

# **A QUANTITATIVE COMPARISON OF STOCHASTIC MORTALITY MODELS USING DATA FROM AUSTRALIA**

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Group 2

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# **Executive Summary**

Mortality has been on a decreasing trend for Australian total, male and female populations. We identify that male mortality is decreasing at a faster rate than female mortality, and therefore aim to address the differences in these mortality experiences. The report will attempt to identify a suitable model to predict Australian mortality data out of eight suitable stochastic mortality models.

We use sample data in the period 1960 - 2016 in the sample ages of 20 to 89 as this captures the mortalities that we typically explore in an actuarial setting - life insurance policyholders and pension fund participants.

We identify period, age and cohort effects in our sample data. When analysing the residuals of the Lee - Carter Model, which lacks a cohort effect, we can clearly distinguish an unaccounted cohort effect. Therefore we expect the model we choose to capture these effects in their prediction.

These models have been analysed, using a range of qualitative (parsimony, transparency, nontrivial correlation structure, ability to generate percentiles etc) and quantitative factors (robustness, BIC, residuals etc). We have selected Model M2 for the total and male populations on the basis of residual randomness, BIC ranking and prediction power. Model M2 is less suitable for the female population because of the poor robustness, which is fulfilled by Model M7 for the female population.

We use the estimated parameters generated by the recommended model to forecast mortality rates and explore the possible changes to mortality for both males and females over the next 20 years as well as the potential drawbacks of mortality modelling based on past data. Lastly, we simulate the change in number of policies to further explore the age and gender effects, and how this affects insurance companies.

## **1.Introduction**

### **1.1 Objective**

The aim of this study is to compare eight stochastic models using both qualitative and quantitative criteria to identify suitable models at predicting Australian male, female and total population data.

### **1.2 Background**

There have been various changes in mortality over the years, with mortality consistently improving due to changes in the fields of technology, medicine and law. As such, these constant

adjustments need to be captured in the modelling of mortality in order for companies to accurately price certain products.

In order for models to accurately be compared and analysed we have used the package “StMoMo” on R to fit these models and test various factors.

### 1.3 Structure

The structure of the report begins with the introduction of both the data and models. This will be followed by an analysis of the criteria and data used to identify an optimal model for Australian male, female and total populations. Using this model, the report will then show a forecast of the population mortality rates over the next twenty years and a simulation of the predicted number of policies which remain out of an initial 10,000 over the next twenty years.

## 2. Analysis of crude data

The data examined, consisting of central exposure  $E_{x,t}^c$  and number of deaths  $D_{x,t}$ , was extracted from the Human Mortality Database (2019).  $x$  represents the age,  $t$  denotes year of observation.

### 2.1 Age and period effect

From Figure 1.1 and 1.2 below, the progression of years are represented by the colours of the rainbow where red represents earlier years and violet represents later years. Here, we observe a fairly consistent period effect for ages between 20 to 89 whereby the log death rate decreases with time and we also observe the age effects in our data where log death rates increase with age.

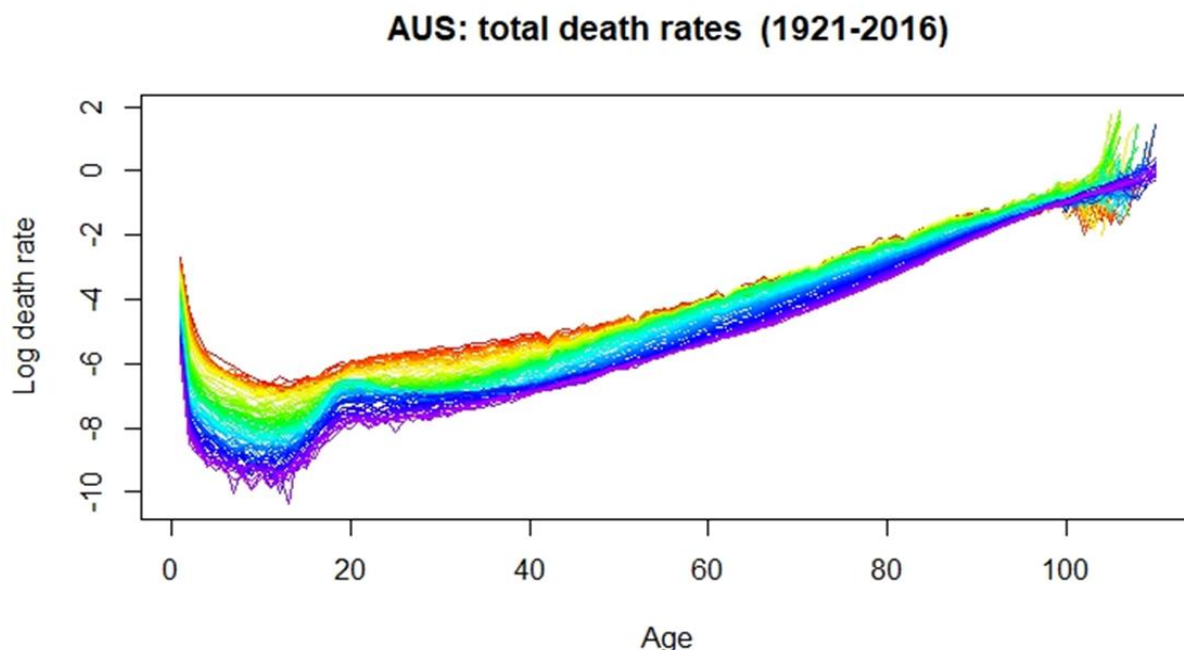


Figure 2.1

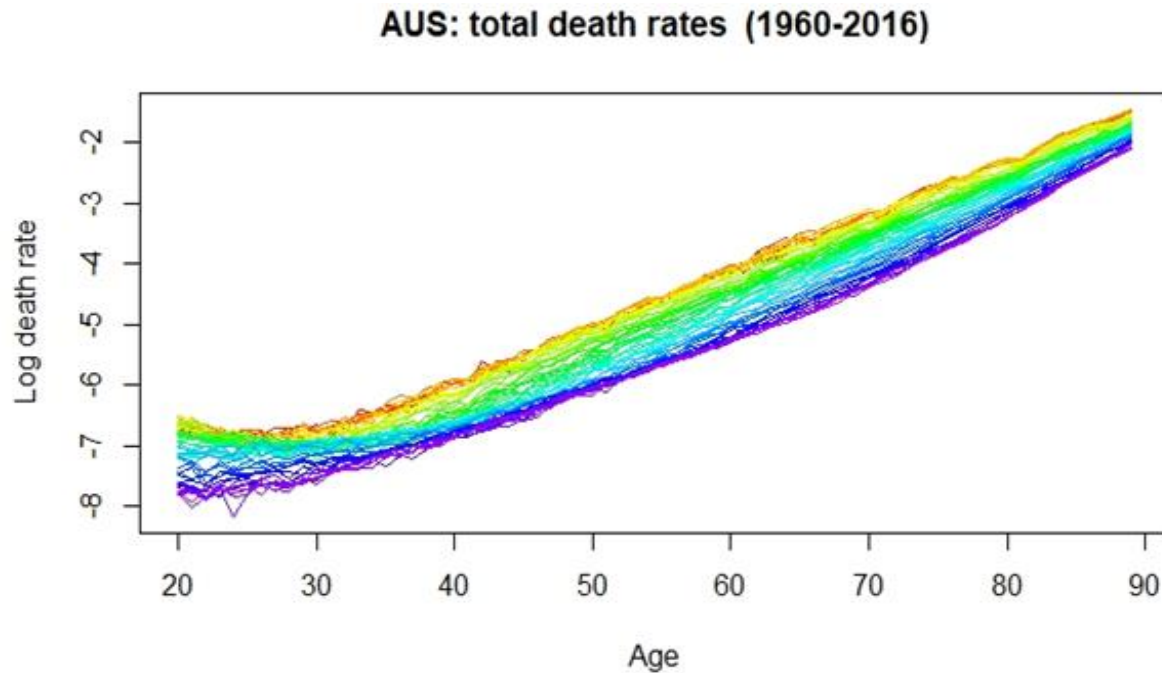


Figure 2.2

## 2.2 Cohort Effect

We observe a cohort effect where the “accident bump” occurs. Even though this effect becomes more pronounced over time, it is most pronounced for the cohorts born between 1950-1955 (Figure 1.1 teal color) where the size is larger than expected. This is further exemplified in Figure 1.2 where the 1950-1955 cohorts (green) have similar or higher mortality in their twenties than lives born 10 years earlier, or 10 years later. This may be due to the fact that as the specific cohort entered the working population during the 1970 economic crisis: they developed a higher mortality rate as a result of increased suicide rates (Chang et. al, 2013). Conversely, the previous cohort 1940-1945 enjoyed the post war economic boom and experienced an opposite effect to the 1950-1955 cohort.

## 2.3 Selected Data

For our analysis, we consider lives aged 20-89 who lived between the years 1960 to 2016.

No omissions were made from the raw data because we did not identify any anomalies that would affect the result in our sample data range. Additionally, since we observed the cohort

effect in our data, we will favor models that incorporate the cohort effect. Hence, we will use data with greater than 5 observations as argued by Cairns et al. (2009).

### **3. Justification for sample period used (1960-2016).**

#### **3.1.1 Advantages of a longer time frame of observation (1921-2016):**

By using a longer sample period, we are able to see trends over time. In particular, causes and effects of mortality changes are clearer over a longer time horizon. Focusing on smaller time frames runs the risk of skewing the parameters due to temporary events. For example, disease outbreaks may spike short term mortality rates whereas trend in mortality depends underlying improvements over time in technology and medicine.

Additionally, a longer time frame provides scale and a bigger perspective. For example, observing mortality changes over the past 10 years (marginal improvement) against a 50 year period (significant decrease in mortality).

#### **3.1.2 Disadvantages of a longer time frame of observation:**

Longitudinal studies require large sample sizes to maintain statistical significance and so it will be rather costly. Data takes a long time to collate and analyse, making it extremely time consuming before insightful conclusions can be made. Additionally, long-term observations may overshadow details in mortality changes as long-term studies focus on trend rather than detail. Data from a long time ago may also be unreliable due to the lack of technology and reliable processing. Lastly, we argue that the inclusion of data from long ago may distort the estimated parameters. In particular, past data on male mortality shows a drastic improvement over the last 50 years, which may not translate into the future. The inclusion of data from a longer time frame also means that parameterisations may include the traits of past data that may not be applicable at present. In essence, mortality of Australians in 1921 may not provide meaningful information of mortality for the 2020's.

Thus, to align with our objectives, we have decided to use the 1960-2016 time frame when fitting our models.

## 4. The mortality models

### 4.1 Assumptions

Our analysis is based on the following assumptions (Cairns et. al, 2009):

- For the purpose of model fitting, we assume that the Australian population is stationary, in that the only mode of decrement is death.
- We use death and exposure data to calculate the crude death rates,

$$m(t, x) = \frac{\text{Number of deaths during calendar year } t \text{ aged } x \text{ last birthday}}{\text{Average population during calendar year } t \text{ aged } x \text{ last birthday}}$$

- The force of mortality is constant over each calendar year for each year of age.
- For integers  $t$  and  $x$ , and for all  $v \geq 0, s < 1, \mu(t + v, x + s) = \mu(t, x)$ .
- This implies that  $m(t, x) = \mu(t, x)$  and we therefore use the relationship,

$$\hat{q}(t, x) = 1 - \exp(-\hat{m}(t, x)).$$

First, we have chosen Poisson model to model death counts (our random component):

$$D(t, x) \sim \text{Poisson}\{m(t, x)E^c(t, x)\}$$

Giving us log-likelihood function:

$$l(\hat{\theta} | D, E) = \sum_{t, x} \{D(t, x) \log(m(t, x | \hat{\theta})E^c(t, x)) - m(t, x | \hat{\theta})E^c(t, x) - \log D(t, x)!\}$$

Where  $\hat{\theta}$  is obtained by maximum likelihood estimation.

Secondly, we assume a **log link function for all our stochastic models**, i.e.

$$\log\{m(t, x)\} = \text{predictor structure}$$

This is to maintain consistency in each model's assumptions during model evaluation as opposed to assuming a Binomial distribution of deaths ( $D(t, x) \sim \text{Binomial}\{E^l(t, x), q(t, x)\}$ ) and the logit ( $q(t, x)$ ) predictor for only certain models.

To justify selecting the Poisson model over the Binomial model of deaths, we forecast mortality rates predicted by M2 (Figure 2.1) for the total population and M7 (Figure 2.2) for the female population, each using both  $\log(m(t, x))$  and  $\text{logit}(q(t, x))$  predictors. From the plots we conclude

that the two different distribution assumptions give very similar forecasts, and therefore the model assumption we choose holds no weight in our report findings.

