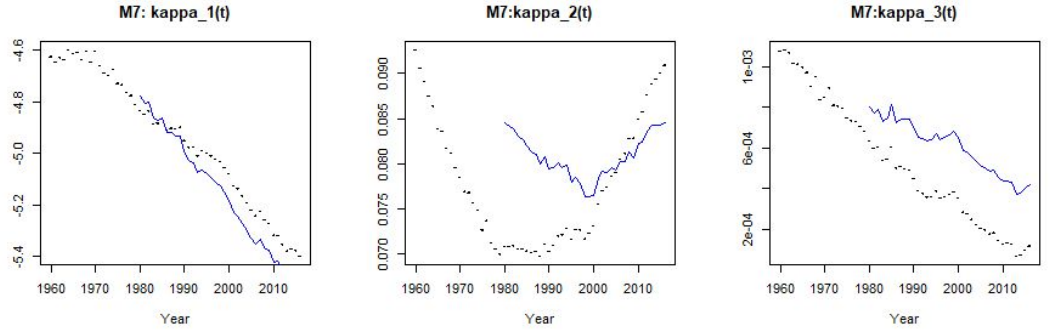

Figure 5.7: Robustness of M7 parameters

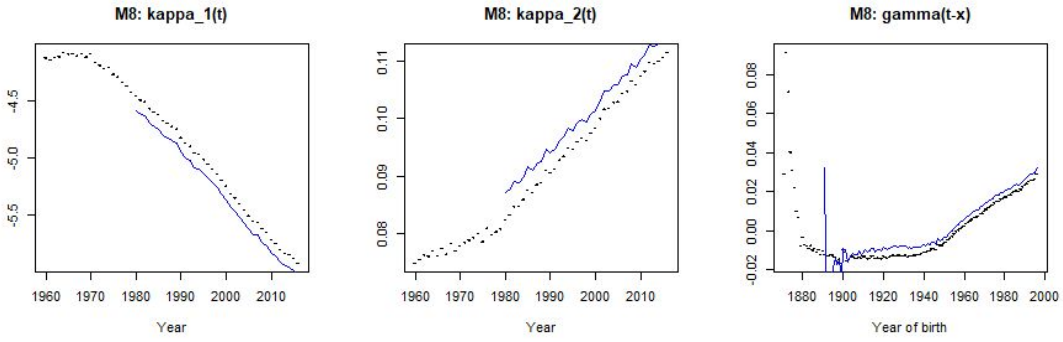

Figure 5.8: Robustness of M8 parameters

- M5 seems to be the most robust when comparing the two data periods; the blue solid line connects every point from the year 1980 onwards and the parameter estimates remains the same when selecting different time period. Since M5 fixes the age effect to 1 and the deviance from the average age, the age effect remains the same when we select the same

range of age, . Also, it does not contain a cohort effect and does not have identifiability issues.

- M3, M6 and M8 are reasonably robust. The plots of the two datasets seem to have similar patterns, however show some differences which may be a result of the constraints $\sum_t \kappa_t = 0$ and $\sum_c \gamma_c = 0$.
- Noticeably, there is a vertical stroke for γ_c of M8, which is due to the chosen x_c representing the basic age when considering cohort effect. In this case, $x_c = 89$, the vertical stroke is on the very left side of the plot.
- M2 seems to lack robustness, as when we choose different periods, the parameter estimates vary a lot. For example, the age related parameter $\beta_x^{(2)}$ shows a decreasing trend after age 70 when using the data from 1960 to 2016; while it is increasing when using the data from 1980 to 2016, shown as the blue solid lines. This cannot be reconciled by changing the constraints.

