Robust Parameter Estimation for the Lee-Carter Model:
A Probabilistic Principal Component Approach

Yiping Guo *and Johnny Siu-Hang Li †

Department of Statistics and Actuarial Science, University of Waterloo

Abstract

As a traditional and widely-adopted mortality rate projection technique, by representing the log mortality rate as a simple bilinear form \( \log(m_{x,t}) = a_x + b_x k_t \). The Lee-Carter model has been extensively studied throughout the past 30 years, however, the performance of the model in the presence of outliers has been paid little attention, particularly for the parameter estimation of \( b_x \). In this paper, we propose a robust estimation method for Lee-Carter model by formulating it as a probabilistic principal component analysis (PPCA) with multivariate t-distributions, and an efficient expectation-maximization (EM) algorithm for implementation. The advantages of the method are threefold. It yields significantly more robust estimates of both \( b_x \) and \( k_t \), preserves the fundamental interpretation for \( b_x \) as the first principal component as in the traditional approach and is flexible to be integrated into other existing time series models for \( k_t \). The parameter uncertainties are examined by adopting a standard residual bootstrap. A simulation study based on Human Mortality Database shows superior performance of the proposed model compared to other conventional approaches.

Keywords: Lee-Carter model; Robust estimation; Multivariate t-distribution; EM algorithm.

1 Introduction

Understanding and modelling human mortality rates are crucial in actuarial science and demography study. Given the time series nature of the data, mortality rates are naturally studied by using stochastic mortality models. There exists numerous stochastic mortality models, in which the Lee-Carter model, first introduced by Lee and Carter (1992) to project

*Email: y246guo@uwaterloo.ca (Yiping Guo)
†Email: shli@uwaterloo.ca (Johnny Siu-Hang Li)
U.S. mortality rates, becomes the “leading statistical model of mortality forecasting in the demographic literature” (Deaton et al., 2007). Although it is proposed to specifically project U.S. mortality rates, now the method is being applied to all types of mortality data and serves as a golden standard in practice. The original Lee-Carter contains two main steps: parameter estimation and forecasting. The estimation step is based on singular value decomposition (SVD) to obtain the first principal component, and then a drifted random walk time series model is used for forecasting.

A variety of extensions to the Lee-Carter model have been proposed. For example, Renshaw and Haberman (2003) studies the feasibility of multiple principal components to extend the deterministic estimation step. Another major type of estimation techniques is under the framework of generalised linear models (GLM), which starts from the Poisson log-bilinear regression setup proposed by Brouhns et al. (2002). To resolve the potential overdispersion issue arisen in the Poisson GLM, Delwarde et al. (2007) proposed a negative GLM structure. A rather complete survey of the GLM framework of the Lee-Carter model can be found in Azman and Pathmanathan (2020). In contrast to the conventional Lee-Carter methods which separate the estimation and forecasting stages entirely, Pedroza (2006) formalizes the Lee-Carter model as a Bayesian model and the forecasting is directly studied through the predictive posterior distribution. Some more recent literature starts to study multiple populations, while traditional Lee-Carter only deals with a single population. Diao et al. (2021) proposed a completely data-driven deletion-substitution-addition (DSA) algorithm to borrow information from multiple populations to make mortality predictions for a single population. Furthermore, a neural network extension of the Lee-Carter model based on the paradigm of representation learning has been developed by Richman and Wüthrich (2021) for forecasting mortality rates for multiple populations simultaneously.

The essence of the Lee-Carter model is relying on the linear extrapolation of the time-varying mortality index \( k_t \), thus the estimation and forecasting quality might be dramatically affected by outliers. Outliers exist naturally in the context of mortality modelling, particularly the pandemics and wars, which result in unexpected movements of the mortality trend. The Lee-Carter model is formulated to capture the long-term mortality rates, thus in many cases one might not prefer to take the outlier effects into account. However, while a vast amount of extensions and improvements of the Lee-Carter method exist, its performance in the presence of outliers attracted little attention. Li and Chan (2005) employ a systematic outlier detection and re-estimation process to the U.K. and Scandinavian countries, which focuses on the time-series modelling for the mortality index \( k_t \). A follow-up study on the U.S. and Canadian mortality data is done by Li and Chan (2007). In addition, Wang et al. (2011) propose to replace the Gaussian innovations by several types of heavy-tailed errors in the Lee-Carter model to overcome the potential issue of outliers. Furthermore, Hunt and Villegas (2015) investigate the robustness and convergence of the Lee-Carter model rigorously and also demonstrate the existence of an unsolved identifiability issue. Among the existing literature concerning the outlier analysis of the Lee-Carter model, most of the focus is being put on the second stage: time series modelling for the mortality index \( k_t \), while keeping the first parameter estimation stage unchanged. However, the mortality index \( k_t \) used to fit the
time series model are directly obtained from the estimation stage, and the estimates of \(a_x\) and \(b_x\) are necessary when doing mortality forecasting, thus more attention should be paid on the robust parameter estimation in the first place.

This paper investigates the robust parameter estimation of the Lee-Carter model, by proposing a multivariate \(t\)-distribution based probabilistic principal component analysis (PPCA) model. The method is motivated by the fact that the traditional SVD approach used in the Lee-Carter estimation is equivalent to principal component analysis (PCA), where PCA it is well known for lacking robustness as the structure of sample variance matrix can be highly influenced by extreme values. PPCA is first proposed by [Tipping and Bishop (1999)], and it reformulates the conventional non-parametric PCA framework as a parametric Gaussian latent model, where the principal components can be exactly recovered by maximum likelihood estimation (MLE). Surprisingly, the PPCA formulation of the Lee-Carter model is highly similar to its state-space representation, and it naturally motivates to improve the robustness of the Lee-Carter estimation by robustifying the PPCA. The first robust PPCA model was proposed by [Archambeau et al. (2006)], by replacing the Gaussian structure by multivariate \(t\)-distributions. Recently, [Guo and Bondell (2021)] introduce a more general formulation of multivariate \(t\)-distribution based PPCA and the corresponding Monte-Carlo expectation-maximization (MCEM) algorithm.

To evaluate the performance of the proposed robust PPCA based Lee-Carter model, we design real data experiments and simulations based on the data from the Human Mortality Database (HMD). The proposed method is first applied to the U.S. mortality data in different time periods, and compared to the two traditional methods: SVD and Poisson GLM. The standard errors of the estimated parameters are obtained through a standard residual bootstrap procedure. Then we create hypothetical outliers by adding the U.S. Covid-19 death numbers to the U.S. mortality data from 1970 to 2019. This design simulates the situations that hypothetical pandemic occurring in the history. The experimental results show strong evidence that our estimation method perform significantly more robustly against outliers compared to the standard SVD and Poisson GLM approaches.

The rest of the paper is organized as follows. Section 2 provides a review of the Lee-Carter model, the standard PPCA and their interconnection. Section 3 introduces the main method in this paper, robust multivariate \(t\)-PPCA, with an efficient EM algorithm for implementation. Outlier detection is also briefly discussed. Section 4 presents both the real data illustration and simulation studies. The conclusion and further remarks are offered in Section 5.