Comparison of log link vs logit link for M2 forecasted for 2017

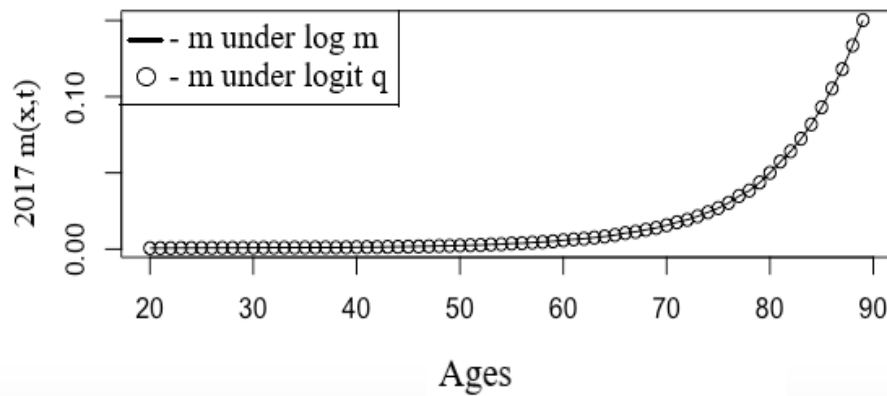


Figure 4.1

Comparison of log link vs logit link for Female M7 forecasted for 2037

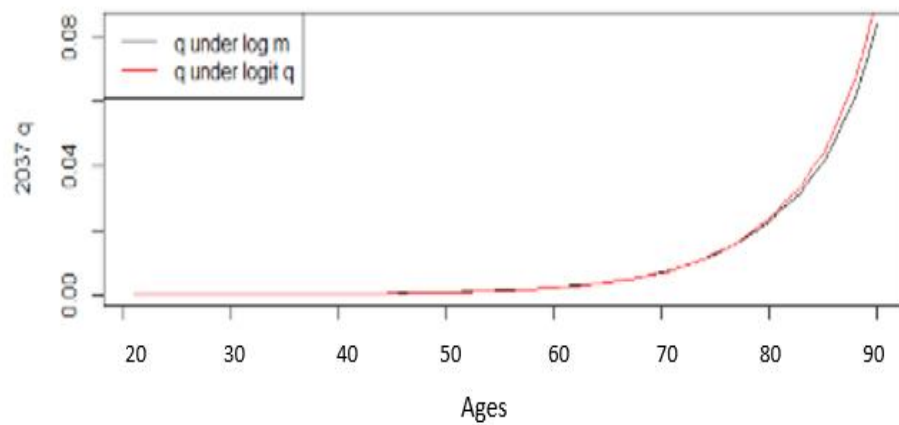


Figure 4.2

## 4.2 Description and comparison of models

### 4.2.1 Description of models

Models	Formula
M1(Lee Carter)	$\log\{m(t, x)\} = \alpha_x + \beta_x^{(I)} \kappa_t^{(I)}$
M2(Lee Carter with cohort effect)	$\log\{m(t, x)\} = \alpha_x + \beta_x^{(I)} \kappa_t^{(I)} + \beta_x^{(2)} \gamma_{t-x}$
M3(APC)	$\log\{m(t, x)\} = \alpha_x + \kappa_t^{(I)} + \gamma_{t-x}$
M4(P-splines)	$\log\{m(t, x)\} = \sum_{i,j} \theta_{i,j} \beta_{i,j}^{ay}(x, t)$
M5(CBD)	$\log\{m(t, x)\} = \kappa_t^{(I)} + (x - \underline{x}) \kappa_t^{(2)}$
M6(CBD with cohort effect)	$\log\{m(t, x)\} = \kappa_t^{(I)} + (x - \underline{x}) \kappa_t^{(2)} + \gamma_{t-x}$
M7(M6 with quadratic age effect)	$\log\{m(t, x)\} = \kappa_t^{(I)} + (x - \underline{x}) \kappa_t^{(2)} + \{(x - \underline{x})^2 - \hat{\sigma}_x^2\} \kappa_t^{(3)} + \gamma_{t-x}$
M8(M6 with decreasing age effect)	$\log\{m(t, x)\} = \kappa_t^{(I)} + (x - \underline{x}) \kappa_t^{(2)} + (x_c - x) \gamma_{t-x}$

Table 4.1: List of candidate models and their respective predictor structure (Cairns et. al, 2009)

- i) The functions  $\alpha_x, \beta_x^{(i)}$  will reflect age-related effects.
- ii) The functions  $\kappa_t^{(i)}$  will reflect period-related effects.
- iii) The functions  $\gamma_c$  will reflect cohort-related effects, with  $c=t-x$  representing cohort.
- iv)  $\underline{x}$  is the mean age of sample range, which is 54.5.
- v)  $\hat{\sigma}_x^2$  is the mean of  $(x - \underline{x})^2$ .
- vi)  $x_c$  is a constant to be estimated.

Model considered	Constraints
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M1(Lee Carter)	$\sum_t \kappa_t^{(1)} = 0, \sum_x \beta_x^{(1)} = 1$
M2(Lee Carter with cohort effect)	$\sum_t \kappa_t^{(1)} = 0, \sum_x \beta_x^{(1)} = 1, \sum_c \gamma_c = 0, \sum_x \beta_x^{(2)} = 1, \sum_c (c - \bar{c})\gamma_c = 0$
M3(APC)	$\sum_t \kappa_t^{(1)} = 0, \sum_c \gamma_c = 0, \sum_c c\gamma_c = 0$
M5(CBD)	—
M6(CBD with cohort effect)	$\sum_c \gamma_c = 0, \sum_c c\gamma_c = 0$
M7(M6 with quadratic age effect)	$\sum_c \gamma_c = 0, \sum_c c\gamma_c = 0, \sum_c c^2\gamma_c = 0$
M8(M6 with decreasing age effect)	$\sum_c \gamma_c = 0$

Table 4.2: List of constraints on each models (Villegas, Kaishev and Millossovich, 2015)

We aim to estimate parameters by maximum likelihood method using generalized non-linear modelling. We also introduce constraints on parameters to present identifiability problems.

Lastly, to estimate future mortality rate, we must extrapolate period and cohort parameters for each model. We do this by selecting the following indices to reflect the period and cohort dynamics for the given population.

Here we use

i) *ARIMA(1,1,0) with a constant on cohort indices:*

$$\gamma_c = \gamma_{c-1} - \alpha_1(\gamma_{c-1} - \gamma_{c-2}) + \varepsilon_c + k, \quad \varepsilon_c \sim N(0, \sigma_c)$$

Where  $k$  is the constant term and  $\varepsilon_c$  is Gaussian white noise with variance  $\sigma_c$ .

ii) *Multivariate random walk with drift on period indices:*

$$\kappa_t = \delta + \kappa_{t-1} + \xi_t^\kappa, \quad \kappa_t = \begin{pmatrix} \kappa_t^{(1)} \\ \vdots \\ \kappa_t^{(N)} \end{pmatrix}, \quad \xi_t^\kappa \sim N(0, \Sigma)$$

where  $\delta$  is an  $N$ -dimension vector of drift parameters and  $\Sigma$  is the  $N \times N$  variance-covariance matrix of the multivariate white noise  $\xi_t^k$ . (Villegas, Kaishev and Millossovich, 2015)

Notable features of models (Cairns et. al, 2009):

- i) All the models M1–M3 and M5–M8 share the same underlying assumption that the age, period, and cohort effects are qualitatively different in nature and hence need to be modelled in different ways.
- ii) M5 to M8 assume a functional relationship (and hence smoothness) between mortality rates over adjacent ages within the same year as opposed to M1 to M3.
- iii) M7 adds a quadratic term to the age effect. The inclusion of the quadratic term is inspired by the possible curvature identified in the logit  $q(t, x)$  plots.
- iv) M8 suggests that the impact of the cohort effect for any specific  $\gamma_{t-x}$  diminishes over time (i.e., is decreasing with  $x$ ) instead of remaining constant.
- v) Also note that:
  - M1 and M3 are special cases of M2.
  - M5 is a special case of M6.
  - M5 and M6 are special cases of M7.
  - M5 and M6 are special cases of M8.

We will be using these relationships for the Likelihood Ratio Test when evaluating the model fits.

## 4.2.2 Qualitative comparison of models

The following table concludes the qualitative features of each model:

Model	M1	M2	M3	M4	M5	M6	M7	M8
Ease of implementation	Y	?	Y	?	Y	Y	Y	?*
Parsimony	Y	?	?	Y	Y	?	?	?
Transparency	Y	Y	Y	?	Y	Y	Y	Y
Ability to generate sample paths	Y	Y	Y	N	Y	Y	Y	Y
Ability to generate percentiles	Y	Y	Y	Y	Y	Y	Y	Y

Allowance for parameter uncertainty	Y	Y	Y	Y	Y	Y	Y	Y
Incorporation of cohort effect	N	Y	Y	Y	N	Y	Y	Y
Non-trivial correlation structure	N	N?	N?	N	Y	Y	Y	Y

Table 4.3: Qualitative comparison of all models considered. (Y) indicates YES, (N) indicates NO and (?) represents some in the middle. (Cairns et. al, 2009)

- i) Ease of implementation: M2 and M8 take longer to converge to MLE. For M2 we introduce a constraint  $\sum_c (c - \underline{c})\gamma_c = 0$  to solve the convergence issue.
- ii) Parsimony: M1 and M5 are comparably parsimonious.
- iii) Transparency: All models except M4 give outputs that allow us to explain from a statistical perspective, change in mortality over time; its output is a smooth surface fitted to historical data and then projected; there is little in the output to allow us to get a feel for the underlying dynamics.
- iv) Ability to generate sample paths: Only M4 fails this point. M4 assumes underlying smoothness to mortality surface and that the only uncertainty in forecast is due to parameter and model uncertainty.
- v) Allowance for parameter uncertainty: Since parameter uncertainty is a significant element of uncertainty in our forecast of future mortality, it is a danger for a model to not allow for it.
- vi) Correlation structure is called trivial when there is a perfect correlation between changes in mortality rates at different ages from one year to the next. This is true for M1 for having only one time series process, and generally true for M2 and M3. M5 to M8 have two time series processes which affect different ages in different ways, thus changes in underlying mortality rates at different ages are not perfectly correlated.

## 5. Analysis of Models using Australia Data

### 5.1 Model Selection Criteria

We will assess the suitability of each of the eight models in fitting each of the total, female and male Australian population mortalities, under both qualitative and quantitative criteria. This involves inherent features of the model as described in the last section and other criteria relating to fit, parsimony and robustness.

M4 has no ability to generate sample paths and therefore lacks predictive power, which is central to finding the best fitting model. We will therefore not be considering M4 further in our report.

We will attempt to filter the candidate models as we set out the assessment criteria.

### **5.1.1 Parsimony**

We will calculate and compare the log-likelihoods as defined under the fitted parameters, with better fitting models having a higher log-likelihood.

Models with a higher number of parameters will naturally have a higher likelihood, but it would not necessarily mean it is a more suitable model as it violates its parsimony. We will therefore take likelihood further by calculating the Bayesian Information Criteria (BIC) and Akaike's Information Criteria (AIC) to penalize over-parameterization.

$$BIC = v \log K - 2L$$

$$AIC = 2v - 2L$$

$v$  being the number of parameters in the model,  $K$  being the number of observations (sample size) and  $L$  being the log likelihood. Lower BIC and AIC are preferable.

We summarize the likelihood, BIC, AIC and Deviance of the models in the tables below.

Total Pop. Models	M1	M2	M3	M5	M6	M7	M8
LogLik	-23758.56	-19850.39	-23572.24	-77173.28	-29074.33	-26013.31	-26105.71
Npar	195	388	250	114	238	294	239
AIC	47907.13(3)	40476.79(1)	47644.47(2)	154574.6(7)	58624.66(6)	52614.62(4)	52689.42(5)
BIC	49133.98(2)	42917.91(1)	49217.36(3)	155291.8(7)	60122.05(6)	54464.33(5)	54193.1(4)
Deviance	13074.92	5258.583	12702.27	119904.4	23706.46	17584.41	17769.21

Female Models	M1	M2	M3	M5	M6	M7	M8
LogLik	-18499.61	-17347.63	-18783.41	-39907.55	-19526.26	-19096.51	-19353.53
Npar	195	388	250	114	238	294	239
AIC	37389.23(2)	35471.27(1)	38066.82(3)	80043.09(7)	39528.51(6)	38781.03(4)	39185.06(5)
BIC	38616.08(2)	37912.39(1)	39639.7(3)	80760.33(7)	41025.9(6)	40630.74(4)	40688.74(5)
Deviance	6513.005	4209.041	7080.592	49328.87	8566.289	7706.803	8220.839

Male Models	M1	M2	M3	M5	M6	M7	M8
LogLik	-22150.68	-18652.38	-21230.52	-64885.73	-28861.46	-22734.29	-22901.17
Npar	195	388	250	114	238	294	239
AIC	44691.36(3)	38080.76(1)	42961.05(2)	129999.5(7)	58198.93(6)	46056.58(4)	46280.35(5)
BIC	45918.21(3)	40521.88(1)	44533.93(2)	130716.7(7)	59696.32(6)	47906.29(5)	47784.03(4)
Deviance	11831.57	4834.971	9991.255	97301.67	25253.14	12998.79	13332.56

Table 5.1

### 5.1.2 Likelihood Ratio Test

As some of the candidate models used are a series of general and nested models (as set out in the model descriptions), we will use the Likelihood Ratio Test to evaluate the Goodness of Fit.

