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Title of paper:

A Spatial Approach to Model Mortality Rates

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Conflicts of interest/Competing interests

We declare that we have no competing interests.

Availability of data and material

The data is available on Human Mortality Database (HMD)
https://www.mortality.org/

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Main text:

Abstract

Human longevity has been experiencing its largest increase since the end of World War II, and modeling the mortality rates is often the focus of many studies. Among all mortality models, the Lee–Carter model is a popular approach since it is easy to use and has good accuracy in predicting mortality rates. However, empirical studies from several countries have shown that the age parameters of the Lee–Carter model are not constant in time. Many modifications of the Lee–Carter model have been proposed to deal with this problem, including adding an extra cohort effect and adding another period effect. In this study, we propose a spatial modification of the Lee-Carter model and use simulation results to explain why the proposed approach can be used to deal with the problem of the age parameters.

Mortality rates are usually recorded by age and time, and thus we can treat mortality rates as 2-dimensional values and apply tools of spatial analysis to them. For example, clusters are areas with unusually high (or low) mortality rates than their neighbors and we use popular cluster detection methods, such as Spatial scan statistics, to evaluate where there are locations with mortality rates that cannot be described well by the Lee–Carter model. We first use computer simulation to demonstrate that the cluster effect is a possible source causing the problem of the age parameters not being constant and adding the cluster effect can solve the non-constant problem. We also apply the proposed approach to mortality data from Japan, France, the USA, and Taiwan. The empirical results show that our approach has better fitting results and smaller mean absolute percentage errors than the Lee–Carter model.

Keywords: Mortality Improvement, Lee–Carter Model, Spatial Statistics, Cluster Detection, Simulation

1. Introduction

Since the beginning of the 20th century, human mortality rates have been declining dramatically for all age groups and for both genders. The prolongation in life has become a common phenomenon in most countries. Many researchers think that the mortality rates will continue to fall in the future (Renshaw and Haberman, 2006; Tuljapurkar et al., 2000), and some even believe that the increment in life expectancy will continue to gain pace (Oeppen and Vaupel, 2002; Wilmoth and Robine, 2003). For instance, from the data of the Human Mortality Database[3] (HMD), the life expectancy of Japanese males was 84.58 in 2000—an increase of about 38% over the second half of the 20th century. Further, Tuljapurkar et al. (2000) showed that the life expectancy of G7 countries is likely to improve by about 8–12% for another 50 years.

Stochastic mortality models are a popular choice to deal with the increased longevity. Among all models, the Lee–Carter model (LC model; Lee and Carter, 1992) is a popular mortality model:

$$log(m_{xt}) = \alpha_x + \beta_x \kappa_t + \varepsilon_{xt}, \tag{1}$$

where m_{xt} is the central mortality rate, x is age, t is period (or time) and the error ε_{xt} is assumed to be normally distributed. The LC model can be treated as simultaneously fitting a group of linear regression equations and the logarithm of age-specific central mortality rates are the dependent variables, sharing same predictor (i.e., time). Each regression equation in the LC model has its own slope and intercept, and they do not change with time. The slope of the regression equation can be interpreted as the mortality improvement over time. The estimation of the LC model is easy to implement (Cairns et al., 2009), and the model has been proved to be accurate in estimation and prediction. For example, Yang et al. (2010) demonstrated that the LC model has very small mean absolute prediction errors on mortality rates of different countries.

There are several modifications to the LC model to improve the mortality estimation and prediction. Some of them focus on adding a third factor, in addition to the factors of age and time, while some attempted to modify the probability structure. For example, Renshaw and Haberman (2003) and Yang et al. (2010) extended the LC

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[3] The website of HMD is http://www.mortality.org/.

model into a two-component model. On the other hand, some scholars tried to add a cohort effect into the LC model (Renshaw and Haberman, 2006; Hyndman et al., 2006). Furthermore, Li and Chan (2005) used the time series model to incorporate possible outliers within the period. All these models have been shown to have improved the LC model to different degrees.

The residual analysis can also be applied to the LC model to improve the model performance, similar to those in regression analysis and time series analysis. The residuals of LC model have been studied before, and it is found that the residuals do not meet the assumption of independence (Hunt and Blake, 2014). Also, the residuals can be presented in two-dimensional space, with respect to age and time, and they are two-dimensionally dependent or spatially dependent (Debón et al., 2021). Although geostatistics techniques were proposed to deal with spatial dependence (Debón et al., 2008 & 2010), in general there is lack of discussion for dealing with the problem in residuals (Basellini et al., 2022).

We can use the mortality data of Japan to demonstrate the properties of LC model residuals. Figure 1 shows the residuals of Japanese mortality rates after fitting the LC model, and the red and blue areas indicate under-biased and over-biased estimates, respectively. There are red clusters (higher mortality rates than expected) in the upper-centered parts for both men and women. The cohort effects may also exist since there are red/blue diagonal stripes in the middle of graphs. It seems that both clusters and cohort effects can be included in the LC model. There are two possible modelling strategies to include the clusters and diagonal stripes. The first approach is by adding cohort component, such as the models proposed by Renshaw and Haberman model (RH) and Age-Period-Cohort (APC) model. These models add the cohort effect in different ways and it can exist alone or interact with age, analogous to the age-period interaction in original LC model. The impact of cohort effect had been discussed in previous studies (Cairns et al., 2011). Another modeling strategy is adding cluster effect to the specific ages and years. For example, the cluster effect can be easily observed in Figure 1 for both Japanese men and women, around years 1960–1985 and ages 60–84.

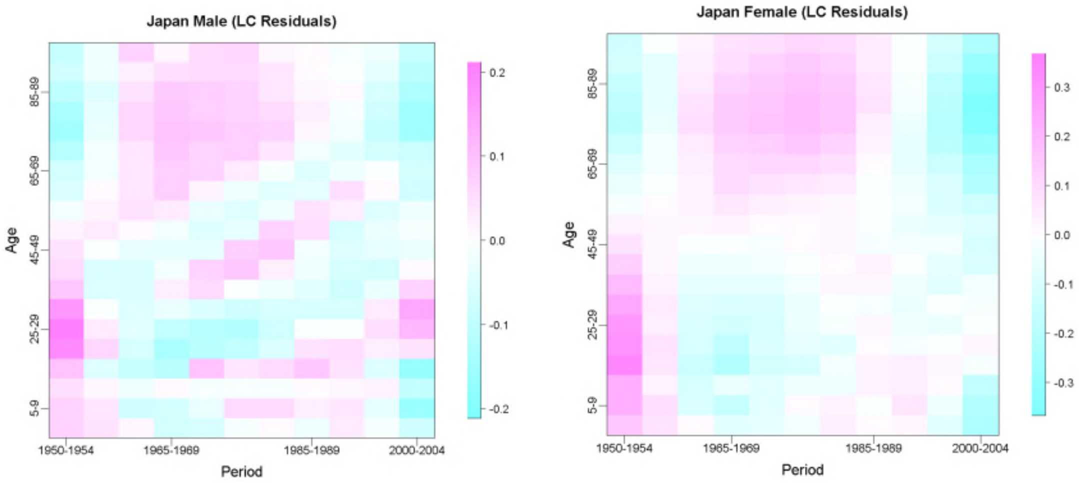


Figure 1. Residuals of LC model (Japan)

On the other hand, several recent studies have addressed unusual mortality events using the Extreme Value Theory (EVT) framework. For example, Gungah and Narsoo (2022) extended the Lee–Carter (LC) model by incorporating extreme mortality events through a Generalized Pareto distribution. Similarly, Chen et al. (2024) examined mortality shocks within a comparable context. These studies highlight that shocks such as wars, pandemics, and earthquakes require special attention in mortality modelling. It is worth noting that these EVT-based approaches are applied to the k_t component which represents time mortality intensity. In contrast, our study conceptualises LC residuals as a 2-dimensional surface over age and time, and applies spatial statistical methods to detect mortality anomalies. This represents a fundamentally different modelling approach.

In addition, several mortality studies have applied spatial statistical techniques. For instance, Cupido et al. (2020) employed spatial filtering on USA mortality data to discover systematic geographic variation. However, while these studies focus on spatial units defined by geographic regions, our analysis considers age–time coordinates as the spatial dimension. Hence, the analytical context is fundamentally different. To the best of our knowledge, this study is the first to integrate the Lee–Carter model with spatial statistical methods in the context of mortality anomaly modeling, more than a decade after the pioneering studies of Debón et al. (2008, 2010).