Final Model Selection

For the BIC criterion, although M2 and M1 are above M3, we cannot choose the former two models since M1 does not incorporate a cohort effect which we require, and as for M2, its parameters are the least robust among all the candidate models, especially for $\beta_x^{(2)}$ and $\beta_x^{(3)}$. Parameter robustness is an essential aspect in model selection since the accuracy of mortality rates projections will be compromised if the parameters of the model are not robust. Also, for the standardised residuals criterion, whilst not having the most random residuals, M3 is still better than most of the other models. It is evident here that no model comes unanimously on top for all criteria and hence we use our qualitative judgement and all the criteria considered.

We select M3 as the most suitable model.

Forecasting

Now that we have selected model M3, we are able to forecast $m(x,t)$. We begin by fixing the arbitrary ages 20, 40, 60, and 80, in order to plot mortality over the 20 year period after our given data range (2017-2036), so that we can analyse how the forecasted mortality rates are expected to fluctuate with age. We plot our point forecasts in red, our observed rates in blue and our fitted rates in black.

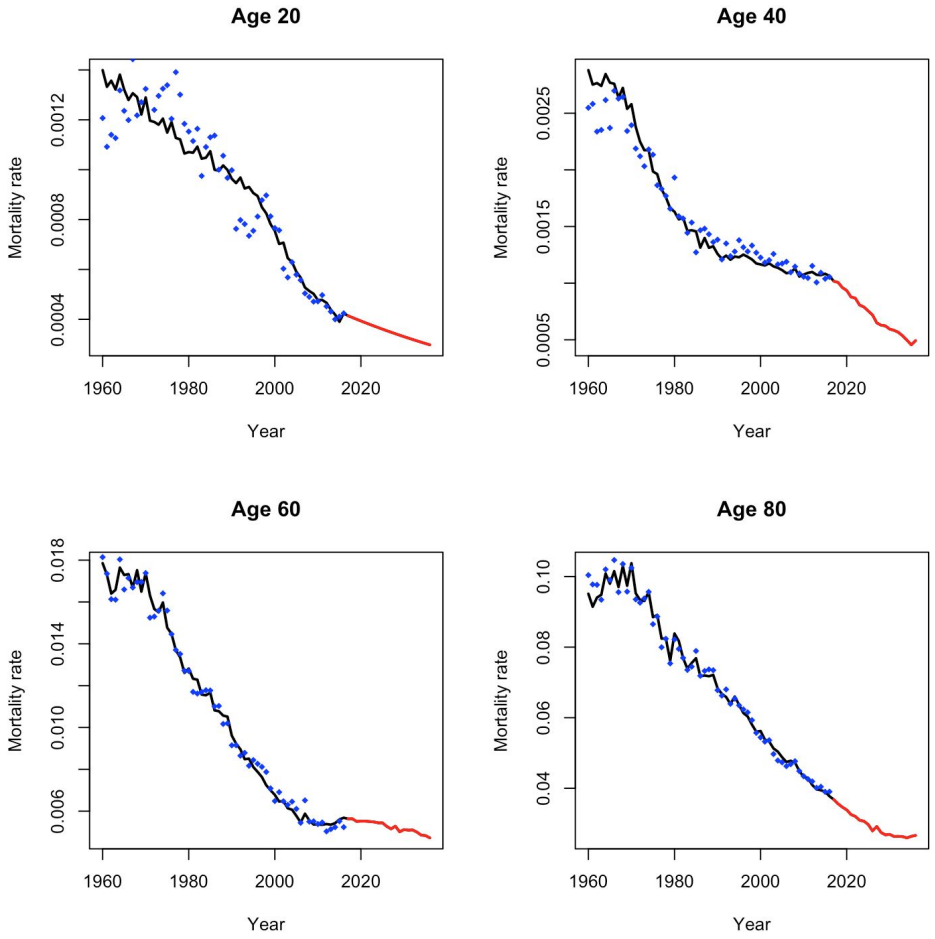

Figure 7.1: Fitted and forecasted mortality rates for ages 20, 40, 60 and 80

Upon visual inspection, it appears that M3 does appear to fit the data well, and projects the mortality rates quite smoothly at each age. Although, it is evident that the projected rates are very smooth at age 20, where smoothness begins to decline as age increases. This is what we would expect to observe, as the mortality for younger ages is presented on a much smaller scale than for

older ages, and thus tends to have lower variability. We also plot the prediction intervals for our forecasts, to understand how reliable our estimates are.