$H_0$ : Accept the smaller (nested) model in favor of the larger model.

$H_1$ : Reject the smaller model in favour of the larger model.

The test statistic will be,  $TS = -2(l_{nested} - l_{general})$  where TS is distributed as a chi-squared distribution with degrees of freedom equals to  $(v_{general} - v_{nested})$ .  $v$  is the number of parameters used in the model.

$H_0$  is rejected if  $TS > \chi^2_{DF,\alpha}$ .

The test will be carried out at a significance level of  $\alpha = 0.05$

The below likelihood ratio test has been completed for the total Australian population, the final results are consistent across male, female and total population data.

H0	H1	LR test stat	d.f.	p-value
M1	M2	7816.339	193	<0.000001
M3	M2	7443.684	138	<0.000001
M5	M6	96197.9	124	<0.000001
M5	M7	102319.9	180	<0.000001
M6	M7	6122.047	56	<0.000001
M5	M8	102135.1	125	<0.000001
M6	M8	5937.245	1	<0.000001

Table 5.2

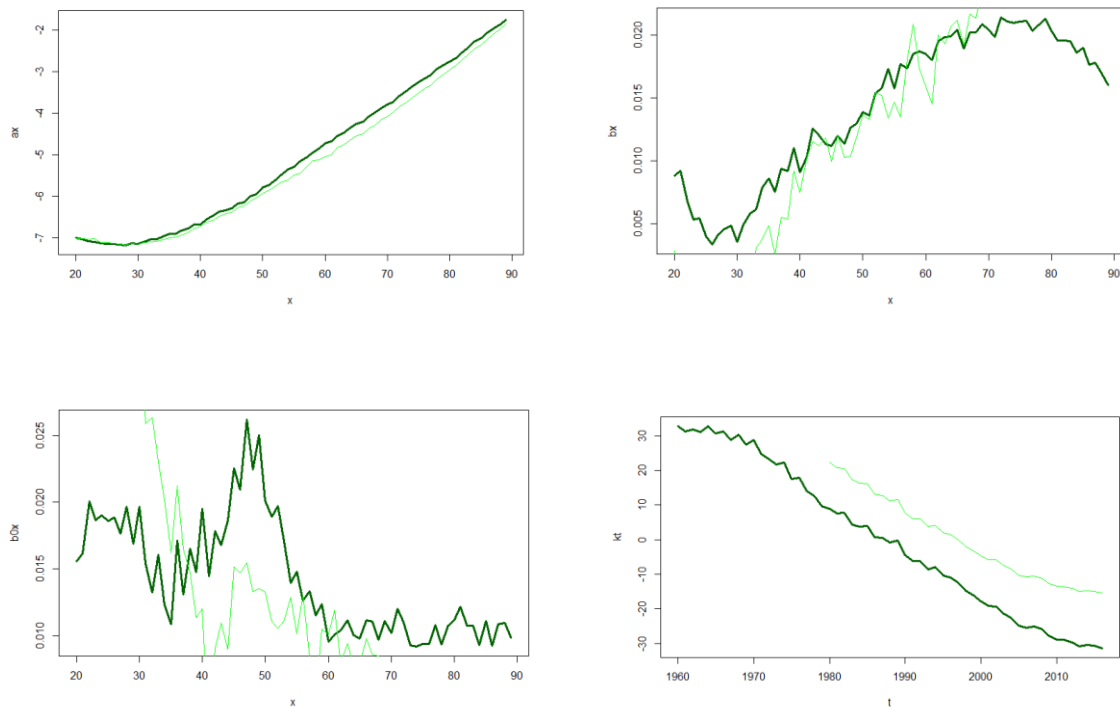
Paired with the rejection from the Likelihood Ratio Test and the lack of cohort effects, we exclude M1 and M5 from further consideration.

### 5.1.3 Robustness

We prefer models that present relatively similar parameter estimates and trends when fitted with a smaller number of observations, as it represents the reliability of projections made using the model.

This will be carried out by comparing plots of our 1960 – 2016 sample parameter estimates against a smaller sample of 1980 – 2016. The candidate model would be robust if the overlap between the two plots are significant.

#### Total Population:



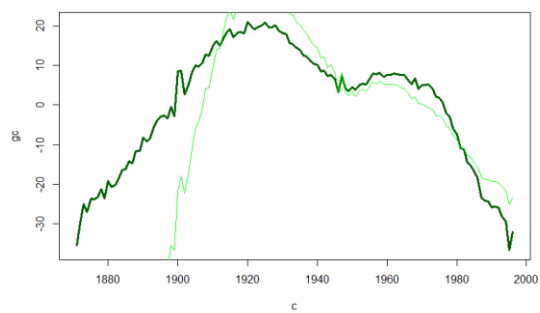


Figure 5.1 Total M2

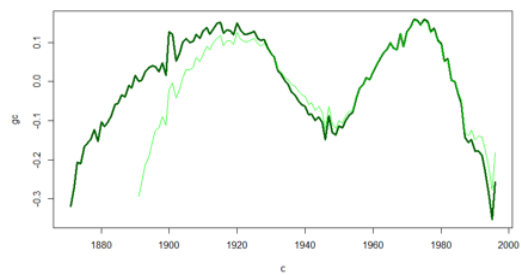
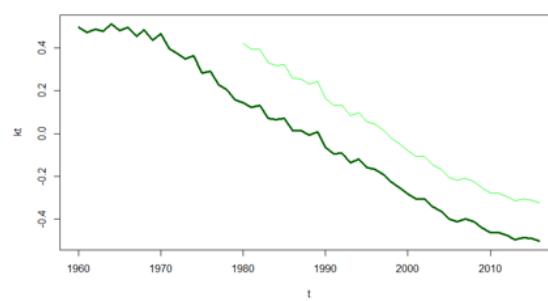
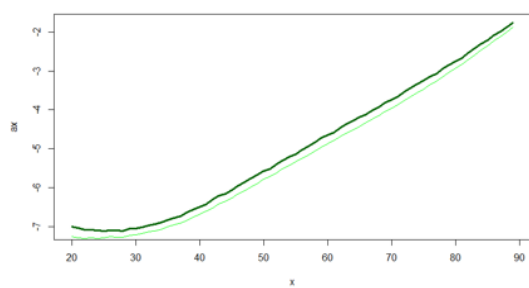


