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Forecasting Mortality Rate Improvements with a High-Dimensional VAR

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Abstract

Forecasting mortality rates is a problem which involves the analysis of high-dimensional time series. Most of usual mortality models propose to decompose the mortality rates into several latent factors to reduce this complexity. These approaches, in particular those using cohort factors, have a good fit, but they are less reliable for forecasting purposes. One of the major challenges is to determine the spatial-temporal dependence structure between mortality rates given a relatively moderate sample size. This paper proposes a large vector autoregressive (VAR) model fitted on the differences in the log-mortality rates, ensuring the existence of long-run relationships between mortality rate improvements. Our contribution is threefold. First, sparsity, when fitting the model, is ensured by using high-dimensional variable selection techniques without imposing arbitrary constraints on the dependence structure. The main interest is that the structure of the model is directly driven by the data, in contrast to the main factor-based mortality forecasting models. Hence, this approach is more versatile and would provide good forecasting performance for any considered population. Additionally, our estimation allows a one-step procedure, as we do not need to estimate hyper-parameters. The variance-covariance matrix of residuals is then estimated through a parametric form. Secondly, our approach can be used to detect nonintuitive age dependence in the data, beyond the cohort and the period effects which are implicitly captured by our model. Third, our approach can be extended to model the several populations in long run perspectives, without raising issue in the estimation process. Finally, in an out-of-sample forecasting study for mortality rates, we obtain rather good performances and more relevant forecasts compared to classical mortality models using the French, US and UK data. We also show that our results enlighten the so-called cohort and period effects for these populations.

JEL Classification: C18, C32, C52, C53.

Keywords: Mortality forecasting; High-dimensional time series; Vector Autoregression; Elastic-Net.

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1 Introduction

Identifying patterns in the mortality dynamics of a population is a hard task due to the complex underlying phenomena that impact the death rates. This problem is of crucial interest for government policies, pension funds and insurance companies. A wide range of models has been developed since the introduction of the famous model proposed by Lee and Carter (1992). Most of these approaches rely on time-series modeling with past data and forecast the main factors influencing the force of mortality, see among other Booth et al. (2002), Brouhns et al. (2002), Cairns et al. (2006), Cairns et al. (2009), Renshaw and Haberman (2008), Plat (2009), and Hunt and Blake (2014). Some reviews are available in the literature, see e.g. Booth and Tickle (2008), Cairns et al. (2008), and Barriau et al. (2012). The purpose of the present paper is to provide a new flexible modeling for the evolution of the mortality. Our high-dimensional vector autoregressive (VAR) approach, combined with an elastic-net penalty estimation method, aims to capture complex demographic effects without imposing a too restricting shape for the dynamics.

In recent years, some advances have been made to improve the forecast of mortality rates compared to the traditional factor-based models inspired by Lee and Carter (1992). This innovation has been provoked in particular by practitioners need for managing longevity risk and responding to the Solvency II requirements in insurance. Indeed, traditional models, even when a cohort effect is considered, have a reasonable fit, but poorer forecasts, indicating that these models may overfit the data. In such a context, one of the major concerns is to avoid the divergence of mortality rates between adjacent ages and different countries. Such inconsistency in the forecasting is pointed out for example by Börger et al. (2014), who explain that these low performances are due to the fact that traditional models mainly focus on the central trajectory projection. Several directions have been explored to overcome this issue. Li et al. (2013) develop an approach letting the age coefficients rotate over time, based on an expert judgment. Hunt and Villegas (2015) add an additional constraint on the cohort effect extensions of the Renshaw and Haberman (2006) model to overcome the convergence and robustness issues induced by the two-stage fitting algorithm for parameters. Regarding mortality trends of multiple populations, a relatively wide literature is organized around the idea of a biological convergence at a long horizon, see Dowd et al. (2011), Jarner and Kryger (2011), Li and Lee (2005), Enchev et al. (2016), and Cairns et al. (2016a) among others. These approaches estimate the mortality model by bringing together the data of several countries. Recently, Bohk-Ewald and Rau (2017) propose to approach the turning points of the mortality problem by combining trends of several countries.

Based on the observation that mortality rates are, in fact, noisy data, other alternative methods have emerged. If no exceptional event occurs, one can assume that the mortality surface is rather smooth over the age and time dimensions. Thus, functional data analysis and nonparametric smoothing techniques have been applied to mortality modeling, leading to a particular family of mortality models (see e.g. Currie et al., 2004; Hyndman and Ullah, 2007; Li et al., 2016; Doku-mentov et al., 2018). These models are known to have good fitting and forecasting performances, however they mostly consider future values as missing ones, making the stochastic generation of multiple prospective mortality scenarios non intuitive.

Other approaches focusing on the age-period dependency have recently been proposed with the constraint of being more data-driven. Christiansen et al. (2015) use spatial statistics to forecast age-period mortality rate improvements using a kriging method. Their approach is parsimonious and provides good performances for short-term projection. However, it seems that their long-term results are more questionable. Doukhan et al. (2017) also focus on the surface of mortality improvements and model it parsimoniously with an AR-ARCH specification for a random field

memory model. A valuable feature of their approach is that both dependencies between cohorts and the conditional heteroscedasticity of mortality are taken into account. Although they have good forecasting results, it is difficult to justify the size of the neighborhoods used to specify the memory process. Li and Lu (2017) choose a VAR process to consider the spatial dependence of mortality rates between neighboring ages adapted to short-term and long-term perspectives. These authors account for sparsity and stationarity in their VAR model by constraining the shape of the Granger causality matrix (Granger, 1969) as a lower triangular. Their model is also able to consider multiple populations.

In this paper, we propose an alternative approach that newly forecasts the age-period dependency using a large VAR specification on the log-mortality improvements. Although a VAR model is suitable for mortality time-series and is able to capture both long-term relationships and short-term shocks (see e.g. Salhi and Loisel, 2017), it is difficult to estimate accurately such models using an ordinary least square (OLS) technique, as these series are highly correlated and histories of data are relatively short. To avoid overparameterization, existing forecasting approaches impose an *a priori* spatio-temporal dependency structure between mortality rates or mortality improvements, which implies that only some selected series can interact. In contrast, our main contribution is the introduction of an estimation framework allowing for a large and flexible VAR structure without excluding potentially relevant relationships. A great feature of such a VAR specification is that all classical mortality models could naturally be included in our specification, especially the so-called cohort and period effects as noted by Li and Lu (2017).

Following recent developments in economics and finance (Fan et al., 2011; Furman, 2014), we develop a penalized VAR method based on the elastic-net (Zou and Hastie, 2005), which allows to take into account the sparsity correctly. Indeed, such a VAR model has a sparse structure in high dimension, which requires an accurate estimation method for shrinking zero coefficients in the Granger causality matrix. Compared to a classical maximum likelihood estimation approach, the key idea behind the elastic-net is to incorporate a penalty, which constrains the parameters. This penalty is a combination of an \mathcal{L}_2 term (as in a ridge regression) to avoid ill-conditioning matrices, and an \mathcal{L}_1 term (as in a LASSO regression) to produce a sparse model. By sparse model, we mean that our data-driven automatic selection produces a model with a relatively small number of non-zero parameters. As noted by Furman (2014), this is an attractive alternative to Bayesian VAR procedures usually considered in an econometrical framework and developed for example by Hahn (2014) for multiple populations modeling. Indeed, such approaches require to introduce relevant priors and do not address the sparsity's issue. The residuals are modeled as a Gaussian vector where the variance-covariance matrix is described using a parametric form for parsimony purposes.

Similarly to Doukhan et al. (2017), but contrary to Li and Lu (2017), our approach models the log of mortality improvements rather than the log of mortality rates. Several empirical elements have been advanced in the recent literature showing the interest of mortality improvements. Haberman and Renshaw (2012) show that a dual approach based on improvement rates can be followed for usual mortality models. They generally obtain quite comparable (but often better) forecasting results with this alternative route for the Lee-Carter model and its variants. As also noted by Bohk-Ewald and Rau (2017), mortality improvements seem to be easier to analyze, which facilitates the identification of divergences in mortality. As our approach is highly flexible, we expect that it can better capture complex patterns of mortality improvements. Another argument is that mortality improvements are generally stationary (see e.g. Chai et al., 2013), which is required for projection as our approach, contrary to Li and Lu (2017), does not impose constraints for guarantying stationarity.

We compare our high-dimensional VAR model to five different benchmark mortality forecasting models: the usual Lee-Carter model (Lee and Carter, 1992) and the M7 model developed by Cairns

et al. (2009) which are standard factor-based models; a reference model in smoothing methodologies developed by Hyndman and Ullah (2007) and the more recent smoothing RESPECT model introduced by Dokumentov et al. (2018); and finally the STAR model, based like ours on a high-dimensional VAR method, developed by Li and Lu (2017). Using the root mean squared error measure, we show that our approach leads to general better fitting (in-sample) and forecasting (out-of-sample) of the mortality rate time series from the three countries we have focused our analysis on. Moreover, our data-driven model implies more stable errors over different countries while the benchmark models tend to have more variable predictive power depending on the considered population.

The remainder of this paper is organized as follows. In Section 2 we describe the VAR model we retained. The high-dimensional estimation of this model is then developed in Section 3. We present the data we used, different results that we obtained and a comparison to other standard mortality models in Section 4. Finally, Section 5 proposes an extension of the VAR model to multi-population modeling, and Section 6 considers some ways of improvement and concludes.

2 A Vector Autoregression approach for mortality rate improvements

In this section, we introduce an econometric model to describe the mortality improvement dynamics jointly. The mortality models we introduce in the literature in Section 1 are initially based on an analysis of the main factors explaining a common trend of mortality rates. For instance, many models have been developed in the past for capturing the cohort effect, observed in the residuals for improvement rates plots (Willets, 2004). Conversely, our approach only imposes an autoregressive structure, which encountered these classical models¹, as shown for example by Salhi and Loisel (2017) or Li and Lu (2017). In particular, the latter authors explain in details how the cohort and period effects can directly be captured in the VAR(1) representation, without defining specific factors explicitly.

Throughout this paper, we focus on the time series $y_{i,t} = \ln(m_{i,t})$, where $m_{i,t}$ is the crude annual death rate at age i and at date t . These rates can be easily computed thanks to annual risk exposures and count of deaths for a country of interest. Those series are usually not stationary, as a trend can be observed in mortality rates and life expectancy. Since we want to apply our vector autoregressive model on stationary series, we compute the first difference of the log-mortality rate $\Delta y_{i,t} = y_{i,t} - y_{i,t-1}$ or, in other words, the log-mortality improvement rates. By working on these quantities, we remove a linear trend in the $y_{i,t}$ series.

With this notation, we specify the mortality rate improvement process by a stationary vector autoregressive model of temporal lag p or a VAR(p). For a minimum age i_{\min} and a maximum age i_{\max} , we define the d -dimensional vector of log-mortality rate improvements, with $d = i_{\max} - i_{\min} + 1$, as $\Delta \mathbf{Y}_t = (\Delta y_{i_{\min},t}, \Delta y_{i_{\min}+1,t}, \dots, \Delta y_{i_{\max},t})^\top$. Next, we assume the following dependence structure dynamic,

$$\Delta \mathbf{Y}_t = \mathbf{C} + \sum_{k=1}^p \mathbf{A}_k \Delta \mathbf{Y}_{t-k} + \mathbf{E}_t, \quad (2.1)$$

where, for $k = 1, \dots, p$, \mathbf{A}_k are $d \times d$ -autoregressive matrices, \mathbf{C} is a d -dimensional vector of constants (an intercept), and \mathbf{E}_t is a d -dimensional Gaussian white noise with mean 0 and Σ the

¹More precisely, it is their alternatives using mortality improvements, as documented by Haberman and Renshaw (2012).

related covariance matrix. We denote by $\epsilon_{i,t}$ its marginals. The matrices \mathbf{A}_k , $k \in \{1, \dots, p\}$, capture the relationship between current mortality improvements and the k^{th} lag of $\Delta \mathbf{Y}_t$. In other words, this corresponds to the Granger causality between different cohorts for the mortality improvement rates. As a result, for a VAR(1) model, the coefficients related to the first subdiagonal of the Granger causality matrix capture a cohort effect for individuals born in the same year. As also noted by Li and Lu (2017), the terms of the diagonal can be interpreted as a period effect, since they measure an effect for a fixed age between periods.