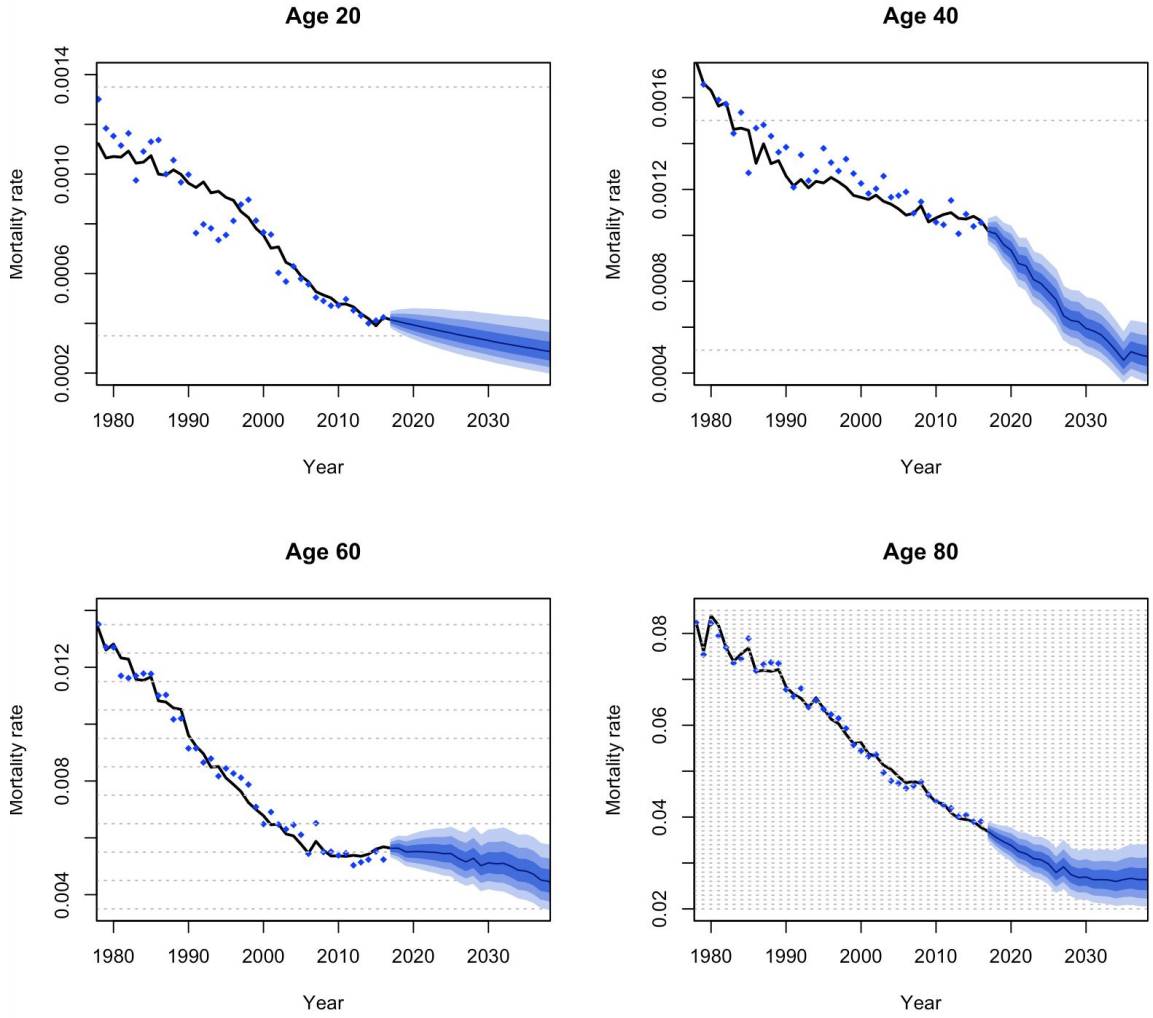

Figure 7.2: Fitted and forecasted mortality rates for ages 20, 40, 60 and 80 with prediction intervals.