2 Background

This section will be devoted to give a review of the Lee-Carter model ([Lee and Carter (1992)]) and the standard PPCA ([Tipping and Bishop (1999)]). The emphasize will be placed on the inherent connection between the Lee-Carter model, PCA and PPCA. It serves as the motivation of our proposed method, the robust multivariate \(t\)-PPCA, which will be introduced in Section 3.
2.1 The Lee-Carter Model

Use $y_{x,t} := \log(m_{x,t})$ to denote the log central mortality rate for age group $x$ ($x = 1, \ldots, p$) and at time $t$ ($t = 1, \ldots, n$), then Lee-Carter model describes $y_{x,t}$ as the following bilinear form:

$$y_{x,t} := \log(m_{x,t}) = a_x + b_x k_t + \varepsilon_{x,t}. \quad (1)$$

In the model, $a_x$ measures the average level of the log mortality rate over time for age group $x$ and the time index $k_t$ is a time-specific parameter which indicates the overall mortality level at time $t$ for the whole population of study. Strong empirical evidence suggests that the overall mortality rate is decreasing, thus $k_t$ normally follows a downwards trend. The age-specific parameter $b_x$ measures the sensitivity of $y_{x,t}$ with respect to the time index $k_t$, for example, a large $b_x$ implies that the log mortality rate for age $x$ declines relatively slowly in response to the decline of $k_t$. $\varepsilon_{x,t}$ is a zero-mean error term which is often assumed to be normally distributed. Two constraints $\sum_x b_x = 1$ and $\sum_t k_t = 0$ are usually imposed to avoid the identification issue.

Let $\hat{a}_x$, $\hat{b}_x$ and $\hat{k}_t$ be the estimates of the parameters $a_x$, $b_x$ and $k_t$. Lee and Carter (1992) seeks the least squares solution to (1), and it immediately implies $\hat{a}_x = y_{x,t} := \frac{1}{n} \sum_t y_{x,t}$. They proposed to estimate $b_x$ and $k_t$ by singular value decomposition (SVD) and the obtained solution can be interpreted as the first principal component of the log mortality rates. To gain more insights on this, we adopt the vector representations: $y_t = (y_{1,t}, \ldots, y_{p,t})^T$, $a = (a_1, \ldots, a_p)^T$, $b = (b_1, \ldots, b_p)^T$ and $\varepsilon_t = (\varepsilon_{1,t}, \ldots, \varepsilon_{p,t})^T$, thus in total it has $n$ observations with dimension $p$ and we can express (1) as:

$$y_t = a + b k_t + \varepsilon_t. \quad (2)$$

By such, we can interpret the original least squares optimization as minimizing the squared reconstruction errors:

$$\min_{a,b,k_t} \sum_{x,t} (y_{x,t} - (a_x + b_x k_t))^2 = \min_{a,b,k_t} \| (y_t - a) - b k_t \|^2_2. \quad (3)$$

The standard PCA theory (Bishop, 2006) gives one optimal solution: the shift $\hat{a} = \bar{y}$, the unit-length principal axis $\hat{b} = \bar{u}$ and the “principal score” (or coordinate) $\hat{k}_t = \bar{u}^T y_t$. Here, $\bar{u}$ is the first left-singular vector of the data matrix $Y := (y_1, \ldots, y_n)$ with $\| \bar{u} \|_2 = 1$ and $\| u \|_2$ denotes the Euclidean norm of $u$, $\| u \|_2 = \sqrt{|u_1|^2 + \cdots + |u_p|^2}$. After normalising the solution under the imposed constraint $\sum_x \hat{b}_x = 1$ (or equivalently $1^T \hat{b} = 1$), we obtain the desired SVD estimates for the Lee-Carter model (2):

$$\hat{b} = \frac{u}{1^T u}, \quad \hat{k}_t = (1^T u) \cdot u^T y_t. \quad (4)$$

For the time index $k_t$, much literature applies a second-stage re-estimation to match the actual death numbers $D_t$ at time $t$, i.e, for all $t = 1, \ldots, n$,

$$D_t = \sum_x D_{x,t} = \sum_x \left( N_{x,t} \cdot e^{\hat{a}_x + \hat{b}_x k_t} \right), \quad (5)$$
where $D_{x,t}$ and $N_{x,t}$ denotes the total number of death and the exposure of risk for age group $x$ at time $t$ respectively. The equations can be solved numerically, for example, by an one-dimensional direct search over a range. As it has been extensively studied, the standard PCA is highly fragile when outliers exist (Huber, 2004), and even an extreme single point can dramatically worsen the quality of the low-dimensional approximation. Therefore, it is expected that the Lee-Carter estimates by SVD also lack robustness in the presence of outliers, and this will be illustrated in our numerical analysis.

As the death numbers are counting random variables, another well-known type of estimating method for the Lee-Carter model is the Poisson bilinear GLM framework:

$$D_{x,t} \sim \text{Poisson}(N_{x,t}m_{x,t}), \text{ with } \log(m_{x,t}) = a_x + b_xk_t. \quad (6)$$

This approach is likelihood-based, thus the parameter estimation is done through MLE, in particular, finding $a_x, b_x, k_t$ to minimize the following log-likelihood function:

$$\ell(a, b, k) = \sum_{x,t} \left( D_{x,t}(a_x + b_xk_t) - N_{x,t}e^{a_x+b_xk_t} \right) + \text{const.} \quad (7)$$

Due to the bilinear term “$b_xk_t$”, (7) cannot be solved using the standard Poisson regression methods. Instead, the estimation is facilitated by adopting a modified iteratively reweighted least square (IRLS), which is first proposed by Goodman (1979). Notice that since the death numbers have been incorporated into (7), there is no need to apply a second-stage re-estimation for $k_t$. Similar to the SVD, the MLE of the Poisson GLM is also sensitive to outliers, as pointed out in Künsch et al. (1989) and Morgenthaler (1992) for instance. Further numerical illustrations will be provided in Section 4.

Once the estimates of $k_t$ are obtained (by either SVD, GLM or other methods), a drifted random walk time series model is suggested by Lee and Carter (1992) to model and forecast:

$$k_t = k_{t-1} + \theta + e_t, \quad (8)$$

where the innovation term is usually assumed to be normally distributed $e_t \sim \mathcal{N}(0, \tau^2)$. This paper focuses only on the estimation step rather than the forecasting.

### 2.2 Standard PPCA and Connections to the Lee-Carter Model

Probabilistic principal component analysis (PPCA), proposed by Tipping and Bishop (1999), is a Gaussian latent model reformulation of the standard non-likelihood based PCA. Firstly, a $d$-dimensional latent variable $z$ is generated from an isotropic Gaussian distribution with zero mean and unit variance for each component:

$$z \sim \mathcal{N}_d(0, I). \quad (9)$$

Then, conditioning on the “latent score” $z$, a $p$-dimensional “data vector” $y$ ($p \geq d$) is generated from another isotropic Gaussian distribution:

$$y|z \sim \mathcal{N}_p(Wz + \mu, \sigma^2 I). \quad (10)$$
Notice that in (9) and (10), only the data vector $y$ is observed, then marginalizing out the unobserved latent variable $z$ immediately implies the marginal distribution:

$$y \sim \mathcal{N}_p(\mu, WW^T + \sigma^2 I).$$

(11)

The MLE of the mean vector can easily be shown to be $\hat{\mu} = \bar{y}$, the sample average of the $d$-dimensional observations. Denote the sample covariance matrix by $S = \sum_n (y_n - \bar{y})(y_n - \bar{y})^T/N$, where $N$ is the sample size and use $S = U\Lambda U^T$ to represent the corresponding eigendecomposition. Also denote the $i$-th largest eigenvalue and the corresponding eigenvector by $\lambda_i$ and $u_i$ respectively. Tipping and Bishop (1999) showed that the MLE of $W$ and $\sigma^2$ equals to

$$\hat{W} = U_d (\Lambda_d - \sigma^2 I_d)^{1/2} R, \quad \hat{\sigma}^2 = \frac{1}{p-d} \sum_{i=d+1}^{p} \lambda_i,$$

(12)

where $U_d$ contains the first $d$ eigenvectors, $\Lambda_d$ is a $d$-dimensional diagonal matrix with the first $d$ eigenvalues $\lambda_1, \cdots, \lambda_d$ of $S$, and $R$ is an arbitrary orthogonal matrix. Therefore, up to a rotation $R$ and a scaling $(\Lambda_d - \sigma^2 I_d)^{1/2}$, the MLE $\hat{W}$ spans the same subspace as $U_d$, which represents the subspace of the first $d$ principal axes of the observed data $y$. This demonstrates the equivalence between the standard PCA and PPCA, where the first one relies on a nonparametric matrix decomposition but the later one utilizes a latent variable-based probabilistic structure.