The VAR(p) model allows taking into account a more complex dependence structure than the usual mortality factor models. First, our model enables a larger flexibility in the long-term spatio-temporal dependence structure through the autoregressive matrices than the standard factor models. For a given square (i, t) in the Lexis diagram, we let the possibility for the improvement mortality rates $\Delta y_{i,t}$ to be dependent of all the ages among the d -dimensional space of ages, and through all the p temporal lags. In particular, we notice that this domain includes a cohort effect for these improvement rates. For each factor $\Delta y_{i-1,t-1}, \dots, \Delta y_{i-p,t-p}$, this effect is indeed captured by the loading coefficients positioned on the k^{th} -subdiagonal of the matrix \mathbf{A}_k for each $k \in \{1, \dots, p\}$. Hence, the VAR(p) structure permits for the shocks to propagate through different periods. Compared to the model proposed by Li and Lu (2017), the lag order p can take a value greater than 1, allowing to capture a more complex dependence structure.

Furthermore, it has the ability to enlighten some effects that are not captured in the standard mortality literature, e.g. between neighboring cohorts, as we do not impose any constraint on the matrices \mathbf{A}_k , $k \in \{1, \dots, p\}$. Compared to most of factor models, the second improvement of our model on the dependence flexibility is that it captures the long-term co-movement by the autoregressive matrices and the short-term dependence through the covariance matrix at the same time.

Nevertheless, the major issue of our VAR(p) model is that it is a natural high-dimensional problem. The number of parameters for the Granger causality matrices is pd^2 , without considering the covariance matrix and the constant vector. In mortality modeling studies, it is common to focus on the age range from 0 to 100, that is to say $d = 101$, while the historical data for estimation rarely exceed 70 years. Given this, a VAR(3) implies 30,704 parameters estimated on only 7,070 observations, which makes the ordinary least-squares estimation not feasible. To avoid over-fitting, additional constraints have to be added. In this direction, Li and Lu (2017) impose that some parameters have to be nil for guarantying that the model is sparse and stationary. Conversely, we choose a less arbitrary high-dimensional selection variables technique, developed in the next section, to ensure sparsity.

Similarly, the covariance matrix estimation is also a high-dimensional problem with $\frac{d(d+1)}{2}$ parameters. In order to estimate prediction intervals, we consider an additional specification for the residuals. Although some high-dimensional techniques do exist for covariance estimation (see e.g. Schäfer and Strimmer, 2005; Opgen-Rhein and Strimmer, 2007; Bickel and Levina, 2008; Bien and Tibshirani, 2011), we rather choose a simple parametric form presented in the following part to reduce the number of parameters.

3 High-dimensional estimation of the VAR model

As highlighted in the previous section, the VAR(p) model estimation is a high-dimensional problem, especially with mortality data. The estimation can be decomposed into two parts: first, we

estimate the pd^2 -dimensional autoregressive matrices, then the d^2 -dimensional covariance matrix. The dimension reduction in the autoregressive matrices is treated through an elastic penalization in Section 3.1. We tackle the problem of the covariance through the choice of a parametric form in Section 3.2.

3.1 Elastic-net

We now described the extension of the elastic-net regularization and variable selection method, proposed by Zou and Hastie (2005), for the high-dimensional estimation of our autoregressive matrices. This technique can be seen as the combination of the LASSO \mathcal{L}_1 -penalty, introduced by Tibshirani (1996), and the ridge \mathcal{L}_2 -penalty developed by Hoerl and Kennard (1970). Elastic-net has similar properties of variable selection as the LASSO. Moreover, it provides a grouping effect: highly correlated variables tend to be selected or dropped together. LASSO and elastic-net have already been extended to VAR model (Gefang, 2014; Basu et al., 2015), mostly with an economic application (see e.g. Song and Bickel, 2011; Furman, 2014).

Therefore, we estimate the VAR(p) model presented in Equation (2.1) with T observations of the process $\Delta\mathbf{Y}_t$ for $t = t_{\min}, \dots, t_{\max}$ by minimizing the criterion

$$\begin{aligned} L(\mathbf{C}, \mathbf{A}_1, \dots, \mathbf{A}_p) &= \frac{1}{T-p} \sum_{t=t_{\min}+p}^{t_{\max}} \|\Delta\mathbf{Y}_t - \mathbf{C} - \sum_{k=1}^p \mathbf{A}_k \Delta\mathbf{Y}_{t-k}\|_2^2 \\ &\quad - \alpha\lambda \sum_{k=1}^p \|\mathbf{A}_k\|_1 - \frac{(1-\alpha)\lambda}{2} \sum_{k=1}^p \|\mathbf{A}_k\|_2^2, \end{aligned} \tag{3.1}$$

where we define for a d -dimensional vector $\mathbf{b} = (b_i)_{1 \leq i \leq d}$

$$\|\mathbf{b}\|_2^2 = \sum_{i=1}^d |b_i|^2,$$

and for a $d \times d$ -dimensional matrix $\mathbf{B} = (b_{i,j})_{1 \leq i \leq d, 1 \leq j \leq d}$

$$\|\mathbf{B}\|_1 = \sum_{i=1}^d \sum_{j=1}^d |b_{i,j}| \text{ and } \|\mathbf{B}\|_2^2 = \sum_{i=1}^d \sum_{j=1}^d |b_{i,j}|^2.$$

The parameter $\alpha \in [0, 1]$ is a hyper-parameter which determines the mix between ridge and LASSO penalties. We use a 10-folds cross-validation method to choose the penalty coefficient λ . It determines the strength of the penalties, for example in the LASSO case, the higher λ gets, the fewer number of variables are selected. The algorithm we used is described in Friedman et al. (2010). In theory, the LASSO \mathcal{L}_1 -penalty part forces most of the coefficients to 0. Nevertheless, in a more practical approach, the algorithm employed does not lead to exact zeroes. Thus, the R-package `glmnet` (Friedman et al., 2010) applies a threshold on the coefficients. Furthermore, following Chatterjee and Lahiri (2011), the `sparsevar` R-package (Vazzoler et al., 2016) enables to apply a more tailor-made threshold for time-series estimation which equals to $\frac{1}{\sqrt{pd \ln T}}$, that we retain for our model.

The hyper-parameter α is determined through a grid search. For every value α_h of a pre-defined grid $\{\alpha_1, \dots, \alpha_H\}$, we estimate the parameters of the VAR model $\{\hat{\mathbf{C}}, \hat{\mathbf{A}}_1, \dots, \hat{\mathbf{A}}_p, \hat{\lambda}\}_{\alpha_h}$, as explained just before, and deduce the residuals $\hat{E}_{\alpha_h, t}$ for $t \in \{t_{\min} + p, \dots, t_{\max}\}$.

In the applications, we estimate the tuning parameters by minimizing the prediction error, that we obtain by computing the root-mean-square error

$$\text{RMSE}(\alpha_h) = \sqrt{\frac{1}{d(T-p)} \sum_{t=t_{\min}+p}^{t_{\max}} \|\hat{E}_{\alpha_h,t}\|_2^2}. \quad (3.2)$$

In our application, we considerate the grid $\{0.5, 0.6, 0.7, 0.8, 0.9, 1\}$ in order to impose a larger weight to the LASSO penalty for sparsity purposes.

The choice of the lag order p for our VAR elastic-net (VAR-ENET) model differs significantly from the usual lag order selection in the standard VAR models. The parameter p does not fully determine the number of parameters, since the LASSO penalty force the less significant coefficients to zero. By increasing the lag order, some non-null coefficients can be forced to zero in favor of other coefficients in autoregressive matrices of higher lag order. Moreover, if there is no significant coefficient above a certain lag order, all autoregressive matrices above the limit order are largely forced to zero. Thus, we chose a relatively large p to capture eventual high order lag effects, without being worried of over-fitting.

3.2 Variance-covariance estimation

The autoregressive matrices are not the only high-dimensional problem of the VAR(p) model, the variance-covariance matrix estimation has $\frac{d(d+1)}{2}$ parameters. This number can quickly get higher than the number of observations while dealing with mortality modeling, and then can cause overfitting, as noted e.g. by Li and Lu (2017).

To overcome this issue, we propose an approach to estimate the covariance matrix with a parametric covariance function, in a manner similar to Spodarev et al. (2013). Firstly, for each age i , we estimate the standard empirical variance $\hat{\sigma}_i^2$ of the residual, and for each couple of ages $(i, j) \in \{i_{\min}, \dots, i_{\max}\}^2$, we estimate the empirical correlation

$$\hat{r}_{i,j} = \frac{\hat{\sigma}_{i,j}}{\hat{\sigma}_i \hat{\sigma}_j},$$

where $\hat{\sigma}_{i,j}$ is the empirical covariance. Then, guided by the form of the empirical correlation matrices and by the approach of Christiansen et al. (2015), we use a parametric form close to the stable family of covariance functions

$$r_{i,j} = \beta e^{-(a_i+a_j) \times |i-j|} \times \mathbb{1}_{\{i \neq j\}} + \mathbb{1}_{\{i=j\}}, \quad (3.3)$$

with $\beta \geq 0$ and $a_i \geq 0$ for each age i . We fit the model based on the empirical correlation as the OLS solution. Thus, after determining $\hat{\beta}$ and $(\hat{a}_{i_{\min}}, \dots, \hat{a}_{i_{\max}})$, we compute our parametric correlation $\tilde{r}_{i,j}$ given by Equation (3.3). Finally, for each couple of ages (i, j) we estimate the covariance by

$$\tilde{\sigma}_{i,j} = \tilde{r}_{i,j} \times \hat{\sigma}_i \hat{\sigma}_j.$$

4 Empirical analysis

In this section, we apply our high-dimensional VAR-ENET model to real data and show its strengths in estimating and forecasting populations. Different populations are considered and we analyze both our in-sample and out-sample results compared to those obtained with retained benchmark models. In the following, the computations are carried out with the R software (R Core Team, 2019). Our scripts are available upon request.

4.1 Data

The datasets that we analyze comes from the Human Mortality Database (2019). We choose to illustrate our approach with historical mortality data from the England and Wales (UK), the United States (US) and France (FR), as these populations have been largely studied, but have specific features. At first, the overall population is considered, and then both males and females are segregated. We select the age-period observation $\{45, \dots, 99\} \times \{1950, \dots, 2016\}$ which was available for these 3 countries when the data was extracted. We begin our analysis by a visual inspection of our data. Figure 1 describes the shape of the period log-mortality improvements for populations on a Lexis diagram where the trajectory of one cohort follows a 45 degree line. Different cohort effects can be observed for these countries with pink (resp. green) shades for positive (resp. negative) improvements, indicating a lower (resp. higher) survival.

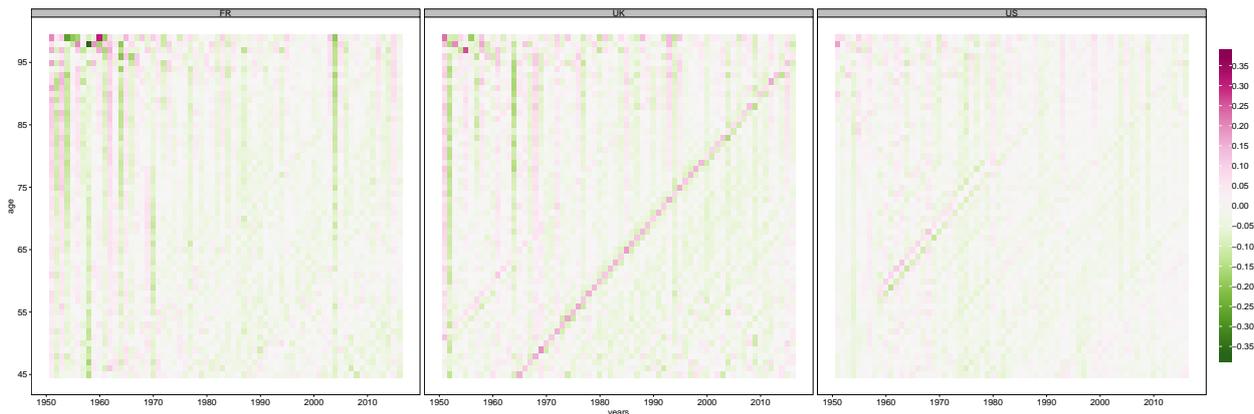


Figure 1: The period log-mortality improvements for England and Wales (UK), the United States (US) and France (FR) on the age-period observation $\{45, \dots, 99\} \times \{1950, \dots, 2016\}$ for overall populations.