In this study, we propose a spatial modification to the LC model and apply spatial techniques to model mortality rates. In specific, the mortality data are recorded in the format of 2-dimension coordinate, i.e., by age and time. Like including the information of time ordering in time series analysis, the target observations and their neighborhood observations will all be considered in estimation of spatial analysis. The idea behind the spatial modification is based on the fact that often nearby observations share similar properties, and this is seemly to be true for mortality modeling since the mortality rates of similar ages and nearby years are likely to share common behaviors.

The rest of the paper is organized as follows. In section 2, we first review the methodology for dealing with the neighborhood observations in spatial analysis and show how to incorporate them into modifying the LC model; we follow these by describing the proposed approach. In section 3, we use a simulation study to evaluate the proposed approach. The empirical analysis is in section 4, where we compare the proposed approach with the LC model and the RH model. We comment and discuss the limitations of the proposed approach in the final section. Note that the goal of the proposed approach is to improve the estimates of parameters (α_x,β_x, and κ_t) for the LC model, by removing the spatial (such as cohort) effects. Forecasting the future spatial effects is not our focus, although it can be done similar to predicting the cohort effect.

2. Spatial Approach and Proposed Modification

As mentioned in the previous section, both the observations and their neighbors are considered in the estimation of spatial analysis. Here, the residuals of the LC model are expressed as a 2-dimensional coordinate, i.e., age and time, and they are expected to behave like white noise. However, the under-biased residuals of Japanese mortality rates in Figure 1 indicate that the residuals are spatially dependent and we can use spatial statistics, such as Moran's I (Moran, 1950; Cressie, 1993) and Getis-Ord G statistics (Getis and Ord, 1992), for verification. Moran's I can be treated as the correlation coefficient in spatial analysis and is used to check whether the observations in the study area are homogeneous. For example, the values of Moran's I are 0.50 (p-value < .001) and 0.71 (p-value < .001) for the cases of Japanese men and women, respectively. Table 1 reports the Moran's I statistics for the remaining countries. All countries exhibit relatively high values and statistically significant, indicating that the residuals are not spatially homogeneous. This suggests that the residuals of fitting the LC model are not random and further analysis is required to improve the model fitting.

Table 1. Moran's I for Residuals under LC Model

	Male	Female
Japan	0.50	0.71
USA	0.63	0.65
Taiwan	0.13	0.12
France	0.44	0.66
England & Wales	0.46	0.68
East Germany	0.33	0.23
West Germany	0.21	0.19

There are quite a lot of methods to deal with dependent residuals in the LC model. Adding clusters is one of possible spatial approaches, which is akin to adding an extra component of the first moment or the second moment into the LC model (Yang et al., 2010). Of course, including autocorrelation is another possible since it is difficult to distinguish whether the residual dependence is due to the first and/or second moment (Wang and Yue, 2013b). For the choice of second moment, Debón et al. (2008) applied the geostatistical technique to the residuals and they modified the covariance structure using distance-decay monotonic function. Note that adding the second moment basically does not change the mean value of mortality rates, which may not solve the problems discovered (i.e., $\alpha_x$and$\beta_x$are not constant of time) in the past studies.

Many studies found that there are trend shifts in mortality rates and this creates uncertainty for mortality prediction (Lee and Miller, 2001; Lunsdström and Qvist, 2004). Adding components (or variables) of the first moment to the LC model would improve the prediction (Renshaw and Haberman, 2006). However, it is not easy to decide which variables are more appropriate and the results tend to be data dependent. As we will show in next section, adding clusters (first moment) will distort the estimation of LC model, resulting in inaccurate predictions. Also, it should be aware that covariance of spatial regression is relied on neighborhood definition, and the model outputs can vary from different neighborhood settings. Furthermore, likelihood function for autocorrelation model is usually highly non-linear, causing the estimation procedure becomes a daunting task. Besides, the spatial weights matrices, derived from neighborhood matrices, needed to be meet some requirements in order to obtain valid solution. (Martellosio, 2011). It is worth noting that the assigned spatial weight to each neighbor is not likely equally distributed. Generally speaking, the correlation between periods is stronger than that of between age. Nevertheless, it is unclear that how the spatial weight should be chosen. From a practical point of view, modelling the autocorrelation is more complicated, compared with that of the original LC. Hence, first order moment modification enjoys its model simplicity and receives more attention.

In this study, we propose adding the first-moment component, that is, cluster(s), to capture the possible mean shifts in the LC model. The shape and size of clusters are not restricted. As shown in Figure 1, cluster can be extended over the age and/or period. We assume that these clusters are not caused by specific outliers but a systematic signal. For example, death toll by wars can cause notably hot spot over adult age groups in some particular periods. Note that the cohort effect can be treated as an elliptic (or oval) cluster of 45 degrees, and adding clusters might help improve the fitting of the cohort effect since, as pointed out in Wong et al. (2004), the cohort effect seems to occur only on some particular ages. On the other hand, many models assume that cohort effect can exist in every cohort, such as RH model and extended CBD model (Crains et al., 2009). Two different perspectives raise the question of whether cohort effect should be partially included or not. The cohort effect can be treated as a special case of cluster, but they show different meanings. Cohort effect is directly related to particular population, causing the effect homogenously spreads over the entire selected population. In contrast, judging from our experience, cluster shape tends to be oval or rectangular. We believe that both cohort and cluster effects can simultaneously exist in mortality dataset, and Crains et al. (2011) also emphasized the fact that cohort effects should never be bypassed. Thus, we consider both cohort and cluster effects in our proposed model.

Renshaw and Haberman (RH) model is an approach adding a cohort component to the LC model, as shown in equation (2):

$$log(m_{xt}) = \alpha_x + \beta_x^{(1)}\kappa_t + \beta_x^{(2)}\gamma_{t-x} + \varepsilon_{xt}, \quad (2)$$

where γ_{t-x} reflects the cohort-related effect, and the rest have same definition as in equation (1). The RH model can be treated as an extension of LC model and its cohort component usually can improve the parameter estimates of LC model and its residuals. Estimation of this model is generally solved by the maximum likelihood methods iteratively. Nevertheless, there are some demerits in the model. First of all, the huge increased number of cohort parameters can lead to over-parameterized and consequently defect the estimation procedure. Cairns et al. (2009) claims that the iterative procedure is very slow, probably due to identifiability problem and some of the outcomes of over-parameterized. Another problem is that the RH model might not fit well empirically since the detected cohort effects occur only on certain period. These drawbacks shed a light to our proposed models.

Here, unlike the RH model, we suggest adding a term to describe cohort effect, analogous to the extended CBD or APC model, and we ignore the possibility of age-cohort interaction, which would create the instability in estimation. For instance, according to pass studies (Crains et al., 2009), the iteration process of the RH model estimation is slow and there might occur identifiability problem. These drawbacks may be caused by flat likelihood function, however, according to Crains et al., the exact reason is still unclear. Currie (2016) reports the same issue substantially in his study by using several empirical data. Similar to these findings, it is worth noting that we also experience the same difficulties during fitting the parameters of RH model.

We refer to the proposed method as the spatial Lee-Carter (SLC) model and it can be written as

$$log(m_{xt}) = \alpha_x + \beta_x\kappa_t + \sum_{r=1}^{s} c_r d_{r,xt} + \gamma_{t-x} + \varepsilon_{xt}, \quad (3)$$

where γ_{t-x} is the cohort parameter corresponded to location(x,t), $d_{r,xt}$is a dummy variable, being 1 if the cluster r is at the location (x,t) and 0 otherwise, andc_r is the cluster parameter of cluster r (cluster effect). For example, consider a lattice in which three cells with coordinates {2,2}, {2,3} and {1,2} are assigned to cluster 1. In this case, $d_{1,\{2,2\}}$= $d_{1,\{2,3\}}$= $d_{1,\{1,2\}}$=1, and all other $d_{1,\{x,t\}} = 0$. Note that, in order to evaluate the influence of cluster detection method, we try two versions of SLC model: one is to detect the clusters using the SaTScan and the other is to assume that the location of the cluster is known, and the observations of the clustered areas are used to estimate the cluster effect in both versions.