Since the SVD method for the Lee-Carter model is equivalent to finding the first principal component of the observed log mortality rates $y_t$ (or log($m_t$)), we can rewrite it as a special case of the PPCA by setting $d = 1$ and denoting $b =: W$, $a =: \mu$ and $k_t =: z_t$:

$$y_t|k_t \overset{iid}{\sim} \mathcal{N}(a + bk_t, \sigma^2 I), \quad k_t \overset{iid}{\sim} \mathcal{N}(0, 1).$$

(13)

or equivalently,

$$y_t \overset{iid}{\sim} \mathcal{N}(a, bb^T + \sigma^2 I).$$

(14)

Denote the MLE of $a$, $b$ and $\sigma^2$ by $\hat{a}$, $\hat{b}$ and $\hat{\sigma}^2$. Letting $d = 1$ immediately implies that

$$\hat{a} = \bar{y}, \quad \hat{b} = u_1 \sqrt{\lambda_1 - \hat{\sigma}^2}, \quad \hat{\sigma}^2 = \frac{1}{p-1} \sum_{i=2}^{p} \lambda_i.$$

(15)

The MLE of $a$ equals to the sample mean $y$ regardless of the choice of $d$, and the MLE of $b$ is equivalent to the first left-singular vector of $Y$ up to scaling. This further reinforces that the MLE of $a$ and $b$ in the PPCA model (14) are equivalent to the SVD estimates of the Lee-Carter model, in which the equivalence between $b$ is up to scaling. The analytical expressions in (15) do not just provide an alternative interpretation to the traditional SVD-based Lee-Carter model, but also serve as good initial values of the numerical optimization in other modified models, as we will point out in Section 3.2.

In the PPCA representation (13), $k_t$ is treated as a latent variable instead of a parameter to be estimated in (2). Once the MLE of $a$ and $b$ are obtained, the estimates of $k_t$ can
be found by the death number matching as in (5), and are fitted using any chosen time series forecasting model such as (8). Notice that the MLE $\hat{b}$ obtained from the PPCA is unnormalised, so one should standardize it by the usually imposed constraint $1^T b = 1$.

There are two motivations to consider the PPCA for the Lee-Carter parameter estimation. First, the PPCA provides exactly the same solution as the SVD method (the standard PCA), but the likelihood-based nature allows for a much more flexible probabilistic formulation. Second, it has the similar probabilistic structure as the state-space representation of the Lee-Carter model, as proposed by Pedroza (2002) and Pedroza (2006):

$$y_t | k_t \overset{iid}{\sim} \mathcal{N}(a + bk_t, \sigma^2 I), \quad k_t | k_{t-1} \overset{iid}{\sim} \mathcal{N}(k_{t-1} + \theta, \tau^2).$$

(16)

Although having rather similar structures, it is worth noticing that the PPCA and the state-space model have fundamental differences. Firstly, the PPCA framework is only applied for estimating $a$ and $b$, but the state-space is an one-in-all model that frames the two stages of estimation and forecasting simultaneously. Secondly, in the state equation in the state-space model (left in (16)), the time indexes $k_t$ are assumed to be dependent as it is equivalent to the drifted random walk time series model (8). However, the latent variable distribution (13) in the PPCA assumes $k_t$ to be independent and identically distributed (i.i.d.), and it does not involve any parameters like $\theta$ and $\tau^2$ in (16).

Understanding what role that the i.i.d. assumption in (13) plays is crucial. It is without any doubt that $k_t$ are not i.i.d. by their time series nature, however, we assume i.i.d. in (13) simply for recovering the first principal axis $b$, rather than estimating and forecasting the time index $k_t$.

3 Robust Multivariate $t$-PPCA Lee-Carter Estimation

3.1 Model Formulation

Same as the conventional PCA, PPCA is also highly sensitive to outliers. When atypical mortality data points exist, for instance due to wars or pandemic, the estimated Lee-Carter parameters $b$ might deviate dramatically. As a result, the succeeding time series modelling and forecasting step for $k_t$ will be affected as well, as $k_t$ are obtained by the death number matching, which directly relies on the estimated value of $a$ and $b$.

As shown in and Archambeau et al. (2006) and Guo and Bondell (2021), one computationally efficient approach to robustify the PPCA is to change the marginal Gaussian distribution (11) to the multivariate $t$-distribution. In particular under the Lee-Carter context, we modify (14) to:

$$y_t \overset{iid}{\sim} t_\nu(a, bb^T + \sigma^2 I),$$

(17)

where $\nu$ is the degrees of freedom. Then, solving the MLE (with normalisation $1^T b = 1$) of (17) gives us the robust parameter estimate of $a$ and $b$ in the Lee-Carter model.

The multivariate $t$-distributions are widely used in a large variety of robust statistical modelling problems. In particular, the maximum likelihood estimates of a probabilistic
model involving $t$-distributions often present stronger robustness against extreme observations (Lange et al., 1989). For the multivariate $t$-PPCA models, the performance against outliers have been studied through both theory and numerical studies, see Archambeau et al. (2006); Chen et al. (2009); Guo and Bondell (2021).

The idea of using the robust multivariate $t$-PPCA in the Lee-Carter model is in fact quite simple, as we will summarize now. The Gaussian PPCA formulation of the Lee-Carter model (15) provides the exactly same estimates of $a$ and $b$ as the SVD method (or essentially PCA), but the results are fragile to outliers. Thus, adopting the robust multivariate $t$-PPCA formulation (17) allows the model to handle outliers in a natural way. Once the MLE of $a$ and $b$ are obtained, then $k_t$ can be calculated by the usual procedure (5) and the time series modelling and forecasting follows.

### 3.2 The Expectation-Maximization (EM) Algorithm

To find the MLE of $a$ and $b$, we write down the probability density function of (17) (Kibria and Joarder, 2006):

$$f(y) = \frac{\Gamma[(\nu + p)/2]}{\Gamma(\nu/2)\nu^{p/2}\pi^{p/2}\left|\Sigma\right|^{1/2}} \left[1 + \frac{1}{\nu}(y - a)^T\Sigma^{-1}(y - a)\right]^{-\frac{(\nu + p)/2}{2}}, \quad (18)$$

where the scale matrix $\Sigma = bb^T + \sigma^2 I$ and $\Gamma(\cdot)$ denotes the gamma function. We can easily see that this density function decays at a polynomial rate, which indicates that $t$-distributions have heavier tails than normal distributions since normal densities decay exponentially.