On the center, UK improvement rates do exhibit some significant diagonal patterns corresponding to the so-called cohort effects. A diagonal stands out, more precisely for individuals aged 45 in 1965. Several vertical patterns corresponding to period effects are also observed, especially for the older ages. Diagonal and vertical structures associated with cohort and period effects also stand out in the American data, even if the patterns are less marked than in the English data. Contrary to English and American mortality, the French mortality data doesn't clearly display any diagonal structures, but only period effects. We note that the cohort effects (also observable on residual plots), which used to appear in the French data, were strongly reduced with the correction developed by Boumezoued (2016), thanks to fertility rates. Female and male data are displayed in Appendix 1.

We have chosen to apply the VAR-ENET to the first difference of log-mortality rates series because they are known in the literature as stationary time series. In order to verify this point, we perform a Phillips-Perron test (Perron, 1988) and an augmented Dickey-Fuller test (Said and Dickey, 1984) on every age mortality series for each of the nine populations of interest. All of these time series satisfy the Phillips-Perron test at a confidence level of 1%, and 93% of them are considered as stationary by the augmented Dickey-Fuller test at a level of 5%. These results strengthen our choice to focus on the first difference of time-series.

4.2 Benchmark models

In this section, we present the benchmark mortality models that we compare to the VAR-ENET. First, we retain two models from the standard factor-based family:

- the usual Lee-Carter (LC) model (Lee and Carter, 1992), estimated with the approach of Brouhns et al. (2002) and given by

$$y_{i,t} = \alpha_i + \beta_i \kappa_t, \quad (4.1)$$

with the hyper-parameters α_i and β_i , and the mortality trend κ_t ,

- the M7 model developed by Cairns et al. (2009), which considers a quadratic and a cohort effect, i.e.

$$y_{i,t} = \kappa_t^{(1)} + (i - \bar{i}) \kappa_t^{(2)} + \kappa_t^{(3)} \left((i - \bar{i})^2 - \hat{\sigma}_i^2 \right) + \gamma_{t-i}, \quad (4.2)$$

where $\kappa_t^{(j)}$, $j = 1, 2, 3$, are period effects, γ_{t-i} is a cohort effect, \bar{i} is the average age in the data, and $\hat{\sigma}_i^2$ is the average value of $(i - \bar{i})^2$.

These last models are estimated using the R-package **StMoMo** (Villegas et al., 2017) following their usual two-stage fitting procedure: first, we estimate the factor coefficients of each model, and then we forecast it using univariate ARIMA processes, automatically selected by the R-package using an AIC criterion. To be comparable with our one-stage fitting approach, the results for these models are those obtained after fitting the time-series parameters.

We also consider two recent models based on smoothing methodologies :

- the classical model proposed by Hyndman and Ullah (2007) (HU) which estimates a non-parametric smoothing function $f_t(i)$ for every period t that smooths mortality rates over the age dimension, and is then decomposed

$$f_t(i) = \mu(i) + \sum_{k=1}^K \beta_{t,k} \phi_k(i), \quad (4.3)$$

where $\mu(i)$ is a measure of location of $f_t(i)$, $(\phi_k(i))_{i=1, \dots, K}$ is a set of orthonormal basis functions of dimension $K \geq 1$. This model is applied thanks to the R-package **demography** (Hyndman, 2019) based on weighted penalized regression splines for smoothing.

- The recent RESPECT model, developed by Dokumentov et al. (2018) and implemented in the R-package **smoothAPC** (Dokumentov and Hyndman, 2018), which uses \mathcal{L}_1 -regularized bivariate smoothing over the age and period dimensions, and further allows identification of period and cohort effects on the smoothing residuals.

Finally, we retain a model closer to the methodology of the VAR-ENET, which is based on a spatial-temporal autoregressive framework: the STAR method, introduced by Li and Lu (2017). It models the dynamic of the log mortality rates through a large first-order VAR, of which autoregressive matrix's parameters are forced to a sparse estimation by the following constraints:

$$y_{i_{min}, t+1} = y_{i_{min}, t} + m_{i_{min}}, \quad (4.4)$$

$$y_{i_{min}+1, t+1} = (1 - \alpha_{i_{min}+1}) y_{i_{min}+1, t} + \alpha_{i_{min}+1} y_{i_{min}, t} + m_{i_{min}+1}, \quad (4.5)$$

and

$$y_{i+1,t+1} = (1 - \alpha_{i+1} - \beta_{i+1})y_{i+1,t} + \alpha_{i+1}y_{i,t} + \beta_{i+1}y_{i-1,t} + m_{i+1}, \quad (4.6)$$

for $i \in \{i_{min} + 2, \dots, i_{max}\}$, m_{i+1} a parameter, and α_{i+1} and β_{i+1} two positive parameters that are smaller than 1. The model is estimated using the benchmark ordinary least square proposed by the authors.

4.3 In-sample analysis

In this section, we present the results of our empirical estimations with the VAR-ENET model for each population. We especially focus on the study of the estimated Granger causality matrices that describe the long-term underlying mortality dynamic of the model. The goodness of fit is analyzed by comparing the in-sample results with the benchmark models presented in Section 4.2.

4.3.1 Parameters estimation

Let us present our estimated results on the period 1950 – 2016. The parameters are estimated as described in Section 3. For the lag order p , we choose the value 7, which represents between 10% and 15% of the observation, depending if we analyze the in-sample or, as in the latter sections, out-sample. Table 1 reports the list of the estimated hyper-parameters for each population of interest. We note that, for some populations, we retain the value 1 for α , i.e. we estimate the model with the LASSO constraint only.

Table 1: The estimated VAR-ENET hyper-parameters.

Country	Population	α	λ
FR	Female	0.8	0.0012
FR	Male	0.6	0.0003
FR	Total	0.8	0.0006
US	Female	0.6	0.0010
US	Male	1.0	0.0005
US	Total	1.0	0.0005
UK	Female	0.6	0.0004
UK	Male	1.0	0.0003
UK	Total	0.8	0.0005

Note: This table displays the estimated hyper-parameters α and λ in Equation (3.1) for the VAR(7) models. We consider males, females and the overall populations for FR, UK and US.

The first Granger causality matrix \mathbf{A}_1 for each population is displayed in Figure 2. These estimated matrices are sparse, i.e. most of the coefficients are estimated to 0 while minimizing the criterion given in Equation (3.1). We identify two main structures by observing the non-zero coefficients. We interpret these patterns in terms of demographic effects, basing our explanations on the underlying mortality dynamic of the model induced by the matrices and described in Equation (2.1).

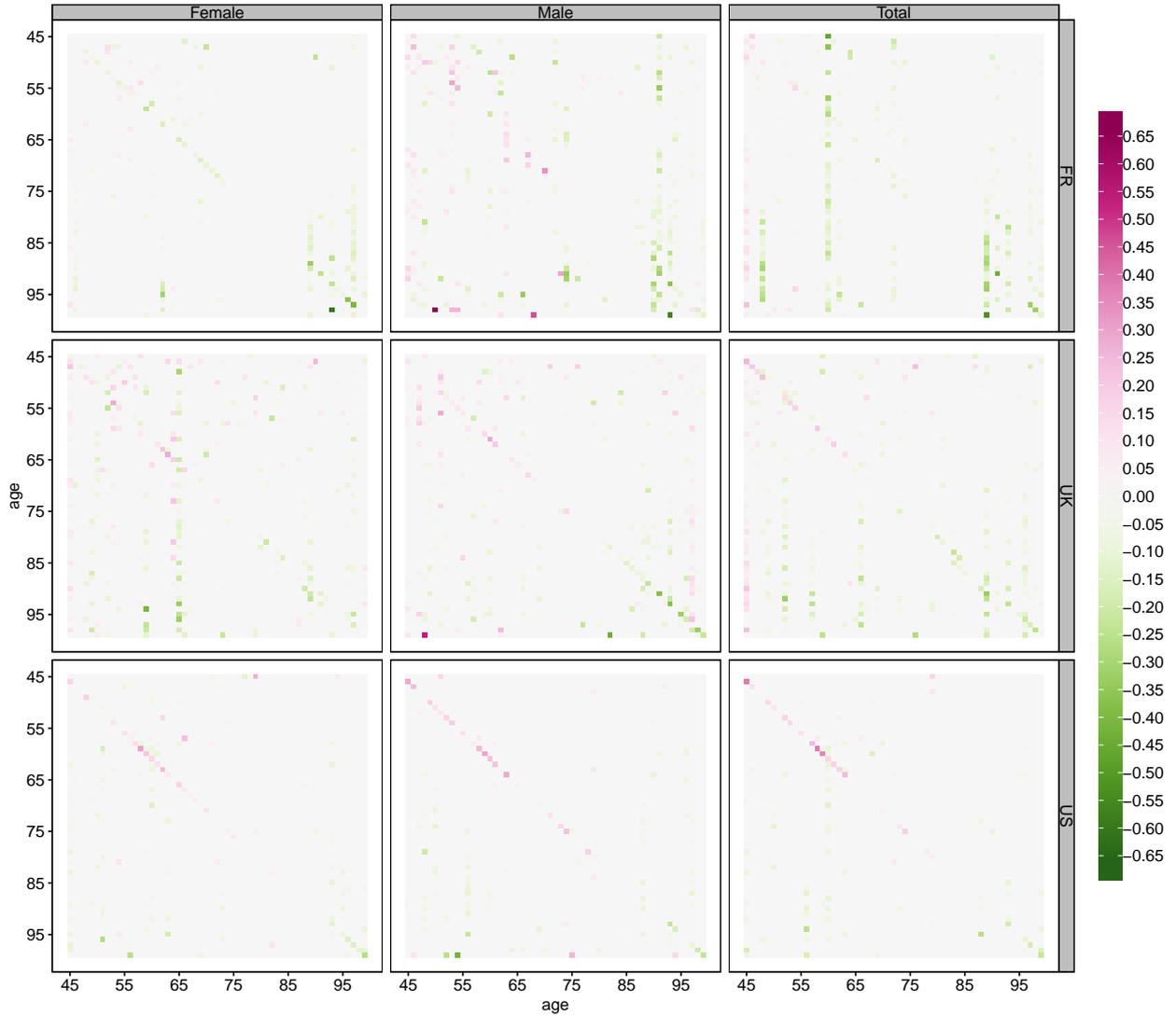


Figure 2: The Granger causality matrix \mathbf{A}_1 for England and Wales (UK), the United States (US) and France (FR) on the age range 45-99 for females, males and the overall population.

First, an expected cohort effect, induced by individuals belonging to the same generation, is highlighted by allocated coefficients on the k^{th} subdiagonal for \mathbf{A}_k for $k \in \{1, \dots, p\}$. Indeed, those coefficients in the VAR model describe the Granger causality of $\Delta y_{i-k,t-k}$ on $\Delta y_{i,t}$. This effect appears positively mainly for the younger ages of our different samples. It is more diffuse between the ages of 65 and 85 years old. In Figure 2, the difference between countries appears clearly and the so-called cohort effect is relatively strong for the US population, compared to the FR and the UK. The cohort effect is also clearly visible for $k \in \{2, \dots, 7\}$ (not shown here).

Second, negative period effects are observed on the main diagonals in just about any population, especially between the ages of 85 and 95. Females in France are more impacted by this effect also for younger ages, whereas almost no cohort effect appears for this group. An opposite situation emerges for the US, where the period effect remains limited to the very older ages.

Third, we notice some age-specific effects corresponding to vertical structure of non-zero co-

efficients. This third type of patterns reveal non-trivial interactions between different cohorts which are non-necessary within a close neighboring. More concretely, a vertical pattern on the i^{th} column of \mathbf{A}_1 reveals a persistent effect from the term $\Delta y_{i,t-1}$ on $\{\Delta y_{j_1,t}, \dots, \Delta y_{j_l,t}\}$, with $\{j_1, \dots, j_l\} \subset \{i_{min}, \dots, i_{max}\}$. It means that the mortality improvement of a single specific age i seems to impact the mortality improvement on a group of ages $\{j_1, \dots, j_l\}$ one year after. Similar structures can be observed on the matrices \mathbf{A}_k for $k \in \{2, \dots, 7\}$ (not shown here).