Figure 5.2 Total M3



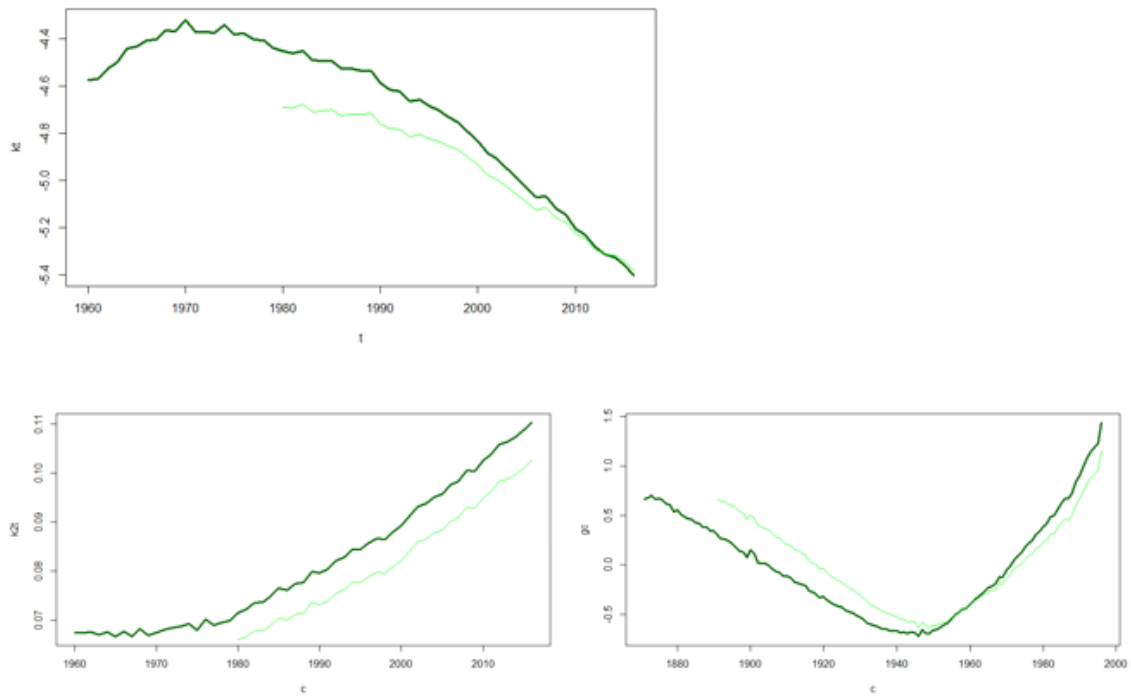


Figure 5.3 Total M6

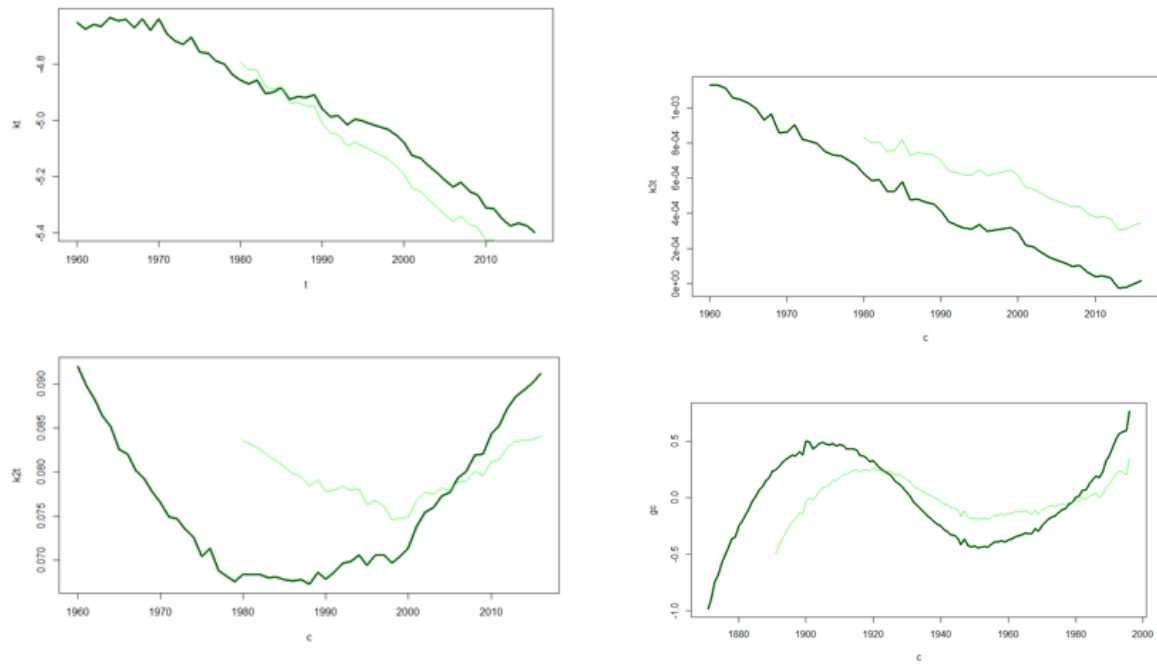


Figure 5.4 Total M7

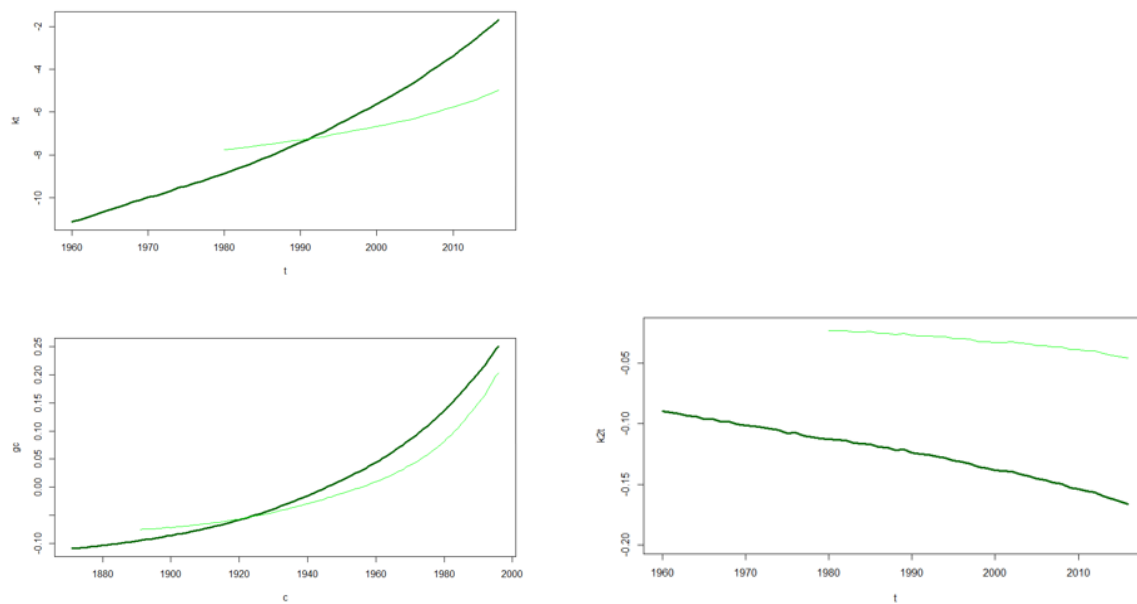


Figure 5.5 Total M8

**Males:**

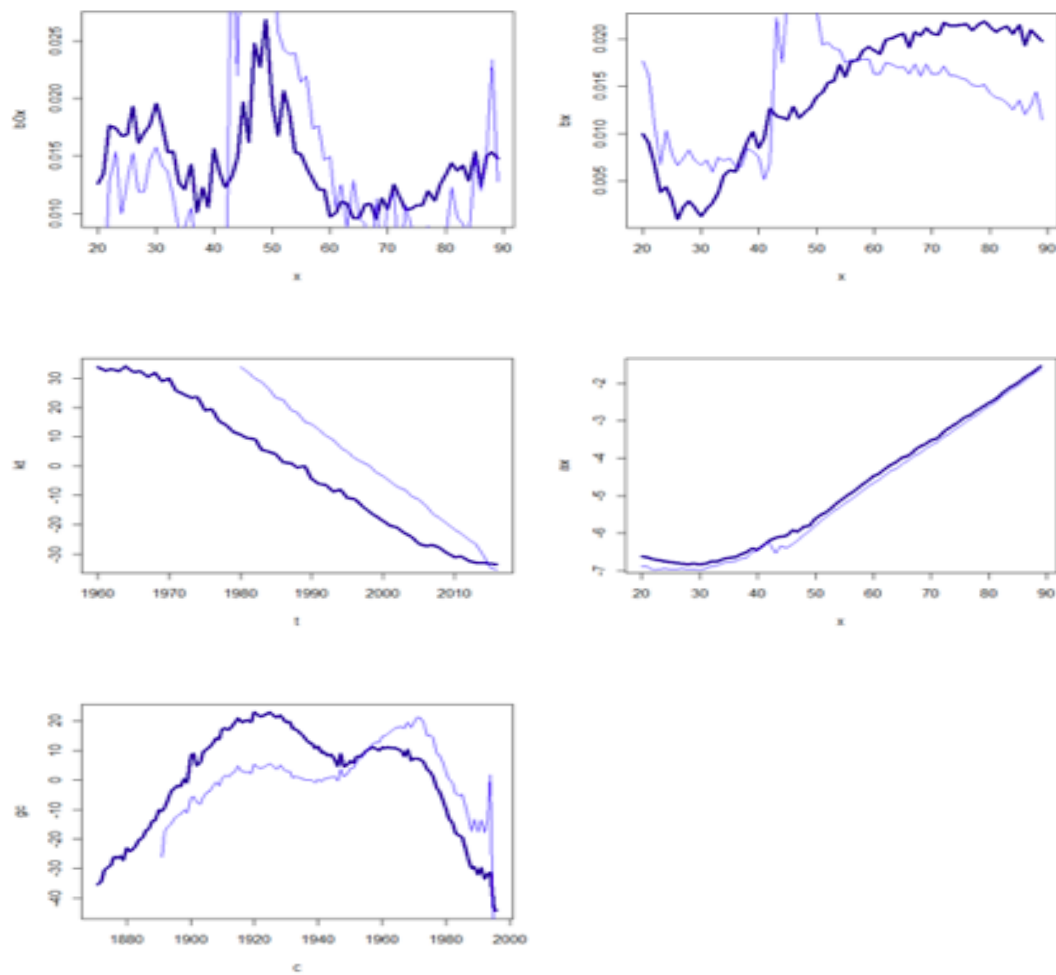


Figure 5.6 Male M2

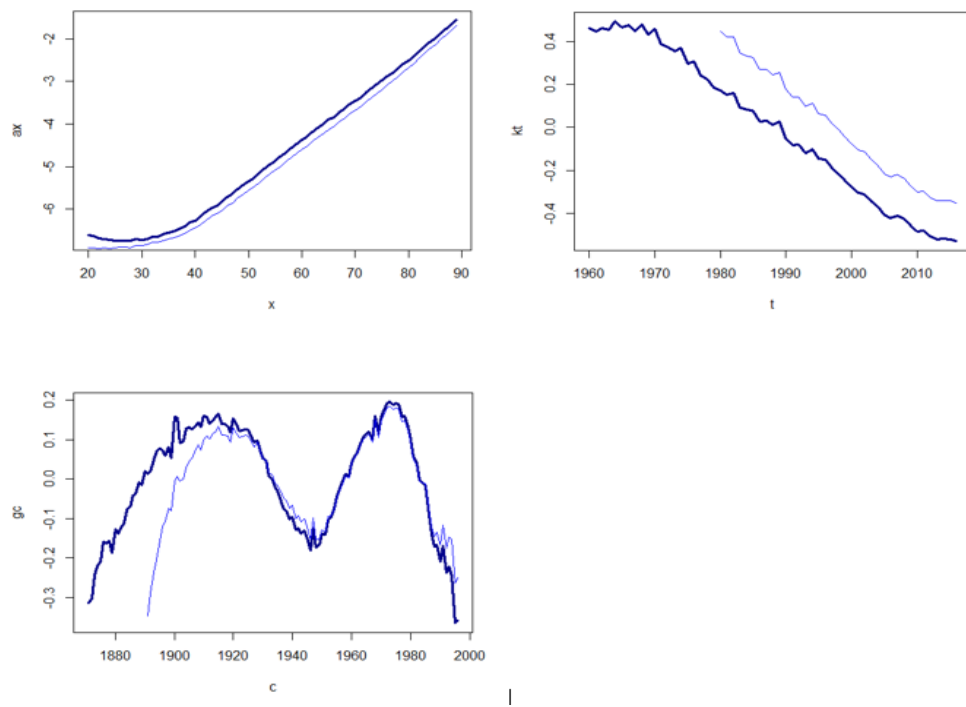


Figure 5.7 Male M3

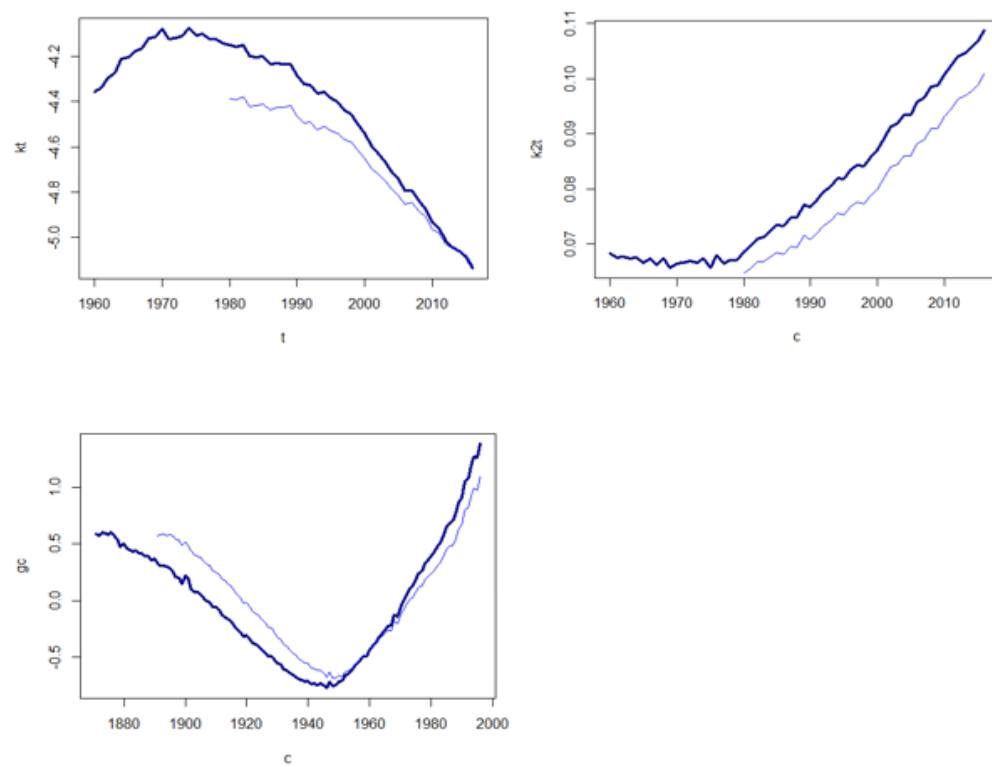


Figure 5.8 Male M6

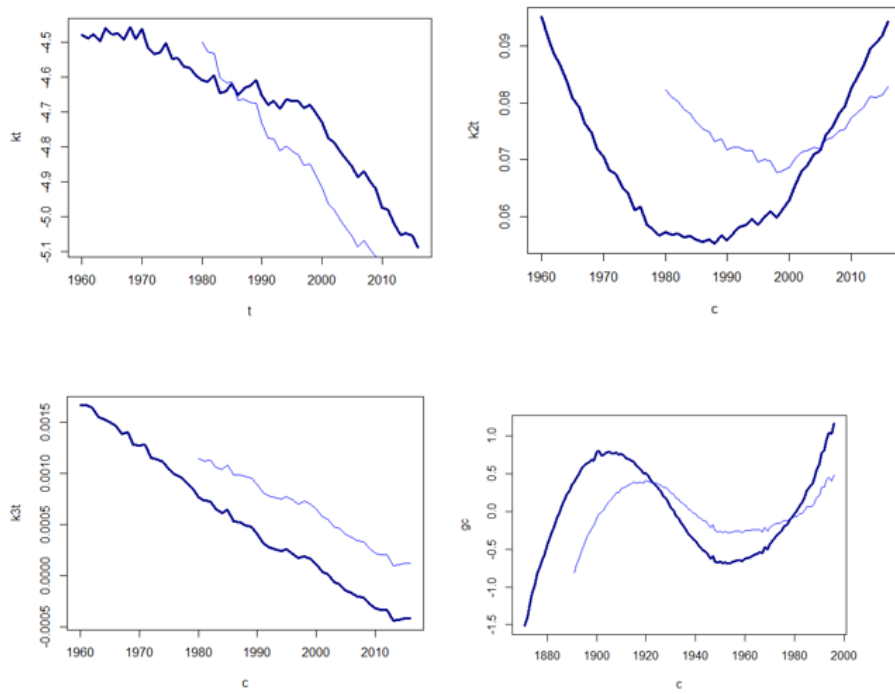


Figure 5.8 Male M7

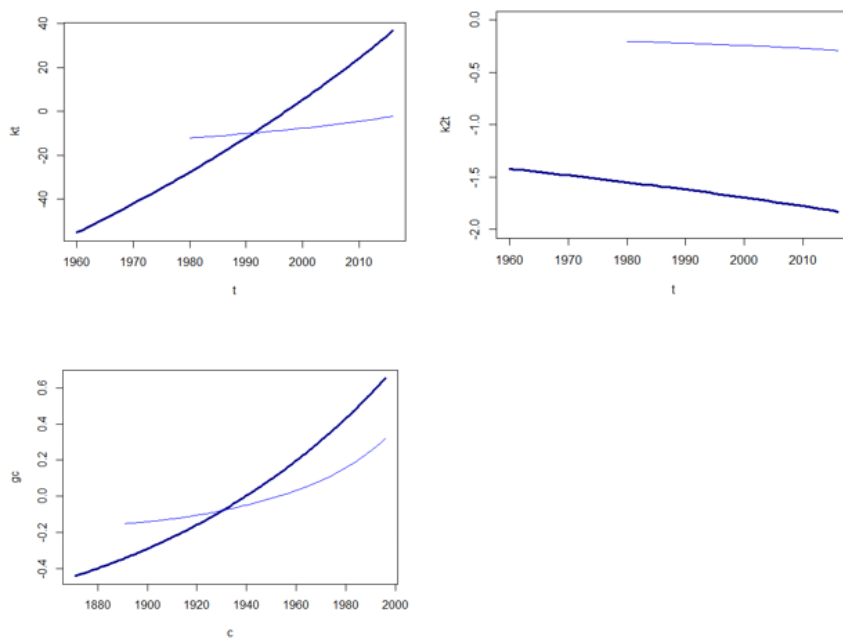


Figure 5.9 Male M8

**Females:**

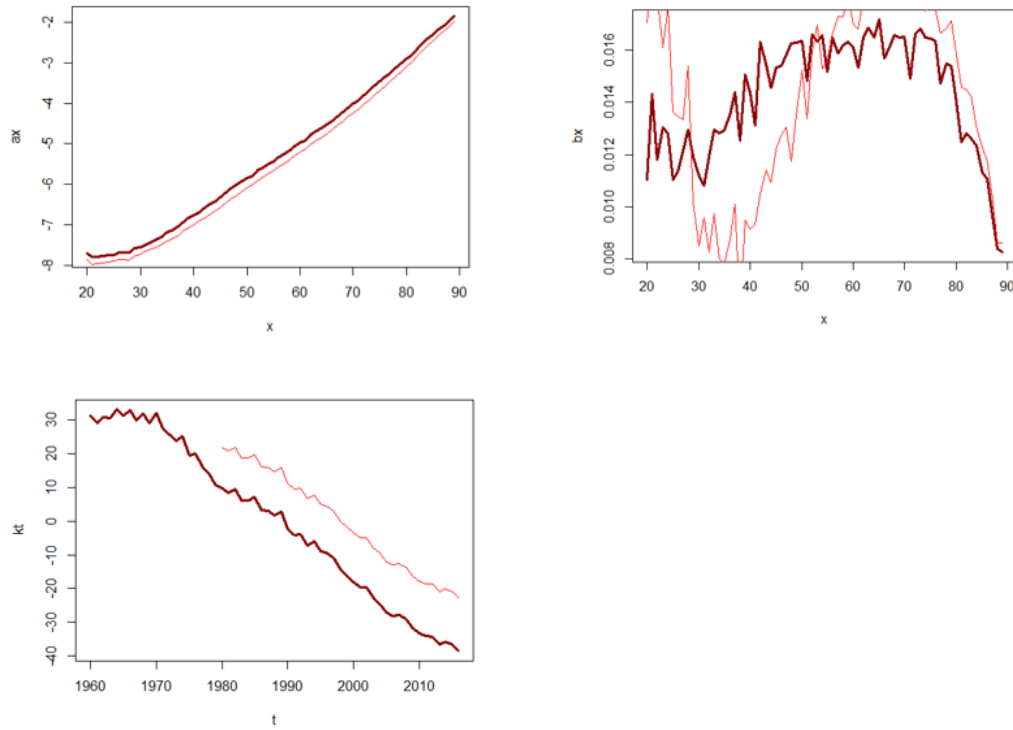


Figure 5.10 Female M1

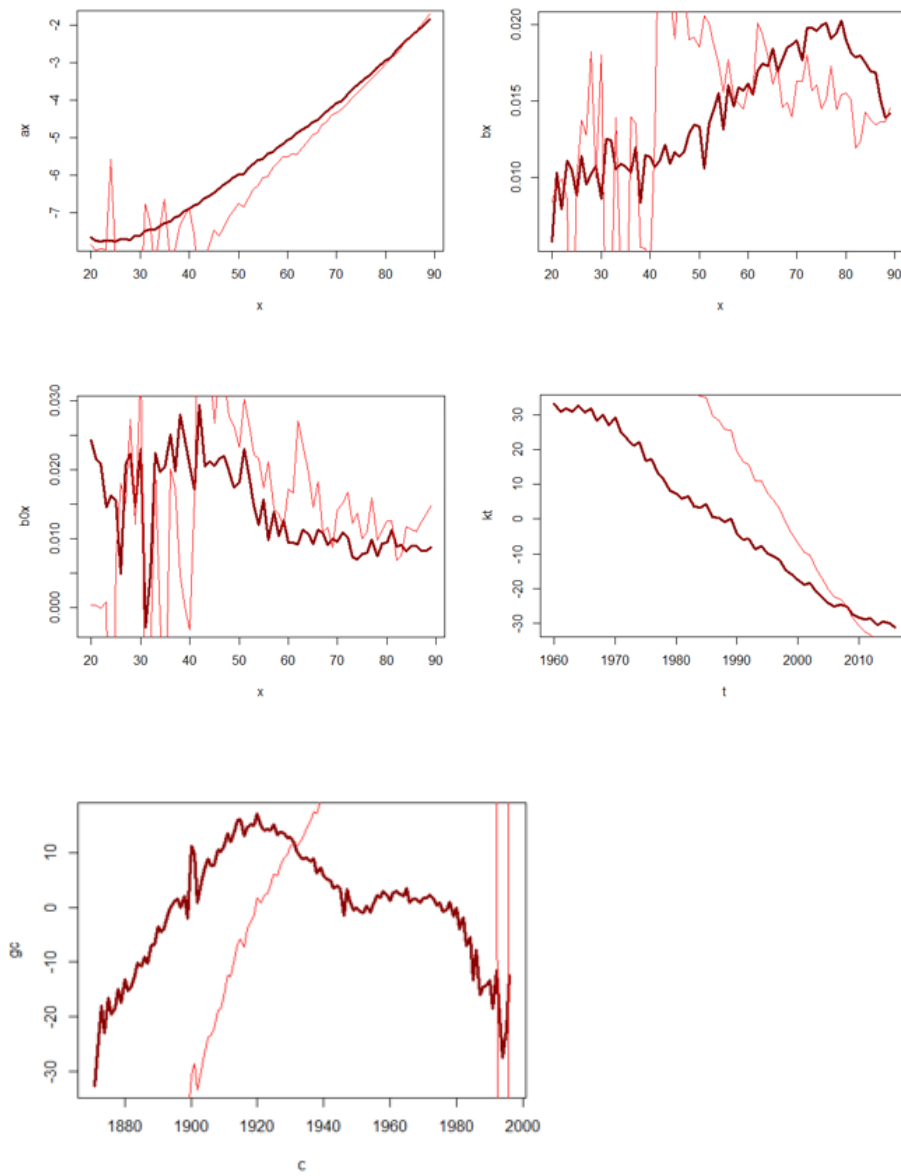


Figure 5.11 Female M2

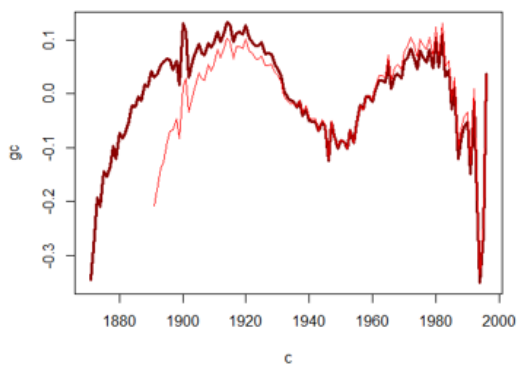