Directly solving the MLE from (18) is impractical, thus a common strategy to solve the MLE involving multivariate $t$-distributions is to adopt their scale mixture Gaussian representations (Liu and Rubin, 1995) and then apply the EM algorithm, in which in each iteration the computation is more tractable. The key step is to represent a multivariate $t$-distribution $t_\nu(\mu, \Sigma)$ as a continuous mixture of Gaussians, with a Gamma weight distribution. Formally,

$$y \sim t_\nu(\mu, \Sigma) \iff y|u \sim N\left(\mu, \Sigma_u\right), \quad u \sim Ga\left(\frac{\nu}{2}, \frac{\nu}{2}\right). \quad (19)$$

Specifically for our proposed robust multivariate $t$-PPCA Lee-Carter model (17), we have the following equivalent hierarchical structure:

$$y \sim t_\nu(a, bb^T + \sigma^2 I) \iff \begin{cases} y|k, u \sim N\left(a + bk, \frac{\sigma^2 I}{u}\right), \\ k|u \sim N\left(0, \frac{1}{u}\right), \\ u \sim Ga\left(\frac{\nu}{2}, \frac{\nu}{2}\right). \end{cases} \quad (20)$$

To see why this equivalence holds, first we notice that the conditional distribution $p(y|u)$ is also a normal distribution since normal prior for the mean parameter conjugates to a normal
likelihood:

\[ p(y|u) = \int p(y|k, u)p(k|u)dk = \int \mathcal{N}(a + bk, \sigma^2I) \cdot \mathcal{N}(0, \frac{1}{u}) \, dk \sim \mathcal{N}(a, \frac{bb^T + \sigma^2I}{u}) \]  \hspace{1cm} (21)

Then, by the Gaussian scale mixture expression of multivariate t-distributions (19), we show that the data vector \( y \) is multivariate t-distributed, which elaborates (20):

\[ p(y) = \int p(y|u)p(u)du = \int \mathcal{N}(a, \frac{bb^T + \sigma^2I}{u}) \cdot \text{Ga}\left(\frac{\nu}{2}, \frac{\nu}{2}\right) \, du \sim t_{\nu}(a, bb^T + \sigma^2I) \]  \hspace{1cm} (22)

It is worth noticing that in much literature about the robust PPCA, there exists a misrepresentation for the hierarchical structure, for example, Archambeau et al. (2006, 2008); Chen et al. (2009). A more detailed discussion regarding to the hierarchical representation can be found in Guo and Bondell (2021).

The EM algorithm was first introduced by Dempster et al. (1977), and has become a powerful iterative optimization technique to find the MLE involving missing data or latent variables. A general introduction of the EM algorithm can be found in many standard textbooks on machine learning, such as Friedman et al. (2001) and Bishop (2006). Instead of maximizing the original log-likelihood function derived from (18), the EM algorithm considers the complete log-likelihood which comprises the observation vector \( y \) and latent variables \( k \) and \( u \):

\[ L_c = \sum_{t=1}^{n} \log[p(y_t, k_t, u_t)] = \sum_{t=1}^{n} \log[p(y_t|k_t, u_t)p(k_t|u_t)p(u_t)]. \]  \hspace{1cm} (23)

In the E-step, we need to find the conditional expectation of the complete log-likelihood \( \langle L_c \rangle \) conditioning on the observed data \( y_t \)'s. Substituting the expressions for \( p(y_t|k_t, u_t) \), \( p(k_t|u_t) \), and \( p(u_t) \) into (23), we obtain:

\[ \langle L_c \rangle = -\sum_{t=1}^{n} \left[ \frac{p}{2} \log \sigma^2 + \frac{\langle u_t \rangle}{2\sigma^2} (y_t - a)^T(y_t - a) - 2\langle u_t k_t \rangle^T b^T (y_t - a) \right] \\
+ \frac{1}{2\sigma^2} \text{tr}(b^T b \langle u_t k_t^2 \rangle) - \frac{\nu}{2} \left( \log \frac{\nu}{2} + \langle \log u_t \rangle - \langle u_t \rangle \right) + \log \Gamma \left(\frac{\nu}{2}\right) + \text{const.}, \]  \hspace{1cm} (24)

where \( \langle \cdot \rangle = \mathbb{E}[\cdot|y] \) denotes the conditional expectation operator. It turns out that all the posterior expectations in (24) have analytical forms, which makes the E-step highly efficient:

\[ \langle u_t \rangle = \frac{\nu + p}{\nu + (y_t - a)^T(b b^T + \sigma^2I)^{-1}(y_t - a)}, \]  \hspace{1cm} (25)

\[ \langle \log u_t \rangle = \psi \left(\frac{\nu + p}{2}\right) - \log \left(\frac{\nu + (y_t - a)^T(b b^T + \sigma^2I)^{-1}(y_t - a)}{2}\right), \]  \hspace{1cm} (26)

\[ \langle k_t \rangle = (b^T b + \sigma^2)^{-1} b^T (y_t - a), \]  \hspace{1cm} (27)

\[ \langle u_t k_t \rangle = \langle u_t \rangle \langle k_t \rangle, \]  \hspace{1cm} (28)

\[ \langle u_t k_t^2 \rangle = \sigma^2 (b^T b + \sigma^2)^{-1} + \langle u_t \rangle^2 \langle k_t \rangle^2, \]  \hspace{1cm} (29)
where $\psi(\cdot)$ is the digamma function. More details for deriving (25)-(29) are given in appendix A.

In the M-step, we maximize $\langle L_c \rangle$ with respect to the parameters $(a, b, \sigma^2, \nu)$, by setting all the first order partial derivatives to 0. This results in the following updating equations:

$$\tilde{a} = \frac{\sum_{t=1}^{n} (\langle u_t \rangle y_t - b \langle k_t \rangle)}{\sum_{t=1}^{n} \langle u_t \rangle},$$

(30)

$$\tilde{b} = \left[ \sum_{t=1}^{n} (y_t - \tilde{a}) \langle u_t k_t \rangle \right] \left[ \sum_{t=1}^{n} \langle u_t k_t^2 \rangle \right]^{-1},$$

(31)

$$\tilde{\sigma}^2 = \frac{1}{np} \sum_{t=1}^{n} \left[ \langle u_t \rangle (y_t - \tilde{a})^T (y_t - \tilde{a}) - 2 \langle u_t k_t \rangle \tilde{b}^T (y_t - \tilde{a}) + \tilde{b}^T \tilde{b} \langle u_t k_t^2 \rangle \right].$$

(32)

The updating of $a$ and $b$ has very nice interpretations to demonstrate why the resulting estimates are more robust. From the scale mixture representation (20) of our multivariate $t$-PPCA model, $y_t \mid k, u \sim \mathcal{N}(a + b k, \sigma^2 I / u)$ and $k \mid u \sim \mathcal{N}(0, u^{-1})$, it is easy to see the scale parameter $u$ turns to be small if $y$ is a potential outlier. Therefore, the updating equations (30) and (31) can be treated as a weighted sample mean and weight least square solution, respectively, where $u_t$ represents a weight parameter to deweight any extreme observations.

Lastly, The maximum likelihood estimate of the degrees of freedom $\nu$ can be found by solving the following equation using an one-dimensional line search:

$$1 + \log \frac{\nu}{2} - \psi \left( \frac{\nu}{2} \right) + \frac{1}{n} \sum_{t=1}^{n} \langle\log u_t \rangle - \langle u_t \rangle = 0.$$

(33)

One detail worth noting is that in (31) we update $b$ using $\tilde{a}$ instead of $a$ (similar to (32) for $\sigma^2$), which means this EM algorithm is actually an expectation conditional algorithm (ECM). Dempster et al. (1977) have shown that the ECM algorithms belong to the generalised EM algorithms (GEM) and share the same convergence properties as the standard EM algorithms.