This latter effect, underlined by our data-driven approach, has not been well documented in the literature yet to our knowledge. These patterns are quite difficult to interpret and to explain within the demographic framework with the available datasets. Disaggregated data would be very useful to explore these effects further. Indeed, these patterns could result from biological, environmental or societal causes, unless it is due to some anomalies in the HMD (Cairns et al., 2016b; Boumezoued, 2016). At this point, we are unable to conclude on the very causes of such age-effects.

On the contrary, the observed cohort and period effects have already been well studied in the literature. However, our model highlights this result in a more data-driven way. Indeed, the existing models either detect these effects in the residuals (e.g. Lee and Carter, 1992; Dokumentov et al., 2018), or force the estimation of specific parameters (e.g. Cairns et al., 2009; Li and Lu, 2017). In our case, we notice these effects by analyzing the parameters estimated without imposing any specific constraints. To exhibit how our data-driven approach can adapt to these effects, we estimate two VAR-ENET(1) models on the French male population over the period 1950-2012, but with the data downloaded from the HMD at two different dates: 2nd October 2017 and 28th January 2019. Indeed, between these two dates, the HMD data had been updated, following the work of Cairns et al. (2016b) and Boumezoued (2016) using fertility rates. With this correction, the residual plots display a cohort effect which is substantially lessened. The two Granger causality matrices estimated are displayed in Figure 3. In the old version, we clearly remark a subdiagonal in the estimated parameters. In the new estimation, where many false cohort effects had been removed, the pattern on the first subdiagonal is virtually nil, whereas the negative period effect on the main diagonal is only slightly reduced.

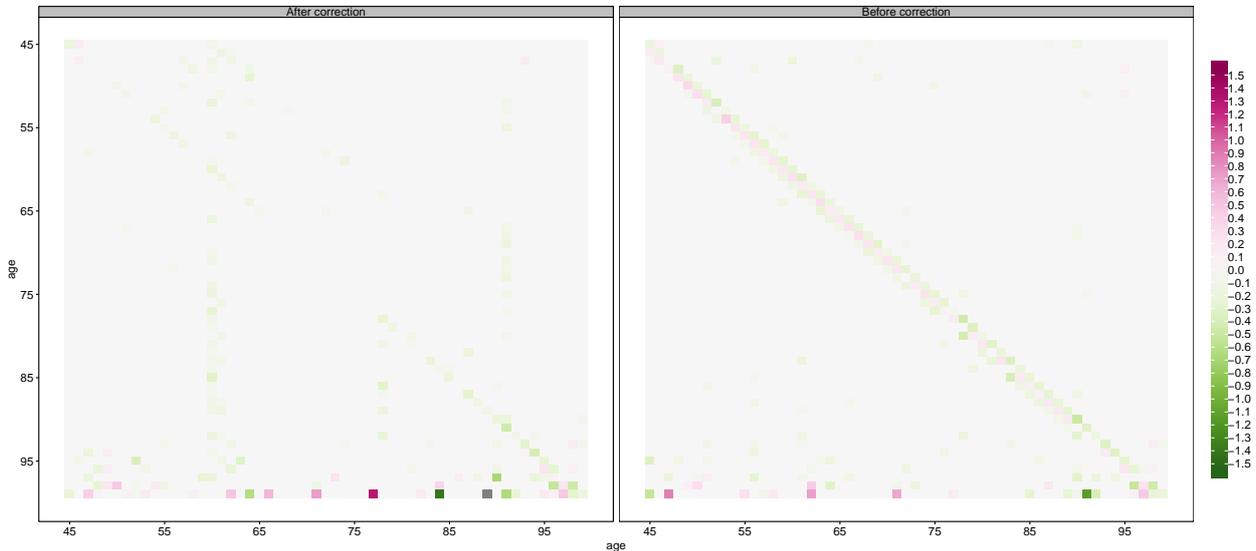


Figure 3: The Granger causality matrix \mathbf{A}_1 for the French males on the age range 45-99 estimated with a VAR-ENET(1) over the period 1950-2012, on the HMD data downloaded on the 2nd October 2017 (Before correction) and the 28th January 2019 (After correction).

4.3.2 In-sample model comparison

We now study how our approach fits well and captures better the mortality pattern on these subsets compared to the benchmark models we retained in Section 4.2. Table 2 contains the values of the RMSE, as defined in Equation (3.2) for each model and each population. Table 3 displays summary statistics of RMSE values over all the populations considered for each model. Benchmark models and the VAR-ENET have quite comparable results. Although the VAR-ENET has not the lowest value for each population, it globally leads to one of the best in-sample results with the HU and RESPECT model (around 2% in average). More particularly, the RESPECT model outperforms the VAR-ENET on the US populations.

Table 2: The RMSE of the VAR-ENET and benchmark models.

Country	Model	RMSE Female	RMSE Male	RMSE Overall
FR	VAR	0.032	0.013	0.021
FR	HU	0.022	0.024	0.017
FR	LC	0.054	0.050	0.041
FR	M7	0.076	0.071	0.065
FR	RESPECT	0.021	0.025	0.022
FR	STAR	0.042	0.045	0.038
UK	VAR	0.014	0.015	0.018
UK	HU	0.024	0.029	0.021
UK	LC	0.052	0.059	0.050
UK	M7	0.058	0.049	0.044
UK	RESPECT	0.022	0.027	0.016
UK	STAR	0.040	0.044	0.035
US	VAR	0.020	0.017	0.017
US	HU	0.017	0.016	0.014
US	LC	0.045	0.049	0.042
US	M7	0.048	0.050	0.046
US	RESPECT	0.010	0.009	0.006
US	STAR	0.025	0.024	0.023

Note: This table reports the RMSE values obtained after fitting the VAR-ENET and the considered benchmark models. We compare this indicator for males, females and the overall populations for FR, UK and US.

The RMSE value is also computed for each age and each year, and the results are displayed respectively on Figures 4 and 5 for all of the overall populations. First, we note that, on top of having one the lowest RMSE with the smoothing models, the VAR-ENET leads to a more stable error over the age. This is clearly noticeable on the higher ages, especially for the French and English data. For example we observe that the M7's fitting error drastically increases for ages above 95. More generally, on these two populations, all the benchmark model tend to have an increasing age-marginal RMSE starting from 90 years old, while our model's fitting error stays relatively stable. On the American data, the results are more nuanced: whereas we still notice an increase of RMSE values at higher ages for the stochastic benchmark models (LC, M7 and STAR), the smoothing ones and the VAR-ENET lead to stable errors.

Table 3: Summary statistics for the RMSE of the VAR-ENET and the benchmark models.

Model	Mean	Standard Deviation	Minimum	Maximum
VAR	0.019	0.006	0.013	0.032
HU	0.020	0.005	0.014	0.029
LC	0.049	0.006	0.041	0.059
M7	0.056	0.012	0.044	0.076
RESPECT	0.018	0.008	0.006	0.027
STAR	0.035	0.009	0.023	0.045

Note: This table reports statistics of the RMSE values obtained after fitting the VAR-ENET and the considered benchmark models over the males, females and the overall populations for FR, UK and US.

The RMSE patterns across periods are more erratic. While the errors of smoothing models (HU and RESPECT) are quite stable over the periods, many peaks are observed for all the stochastic models. More particularly, we note that these peaks tend to occur at the same period for all the concerned models, especially on the French and American data. We remark that, among the stochastic models, the VAR-ENET is the one producing the peaks of the lowest amplitude, and is the closest of the smoothing models in terms of goodness-of-fit. Finally, we notice that, on the American data, the errors of the VAR-ENET and the STAR model are highly correlated, mainly starting from 1985. This shows the methodological closeness of these two methods. The results for females and males are given in [Appendix 2](#) with similar findings.

Some of the period peaks may be explained by specific events that have an unexpected impact on the mortality rates, such as an influenza epidemic or a heat wave (Huynen et al., 2001). Indeed, this type of exogenous stresses is difficult to predict with only mortality rate series, which explains why the peaks are observable for the three models. For example, we try to explain the relatively high RMSE in France in 2004. In 2003 a heat wave led to one of the hottest summer ever recorded in France and, as a direct consequence, to higher mortality rates during this year, especially for the elderly. Then, the mortality was much lower in 2004 due to the so-called harvesting effect (Toulemon and Barbieri, 2008; Izraelwicz, 2012). On the contrary, in the calculation of the RMSE, the mortality rates of the year 2004 are forecasted from the observation of the 2003 rates in accordance with the temporal dynamics we have imposed; in this way, the 2004 mortality was expected to be relatively high. This must explain why we observe a RMSE peak in 2004 for the French population.

4.4 Out-of-sample performance

For risk management in insurance or more generally for demographers or public policy purposes, mortality rates require being predicted based on the past information. A quite usual test for accuracy is to analyze how the model is able to reproduce the mortality rates correctly. Note that this objective is more demanding than measuring the prediction power on the residual life expectancy. A reasonable model should be able to predict a kind of convergence for mortality at a similar level.

We focus on the prediction power of the VAR-ENET model compared to the benchmark models through an analysis of the out-sample forecasting performance on the same age-period space. To this end, we first estimate each model based on the observations from 1950 to 2000, then we forecast

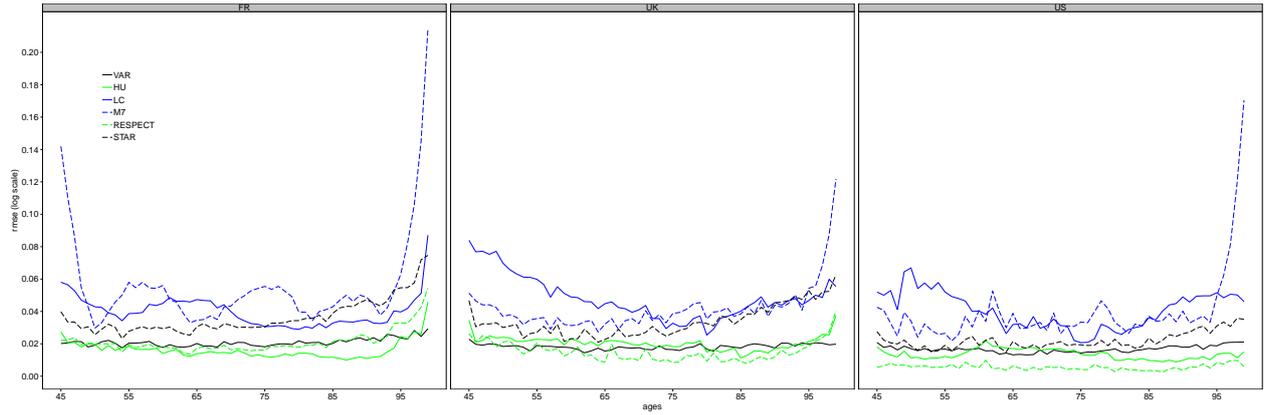


Figure 4: The RMSE for England and Wales (UK), the United States (US) and France (FR) grouped by age for the overall populations.