The solid lines show fitted and forecasted rates, the blue dots show observed rates and the prediction intervals are at confidence levels of 50%, 90%, 95% (darkest to lightest). Dotted lines are shown to be used as a scale, separated by 0.001 on all plots

In the above Figure 7.2, scales with distance 0.001 have been added to avoid comparing variability across ages incorrectly. It is evident that as age increases, the prediction intervals for our estimates become much wider. Using the same reasoning as before, this result is expected, and does not necessarily indicate that forecasts for older ages are unreliable. In fact, for all

plotted ages, the width of the prediction intervals do not diverge much when viewed in comparison to the observed mortality rates.

Since we are going to simulate mortality for ages 30, 40 and 50, it's worth having a look at the forecasts for these ages to view the predicted behaviour of the mortality rates. All visual features correspond to Figure 7.1 and Figure 7.2.

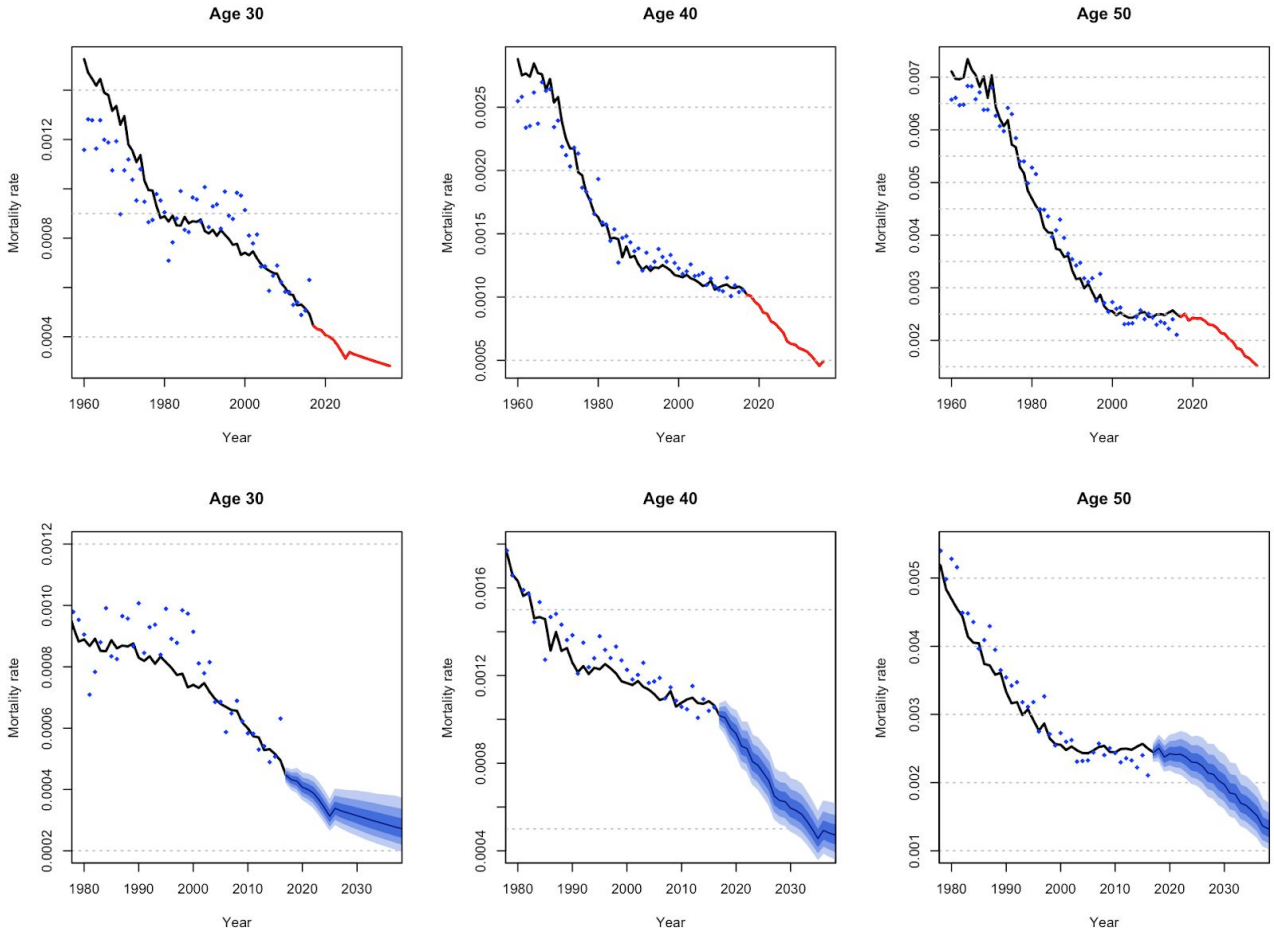

Figure 7.3: Fitted and forecasted mortality rates for ages 30, 40 and 50, with prediction intervals below.

The features of Figure 7.3 reflect what was previously explained with respect to the features of Figures 7.1 and 7.2. Across all 3 ages, projections look reliable with relatively stable prediction intervals.

Simulation

Given the number of policies in force at the beginning of 2017 for an insurance company (Table 8.1), and assuming death is the only cause of policy termination, we can use our fitted M3 to simulate the number of policies expected to be remaining in force for the following 10 year period.

	Age at start of 2017		
	30	**40**	**50**
Male	3000	2000	1000
Female	2000	1000	500

Table 8.1: Policies in force at the beginning of 2017 by age and gender