The proposed method consists of two stages: (1) fitting the original LC model along with cohort parameters (2) applying the cluster detection methods to the residuals of previous step. The first stage is to acquire the residuals of the LC model: we omit the fitting procedure, since the LC model has been well studied. Basically, we suggest using the singular value decomposition (SVD) method if possible; otherwise, we suggest using the approximation method first, followed by the weighted least squares estimation (Wilmoth, 1993). For the second stage, there are quite a few methods for detecting clusters and we choose the most popular method to illustrate our approach: Spatial scan statistics (SaTScan; Kulldorff et al., 2009), which is recommended by the American Cancer Society.

The reason for choosing the SaTScan is its detection power and the computational tool available. SaTScan is popular and is shown to be powerful in detecting clusters. For example, Song and Kulldorff (2003) compared various detection methods and concluded that SaTScan is preferable if there are no prior knowledge about the size and scale of cluster. Also, the software of performing SaTScan is available in public. (http://www.satscan.org/) However, the SatScan tends to detect more clusters (or false clusters) and we suggest reexamine the clusters detected.

Scan statistics is a parametric test, comparing the suspicious area and the global region with a large set of scanning windows. It is based on maximum likelihood ratio test, as shown in equation (4):

$$\lambda = \frac{sup_{z \in Z, \theta_Z \neq \theta_{Z^c}} L(Z, \theta_Z, \theta_{Z^c})}{sup_{\theta_Z = \theta_{Z^c}} L(Z, \theta_Z, \theta_{Z^c})} = \frac{L(\hat{Z})}{L_0} \tag{4}$$

whereθ_Z and$\theta_{Z^c}$is the parameters inside and outside the suspicious region, respectively, $\hat{Z}$ is the region where maximizes the test statistics L, and L_0 is the likelihood function under spatial homogeneity. Note that the exact p-value of the likelihood ratio statistics is difficult to derive and usually is computed via Monte-Carlo procedure. The scan statistics can be performed with SaTScan, software created by Kulldorff et al.

(2009). Several well-known parametric models, such as Poisson and Normal distribution can be implemented into SaTScan software.

The SLC model can be iteratively derived by the following procedure:

Step 0. Let $log(m_{xt}) *= log(m_{xt})$. Note that$log(m_{xt})$is the logarithm of observed central mortality rate and$log(m_{xt}) *$represents the logarithm of updated central mortality rate during the iteration process.

Step 1. Apply SVD to $log(m_{xt}) *$, and obtain $\hat{\alpha}_x$, $\hat{\beta}_x$, and $\hat{\kappa}_t$, which is like the standard estimation procedure of the Lee-Carter model.

Step 2. Adjust $\hat{\kappa}_t$ in order to let D_t equal to estimated death counts $\widehat{D}_t$. That is, let a_t such that $D_t = \sum_x E_{xt}\, exp(\hat{\alpha}_x + \hat{\beta}_x \cdot a_t\hat{\kappa}_t)$ and thus $\hat{\kappa}_t^* = a_t\hat{\kappa}_t$, where E_{xt} is the exposure population. And finally let $\hat{k}_t$equal to the new$\hat{k}_t^*$.

Step 3. Estimate the cohort effect, using the residuals from Step 2. That is, $\hat{\gamma}_{t-x} = \frac{\sum_{x,t} r_{xt} I\{(x,t)\in t-x\}}{\sum_{x,t} I\{(x,t)\in t-x\}}$. The r_{xt}defined in this step is given by $r_{xt} = log(m_{xt}) * -\hat{\alpha}_x - \hat{\beta}_x\hat{\kappa}_t$. The indicator function indicates the cells that fall into cohort index $\{t\text{-}x\}$. In other words, the $\hat{\gamma}_{t-x}$ is the average residual values of the corresponded cohort $\{t\text{–}x\}$.

Step 4. Re-calculate the residuals from Step 3, as shown as below:

$r_{xt} = log(m_{xt}) * -\hat{\alpha}_x - \hat{\beta}_x\hat{\kappa}_t - \hat{\gamma}_{t-x}$. After that, compute the sample mean of each cluster area, using the residuals to get the estimate of the cluster effectc_r; that is, $\hat{c}_r = \sum_{x,t} r_{xt} d_{r,xt} / \sum_{x,t} d_{r,xt}$. Similar to step 3, the $\hat{c}_r$represents the average residual values of the corresponded cluster area index by$\{r\}$. For example, consider c_1, if the lattice cell {1, 3, 4} belong to cluster 1. Then, the average residuals value from these cells, obtained from step 3 are calculated as c_1.

Step 5. Update $log(m_{xt}) *$ with $log(m_{xt}) *= log(m_{xt}) - \hat{\gamma}_{t-x} - \sum_{r=1}^{s} \hat{c}_r d_{r,xt}$.

Step 6. Repeat Steps 1 to 5 until the change in the error sum of squares (SSE) for the residuals meets some stopping criterion. In this study, the stopping criterion is chosen as 0.001, or $\left|SSE_{i+1} - SSE_i\right| / SSE_i < 10^{-3}$, where SSE_i is the SSE for the i^{th} iteration.

The preceding iteration process usually converges rapidly. For instance, the estimation process is done in few seconds for the Japanese data. It is worth mentioned that this procedure is analogy to the algorithm in Yue et al. (2022) to deal with the selection effect. We will use computer simulation and empirical data to evaluate the proposed SLC for the next two sections. In the next section, assuming that there is a cluster, we want to know if the LC model would produce biased mortality estimates and whether the SLC model can correctly capture the cluster.

3. Simulation Study

In this section, we use computer simulation to evaluate the performance of the SLC model when there is a cluster. There are two parts in this section. First, we focus on the slope parameter β_x , from the LC models. The slope parameter β_x decides the mortality improvement rate of age x. The main objection is that to demonstrate slope distortion when the underlying true model has a cluster. Next, we will compare three models (LC, SLC and RH) with respect to to the unbiased property. The true model incorporates a cluster along with cohort. Also, two different cluster identifying method are compared in this part. One is known cluster location ($d_{1,xt}$ known), and another is unknown position ($d_{1,xt}$ to be estimated). Thus, for the latter, the cluster location is detected by SatScan, as mentioned in Section 2.

We assume that the true mortality rates satisfy the LC model but with a cluster, or satisfy the SLC model. The parameters of the SLC model mimic the age-specific mortality rates of Japanese females. Further, in order to reduce the computation time, the mortality data are in the format of five-age groups and five-year intervals. There are 21 age groups (ages 0,1–4, 5–9, …, 95–99) and 12 periods (1950–54, 1955–59, …, and 2005–09), which consist of 252 observations and can be treated as a 21 × 12 regular lattice surface.

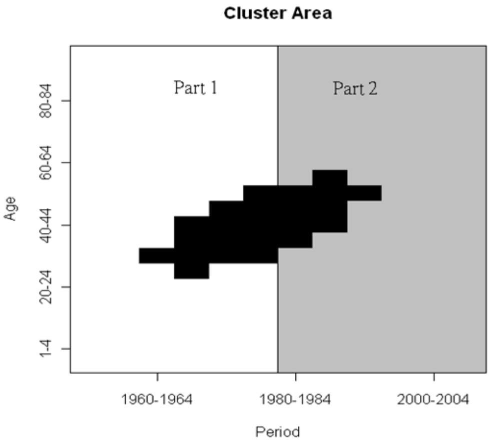


Figure 2. Cluster location in the simulation Study

To create a cluster effect, we add a mean shift at the center of the surface, as shown in Figure 2. The black ellipse corresponds to the cluster location. We let the mortality rates of the clustered area be 20% higher than the original rate under the LC model. In other words, the cluster effect is log(1.2) from equation (3); alternatively, we can say that the clustered area has a relative risk (RR) of 1.2. The term RR is often used in epidemiology to describe if there are areas with death/occurrence rates, which are higher or lower than the average value. For each simulation run, we assume that the death counts D_{xt} are generated from the Poisson assumption (Brouhns et al., 2002):

$$D_{xt} \sim Poi(E_{xt}\mu_{xt}),\ \mu_{xt} = exp\{\alpha_x + \beta_x\kappa_t + c_1 d_{1,xt}\},\ c_1 = log(1.2) \qquad (5)$$

where$E_{xt}$is the exposure population at location (*x,t*). After that, the central mortality rates m_{xt} isD_{xt} divided by E_{xt}. The μ_{xt} is 1.2 times of original mortality rate, That is, $\mu_{xt} = 1.2\, exp\{\alpha_x + \beta_x\kappa_t\}$implies $c_1 = log(1.2)$. All parameters are given from the LC or SLC estimated values for Japanese females. The computer simulation is repeated 1,000 times. Note that the parameter estimates of other countries can be used in the simulation study and the results are similar. Therefore, we use the Japanese female data as the illustrative example in the simulation study.