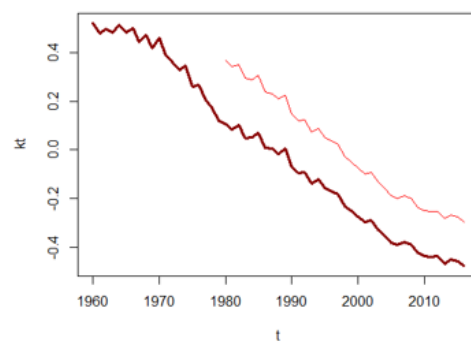
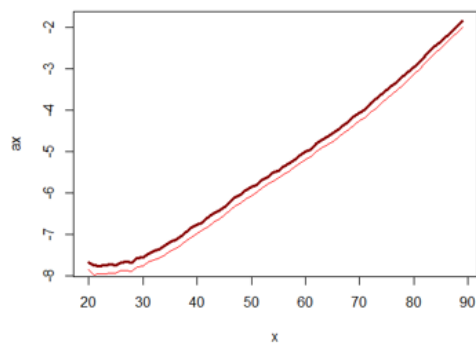


Figure 5.12 Female M3

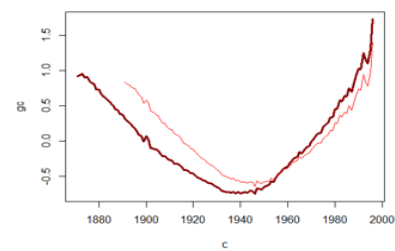
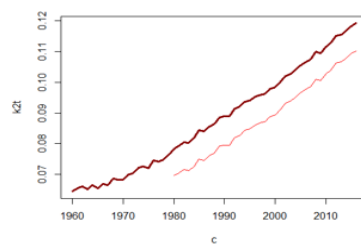
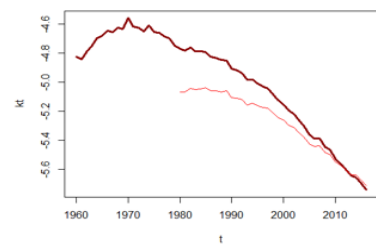




Figure 5.13 Female M6

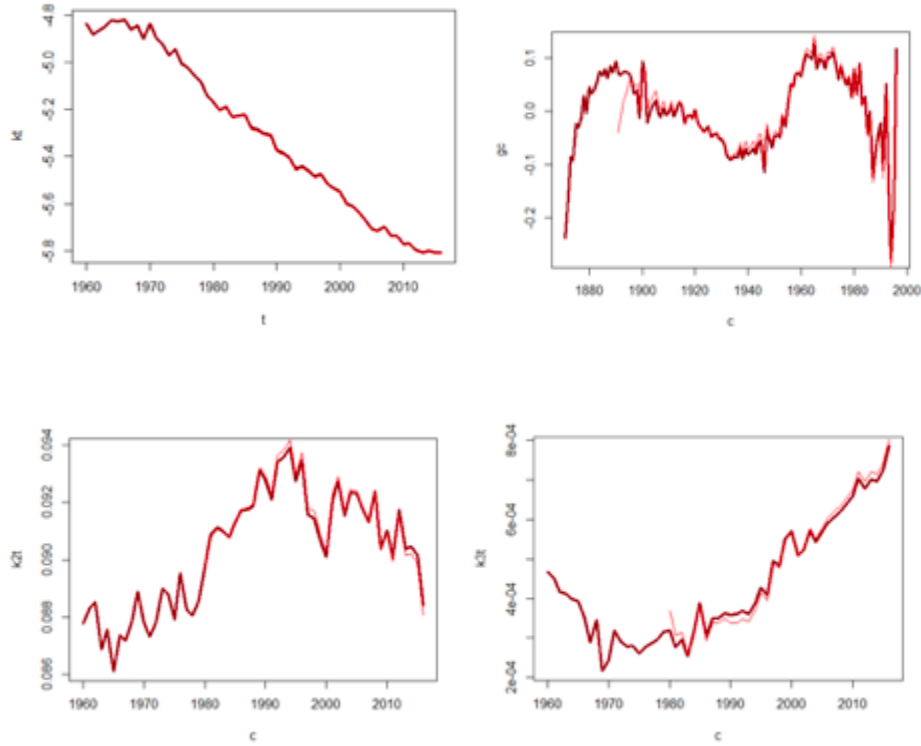


Figure 5.14 Female M7

Robustness	M2	M3	M6	M7	M8
Total Data	medium	medium	medium	low	low
Female Data	medium	medium	medium	low	low
Male Data	low	medium	medium	high	low

Figure 5.14 Robustness table

### 5.1.3 Standardised Deviance Residuals

SDRs are the standardised differences between actual and fitted deaths under a model, shown as

$$Z(t, x) = \frac{D(t, x) - E^c(t, x) * \hat{m}(t, x|\hat{\theta})}{\sqrt{E^c(t, x) * \hat{m}(t, x|\hat{\theta})}}$$