The implementation of the EM algorithm requires a properly selected initial value for the parameters. For the $t$-PPCA model $y_t \overset{iid}{\sim} t_{\nu}(a, bb^T + \sigma^2 I)$, the MLE of $(a, b, \sigma^2)$ fitted from the standard PPCA $y_t \overset{iid}{\sim} \mathcal{N}(a, bb^T + \sigma^2 I)$ gives a natural starting value, which is stated in (15). The initial value of the degrees of freedom $\nu$ is fairly arbitrary, and we choose $\nu_0 = 3$ by following Guo and Bondell (2021). The main steps of estimating the parameters in the robust multivariate $t$-PPCA Lee-Carter model are summarized in Algorithm 1. After the parameter estimates are obtained, one can adopt any preferred time series model, for example the drifted random walk, to fit the time index $k_t$ and make mortality forecasting.

### 3.3 Outlier Detection

Without being the main focus of this paper, we briefly make some remarks on the outlier detection. Under the robust $t$-PPCA Lee-Carter scheme, two main types of strategies exist...
Algorithm 1 Robust Multivariate t-PPCA Lee-Carter Estimation

1. Fit a standard PPCA model (14) to the log mortality rate data \(y_t\), where \(t = 1, \ldots, n\), and obtain the MLE of \((a, b, \sigma^2)\) as shown in (15).

2. Estimate \(a\) and \(b\) by the EM algorithm introduced in Section 3.2.
   (a) Take the MLE obtained in Step 1 as the initial value of \((a, b, \sigma^2)\), and choose a initial value of \(\nu\).
   (b) Given the current estimates of the parameters \((a, b, \sigma^2, \nu)\), compute the posterior conditional expectations (25)-(29) in the E-step.
   (c) Update the parameters \((a, b, \sigma^2, \nu)\) by (30)-(33) in the M-step.
   (d) Repeat Step 2(b) and Step 2(c) until convergence. Normalise \(b\) by \(1^T b = 1\).

3. Using the final MLE obtained from the previous EM algorithm and the historical death numbers \(D_{x,t}\), compute the time index \(k_t\) by matching the actual death numbers, as shown in (5):

\[
\sum_x D_{x,t} = \sum_x \left( N_{x,t} \cdot e^{\hat{a} x + \hat{b} x k_t} \right).
\]

for detecting outliers. One is to detect the outliers directly through the estimation step, and consequentially the resulting time indexes \(k_t\) for modelling are expected to be statistically outlier-free. As the original mortality data are multidimensional \((p\)-dimensional, where \(p\) is the number of age groups\), a large number of techniques for outlier detection do not apply. One of the advantages of the \(t\)-PPCA model is to provide a closed-form likelihood-based confidence region, to measure how far one point deviates from the majority of the data set in high dimension. In our proposed robust \(t\)-PPCA model (17), the marginal distribution of the log mortality rate \(y \sim t_\nu(a, bb^T + \sigma^2 I)\). We use the fact that for a \(p\)-dimensional random vector \(y \sim t_\nu(\mu, \Sigma)\), its scaled square Mahalanobis distance is \(F\)-distributed: \((y - \mu)^T \Sigma^{-1} (y - \mu) / p \sim F_{p,\nu}\) \cite{Lin1972}. By such, we have the following explicit decision rule based on the scaled square Mahalanobis distance \(D^2 / p\): an observation \(y\) is classified as an outlier at level \(\alpha\) if

\[
\frac{D^2}{p} = \frac{(y - a)^T (bb^T + \sigma^2 I)^{-1} (y - a)}{p} > F_{p,\nu}(\alpha),
\]

where \(F_{p,\nu}(\alpha)\) is the \(\alpha\)-quantile of the \(F\)-distribution with degrees of freedom \(p\) and \(\nu\) and the predetermined parameter \(\alpha\) controls the tolerance level for outliers. The unknown parameters \((a, b, \sigma, \nu)\) are replaced by their MLE obtained from the EM algorithm.

However, the outlier detection rule (34) is not recommended in practice. Recall that the \(t\)-PPCA is adapted not because the underlying multivariate \(t\)-distribution captures the true structure of the log mortality data and in general it does not provide a sound fit. This can also be noticed by the high-dimensionality of the data, where the dimension \(p\) (number of age groups) is close to the sample size \(n\) (number of years). On contrast, the \(t\)-PPCA formulation
of the Lee-Carter model provides a pathway to find the robust least-square estimates of $a$ and $b$, i.e., the first principal component.

An alternative strategy to detect the outliers is adapting the robust estimates obtained from the estimation stage, then process the outlier detection in the time series modelling of the time indexes $k_t$. For example, Li and Chan (2005) proposed a refined ARIMA model for $k_t$ to systematically detect and adjust the outlier effects, in which the $k_t$ is obtained from the standard SVD procedure. Since the robust $t$-PPCA algorithm focuses only on the estimation stage, it can be naturally combined with other robust time series models (for example, Li and Chan (2005)). Moreover, with more robust estimates of $k_t$, it could potentially reduce the false positive rate for the second-stage outlier detection.

4 Numerical Analysis

4.1 Illustration: The United States Mortality Rates

In this section, we apply the proposed $t$-PPCA method to the U.S. mortality data from the Human Mortality Database (HMD), a database that has been widely applied to various actuarial science and demographic research. All the death numbers ($D_{x,t}$), exposure-to-risk ($E_{x,t}$) and central mortality rates ($m_{x,t}$) are for all sexes and indexed by single year of age (0-100). Throughout the entire numerical analysis, the standard SVD (Lee and Carter, 1992) and Poisson GLM (Brouhns et al., 2002) are used as the benchmarks for comparison. The Poisson GLM method is implemented by means of the “StMoMo” package in R.

Two ranges of time periods are considered, 1933-2019 and 1970-2019, where the first one contains a large number of “outliers” such as the WWII and Korean War, and the second one does not involve any significant historical events affecting the mortality. The fitting results for are shown in Figure 1. We observe that all three methods produce highly similar estimates for the time period from 1970 to 2019, which is in line with our intuition. Given we are considering the post-war time period and no severe pandemic happened during this time, no significant outliers are expected to present. As a result, little improvements can be achieved by robustification.