Using our model M3, we can simulate $m(x,t)$ for the relevant ages over the 10 year period following 2017. Applying our simplifying assumptions as explained in the Basis Section, we can use $\mu(x,t) = m(x,t)$ to treat the simulated values as values of $\mu(x,t)$, and then convert these to simulated survival probabilities using the relationship $p(x,t) = exp\,[-\mu(x,t)]$. To get the survival probabilities over a range of years, we compute the product of each individual survival probability within that time frame. Finally, the corresponding survival probabilities are multiplied to the relevant number of initial policies in force, where we obtain the simulated remaining policies in force in Table 8.2.

Year	Male, 30	Male, 40	Male, 50	Female, 30	Female, 40	Female, 50
2017	3000	2000	1000	2000	1000	500
2018	2998	1997	997	1999	999	499
2019	2996	1995	994	1999	999	498
2020	2994	1992	990	1998	998	497
2021	2993	1988	986	1998	997	496
2022	2991	1985	982	1997	996	495
2023	2989	1981	978	1996	995	494
2024	2987	1977	973	1995	994	492
2025	2985	1973	968	1995	992	491
2026	2982	1969	962	1994	991	489
2027	2980	1964	956	1993	989	488

Table 8.2: Simulated policies in force at the beginning of each year from 2018 to 2027, given the policies in force at 2017.

	Age at start of 2017		
	30	**40**	**50**
Male	0.9934019	0.9819140	0.9562986
Female	0.9962789	0.9894676	0.9755077

Table 8.3: Simulated 10 year survival probabilities for each cohort

We refer to table 8.3 to make accurate comparisons between the simulated data. Overall, the 10 year survival probabilities are quite high across all ages and genders, as to be expected since our starting ages are quite young. We also note that the simulated survival probabilities decrease with age, of course due to age effect. Finally, across each age, survival probabilities are higher for females compared to males, with the difference becoming more drastic as age increases.

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