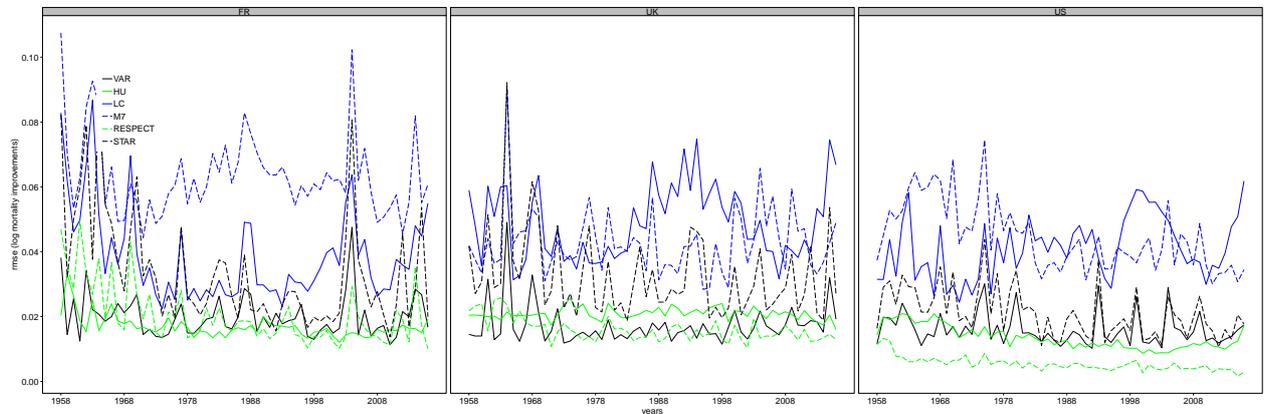


Figure 5: The RMSE for England and Wales (UK), the United States (US) and France (FR) grouped by period for the overall populations.

the mortality rates for the period 2001-2016. Note of course that the mortality rates can be easily calculated using the VAR model, based on the predicted improvement rates and the initial values known for the last year of the training sample. We choose a similar measure to the one taken for the in-sample analysis, the root mean squared forecast error (RMSFE) that we define for a projection horizon h as

$$\text{RMSFE} = \sqrt{\frac{1}{dh} \sum_{i=i_{\min}}^{i_{\max}} \sum_{t=t_0+1}^{t_0+h} (y_{i,t} - \hat{y}_{i,t})^2}, \quad (4.7)$$

where t_0 is the year 2000 and h equals to 16 years in our study.

We compare the predictive power of the different models on the period 2001 – 2016 for the 3 populations (overall, female, male) of the 3 countries of interest. The results are displayed in Table 4 and 5 (we also display the results for different estimation years but with the same forecasting period in Appendix 3). We note in Table 5 that the average RMSFE is smaller with the VAR-ENET than with the benchmark models, indicating that the former one has higher predictive power in general. However, it is locally outperformed by other models for some populations. Thus, we note for example that the RESPECT model slightly outperforms the VAR-ENET on the French data, and

the STAR’s RMSFE value on the US male population (5%) is significantly lower than the one obtained with the VAR-ENET (11.6%) and the other models.

Furthermore, we observe that, in the VAR-ENET applications, all the forecasting errors are of the same order of magnitude, no matter the selected population. This point is highlighted by the standard deviation of RMSFE values over the 9 populations displayed in Table 5 for each model. Although the RESPECT and STAR models locally outperform the VAR-ENET, they are more sensible to population considered, leading to a significantly higher standard deviation (respectively 9.4% and 11.3% against only 1.4% for our model). The M7, and to a lesser extent the LC and HU models, also tend to have more variable forecasting errors, depending on the considered population. These results highlight the stability of the prediction error of the VAR-ENET over different populations compared to the other benchmark models due to the more data-driven approach of the first one, allowing it to better capture the features of each populations’ mortality dynamic. By analyzing the results displayed in Appendix 3, we also notice a better stability of the VAR-ENET over different estimation periods.

Table 4: The RMSFE of the VAR and the benchmark models estimated on the period 1950 – 2000.

Country	Model	RMSFE Female	RMSFE Male	RMSFE Overall
FR	VAR	0.088	0.110	0.078
FR	HU	0.082	0.112	0.067
FR	LC	0.111	0.113	0.067
FR	M7	0.676	0.193	0.257
FR	RESPECT	0.083	0.091	0.071
FR	STAR	0.098	0.127	0.417
UK	VAR	0.095	0.087	0.080
UK	HU	0.109	0.138	0.122
UK	LC	0.142	0.141	0.138
UK	M7	0.228	0.099	0.145
UK	RESPECT	0.281	0.230	0.296
UK	STAR	0.083	0.115	0.156
US	VAR	0.078	0.116	0.078
US	HU	0.061	0.141	0.085
US	LC	0.085	0.122	0.087
US	M7	0.237	0.144	0.135
US	RESPECT	0.110	0.081	0.075
US	STAR	0.071	0.050	0.049

Note: This table reports the out-of-sample performance *via* the RMSFE values for the HU, the LC, the M7, the RESPECT, the STAR and the VAR-ENET models estimated on the period 1950 – 2000. We compare this indicator for males, females and the overall populations for FR, UK and US.

We plot the RMSFE in Figure 6 for the overall population of our three countries of interest. The results for female and male populations are postponed in Appendix 3. First, we note that the forecasting errors from most models tend to converge with the projection horizon, suggesting that obtaining a significant enhancement of the forecasting accuracy on the long term seems very challenging. However, we observe that for specific population, some models fail to capture the mortality

Table 5: Summary statistics for the RMSFE of the VAR-ENET and the benchmark models.

Model	Mean	Standard Deviation	Minimum	Maximum
VAR	0.090	0.014	0.078	0.116
HU	0.102	0.030	0.061	0.141
LC	0.112	0.027	0.067	0.142
M7	0.235	0.174	0.099	0.676
RESPECT	0.146	0.094	0.071	0.296
STAR	0.129	0.113	0.049	0.417

Note: This table reports statistics of the out-of-sample performance *via* the RMSFE values for the VAR-ENET and the considered benchmark models estimated on the period 1950 – 2000 over the males, females and the overall populations for FR, UK and US.

dynamics, therefore the RMSFE strongly diverges, see e.g. M7 and STAR on the French data or HU on the English data. Nevertheless, our model doesn't suffer from this drawback. Furthermore, it always belongs among the best models for any population and any period considered in this study.

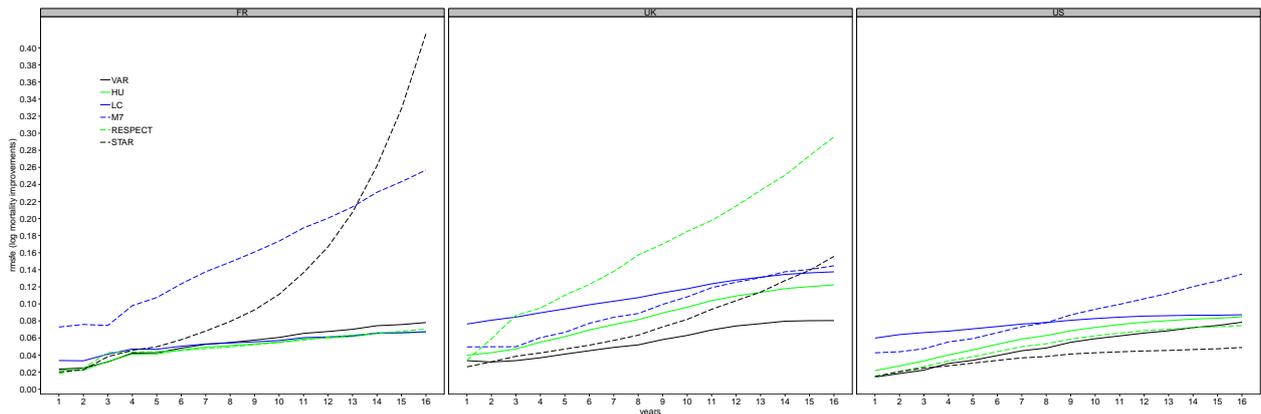


Figure 6: The RMSFE for England and Wales (UK), the United States (US) and France (FR) grouped by period for the overall populations.

We now focus on the forecasting error by age groups. We choose to separate the age dimension into 5 classes and compute the RMSFE at a projection horizon of 10 years. By doing so, we compare the predictive power over the different ages. Indeed, depending on the purpose of the mortality forecasting application, one could be more interested in producing accurate predictions for some specific ages. We show the results of the three models in Figure 7.

Yet again, we observe that the VAR-ENET is the most stable model over the age classes, when analyzing the forecasting errors at a 15 years projection horizon. While the M7 consistently fails to capture the mortality dynamic at higher ages, the other models have more local issues. For example, we note poorer predictions for the STAR on the French age class 85-94. On the English mortality, the two models LC and HU, and the RESPECT methodology, have respectively higher RMSFE on the age classes 65-74 and 85-94. This point highlights the capacity of our model to uniformly forecast the mortality rates over the age dimension for any of the considered populations.

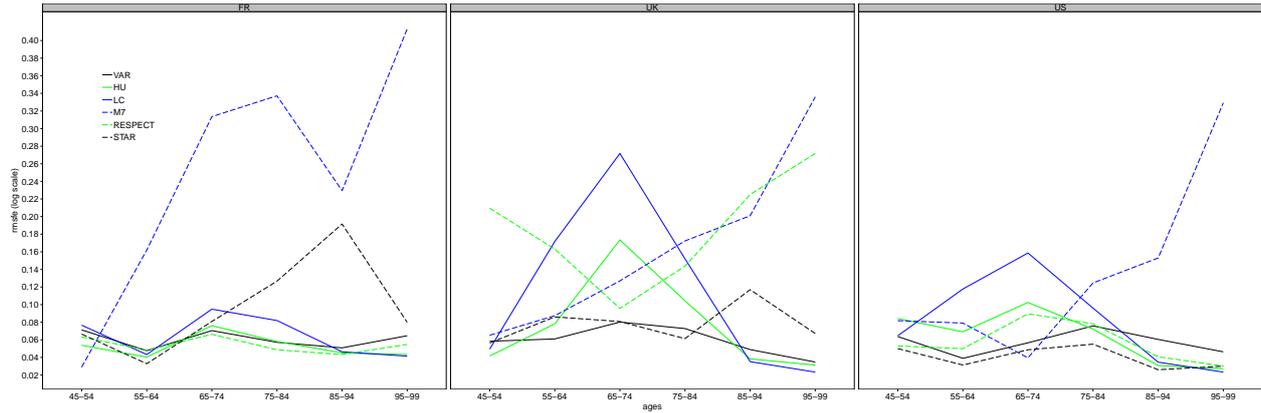


Figure 7: The RMSFE for England and Wales (UK), the United States (US) and France (FR) grouped by age for the overall populations.

The results presented in this section suggest that our model slightly outperforms the benchmark methodologies in average for the considered data, even though it doesn't lead to the best accuracy for every population. In all the tested situation, it is at least a credible competitor compared to the best model. More importantly, the VAR-ENET seems to be more stable according to the selected population. This last point is the most noticeable difference between our in and out-of-sample results. Whereas, in our in-sample study, the models' fit seems to be relatively equally stable in respect of the considered population, the out-of-sample analysis emphasizes a noticeable heterogeneity in the outcomes depending on the selected dataset. In that regard, the VAR-ENET tends to provide significantly more consistent forecasts.

4.5 Forecasting application

Figure 8 displays the median forecasts of the log of death rates for ages in $\{45, 65, 85, 95\}$ using the VAR-ENET model from 2017 to 2066. We note that the trends seem rather realistic. We remark that the male and female mortality rates tend to converge rapidly for the UK population. This forecasting result has already been observed in the literature with other models with a similar estimation period (see e.g. Bohk-Ewald and Rau (2017)). We note on the forecasted series that there are some limited shocks during the first projection years, followed by a linear trend. This effect is characteristic of the VAR model and shows how it can propagate innovation shocks among a cohort for example.

Figure 9 compares the median forecasts of the log of death rates of two popular models LC, the HU model with the VAR-ENET model from 2013 to 2062. First, we note that for many of the forecasted series, the three models produce very similar projections, especially on the female populations at higher ages. On the contrary, for the British male mortality dynamics, the forecasts are noticeably different. While the LC and HU models predict a stabilization of the mortality rates, and even a slight increase at age 45 for the smoothing methodology, our VAR-ENET forecasts a decrease consistent with the average longevity improvement over the last decades. The two benchmark models seems to be more impacted by the slowdown of this enhancement observed during the very recent years. To a lesser extent, we also notice a comparable results on the French male population.