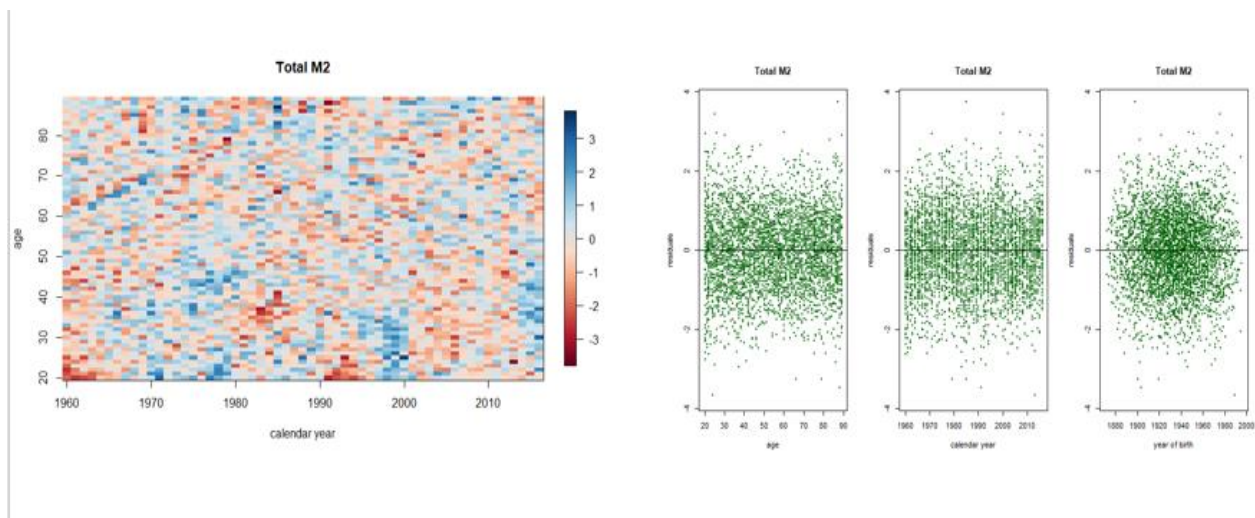
Following our assumption of independent deaths for each  $x$  and  $t$  and the Poisson distribution of deaths, we assume an i.i.d standard normal distribution for the SDRs.

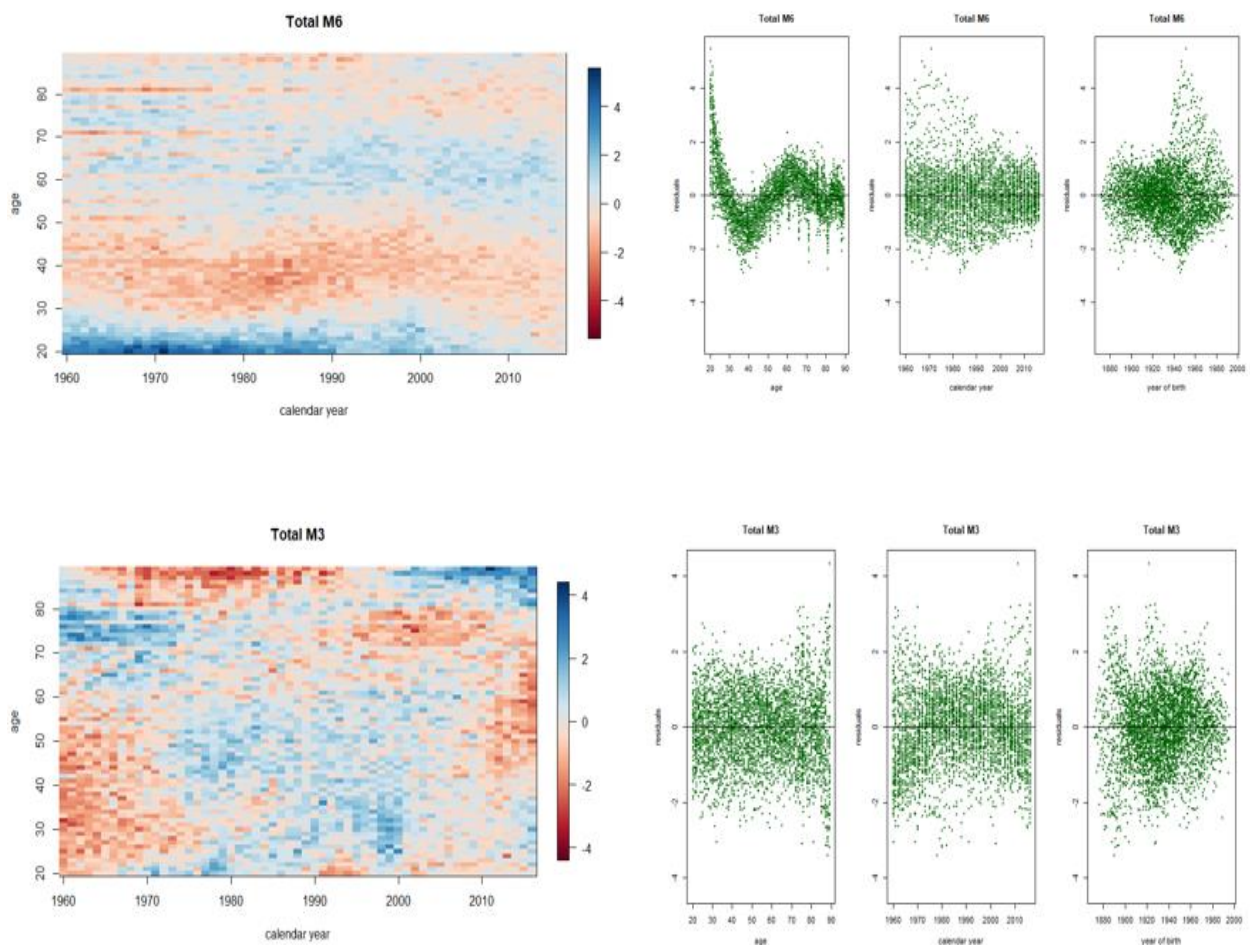
We will analyse models based on the variance and pattern of SDRs.

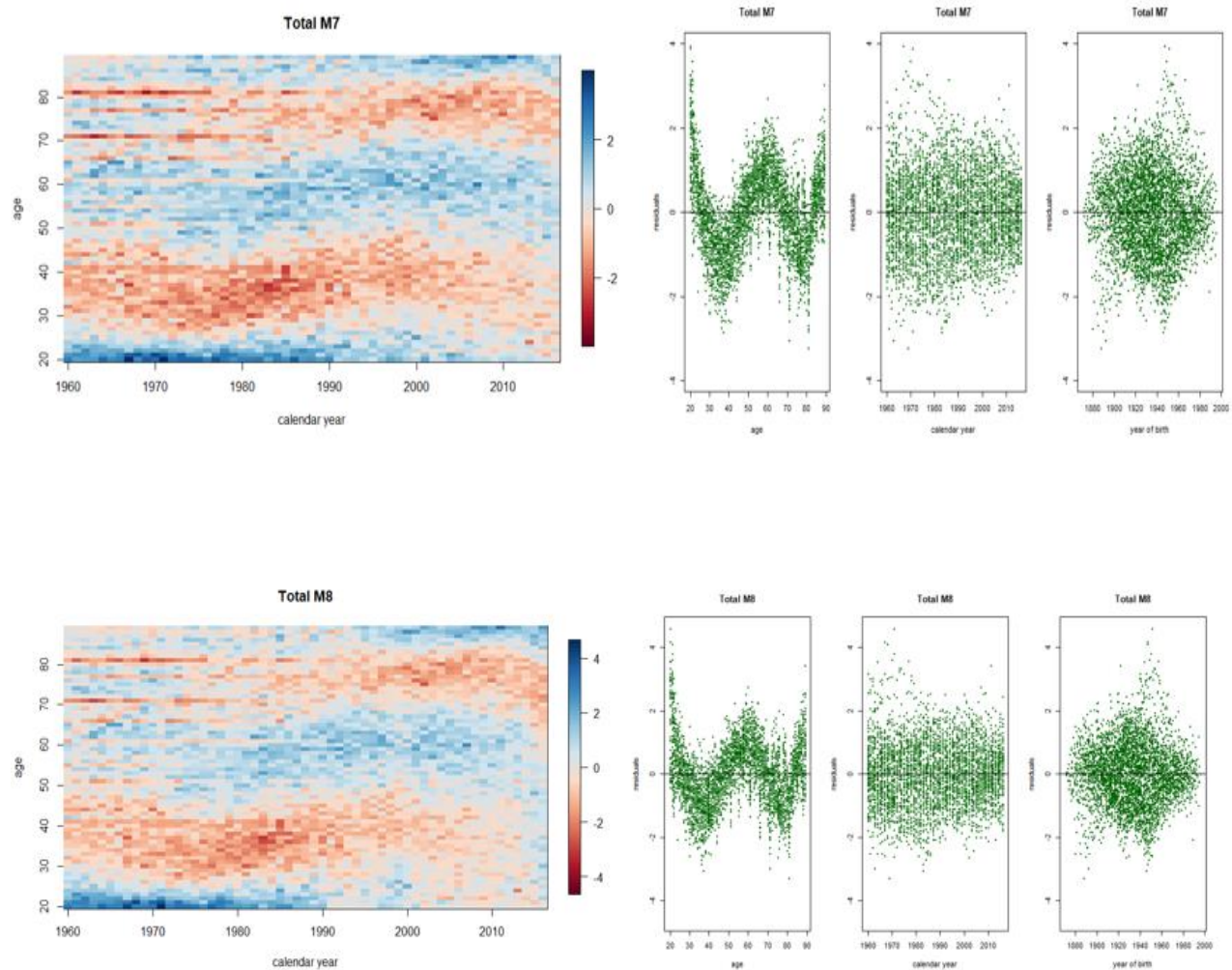
In terms of variance, we expect better fitting models to have lower variance of residuals.

In terms of analysing the pattern of SDRs, we will conduct visual tests using ‘colourmaps’ or ‘heatmaps’ of the residuals to observe whether they are randomly scattered close to 0, and whether an identifiable cohort (clustered diagonals) or period effect (vertical lines) has not been accounted for by the model.