On the other hand, for the scenario concerning year 1933-2019, the $t$-PPCA model presents different estimates from the two benchmarks. More specifically, $b_x$ estimated from the $t$-PPCA turns out to be more robust, in the sense that being similar to the counterpart in 1970-2019, where no significant outliers are involved. On contrast, the conventional SVD and Poisson GLM approaches estimate $b_x$ close to flat line for age from 20 to 80, which is dramatically deviate. It is also worth looking at the plot for the time index $k_t$, in which the $t$-PPCA model gives slightly lower estimates than the SVD and Poisson GLM for the early years. This is also consistent with our prior expectation, since both the WWII and Korean War produced higher mortality rates than normal. We admit that this single case study serves more like an illustration rather than a full investigation of the robustness of our proposed method. Thus, a more systematic and practical simulation study will be conducted in the next section, where we quantitatively measure the quality of parameter estimation of
Figure 1: Estimates of $a_x$ (top), $b_x$ (middle) and $k_t$ (bottom) for real U.S. mortality data. Left: 1933 to 2019; right: 1970 to 2019
| Year       | Standard error | 95% CI width | Year       | Standard error | 95% CI width |
|------------|----------------|--------------|------------|----------------|--------------|
| 1933-2019  |                |              | 1970-2019  |                |              |
| $a_1$      | 0.02162        | 0.01617      | 0.01960    | 0.00638        | 0.01117      |
| $a_{30}$   | 0.02050        | 0.01326      | 0.01697    | 0.00638        | 0.01117      |
| $a_{60}$   | 0.00540        | 0.00545      | 0.00789    | 0.00638        | 0.01117      |
| $a_{100}$  | 0.00638        | 0.02555      | 0.01187    | 0.00638        | 0.01117      |
| $b_1$      | 0.00034        | 0.00039      | 0.00060    | 0.00638        | 0.01117      |
| $b_{30}$   | 0.00043        | 0.00035      | 0.00042    | 0.00638        | 0.01117      |
| $b_{60}$   | 0.00021        | 0.00014      | 0.00021    | 0.00638        | 0.01117      |
| $b_{100}$  | 0.00017        | 0.00061      | 0.00032    | 0.00638        | 0.01117      |
| $k_{1970}$ | 1.59490        | 0.63744      | 1.65241    | 8.34054        | 2.49150      |
| $k_{1990}$ | 1.61802        | 0.67491      | 1.71105    | 7.87089        | 2.65508      |
| $k_{2005}$ | 1.99477        | 0.68491      | 2.05185    | 9.40136        | 2.67959      |
| $k_{2019}$ | 2.60678        | 0.67347      | 2.74572    | 11.70851       | 2.67508      |
|           |                |              |            |                |              |
| 1970-2019  |                |              | 1990-2019  |                |              |
| $a_1$      | 0.01105        | 0.01876      | 0.01765    | 0.04342        | 0.07292      |
| $a_{30}$   | 0.01571        | 0.01299      | 0.02005    | 0.06210        | 0.05138      |
| $a_{60}$   | 0.00673        | 0.00523      | 0.01025    | 0.02676        | 0.02058      |
| $a_{100}$  | 0.00801        | 0.01470      | 0.01325    | 0.03130        | 0.05769      |
| $b_1$      | 0.00047        | 0.00096      | 0.00076    | 0.00183        | 0.00383      |
| $b_{30}$   | 0.00075        | 0.00072      | 0.00088    | 0.00293        | 0.00283      |
| $b_{60}$   | 0.00022        | 0.00028      | 0.00040    | 0.00085        | 0.00110      |
| $b_{100}$  | 0.00040        | 0.00077      | 0.00061    | 0.00155        | 0.00296      |
| $k_{1970}$ | 1.26083        | 0.49462      | 1.38760    | 5.53323        | 1.93144      |
| $k_{1990}$ | 0.52567        | 0.44772      | 0.72850    | 2.16245        | 1.78538      |
| $k_{2005}$ | 0.52726        | 0.44354      | 0.80504    | 2.10271        | 1.76693      |
| $k_{2019}$ | 0.87203        | 0.46698      | 1.16973    | 3.40213        | 1.81933      |

Table 1: Selected standard errors and widths of 95% CI of $\hat{a}_x$, $\hat{b}_x$ and $\hat{k}_t$ for fitting the two U.S. mortality datasets by SVD, Poisson GLM and $t$-PPCA. The results are obtained from 5000 bootstrap samples.
different methods under the presence of outliers.

As for any stochastic mortality models, it is of huge importance to understand the parameter uncertainties, i.e., the standard error of the estimators. There is no analytical solution for the standard error of the parameters in the multivariate $t$-PPCA, so is for our proposed $t$-PPCA Lee-Carter model. Since the prediction errors for the log mortality rate $y_t$ can be directly obtained, we follow Lee and Carter (1992) to adopt a nonparametric residual bootstrapping approach. In each bootstrap simulation, we build a hypothetical-data matrix by adding the residuals to the fitted-data matrix $\hat{Y} = (\hat{y}_1, \cdots, \hat{y}_n)$, where the residuals are obtained by sampling with replacement from the vectors of fitting errors $y_t - \hat{y}_t$ among all $t$. Then, we reestimate the parameters $a$, $b$ and $k$ using the pseudo-observation matrix.

We conduct 5000 bootstrap simulations for both the proposed $t$-PPCA method and the benchmarks. For the standard SVD, we adopt a residual bootstrapping method in Lee and Carter (1992), which directly samples the prediction residual vectors with replacement. On the other hand, the Poisson GLM adopts another residual bootstrapping proposed by Koissi et al. (2006), which first samples the deviances from the Poisson GLM fitting, and recovers the prediction errors through a properly chosen inverse transformation. The bootstrap standard errors and 95% confidence intervals (CI) of parameters are computed to demonstrate the parameter uncertainties, in which the confidence intervals are obtained symmetrically by taking the 2.5% and 97.5% sample quantile. A selection of results are shown in Table 1.

For each $\hat{a}_x$ or $\hat{b}_x$, all three methods produce estimates with a similar magnitude of uncertainties, in terms of both the standard error and width of CI. We notice that the uncertainties obtain from the dataset concerning year 1933-2019 are uniformly larger than that for 1970-2019. It is because year 1933-2019 contains more extreme mortality rates (at early years), and so for the bootstrap residuals and samples, which results in larger standard errors and wider CIs. It is worth noting that the relative size of the quantities among different parameters are not of primary interest, since magnitude of each parameter differs.

For the time index $k_t$, it is observed that the $t$-PPCA method involves similar level of uncertainties as the SVD approach, but both are significantly higher than that for the Poisson GLM. This phenomena is caused by the second-stage reestimation of $k_t$ in SVD and $t$-PPCA, $\sum_x D_{x,t} = \sum_x (N_{x,t} \cdot e^{\hat{a}_x + \hat{b}_x k_t})$. In each bootstrap simulation, after obtaining a bootstrap log mortality rate, we recalculate the death numbers $D_{x,t}$ based on the corresponding exposure to risk $N_{x,t}$. This implies that the standard error of estimating $k_t$ depends on both the uncertainties of the data $y_t$ (or equivalently, $D_{x,t}$) and the estimators ($\hat{a}, \hat{b}$). On the other hand, the Poisson GLM approach estimates all the parameters $(a, b, k)$ simultaneously and no second-stage reestimation is needed, so the uncertainty of $\hat{k}_t$ depends only on the variation of the observation $D_{x,t}$.

### 4.2 Simulation Study: Hypothetical Pandemic

In this section, we design a number of simulation experiments to evaluate the robustness of our proposed $t$-PPCA Lee-Carter model more comprehensively. Covid-19 is with no doubt one of the most important public health events since 2020, and causes an unexpectedly high
death number/rate in many countries. However, when making mortality forecasting for a relatively far future, for example 2030, the years that are mostly affected by Covid-19 should be considered as outliers. Therefore, the basic idea of the simulation studies is assuming a severe pandemic such as Covid-19 happened in the history, and then examine how robust our proposed method performs compared to the SVD and Poisson GLM.