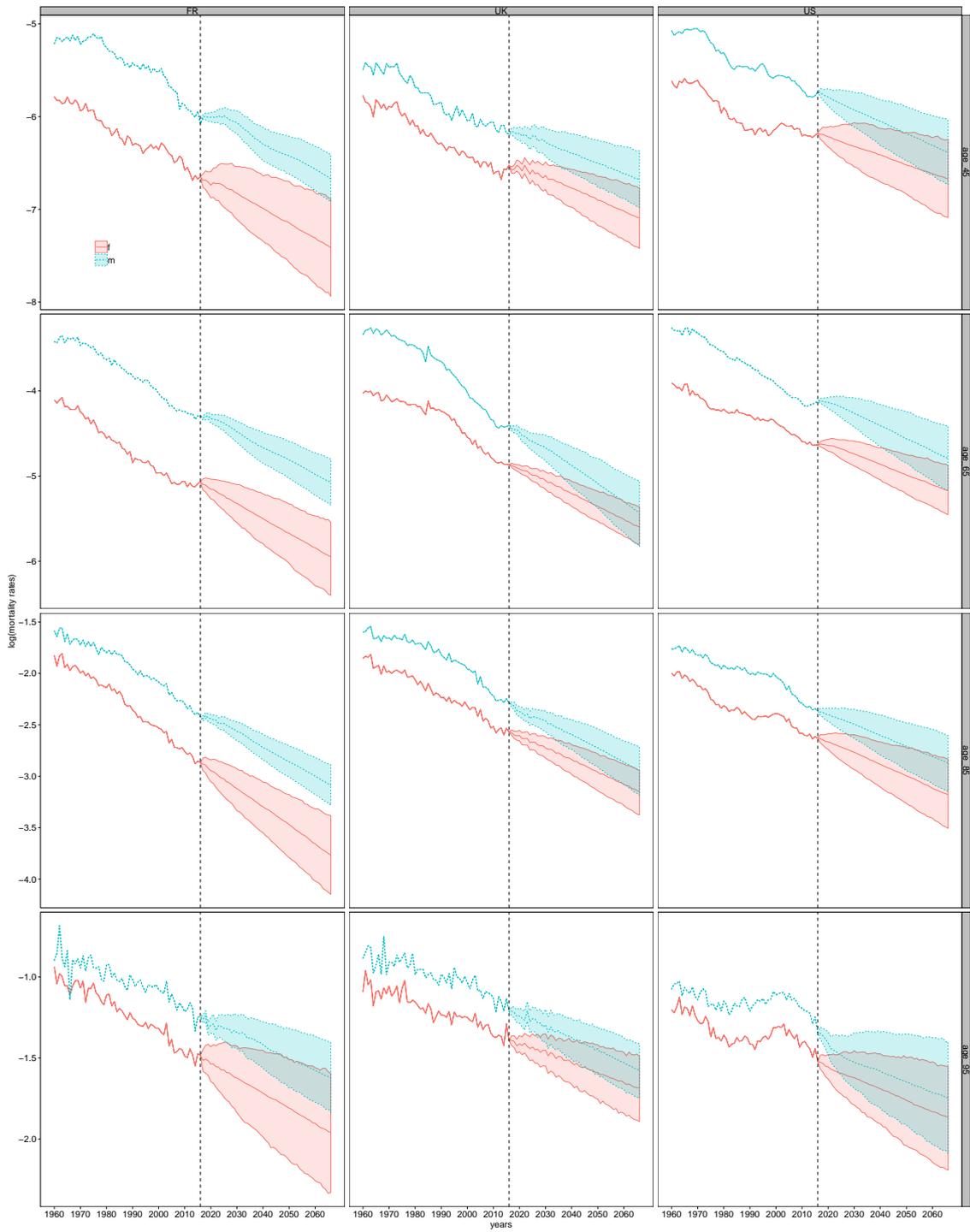


Figure 8: The observed and the projected log of death rates for British (UK), American (US) and French(FR) females and males with the 97.5% prediction intervals, obtained from the VAR-ENET model.

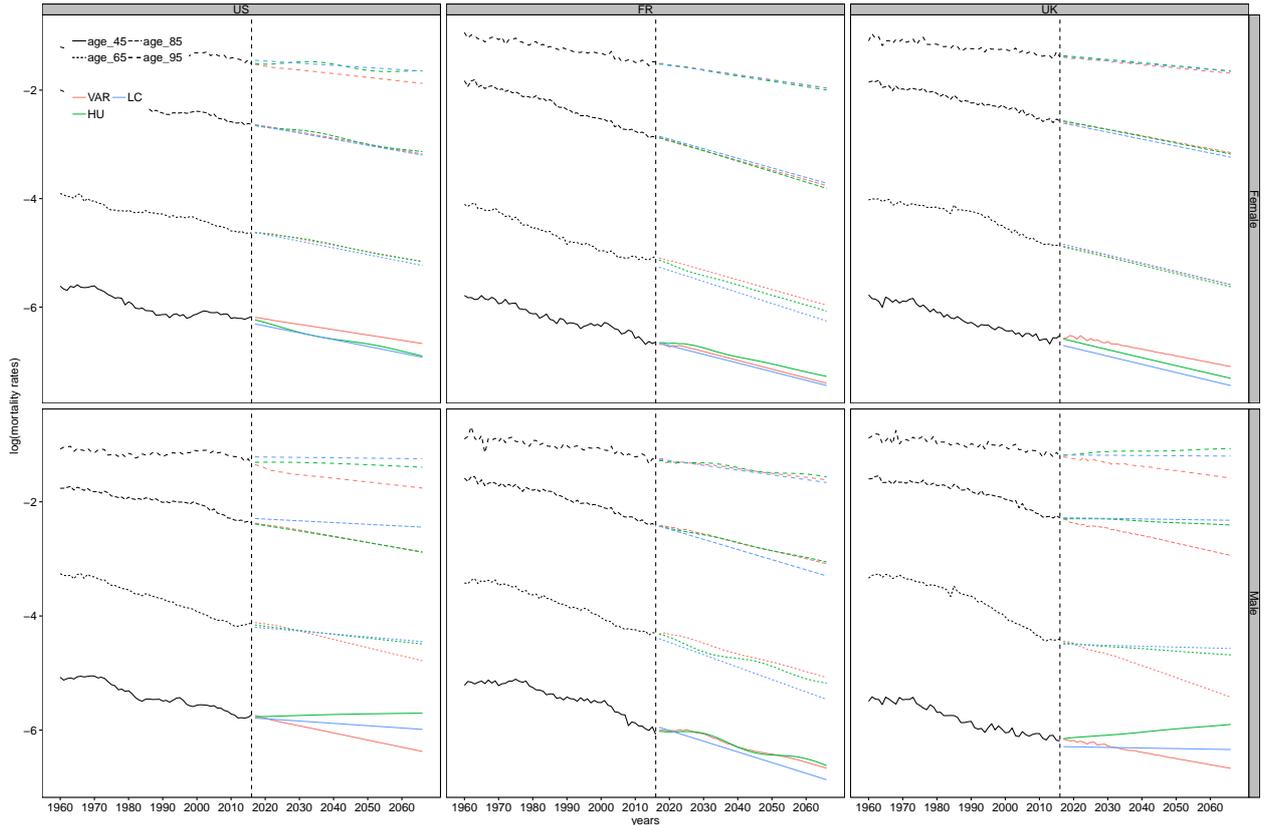


Figure 9: The observed and the projected log of death rates for British (UK), American (US) and French (FR) females and males. This figure compares trends obtained with the HU, the LC and the VAR-ENET models.

5 A multi-population extension

Some of the standard mortality forecasting models can be extended to multi-population. However, many of these extensions suffer from limits. One of the recurrent limits in multi-population mortality modeling is the restriction of the extension to only 2 populations. For example, we can note the GRAVITY model of Dowd et al. (2011) or the Bayesian model of Cairns et al. (2011). Another restriction imposed by some existing multi-population models is the necessity to determine a dominant population and sub-populations, see e.g. the SAINT model of Jarner and Kryger (2011), or a common trend for the different populations like in Li and Lee (2005). In this section, we explore the possibility of extending our model for multi-population mortality forecasting and we give the needed details.

We denote M the number of selected populations and $y_{m,i,t}$ the log of mortality rates for the m^{th} population. We suppose that the pair (i_{\min}, i_{\max}) is the same for all the populations to avoid exaggerated notations, although we could have chosen M different pairs of age limits. Thus, we define M different d -dimensional vectors $\Delta \mathbf{Y}_{m,t}$ that we concatenate into a single Md -dimensional vector $\Delta \mathbf{Y}_t = (\Delta y_{1,i_{\min},t}, \dots, \Delta y_{1,i_{\max},t}, \Delta y_{2,i_{\min},t}, \dots, \Delta y_{M,i_{\max},t})^\top$. We then apply the same model as in Equation (2.1) except that the dimension equals now to Md .

The $(Md) \times (Md)$ -dimensional autoregressive matrices and the Md -dimensional vector of con-

stants are estimated through the same elastic-net methodology as in the single population problem. However, the covariance matrix estimation needs to be extended since its structure may change significantly compared to the single population case.

In the multi-population context, the covariance matrix Σ is $(Md) \times (Md)$ -dimensional. Firstly, we propose to consider this matrix as a block matrix broken into M^2 different $d \times d$ -dimensional submatrices noted $\Sigma_{m,n}$ for each population couple $(m, n) \in \{1, \dots, M\}^2$. Then, for each population m , we estimate the diagonal submatrix $\Sigma_{m,m}$ through the same methodology as in the single population, obtaining in this way $\tilde{\Sigma}_{m,m}$. Since $\tilde{\Sigma}_{m,m}$ is a positive-definite matrix, we define its Cholesky decomposition

$$\tilde{\Sigma}_{m,m} = \tilde{R}_m^\top \tilde{R}_m,$$

where \tilde{R}_m is an upper triangular matrix. Finally, for a couple of populations (m, n) we estimate the covariance submatrix as

$$\tilde{\Sigma}_{m,n} = \rho_{m,n} \times \tilde{R}_m^\top \tilde{R}_n,$$

where $\rho_{m,n} \in [-1, 1]$ is the empirical Pearson's correlation coefficient between the observations of residuals $(\epsilon_{m,i,t})_{(i,t)}$ and $(\epsilon_{n,i,t})_{(i,t)}$ for $(i, t) \in \{i_{\min}, \dots, i_{\max}\} \times \{t_{\min} + p, \dots, t_{\max}\}$.

Thus, our extended covariance model has only $M(2d + 1) + \frac{M(M-1)}{2}$ parameters. The number of ages, d , being generally much larger than the number of populations in mortality modeling, we note that $M(2d + 1) \gg \frac{M(M-1)}{2}$, meaning that we do not add many parameters for covariance estimation while modeling M populations together compared to fitting M single models.

6 Conclusions

In this paper, we have proposed a vector-autoregression elastic-net (VAR-ENET) model on the differentiated log-mortality, leading to three key results. First, this new high-dimensional time series analysis outperforms in fitting the mortality rate series of each of the nine populations we considered, compared with the three stochastic benchmark models (LC, M7 and STAR). Moreover, in average, it leads to in-sample errors of same order as the two smoothing benchmark models (HU and RESPECT). Even though our model doesn't produce the most accurate forecasts on each population, it leads to relatively close results compared to the best model each time. In addition, the average RMSFE over the 9 population is lower than the one obtained with any other benchmark models. Furthermore, thanks to its data-driven approach, the VAR-ENET leads to more stable errors than the benchmark models over populations, showing its power of adaptability to the specific mortality dynamics of different populations. Compared to the usual strategy which requires to compare a variety of possible models and then select the best for a particular age-period population, our approach gives directly and with little effort a serious candidate for a consistent modeling of the mortality, regardless of the population features. The second key result is that, although we let a large freedom in the spatio-temporal dependence structure without imposing a priori constraints, the VAR-ENET model enlightens three main effects: the so-called cohort and period effects and a specific age effect. While the first two models have already been well studied in many papers on mortality modeling, we develop in this paper a new ways for detect the effects for any population. The last effect is less known or possibly even unknown in the literature. Future researches are needed, probably on a finest dataset to understands such a phenomena. Finally, the proposed extension of the VAR-ENET to multi-population mortality modeling seems a priori

straightforward, without raising unavoidable issues on the number of populations or on the hierarchy between them, considering the estimation process.

Some points should however be improved and need further researches. The first one concerns the interpretation of the results given by our VAR-ENET model. Although it seems to have a better forecasting and adaptability power than the standard factor-based models, the last ones do benefit from a greater interpretability. Indeed, even if most of the coefficients in the autoregressive matrices are estimated to zero in the VAR-ENET and that the non-null coefficients seems to form specific patterns, the comprehension of the underlying dynamics remains complex. On the contrary, it is much easier to understand the mortality dynamics in terms of period, age and cohort effects, which are directly visible through the use of the classical factor-based models.