Slope distortion

Since there is a cluster at the center of the study region, we would expect biased estimates of age parameters for the LC model to occur at around ages 40–44. We divide the data into two periods (white and dark) to inspect the estimates of the parameters, as shown in Figure 2. We first check the estimates of the slope parameter β_x from the LC model. Figure 3 shows the true β_x value (dots) and its estimates (including confidence intervals calculated from 1,000 simulation runs) from the LC model. We divide the study period into two segments: period 1 (part 1), covering 1950 to 1979, and period 2 (part 2), covering 1980 to 2009. The black and red lines represent the fitted results of using only period 1 (part 1) and period 2 (part 2), respectively. Clearly, the estimates derived from the two periods produce opposite results: the fitting outcomes based on Period 1 tend to be overestimated, whereas those based on Period 2 tend to be underestimated. As expected, the LC estimates are particularly over-biased around the middle age groups, or ages 30–44, indicating the influence of the cluster. In fact, it is easy to understand this phenomenon with respect to regression analysis (since we can use a regression equation to interpret the LC model). For example, if there are positive outliers at the end of the study period (such as ages 40–44 at the first period), then the slope estimates will jump up due to the leverage effect.

Figure 3. β_x and its estimates via the SVD in two periods

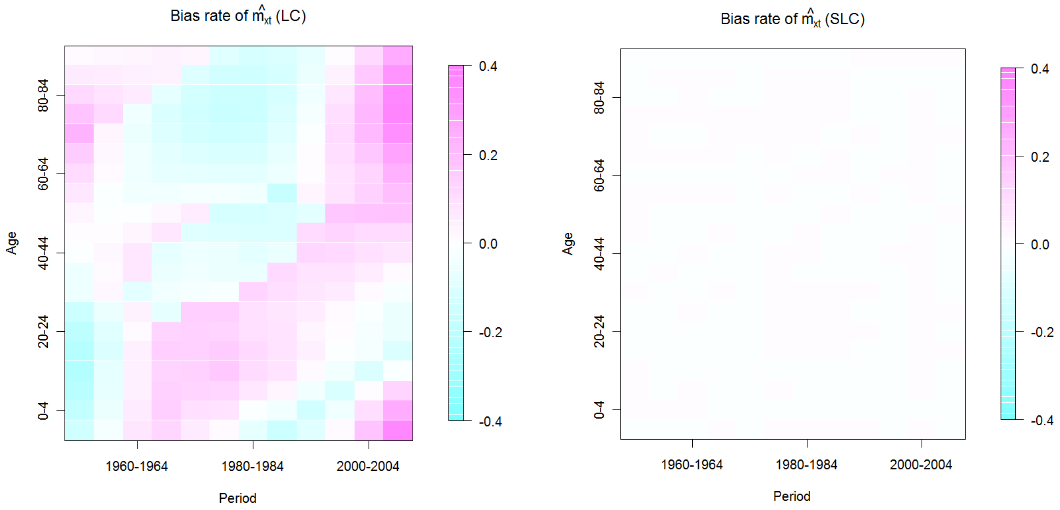
Bias of mortality rates

In this part, we will carry out the bias investigation to access our proposed estimation procedure is proper. Despite our estimation formula doesn’t have straightforward closed form, however, the concept is based on maximum likelihood approach. Therefore, under some mild condition, we expect the estimation will unbiased due to the consistency property of maximize likelihood estimator, given that the model is correctly specify. The comparison is based on the bias rate of the parameter estimate, which is defined as

$$Bias\ Rate = \frac{Ave.\hat{\theta} - \theta}{\theta}, \tag{6}$$

where θ and $\hat{\theta}$ are the parameter and its estimate, respectively.

Figure 4 shows the bias rate of mortality rate (i.e. $\hat{m}_{xt}$) when the cluster effect is log(1.2). The estimates from the SLC using the SaTScan (whether the cluster location is known or not) are better than those of the LC and RH models. As expected, the estimates from the SLC model with unknown cluster location are not as good as those with known location, but they are still much better than those of LC and RH models. The estimates of RH model produce smaller bias than those of LC model, but the cohort component cannot produce estimates similar to a cluster. Another possibility of producing larger bias in the RH model is that its iteration process does not always converge to the true MLE, according to Currie (2014).



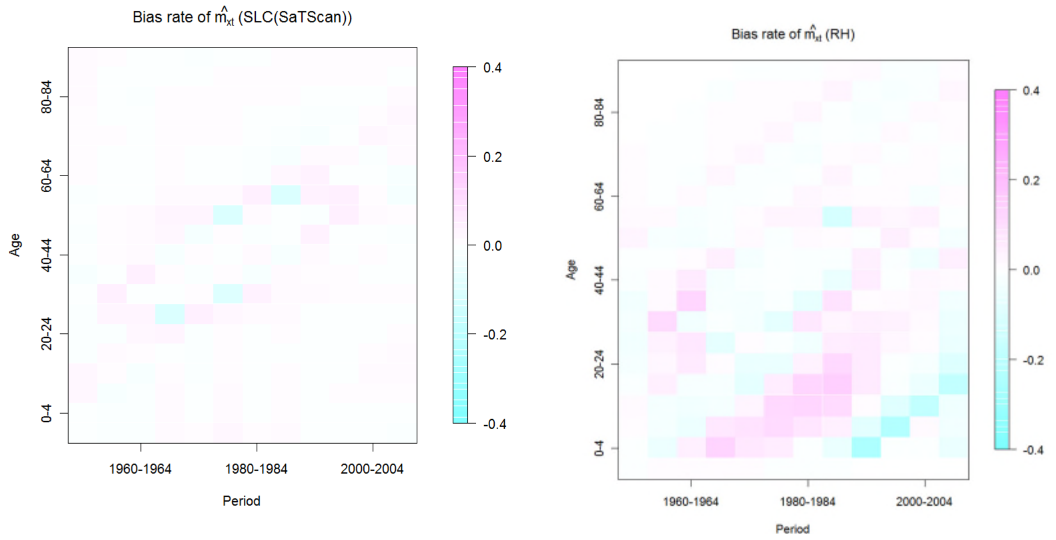


Figure 4. Bias rate of $\hat{m}_{xt}$ for the LC and SLC SaTScan models

Next, we check the estimates of the cluster effect of the SLC models. The differences between the true cluster effect c_1 and its estimate via the SLC model (assuming the location is known) are not large when we know the cluster location. The differences from the true parameter are mostly between -0.01 and 0.01 and they are about 3% of the cluster effect $\log(1.4) \cong 0.34$. It seems that, if we know cluster location, a simple average over all observations of the clustered area is very reliable. On the other hand, the differences from the true parameter via the SLC model (SaTScan) is under-biased, about 23% ($\cong 0.08/0.34$), and has a larger spread when we use SaTScan to detect the cluster. The bias might be due to that the SaTScan suffers from a higher false-positive rate (Wang and Yue, 2013a) and the false clusters are usually located at the edges or corners, which can also be verified in Appendix B. In practice, we can use the sizes of RR and the locations of the clusters to judge if we should include the suspected clusters. We further investigate the Moran's I statistics from SLC fitting. Among 1000 simulations, all of them shows that statistical non-significant, indicating that the spatial heterogeneity no longer exists.

4. Empirical Study

We now employ both mortality models to empirical data, checking the performance of prediction and residual analysis. The mortality data considered in study include seven countries, such as Japan, USA, England & Wales, and Germany.[4] Similar to the setting of the simulation study, the data are in the format of five-year age groups and five-year intervals. Table 2 shows the fitting and prediction periods for these countries. Furthermore, there are 21 age groups (age 0, 1–4, 5–9, …, 95–99) in the data. The fitting period varies by country. For example, the data for Japan span 1947 to 1999, covering a total of 11 periods. While most periods are five years in length, some are shorter due to limitations in the HMD database. Consistent with common mortality modeling practices, a few periods are reserved for evaluating prediction performance. Before showing the results of data analysis, we should first check if there is a need to implement the SLC model.