The experiments are based on the U.S. mortality data from 1970 to 2019 from HMD. As we see from Section 4.1, this time period contains few pre-existing extreme observations so is appropriate to be used in the simulation to control the artificial outlier effect. To introduce hypothetical outliers, we add the death number for all sexes involving Covid-19 in 2020 in U.S. back to the historical mortality data. The Covid-19 data are obtained from the website of Centers of Disease Control and Prevention (CDC) and are displayed in Table 2. Notice that the Covid-19 deaths are not indexed by single year of age, while other death data are. Thus, we distribute the deaths in each group to each age based on the empirical distribution implied by the U.S. 2020 total deaths.

| Age Group | < 1 | 1-4 | 5-14 | 15-24 | 25-34 | 35-44 |
|-----------|-----|-----|------|-------|-------|-------|
| Deaths    | 52  | 25  | 68   | 615   | 2,621 | 6,785 |
| Age Group | 45-54 | 55-64 | 65-74 | 75-84 | > 85 | N/A |
| Deaths    | 18,327 | 45,572 | 82,286 | 106,259 | 122,820 | N/A |

**Table 2:** U.S. Covid-19 Deaths for all sexes in 2020

As the first illustration, we start by considering the scenario that the “hypothetical Covid-19” happened for three years during 1970-1972. In terms of the data, we add the re-distributed Covid-19 deaths (U.S. 2020) into the total deaths in 1970, 1971 and 1972. It is worth noting that in practice, the death number from a pandemic will be different for each year. However, in this simulation we assume it kept unchanged for simplicity, since our goal is to create outliers instead of concerning their exact values. For each of the SVD (Figure 2, top), Poisson GLM (Figure 2, middle) and the proposed robust $t$-PPCA (Figure 2, bottom), we estimate the parameters with and without the added outliers and compare the results.

In this experiment, the estimates of $a_x$ are basically unaffected when adding outliers for all the three methods (see plots in Appendix B), which is consistent with Figure 1, and implies that $a_x$ seems to inherently be robust to outliers. This observation can be formally demonstrated later in Table 3. On the other hand, both the SVD and Poisson GLM methods produce highly fragile estimates for $b_x$ in the presence of outliers, which can be observed in Figure 2. Clearly $b_x$ are overestimated for old ages, which makes perfect sense since most of the deaths in the added outlier (hypothetical Covid-19) are for the old ages (from Table 2) and at the starting of the experiment period (1970-1972). Recall that $b_x$ represents the sensitivity of the death rates with respect to the time index $k_t$, thus a positive outlier at the beginning will inflate the overall sensitivity $b_x$. On contrast, the proposed $t$-PPCA approach gives extremely robust estimates over all ages $x = 0, \cdots, 100$ for $b_x$ even though the outliers are inserted.
Figure 2: Estimates of $b_x$ (Left) and $k_t$ (Right) for the simulated U.S. mortality data from 1970 to 2019, with Covid-19 outliers added to year 1970-1972: SVD (top); Poisson GLM (middle); $t$-PPCA (bottom)
It is worth studying the plots for \( \hat{b}_x \) for SVD and Poisson GLM in more detail. Again from Figure 2, it seems like the SVD and Poisson GLM also underestimate \( b_x \) for young age groups in the simulated scenario, but this interpretation is not correct. Notice that the death number in the outlier is generally increasing with age (and always positive), so \( b_x \) should be overestimated for all ages and with a growing extent as age goes up. However, the imposed parameter constraint \( \sum_x b_x = 1 \) re-scales the overall overestimation such that the less overestimated \( b_x \) part (younger age groups) will look like an “underestimation”.

In terms of the time index \( k_t \), we can see from Figure 2 that all methods yield extremely distorted estimates at \( t = 1970, 1971, 1972 \) (the years containing outliers), which makes intuitive sense. For SVD and \( t \)-PPCA, \( k_t \) are obtained from the death number matching \( D_t = \sum_x N_{x,t} \cdot e^{\hat{a}_x + b_x \cdot k_t} \) after obtaining \( \hat{a}_x \) and \( \hat{b}_x \). As a result, for a positive outlier with larger \( D_t \) will naturally produce a positively deviated \( \hat{k}_t \), regardless of the estimation quality of \( \hat{a}_x \) and \( \hat{b}_x \). Similarly, an abnormal \( D_t \) of the outliers will be directly used in the Poisson likelihood structure, which consequentially leads to a poor \( \hat{k}_t \). Despite of the distorted estimates \( k_t \) for the outliers, our proposed \( t \)-PPCA still outperforms the traditional SVD and Poisson GLM. The \( t \)-PPCA are able to give highly robust estimates for \( k_t \) where \( t \) is not an outlier point (in Figure 2 bottom, year 1973-2019), which means the outlier effect does not significantly propagate beyond the originally affected time region. However, the estimated \( k_t \) in the “normal time region” obtained from SVD and Poisson GLM (in Figure 2 top/middle, year 1973-2000) are still influenced, or equivalently to say, the outlier effect propagates much further.

To further examine the performance of three estimating methods, we consider three different scenarios, where the “hypothetical Covid-19” (added outlier) lasted for one, three or five years in the history. We conduct a set of experiments for each scenario, and the outlier data still follows Table 2, the Covid-19 deaths in 2020 in U.S. To be more concrete, consider the set of experiments where the outlier is of one year, we put this one-year outlier into each of year 1970-2019, thus in total we have \( N = 50 \) experiments. For another set of experiments where the outlier is of three years, we insert the outlier into year 1970-1972, 1971-1973, 1972-1974, \( \cdots \), 2017-2019, which results in totally \( N = 48 \) experiments. The scenario for 5-year outliers is similar to the 3-year case and involve \( N = 46 \) experiments. The essence of the simulation is to examine the robustness of the three methods if assuming “hypothetical Covid-19” happening in the history, which lasted one, three or five years respectively.

For each scenario (outlier duration), we estimate \( a_x, b_x \) and \( k_t \) for each experiment (outlier location). To compare the performance between different methods, we adopt two mean types of error metrics: mean absolute percentage error (MAPE) and root mean square percentage error (RMSPE), which are defined as follows:

\[
\text{MAPE}(\hat{a}) = \frac{1}{p} \sum_{x=0}^{100} \left| \frac{a_x - \hat{a}_x}{a_x} \right|, \quad \text{RMSPE}(\hat{a}) = \sqrt{\frac{1}{p} \sum_{x=0}^{100} \left( \frac{a_x - \hat{a}_x}{a_x} \right)^2}, \quad (35)
\]

\[
\text{MAPE}(\hat{b}) = \frac{1}{p} \sum_{x=0}^{100} \left| \frac{b_x - \hat{b}_x}{b_x} \right|, \quad \text{RMSPE}(\hat{b}) = \sqrt{\frac{1}{p} \sum_{x=0}^{100} \left( \frac{b_x - \hat{b}_x}{b_x} \right)^2}, \quad (36)
\]
| Outliers | Method       | MAPE($\hat{a}$) | RMSPE($\hat{a}$) | MAPE($\hat{b}$) | RMSPE($\hat{b}$) | MAPE($\hat{k}$) | RMSPE($\hat{k}$) |
|----------|--------------|-----------------|-----------------|-----------------|-----------------|-----------------|-----------------|
|          |              | Sample mean     | Sample s.d.     | Sample mean     | Sample s.d.     | Sample mean     | Sample s.d.     |
| 1-year   | SVD          | 0.10%           | 0.03%           | 0.18%           | 0.09%           | 4.48%           | 5.07%           |
|          | Poisson GLM  | 0.13%           | 0.04%           | 0.27%           | 0.10%           | 7.05%           | 4.49%           |
|          | t-PPCA       | 0.06%           | 0.03%           | 0.08%           | 0.05%           | 1.70%           | 1.36%           |
| 3-year   | SVD          | 0.29%           | 0.09%           | 0.54%           | 0.25%           | 12.20%          | 13.03%          |
|          | Poisson GLM  | 0.38%           | 0.10%           | 0.79%           | 0.26%           | 19.67%          | 11.73%          |
|          | t-PPCA       | 0.17%           | 0.08%           | 0.23%           | 0.13%           | 4.79%           | 3.30%           |
| 5-year   | SVD          | 0.48%           | 0.14%           | 0.89%           | 0.40%           | 18.51%          | 18.42%          |
|          | Poisson GLM  | 0.60%           | 0.14%           | 1.24%           | 0.39%           | 29.09%          | 16.72%          |
|          | t-PPCA       | 0.28%           | 0.12%           | 0.38%           | 0.19%           | 7.46%           | 4.60%           |