Second, we are also aware that some of the hyper-parameter selection techniques we applied can be improved. Firstly, we imposed the lag order p equals to 7 for all the population. In a sensibility analysis, we have noted that according to the considered population, the highest predictive power of the VAR-ENET(p) model is not reached at the same lag order p . These results suggest that an optimization on the hyper-parameter p could be developed. The second hyper-parameter to be improved is the mixing weight parameter α between the LASSO and ridge penalties. In the general context of elastic-net regression, it is usually selected with a grid search. However, Friedman et al. (2010) propose to optimize it through a cross-validation by following the same methodology as the λ selection.

Third, the log-mortality rates series $y_{i,t}$ are known to not be stationary, but also to be cointegrated (see e.g. Chen et al., 2015; Salhi and Loisel, 2017; Li and Lu, 2017). In our paper, we choose to study the first difference in the log mortality-rates and, by doing so, we lose some information about the long-term co-movement. Another way that we can deal with the non-stationarity and co-integration is to rather select the Vector Error Correcting Model (VECM). Nevertheless, although high-dimensional VAR model has been relatively well studied and recently documented especially in financial econometrics, VECM sparse estimation with elastic-net or other techniques seems to be a new field (see e.g. Wilms and Croux, 2016), and could be developed further for the mortality projection. A major improvement of our model would be to implement the elastic-net procedure to VECM estimation and apply it to the log-mortality series.

Finally, even though we introduce an extension to multi-population mortality forecasting of our model, we don't show any empirical studies on that subject in this paper, which rather focuses on the single population case. Many points need to be analyzed in greater detail to correctly assess the behavior of the VAR-ENET model applied to multi-population. It notably includes the examination of a broader list of countries, the specific case of sub-regional populations and the comparison of forecasts to recent multi-population models. Further more specific studies should be conducted to examine the multi-population model.

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Appendix 1 Improvement rates data for females and males

Figures 10 and 11 describe the log-mortality improvements for females and males.

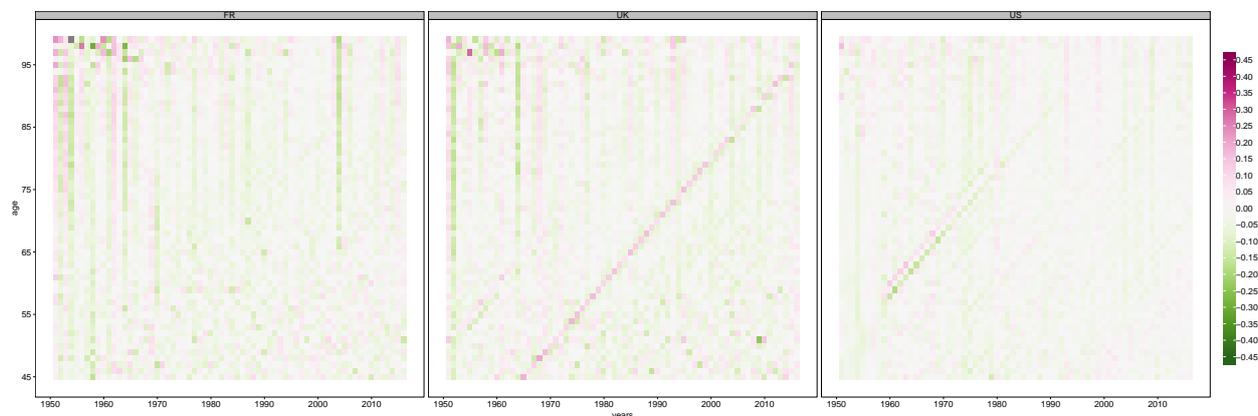


Figure 10: The period log-mortality improvements for England and Wales (UK), the United States (US) and France (FR) on the age-period observation $\{45, \dots, 99\} \times \{1950, \dots, 2016\}$ for females.

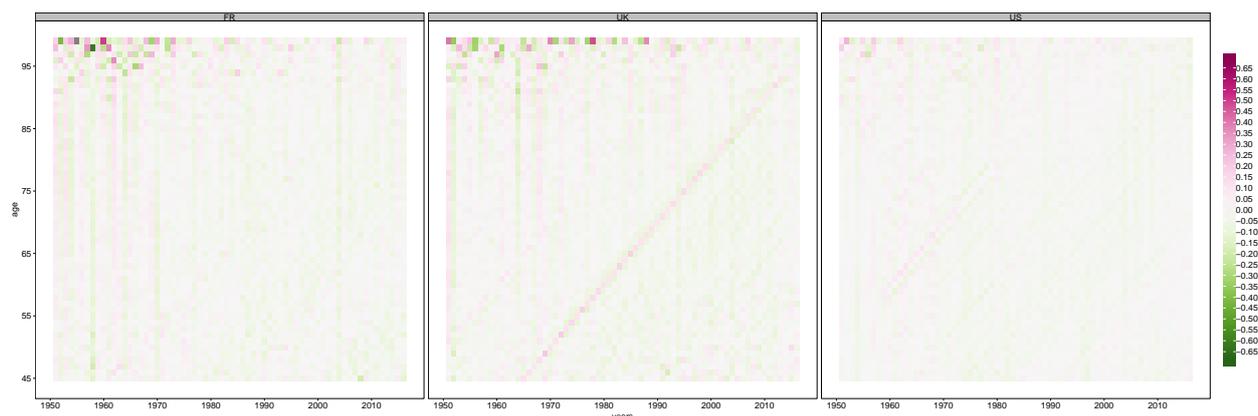


Figure 11: The period log-mortality improvements for England and Wales (UK), the United States (US) and France (FR) on the age-period observation $\{45, \dots, 99\} \times \{1950, \dots, 2016\}$ for males.

Appendix 2 In-sample analysis for females and males

Figures 12 and 13 present the in-sample performance in terms of RMSE for females. Figures 14 and 15 present the in-sample performance in terms of RMSE for males.

Appendix 3 Out-of-sample analysis for females and males

Tables 6 and 8 present the out-of-sample performance in terms of RMSFE for different model estimation period, respectively $\{1970, \dots, 2000\}$ and $\{1980, \dots, 2000\}$. Tables 7 and 9 outlines the

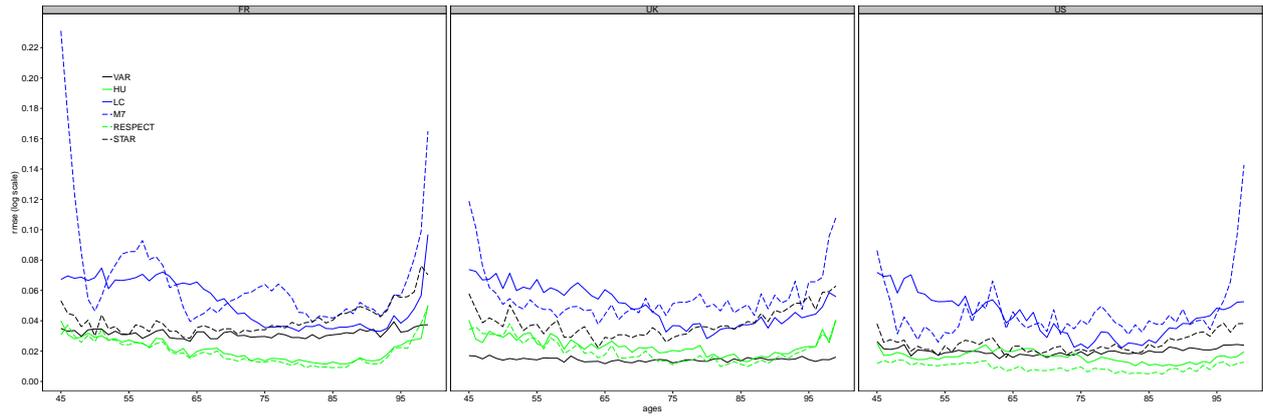


Figure 12: The RMSE for England and Wales (UK), the United States (US) and France (FR) grouped by age for the female populations.

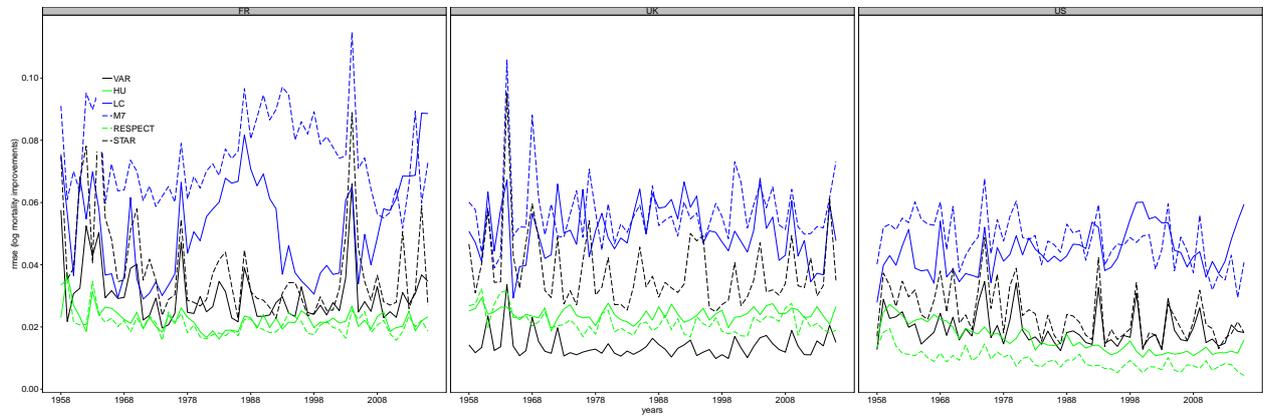


Figure 13: The RMSE for England and Wales (UK), the United States (US) and France (FR) grouped by period for the female populations.

global statistics of out-sample performance in terms of RMSFE.

Figures 16 and 17 present the out-of-sample performance in terms of RMSFE for females. Figures 18 and 19 present the out-of-sample performance in terms of RMSFE for males.

Table 6: The RMSFE of the VAR and the benchmark models estimated on the period 1970 – 2000.

Country	Model	RMSFE Female	RMSFE Male	RMSFE Overall
FR	VAR	0.088	0.092	0.068
FR	HU	0.081	0.085	0.058
FR	LC	0.085	0.086	0.055
FR	M7	0.266	0.137	0.139
FR	RESPECT	0.077	0.085	0.074
FR	STAR	0.101	0.110	0.172
UK	VAR	0.074	0.091	0.067
UK	HU	0.116	0.134	0.126
UK	LC	0.133	0.146	0.129
UK	M7	0.148	0.111	0.097
UK	RESPECT	0.321	0.232	0.260
UK	STAR	0.073	0.083	0.069
US	VAR	0.105	0.116	0.092
US	HU	0.105	0.118	0.087
US	LC	0.133	0.123	0.090
US	M7	0.192	0.133	0.133
US	RESPECT	0.148	0.081	0.077
US	STAR	0.120	0.070	0.079

Note: This table reports the out-of-sample performance *via* the RMSFE values for the HU, the LC, the M7, the RESPECT, the STAR and the VAR-ENET (4) models estimated on the period 1970–2000. We compare this indicator for males, females and the overall populations for FR, UK and US.

Table 7: Summary statistics for the RMSFE of the VAR-ENET and the benchmark models estimated on the period 1970 – 2000.

Model	Mean	Standard Deviation	Minimum	Maximum
VAR	0.088	0.017	0.067	0.116
HU	0.101	0.025	0.058	0.134
LC	0.109	0.031	0.055	0.146
M7	0.151	0.051	0.097	0.266
RESPECT	0.151	0.096	0.074	0.321
STAR	0.097	0.033	0.069	0.172

Note: This table reports statistics of the out-of-sample performance *via* the RMSFE values for the VAR-ENET and the considered benchmark models estimated on the period 1970 – 2000 over the males, females and the overall populations for FR, UK and US.

Table 8: The RMSFE of the VAR and the benchmark models estimated on the period 1980 – 2000.