Table 2. Data description of empirical study

Country	Fitting Period		Prediction Period	
	Period	# of periods	Period	# of periods
Japan	1950-2004	14	2005-2019	3
USA	1935-2004	17	2005-2019	3
Taiwan	1970-2004	10	2005-2019	3
France	1900-2004	24	2005-2019	3
England & Wales	1900-2004	24	2005-2019	3
East Germany	1960-2004	12	2005-2019	3
West Germany	1960-2004	12	2005-2019	3

As in Section 2, we use Moran's I to check the homogeneity of residuals for fitting the LC model. Table 3 shows the values of Moran's I and all are significantly different

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[4] The data are obtained from 5x5 period data in the HMD database.

from zero (p-value < .001 for most cases), indicating that there is clustering or autocorrelation. The residuals from RH model also show the similar results in certain cases due to high Moran's I values, suggesting that cohort component might not capture all inherent signals within mortality rates. Also, in the empirical study, we use two criteria to evaluate the model fitting: MAPE and Bayesian information criterion (BIC). MAPE is defined as

$$MAPE = \frac{1}{n}\sum_{i=1}^{n}\frac{\left|m_{xt} - \hat{m}_{xt}\right|}{m_{xt}} \times 100\%, \tag{7}$$

where m_{xt} and $\hat{m}_{xt}$ are the observed and estimated mortality rates, respectively, and n denotes the sample size. On the other hand, we also include spatial homogeneity index such as Moran's I into our evaluation.

Another concept we would take into consideration is transparency reason, which was proposed by Cairns et al. (2009). The principle of model transparency is to avoid 'black box' outcome from any model. In order to gain better understanding from model, the output should be somewhat explainable in sense of plausible factors such as biological factors, medical advances and environmental changes. Although the judgement of this criterion is quite subjective, we can still focus on some features like model complexity and coefficient meaning to make an assessment. Often, simpler model such as less interaction terms or linear-structure yields better straightforward insight. Clearly, SLC is benefited from these merits. For example, a higher values for parameter c or γ indicates higher rates of mortality clusters/cohort, vice versa. We would further investigate SLC and see whether the cluster/cohort has substantial meaning. To sum up, a good model should have small prediction MAPE values, small Moran's I and good transparency.

Table 3. Moran's I for Residuals under Different Models

	Male			Female		
	LC	SLC	RH	LC	SLC	RH
Japan	0.50	0.15	-0.02*	0.71	0.04*	0.11

USA	0.63	0.32	0.38	0.65	0.35	0.45
Taiwan	0.13	-0.07*	-0.14*	0.12	-0.01*	-0.08*
France	0.44	0.22	0.36	0.66	0.29	0.32
England	0.46	0.44	0.47	0.68	0.42	0.33
East Germany	0.33	-0.01*	-0.01*	0.23	-0.02*	0.04*
West Germany	0.21	-0.07*	0.01*	0.19	0.08	0.20

Note: Numbers with * are not statistically significant

The cluster location, or $d_{r,xt}$, of the SLC model is decided by SaTScan, which has been shown to have high power in cluster detection though it was originally designed to detect ellipse-shaped clusters. Further, although SaTScan is for normally distributed data, we can use the Freeman–Tukey transformation (Cressie and Read, 1989) to transform the mortality data into normal data. For the estimation of the RH model, we apply '*StMoMo'* package in R software (Villegas et al., 2018). An important feature regard to the cohort estimation is that '*StMoMo'* package omits the estimation if the cohort sample sizes is below 5 or under (i.e., the upper left corner and lower right corner of residuals plot). It is likely instable estimation might be occurred if sample size is too small. We also follow this setting in our proposed cohort parameters. Furthermore, κ_t in all three models is specified as random walk with drift, which is also the default setting in '*StMoMo'* package. The prediction sample path of cohort parameter follows ARIMA(p,d,q) model, where values of (p, d, q) are equal to 0 or 1.

Table 4 summarizes the prediction performances. As shown in Table 3, the residuals of the LC model are not homogeneous and we subsequently discover that there are clusters over half of all countries. The SLC yields more accurate prediction with respect to the MAPE than other model in six out of fourteen datasets. Note that the SLC also has advantage in terms of the Bayes Information Criterion (not shown here), but it is not appropriate to compare since the SLC and RH models have different probability measures. Although the RH model shows better predictive performance in some datasets, it fails in certain cases, exhibiting substantial prediction errors. The lack of parameter constancy raises concerns about its generalizability. In contrast, the SLC model performs robust predictions across all datasets. Appendix A illustrates the detected clusters. We also compare the MAPE of each prediction year (Appendix B), and find that on average, the SLC estimation is quite stable over the years and exhibits some improvements over the LC model with respect to MAPE.

Table 4. Forecast MAPE of Various Models

	Male			Female		
	LC	SLC	RH	LC	SLC	RH
Japan	11.4%	14.6%	26.8%	18.0%	12.9%	9.5%
USA	12.9%	10.6%	11.5%	11.1%	9.4%	21.2%
Taiwan	14.1%	14.5%	81.4%*	11.2%	8.1%	542%*
France	48.4%	29.7%	16.6%	29.2%	16.0%	14.8%
England	52.6%	34.5%	23.1%	23.2%	20.7%	19.9%
East Germany	36.0%	32.2%	109.8%*	13.5%	13.0%	16500%*
West Germany	16.9%	13.0%	10.3%	9.6%	8.1%	9.2%

Note: Shaded numbers indicate the smallest prediction errors and * denotes bad estimation values.

We show the Moran's I statistics for the residuals in all models in Table 3 and the residuals from SLC model are often less deviate from spatial homogeneity assumption. Yet, although the SLC model greatly reduces the systematic spatial patterns, it is still not able to capture all the hidden patterns, suggesting that a further investigation of independent error assumption is needed. We found some interesting information from residuals plots and some clusters begin to emerge on the residuals plot, after fitting the data with age, period and cohort effects. We use the residual plots of England & Wales and France as a demonstration (Figure 5). The estimation of SLC model for both cases show very similar clusters during 1915-1919. We believe this is not a coincidence since there are two major events happened on that period – World War I and 1918 Flu Pandemic (or Spanish Flu), both causing a lot of deaths. In fact, although it is not shown here, we did find that Italy mortality data has the same pattern as these countries. For the East Germany data, there is a cluster appears during 1990-1994 (Appendix A) and we might think that this cluster is related to demolition of Berlin wall.

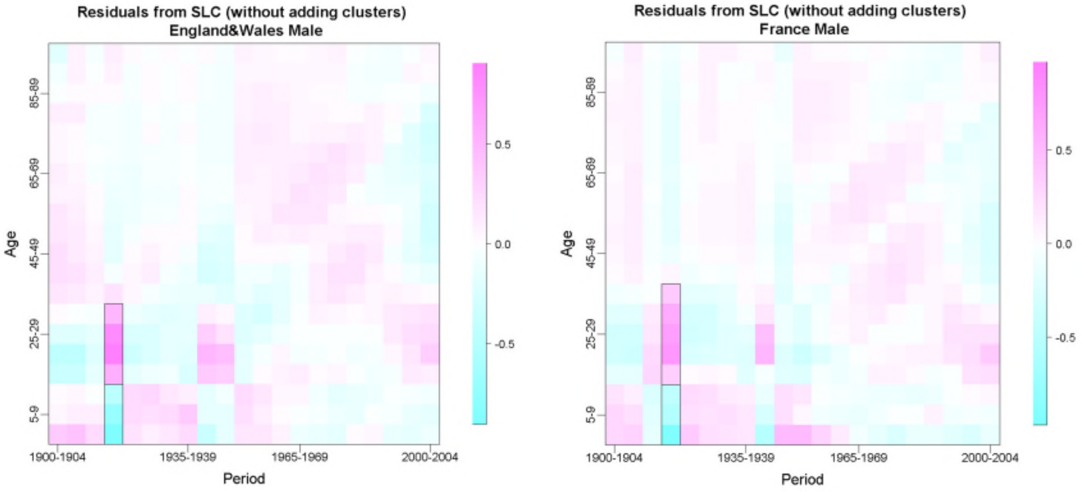


Figure 5. Residual of SLC plot (without clusters) from Western Europe countries.

Additionally, the cohort effect can be considered a special case of the cluster effect, where the effect occurs within a specific cohort. This effect is implicitly captured in the cohort parameter. In this sense, we also examine the cohort effect. Figure 6 illustrates the trend of cohort parameters from the SLC model. Note that the y-axis in Figure 6 represents the estimated cohort parameter. It seems that the estimated cohort effects of West Germany and East Germany are different from those of other countries and the death rates of West and East Germany are generally higher, especially for East Germany. This might be the consequences of World War I and World War II. However, the interpretation should be drawn with caution since our data is period-based. The cohorts, before the observation period (i.e. cohort that has not observed since age 0 throughout the lifetime) might results in bias estimation due to population selection.