Table 3: Estimation error of $\hat{a}_x$, $\hat{b}_x$ and $\hat{k}_t$ (outliers excluded) under different scenarios of outlier settings (hypothetical pandemic). The number of simulations $N = 50/48/46$ for each outlier setting.
\[
\text{MAPE}(\hat{k}) = \frac{1}{n} \sum_{t \in T} \left| \frac{k_t - \hat{k}_t}{k_t} \right|, \quad \text{RMSPE}(\hat{k}) = \sqrt{\frac{1}{n} \sum_{t \in T} \left( \frac{k_t - \hat{k}_t}{k_t} \right)^2},
\] (37)

where \( T = \{1970, \cdots, 2019\} \setminus \{t | y_t \text{ is an outlier}\} \), and \( \{a_x, b_x, k_t\} \) represents the estimates obtained from no outliers. We adopt these two risk metrics, which both measure the estimation errors in a percentage sense, because the magnitude of different parameters differs dramatically. Furthermore, MAPE has a very natural interpretation of percentage estimation error, while RMSPE penalizes more strictly to large errors, and one could also understand them as \( L_1 \) and \( L_2 \) percentage error. In each experiment, errors for \( \hat{a}_x \) and \( \hat{b}_x \) are calculated by averaged over all ages \( x = 0, \cdots, 100 \), and error for \( \hat{k}_t \) is averaged over all time \( t = 1970, \cdots, 2019 \) but excluding the time period for the outliers. Then, we compute the sample means and sample standard deviations (s.d.) over all \( N \) experiments in each outlier scenario, where \( N = 50/48/46 \) for each outlier setting as stated before. The results are shown in Table 3.

First from the top part of Table 2, the estimates of \( a_x \) are highly robust for all scenarios, with an MAPE uniformly smaller than 1%, even if a very severe 5-year outlier is added. This phenomena holds for all three approaches, thus our \( t \)-PPCA method is not attractive in estimating \( a_x \). Instead, our major focus is on the performance of estimating sensitivity index \( b_x \). Under all three outlier scenarios, \( \hat{b}_x \) obtained from the Poisson GLM is the most fragile, followed by the SVD, and \( t \)-PPCA gives the most robust estimates by improving the average MAPE by at least 60% compared to the SVD and Poisson GLM. In addition, the standard deviations of the risk metrics are also notably smaller than the traditional approaches, which implies the superior stability of the \( t \)-PPCA method. Furthermore, it is worth noting that the \( t \)-PPCA also results in an even finer improvement of RMSPE, indicating that our proposed method manages to control the estimation errors of large magnitude.

Regarding to the estimation of the time index \( k_t \), the \( t \)-PPCA also reduces the MAPE and RMSPE, which yields more robust \( \hat{k}_t \) and deflates the outlier effects in the second-stage time series modelling. Notice that although the extent is relatively conservative compared to that of \( b_x \), however, this should not be a concern when adapting our method to estimate the parameters. One benefit of the \( t \)-PPCA is that it only focuses on estimation stage, and can be naturally combined with any existing time series model in the forecasting stage with no conflict.

5 Further Comments and Conclusion

Lee-Carter model plays an important role in both actuarial practice and research, since it is adapted as the one of the most standard benchmark methods for mortality modelling and forecasting. This paper proposes a systematic approach to estimate the parameters in the Lee-Carter model. Outliers arise naturally in mortality data and their influences are expected to be diminished when making long-term mortality projections. By noticing an equivalence between the traditional SVD approach and the PPCA formulation, a modified multivariate \( t \)-distribution based PPCA model is proposed to robustify the estimating quality under the
presence of outliers. A computationally efficient EM algorithm has been proposed for imple-
mentation and residual bootstrap can be adopted to examine the parameter uncertainties. An empirical study and simulation experiments are designed, and the results show that the proposed $t$-PPCA model can significantly improve the parameter robustness, particularly for $b_x$, while keeping the standard errors at the same level as the conventional methods.

Existing literature concerning the outlier analysis of the Lee-Carter model mostly focuses on the time series modelling step of the time index $k_t$, and assumes the sensitivity parameter $b_x$ obtained from the estimation stage is correct. This assumption can potentially lead to distorted mortality projections even though a convincing model for $k_t$ is constructed. Our proposed $t$-PPCA model focuses only on the estimation stage and mainly aims to provide a robust estimates for $b_x$. Any suitable time series model for $k_t$ can be flexibly combined with the $t$-PPCA estimation procedure to produce robust mortality projections against outliers.

Finally, it is worth commenting on the appropriateness of adopting the robust methods in mortality modelling. As mentioned in Chan (2002); Li and Chan (2005, 2007), if the goal is to capture the long-term mortality trend, then the robust models are preferred as the outlier effect can be diminished. On the other hand, when the quantity of interest is closely related to the extreme stochastic fluctuations, such as the highest attained age, the existence of outliers and the corresponding effect should be retained.
Appendix A: Derivations of the posterior expectations in the E-step

In the appendix, we present the detailed derivations for the posterior expectations (25)-(29) in the E-step in Section 3.2.

First from (19) and (20), we have $y|u \sim N(a,(bb^T + \sigma^2 I)/u)$ and $u \sim Ga(\nu/2, \nu/2)$. By the conjugacy between of normal likelihood and gamma prior, we obtain

$$u|y \sim Ga\left(\frac{p + \nu}{2}, \frac{(y_t - a)^T(bb^T + \sigma^2 I)^{-1}(y_t - a) + \nu}{2}\right), \quad (38)$$

which immediately implies (25) and (26).

To derive (27), we apply the Bayes’ rule for multivariate normal distributions to $y|k,u \sim N(a + bk, \sigma^2 I/u)$ and $k|u \sim N(0, u^{-1})$ in (20), then obtain

$$p(k|y, u) \propto p(y|k, u)p(k|u) \sim N\left((b^T b + \sigma^2)^{-1}b^T(y_t - a), \frac{\sigma^2(b^T b + \sigma^2)^{-1}}{u}\right). \quad (39)$$

Combining with $u \sim Ga(\nu/2, \nu/2)$ and the scale mixture Gaussian representation (19), it leads to

$$p(k|y) \sim t_{\nu} ((b^T b + \sigma^2)^{-1}b^T(y_t - a), \sigma^2(b^T b + \sigma^2)^{-1}) \quad (40)$$

The two equations above imply that $\langle k_t \rangle = E[k_t|y_t] = E[k_t|y_t, u_t]$ and thus (27). Finally, by the law of total expectations:

$$\langle u_t k_t \rangle = E[E(u_t k_t|u_t, y_t)|y_t] = \langle u_t \rangle \langle k_t \rangle, \quad (41)$$

$$\langle u_t k_t^2 \rangle = E[E(u_t k_t^2|u_t, y_t)|y_t] = E[u_t(E^2(k_t|u_t, y_t) + Var(k_t|u_t, y_t))|y_t]
= \sigma^2(b^T b + \sigma^2)^{-1} + \langle u_t \rangle \langle k_t \rangle^2. \quad (42)$$

By such, we obtain the cross moments (28) and (29).
Appendix B: Plots for the estimation of $a_x$ in Section 4.2

Figure 3: Estimates of $a_x$ for the U.S. mortality data from 1970 to 2019, with Covid-19 outliers added to year 1970-1972. Left top: SVD; right top: Poisson GLM; left bottom: $t$-PPCA.
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