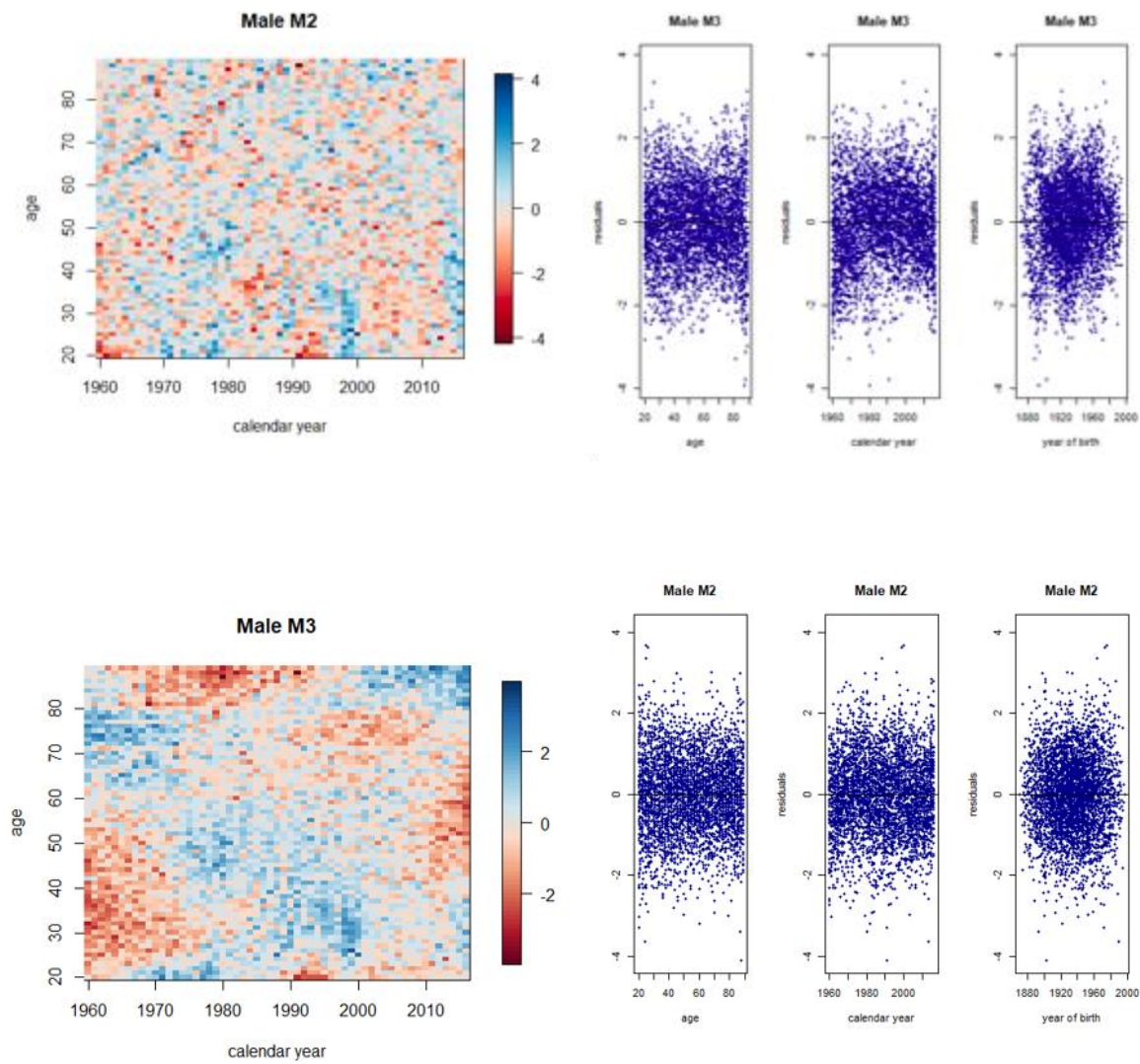
#### Total Data: Residuals



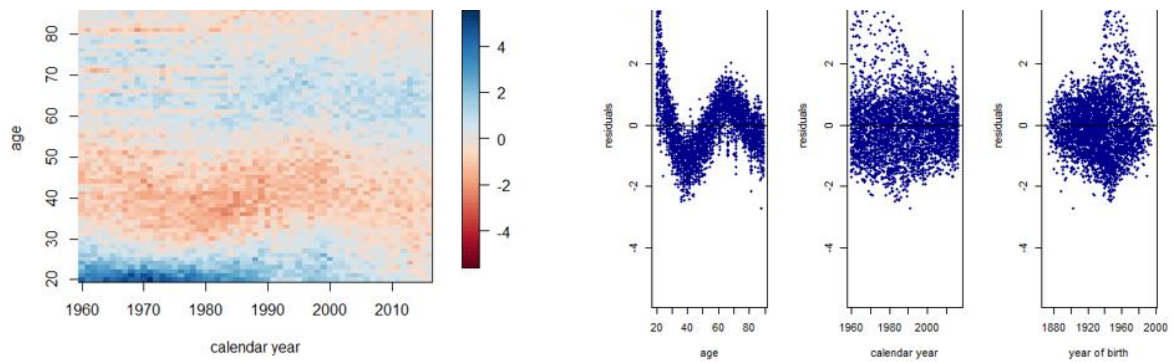
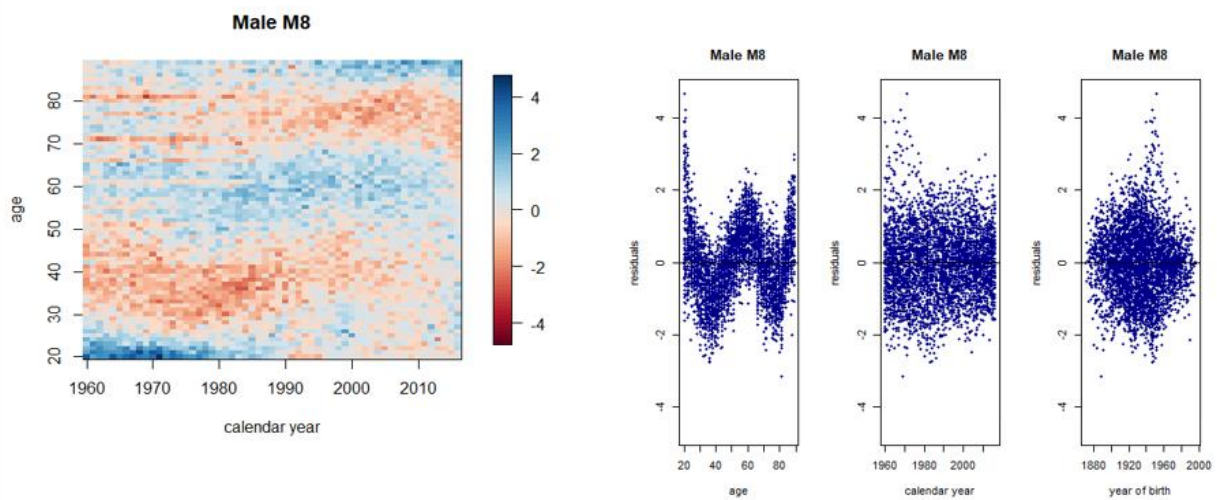
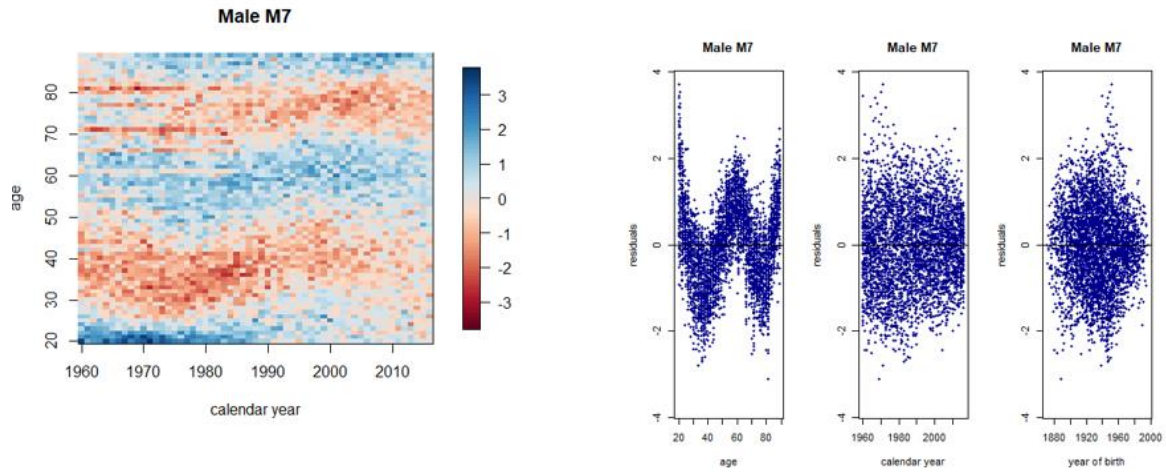




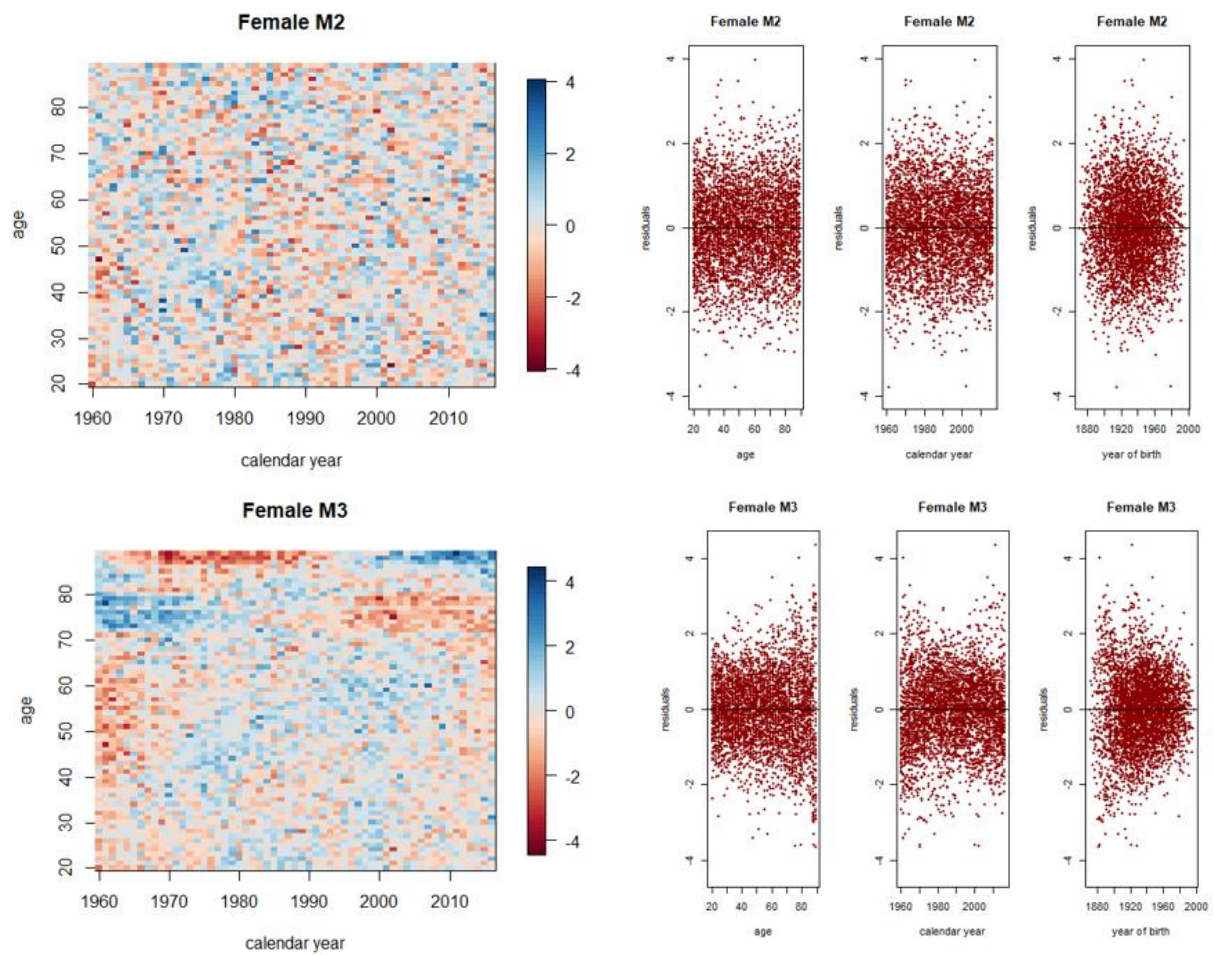
Male Data: Residuals



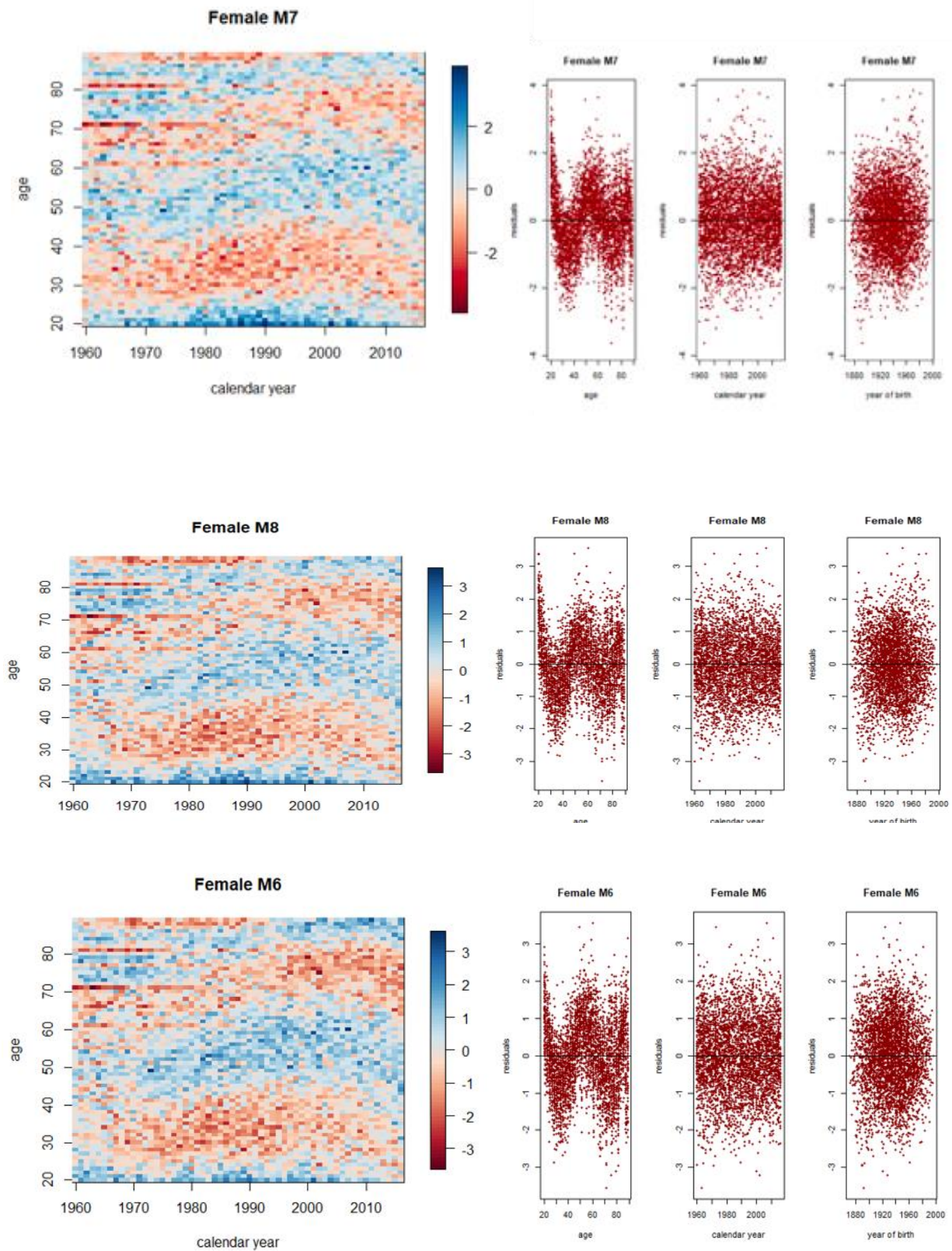




## Female Data: Residuals









<u>Randomness of Residuals</u>	<u>M2</u>	<u>M3</u>	<u>M6</u>	<u>M7</u>	<u>M8</u>
Total Data	<b>high</b>	medium	low	low	low
Male Data	<b>high</b>	medium	low	low	low
Female Data	high	medium	low	<b>low</b>	low

Considering both the distribution of residuals and a model's robustness we would suggest that the best model for males and the total population is M2 whilst the best model for the female population is M7.