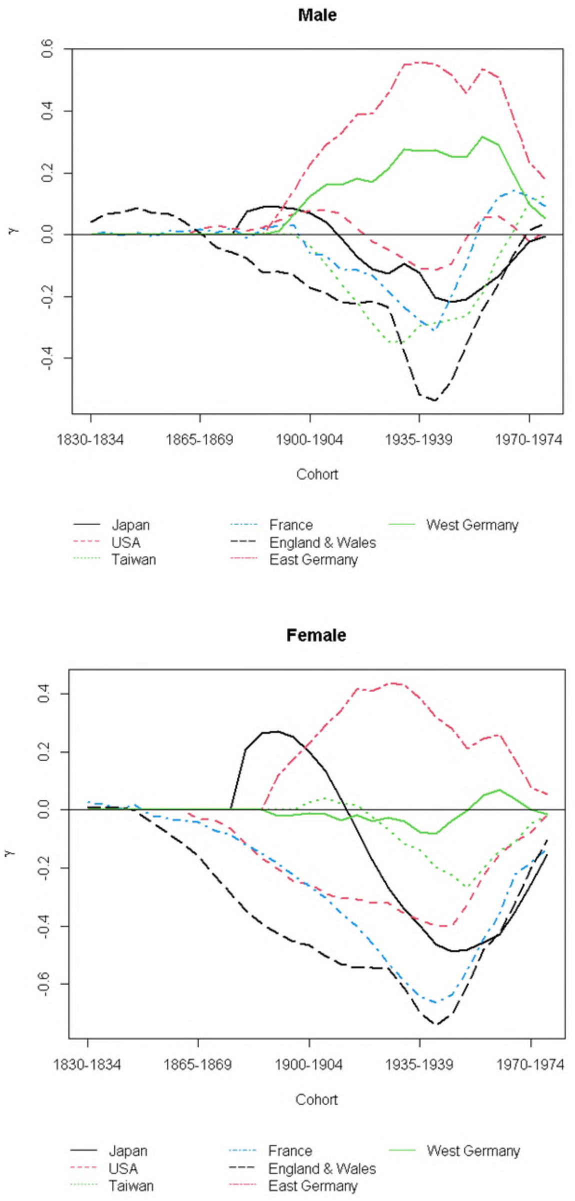
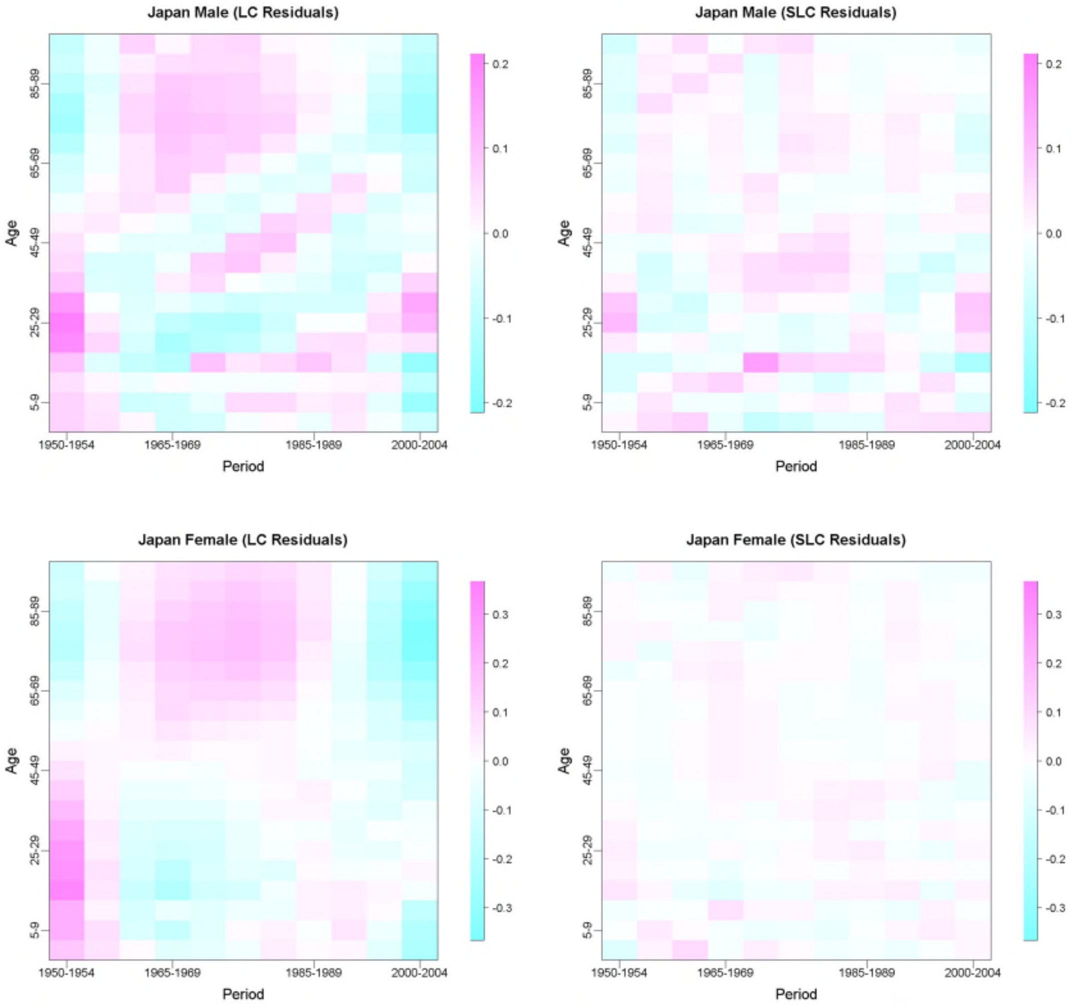


Figure 6. Cohort parameters from SLC model.

Finally, we examine the residuals obtained from the SLC model. As shown in Table 3, the spatial patterns are substantially reduced compared to the original LC model. Compared with the RH model, the average absolute Moran's I across all countries is 0.20 for the SLC model and 0.22 for the RH model (female), indicating a modest improvement in spatial homogeneity. Furthermore, Figure 6 presents a visual comparison of the residuals before and after fitting the SLC model. Several pronounced hot spots and cold spots have been eliminated, and the overall spatial variation in residuals has diminished. These findings suggest that the SLC model effectively captures both clustering and cohort-related components in mortality patterns.



Japan Male (LC Residuals)

Japan Male (SLC Residuals)

Japan Female (LC Residuals)

Japan Female (SLC Residuals)

Figure 7. Residuals of LC and SLC model (Japan)

5. Concluding Remarks and Discussions

Modelling mortality rates is a popular research topic and the LC model is a popular approach. It includes the age and time effects in the model and usually produces stable and reliable mortality predictions. However, it is shown, from past empirical studies, that there may exist possible cluster/cohort effects in mortality data, which causes the age parameters of the LC model to vary with time. Despite the many modifications proposed for the LC model, few confront this problem. In this paper, we propose a spatial modification, namely the SLC model, to deal with the problem of non-constant age parameter. In specific, we suggest adding cluster effect to the LC model, using an iterative process for parameter estimation to deal with the linear dependence of parameters. Both the computer simulation and empirical studies support the proposed model, and adding the cluster effect is a feasible modification to the LC model. The SLC model can be treated as a generalization of adding a cohort effect to the LC model (Renshaw and Haberman, 2006). Adding a cluster/cohort factor can help to solve the problem of the age parameters of the LC model not being time constant.

We found that adding a cluster effect in the SLC model not only yield improvements in model fitting but also help interpret the trends in mortality rates. Based on the detected clusters, epidemiologists and demographers can decide whether there are diseases or factors that influence the mortality rates, and this information can be used to explore if there are undiscovered risk factors or problems that should be taken considered. For example, as shown in Appendix A, Taiwan data have one cluster (in blue) for males and females and it is caused in the change of official records for reporting infant deaths in 1994. Stillbirth and miscarriage are treated as misfortune in the past and many Taiwan family chose to report newborns after the babies survive to certain age (e.g., reaching three months old). As a result, the infant mortality rates were under-reported before 1994.