Country	Model	RMSFE Female	RMSFE Male	RMSFE Overall
FR	VAR	0.092	0.092	0.077
FR	HU	0.071	0.093	0.068
FR	LC	0.068	0.088	0.065
FR	M7	0.219	0.113	0.125
FR	RESPECT	0.091	0.086	0.072
FR	STAR	0.295	0.081	0.764
UK	VAR	0.088	0.095	0.079
UK	HU	0.106	0.124	0.110
UK	LC	0.114	0.125	0.113
UK	M7	0.111	0.099	0.097
UK	RESPECT	0.286	0.269	0.197
UK	STAR	0.236	0.065	0.288
US	VAR	0.122	0.122	0.109
US	HU	0.106	0.121	0.096
US	LC	0.107	0.121	0.097
US	M7	0.161	0.129	0.141
US	RESPECT	0.101	0.085	0.080
US	STAR	0.942	0.088	0.322

Note: This table reports the out-of-sample performance *via* the RMSFE values for the HU, the LC, the M7, the RESPECT, the STAR and the VAR-ENET (4) models estimated on the period 1980–2000. We compare this indicator for males, females and the overall populations for FR, UK and US.

Table 9: Summary statistics for the RMSFE of the VAR-ENET and the benchmark models estimated on the period 1980 – 2000.

Model	Mean	Standard Deviation	Minimum	Maximum
VAR	0.097	0.017	0.077	0.122
HU	0.099	0.020	0.068	0.124
LC	0.100	0.022	0.065	0.125
M7	0.133	0.038	0.097	0.219
RESPECT	0.141	0.086	0.072	0.286
STAR	0.342	0.309	0.065	0.942

Note: This table reports statistics of the out-of-sample performance *via* the RMSFE values for the VAR-ENET and the considered benchmark models estimated on the period 1980 – 2000 over the males, females and the overall populations for FR, UK and US.

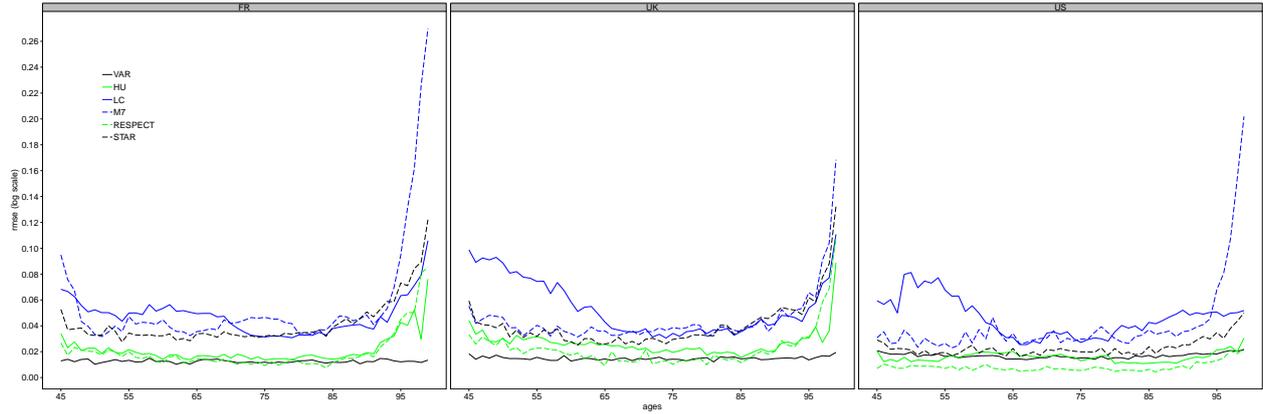


Figure 14: The RMSE for England and Wales (UK), the United States (US) and France (FR) grouped by age for the male populations.

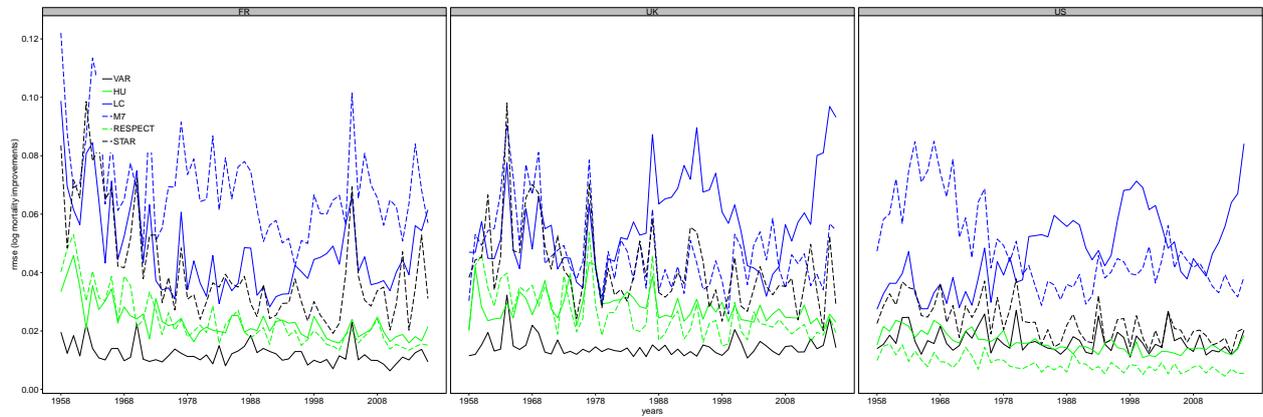


Figure 15: The RMSE for England and Wales (UK), the United States (US) and France (FR) grouped by period for the male populations.

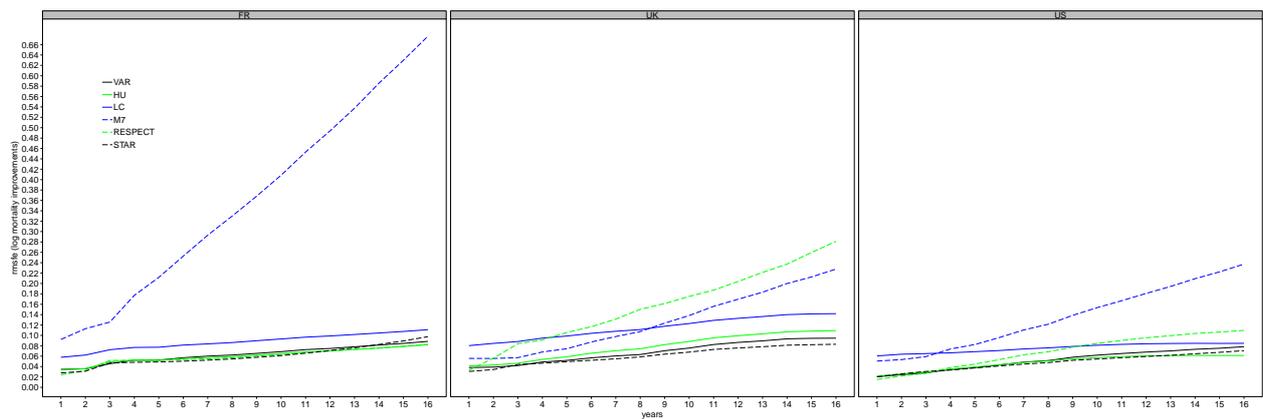


Figure 16: The RMSFE for England and Wales (UK), the United States (US) and France (FR) grouped by period for the female populations.

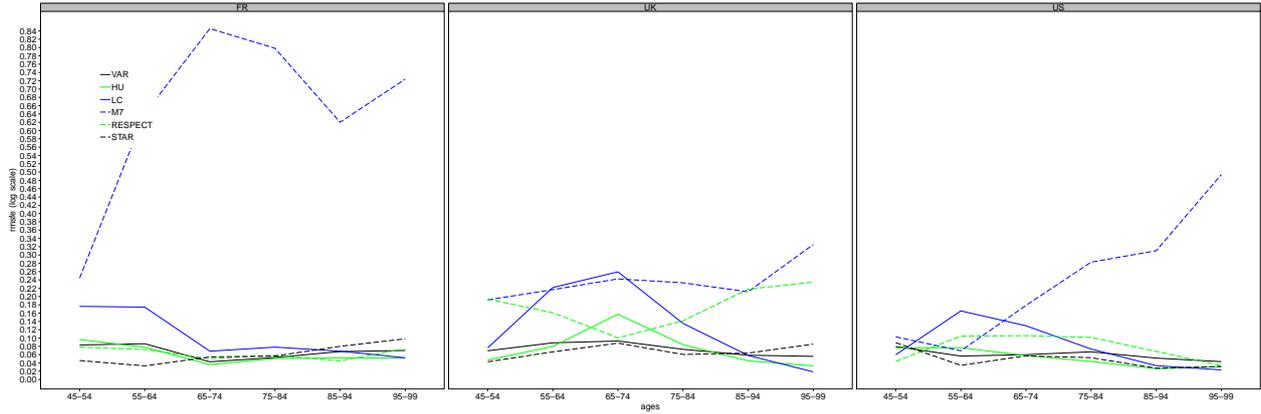


Figure 17: The RMSFE for England and Wales (UK), the United States (US) and France (FR) grouped by age for the female populations.

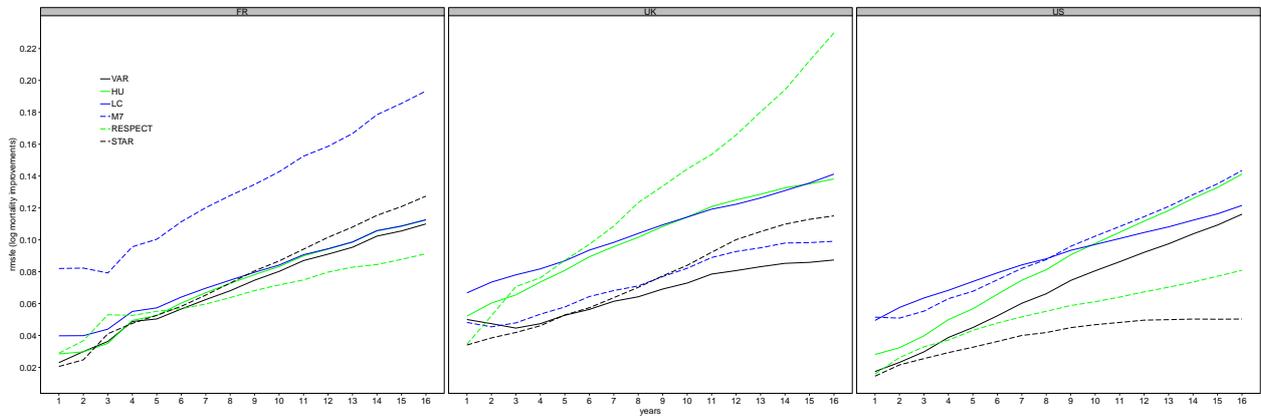


Figure 18: The RMSFE for England and Wales (UK), the United States (US) and France (FR) grouped by period for the male populations.

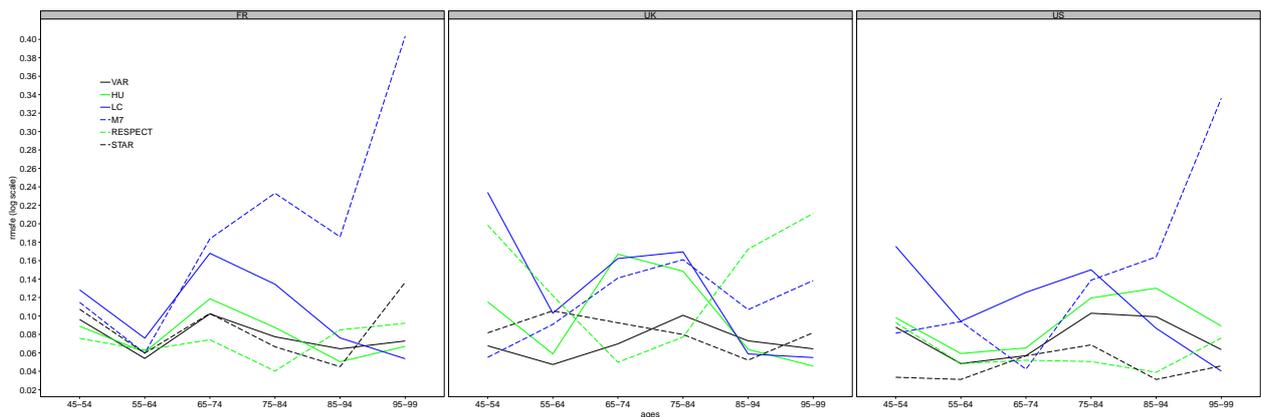


Figure 19: The RMSFE for England and Wales (UK), the United States (US) and France (FR) grouped by age for the male populations.