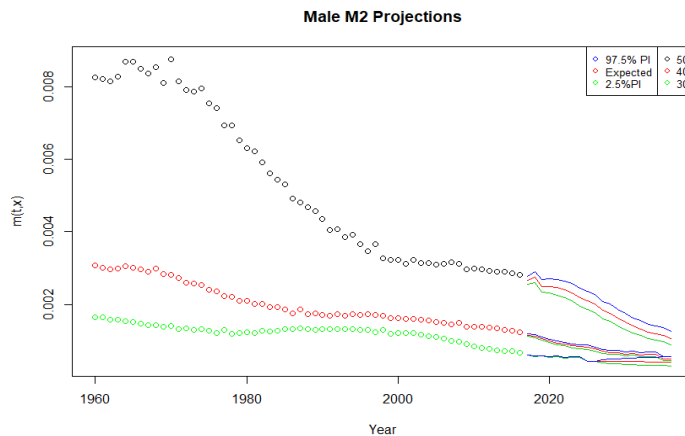
Although M2 dominates based on AIC and BIC for all populations, M7's robustness (Figure 5.14) is much stronger than M2 for the female population (Figure 5.12). Robustness for M2 is strong for both the male and total populations.

Supporting this, upon analyzing the residuals for M2 and M7 we find that the distribution is quite random with the only potential issue lying within the oscillating pattern in M7's age factor for females. However, we conclude that the robustness of model M7 overrides this factor making it our suggested model for the female population.

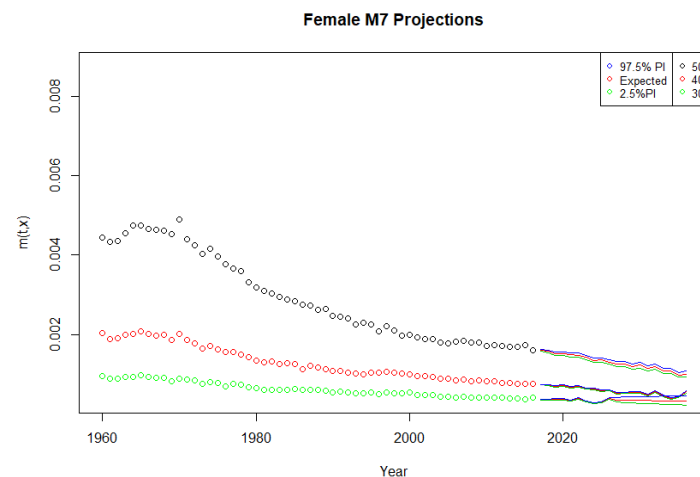
Ultimately, while we suggest M2 for the total population and male data and M7 for the female population, there is no definitive best model as one's choice of model is dependent on their goals. As our goal is to predict future mortality rates, we have opted to use models M2, and M7 for our predictions, as they perform reasonably well in both fit and robustness. This ensures that our predictions are accurate and our parameters will remain consistent despite the data set chosen.

## 6. Prediction and Applications

### 6.1 Forecasting Australian mortality rates for the next 20 years

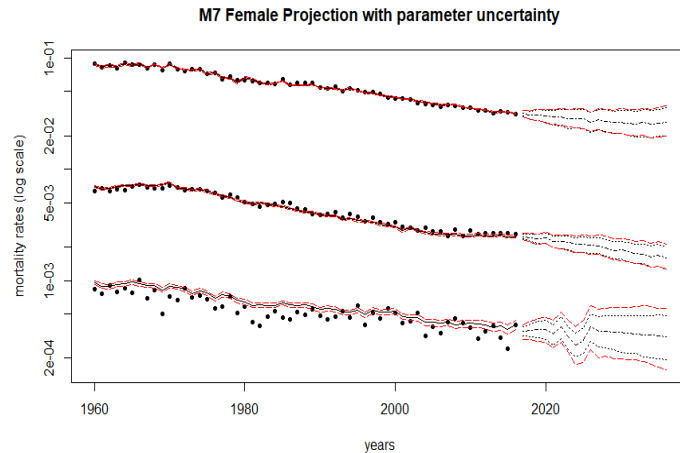


From the outset, men experience higher mortality at all ages but is especially pronounced in older ages. This could be directly attributed to occupational risks in male-dominant industries such as labour. However, there is a greater improvement over time for male mortality due that could be attributed to advancements in the workforce safety that reduces workplace risk.

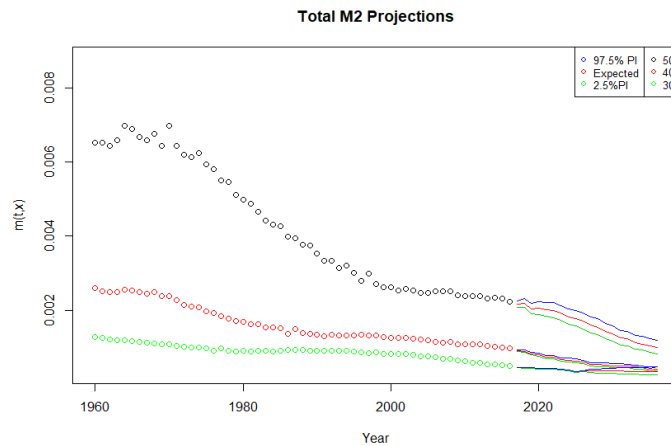


Across all ages, females historically experience lower mortality that could be attributed to environmental and social factors, in particular the lower occupational hazards women are subject to. Additionally, the more gradual decline in mortality for women could be due to parameterisation as the model is based on historical data. Hence, there must be consideration of the influences of historical data on parameters and their projections when

used in application.



In practise, bootstrapping would be more effective as it incorporates parameter variability in its prediction intervals as shown on the left. We can see that for younger ages, bootstrapped prediction intervals are wider than older ages, which is consistent with the higher variability and uncertainty of mortality at younger ages.



The combined mortality appears to be an average of the male and female mortality rates, in both magnitude and shape. The visible differences between male and female mortality emphasises the need to identify gender when pricing products as the genders experience vastly different mortality. Thus, careful consideration of gender when valuing insurance products enables more effective risk control and increases the risk appetite insurance

firms may have.

## 6.2 Simulated change in number of policies from 2018-2027

A further application involves predicting male and female policy numbers over the years from 2018-2027

As death is the only cause for policy termination, number of policies will only be affected by survival probability. The data of survival probability are generated from the mean of 10,000 central mortality rate simulations and converting  $m(x,t)$  to  $p(x,t)$  based on the relationship between  $m(x,t)$  and  $p(x,t)$ .

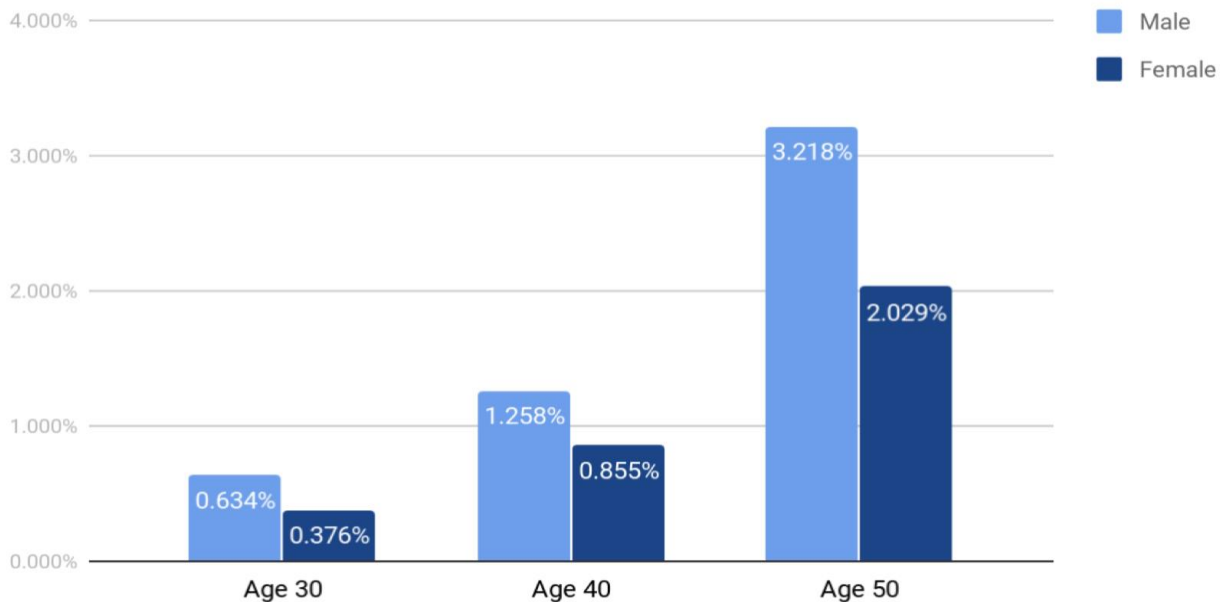
The policy number in 2018 and 2027 for each age and gender group is illustrated below:

Year	Male 30	Male 40	Male 50	Female 30	Female 40	Female 50
2018	2998	1998	997	1999	999	499
2027	2979	1973	965	1992	991	489
% change in number of policies	0.63	1.26	3.22	0.38	0.86	2.03

Table 6.1

The plot below shows the percentage change in policy numbers for each age and gender group

### Simulated percentage change in number of policies from 2018-2027



The overall highest rate of change 3.22% and 2.03% for male and female respectively occurs at age 50. This means as people get older, the rate of change in number of policies increase.

On the other hand, between female and male data, male's rates of policy change is always slightly higher than females. This implies the gender effect where the mortality rate for females and males decrease at a different rate under the same age group. Insurers should thus consider age and gender effect when pricing premiums and estimating risk as mortality rates varies for different age and gender.

## 7. Conclusion

Our research reinforces the general perception that mortality rates are expected to continue to decline at all ages for both genders. This will be a direct result of advancements in all facets of society. However, the details of our results indicate a need for further investigation into the modelling and forecasting of mortality as the models used appears to lack a key mechanism which tracks real-time changes in factors that may determine our lifespan. Intrinsically, the modelling process simply fits historical data and assumes that the trends that have dominated mortality changes will continue to do so. More and more, this may not be the case. Hence, our results should be used and applied in conjunction with additional consideration of this flaw. Ultimately, our findings should simply set a benchmark for further analysis on survivor index projections.

## 8. Reference List

Cairns, A.J., Blake, D., Dowd, K., Coughlan, G.D., Epstein, D., Ong, A. and Balevich, I., 2009. A quantitative comparison of stochastic mortality models using data from England and Wales and the United States. *North American Actuarial Journal*, 13(1), pp.1-35.

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Villegas, A., Kaishev, V.K. and Millossovich, P., 2015, December. StMoMo: An R package for stochastic mortality modelling. In *7th Australasian Actuarial Education and Research Symposium*.