The SLC model has a lot of room for further improvement although it produces smaller estimation errors than the original LC model. Currently, we use SaTScan to detect cluster effect and we can choose other cluster detection methods, for example, Local Getis-Ord statistics (Getis and Ord, 1992) and FlexScan (Tango et al., 2005). The reason for choosing SaTScan (Kulldorff et al., 2009) is its fine performance in cluster detection and availability (e.g., the SaTScan software can be downloaded for free). Nevertheless, although SaTScan is believed to have larger power in detecting clusters, it also suffers from detecting too many false clusters. Usually we can reexamine the clusters detected by the SaTScan and remove those clusters which are not highly significant (e.g., p-value larger than 0.01). In addition, SaTScan tends to detect circular clusters and has smaller power in detecting clusters of irregular shape (e.g., Y-shaped or intersections of two rivers, as shown in Wang and Yue, 2013a & 2013b).

The goal of the proposed method is to improve the parameters' estimates of LC model by removing clusters, and predicting future clusters is not the focus. Still, the prediction of future clusters is possible if the clusters behave like the cohort effect, and the mortality improvement is likely to continue for some birth cohorts. Another possibility for cluster prediction is to include expert opinions which can provide useful clues about the location of future clusters. For instance, a policy change of social medical insurance might have a noticeable impact on the elderly and their mortality rates. Nonetheless, the prediction of future clusters should be applied with care, similar to predicting the cohort effect in the RH model. According to Kevin et al. (2010), the estimation of cohort effect in the RH model is sometimes unstable, depending on the sample structure, and thus influences the forecast of cohort variables.

Further, it should be noted that the proposed method is quite flexible, and we can plug other models into the SLC model with a similar modification. For example, we can use a principal component analysis (PCA) approach to replace SVD in step 1 of the SLC model. Another issue to consider is about cluster heterogeneity, and the observations within a cluster are assumed to be homogenous in this study. However, based on the residuals plots of the empirical study (and past work on cluster detection), the relative risk seems to decrease from the center to the outer boundary of clusters. This suggests that the clusters can be anisotropic (in-homogenous) but this would require a further and thorough study.

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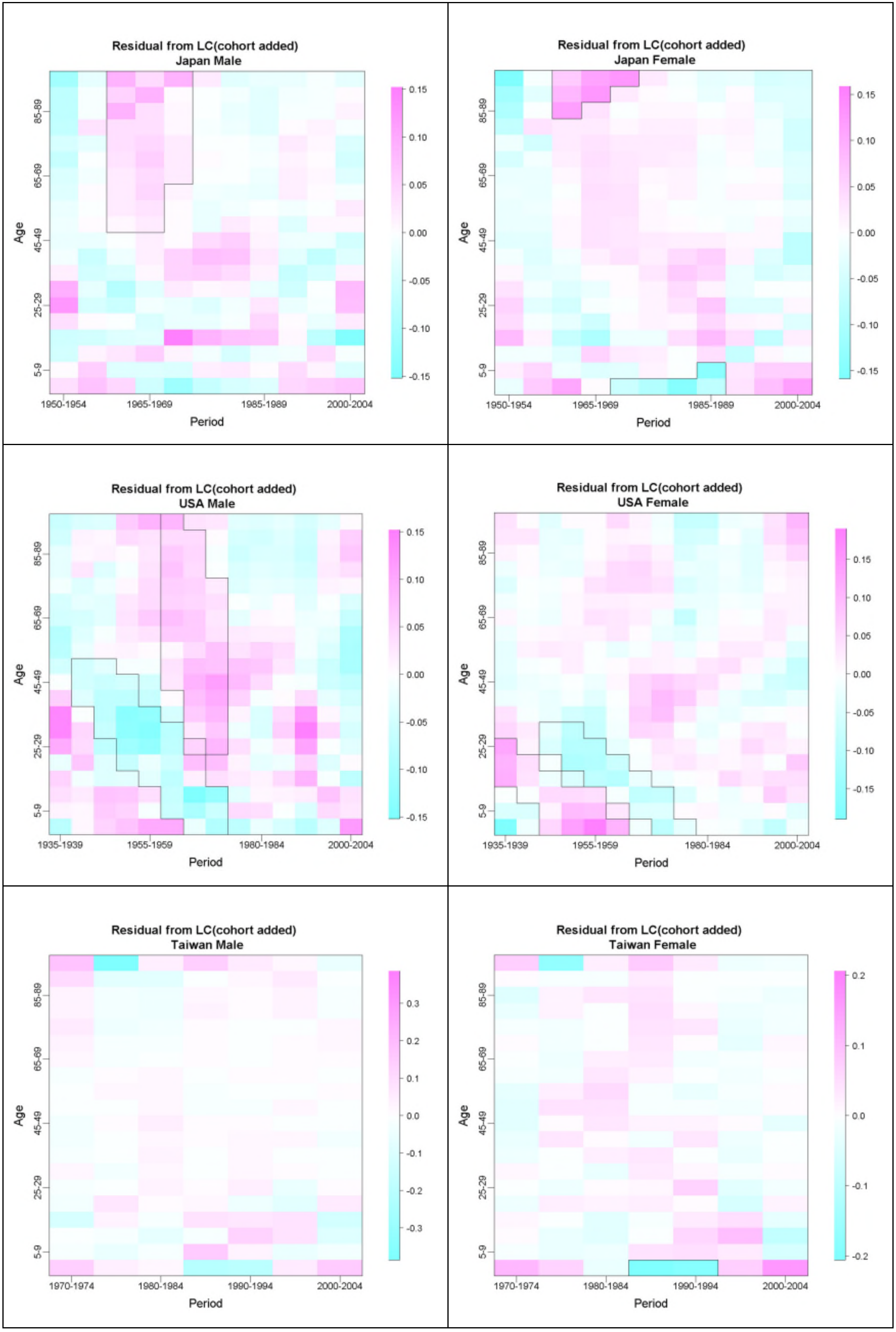
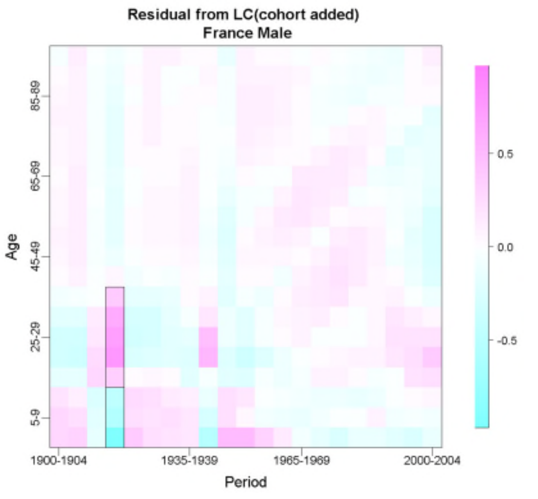
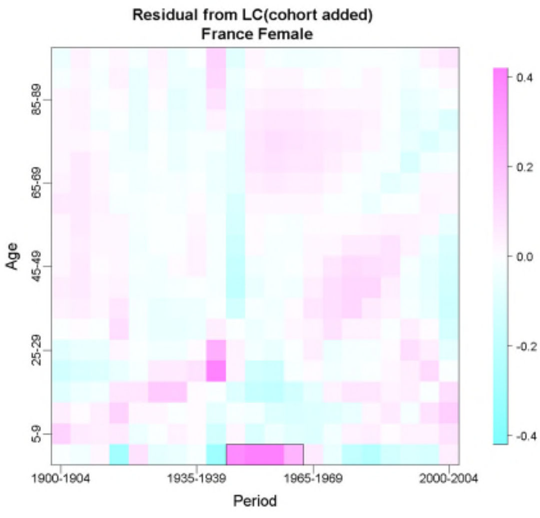
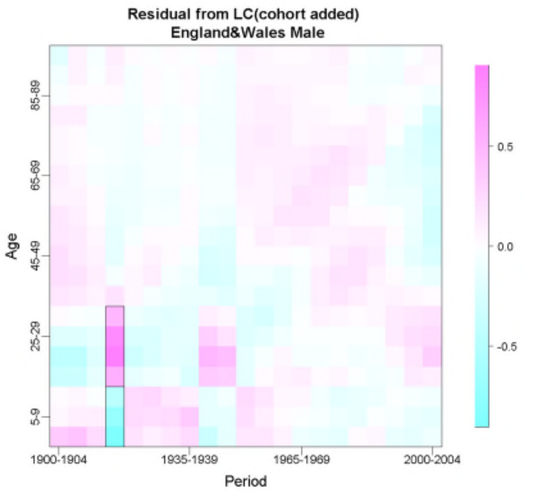
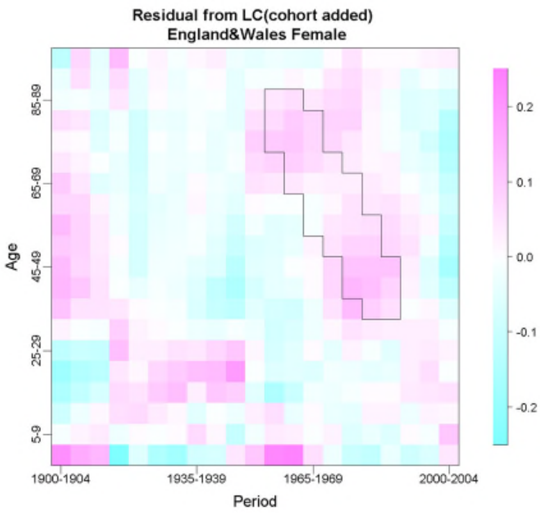
Appendix A. Graphs of residuals plot for each country




Residual from LC(cohort added)
France Male
Age
85-89
65-69
45-49
25-29
5-9
1900-1904
1935-1939
1965-1969
2000-2004
Period
0.5
0.0
-0.5


Residual from LC(cohort added)
France Female
Age
85-89
65-69
45-49
25-29
5-9
1900-1904
1935-1939
1965-1969
2000-2004
Period
0.4
0.2
0.0
-0.2
-0.4


Residual from LC(cohort added)
England&Wales Male
Age
85-89
65-69
45-49
25-29
5-9
1900-1904
1935-1939
1965-1969
2000-2004
Period
0.5
0.0
-0.5


Residual from LC(cohort added)
England&Wales Female
Age
85-89
65-69
45-49
25-29
5-9
1900-1904
1935-1939
1965-1969
2000-2004
Period
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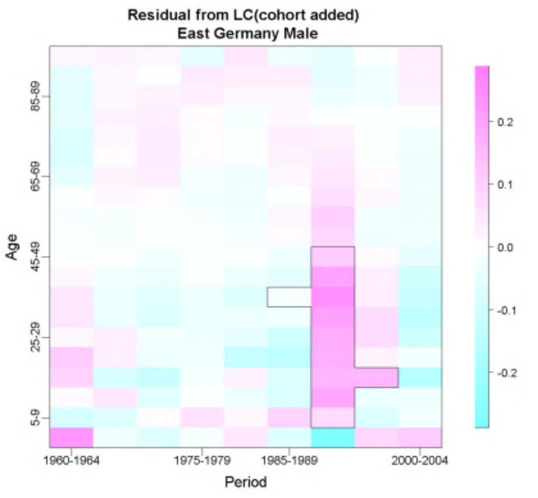
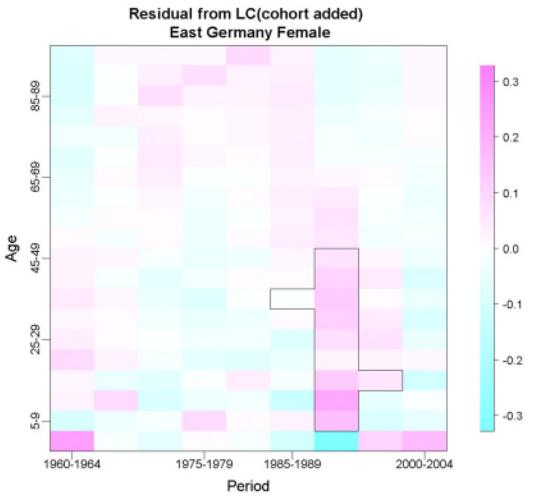
0.1
0.0
-0.1
-0.2


Residual from LC(cohort added)
East Germany Male
Age
85-89
65-69
45-49
25-29
5-9
1960-1964
1975-1979
1985-1989
2000-2004
Period
0.2
0.1
0.0
-0.1
-0.2


Residual from LC(cohort added)
East Germany Female
Age
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65-69
45-49
25-29
5-9
1960-1964
1975-1979
1985-1989
2000-2004
Period
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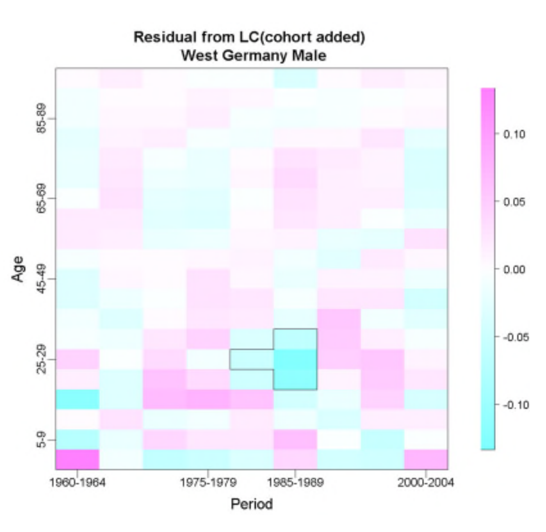
Residual from LC(cohort added)
West Germany Male
Age
85-89
65-69
45-49
25-29
5-9
Period
1960-1964
1975-1979
1985-1989
2000-2004
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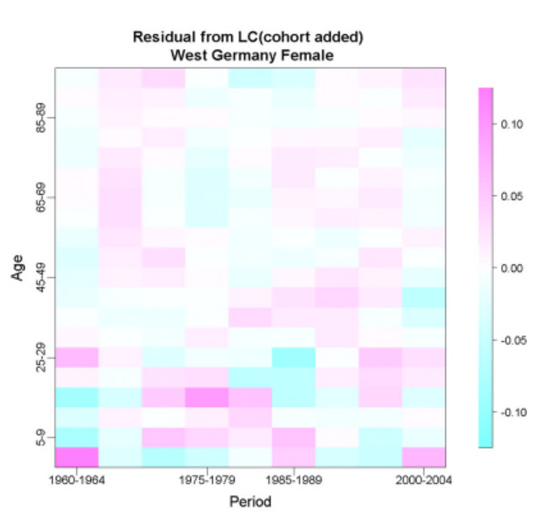
0.05
0.00
-0.05
-0.10


Residual from LC(cohort added)
West Germany Female
Age
85-89
65-69
45-49
25-29
5-9
Period
1960-1964
1975-1979
1985-1989
2000-2004
0.10
0.05
0.00
-0.05
-0.10

Appendix B. Prediction MAPE (proportion form) for various years

Country	Predicted Period	Male			Female		
		LC	SLC	RH	LC	SLC	RH
Japan	2005–2009	0.097	0.084	0.159	0.185	0.084	0.073
	2010–2014	0.117	0.157	0.288	0.177	0.13	0.105
	2015–2019	0.129	0.196	0.356	0.177	0.175	0.107
USA	2005–2009	0.098	0.077	0.058	0.079	0.064	0.099
	2010–2014	0.120	0.103	0.096	0.104	0.093	0.193
	2015–2019	0.169	0.138	0.190	0.151	0.126	0.344
Taiwan	2005–2009	0.101	0.094	0.089	0.088	0.064	0.201
	2010–2014	0.145	0.15	0.221	0.116	0.079	5.01**
	2015–2019	0.177	0.19	2.133**	0.132	0.101	11.07**
France	2005–2009	0.386	0.217	0.111	0.292	0.107	0.112
	2010–2014	0.498	0.307	0.163	0.307	0.169	0.158
	2015–2019	0.568	0.368	0.223	0.277	0.204	0.175
England & Wales	2005–2009	0.438	0.231	0.116	0.203	0.134	0.128
	2010–2014	0.563	0.376	0.285	0.258	0.236	0.214
	2015–2019	0.576	0.427	0.29	0.236	0.251	0.255
East Germany	2005–2009	0.277	0.23	0.295	0.112	0.074	0.448
	2010–2014	0.385	0.325	0.652	0.141	0.132	16.33**
	2015–2019	0.475	0.412	2.347**	0.153	0.184	479.77**
West Germany	2005–2009	0.132	0.095	0.077	0.075	0.058	0.062
	2010–2014	0.181	0.137	0.116	0.093	0.073	0.093
	2015–2019	0.194	0.158	0.116	0.122	0.112	0.122

Note: Shaded numbers have the smallest errors and ** indicates values failed to predict.