

Modeling mortality with pandemics: a Bayesian transitory vanishing jump approach

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- The Lee-Carter approach by Lee and Carter (1992) is among the earliest model for stochastic mortality forecasting. With many extensions thereof in recent years.
- Lee-Carter model is effective in capturing a general mortality trend
→ does not account for large, unexpected jumps caused by e.g. pandemics or wars.
- Lee and Carter (1992) treat the 1918 influenza (spanish flu) as an anomaly and use an intervention model, effectively removing its influence.

- Earliest methods relied on outlier techniques (e.g. Li & Chan, 2005) and remove potential data points.
- H. Chen and Cox (2009) incorporate a jump processes into the Lee-Carter model.
→ either permanent or transitory mortality shocks.
- Adaptation by Liu and Li (2015) to account for age dependent shock.
- More recently, other approaches haven been introduced (e.g. F.-Y. Chen et al., 2022; Robben & Antonio, 2023; van Berkum et al., 2022).
→ All assume that the shock completely disappears the next period
- We introduce a model, where the shock effect slowly vanishes over time.

Vanishing Effects

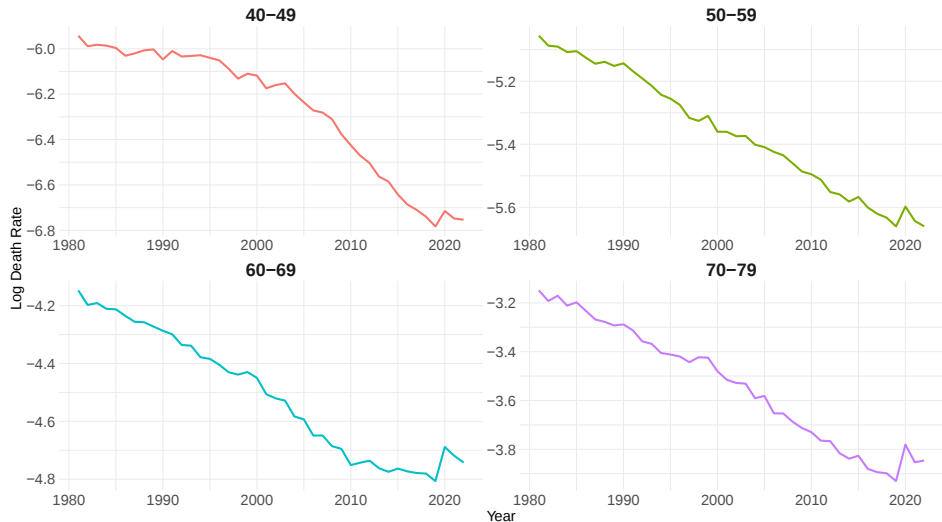


Figure: Log Death Rates for Spain

- Let $D_{x,t}$ denote the total number of deaths and $E_{x,t}$ central exposure to risk, with $x = x_1, x_2, \dots, x_A$ and $t = t_1, t_2, \dots, t_T$.
- We denote $m_{x,t}$ to be the central mortality rate given by

$$m_{x,t} = \frac{D_{xt}}{E_{xt}}.$$

- The Lee-Carter model including a centered error term is as follows

$$\ln(m_{x,t}) = \alpha_x + \beta_x \kappa_t + e_{x,t},$$

where $e_{x,t} \stackrel{iid}{\sim} \mathcal{N}(0, \sigma_e^2)$.

- Extension of κ_t by H. Chen and Cox (2009) that allows for transitory effects.
- Adaption of Chen and Cox by Liu and Li (2015) to account for an age dependent shock.
- Liu and Li (2015) defined three different variants of their shock model. The one closest to our adaptation is given by

$$\ln(m_{x,t}) = \alpha_x + \beta_x \kappa_t + \quad + e_{x,t}. \quad (1)$$

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- Adaption of Chen and Cox by Liu and Li (2015) to account for an age dependent shock.
- Liu and Li (2015) defined three different variants of their shock model. The one closest to our adaptation is given by

$$\ln(m_{x,t}) = \alpha_x + \beta_x \kappa_t + \beta_x^{(J)} N_t Y_t + e_{x,t}. \quad (1)$$

- $N_t \in \{0, 1\}$ represents a binary variable that equals one if a mortality jump occurs in year t and zero otherwise.
- Y_t denotes a jump severity variable, measuring the effect of the mortality jump.
- The parameters $\beta_x^{(J)}$ denote a new age pattern of shocks

- Our model extends the variant of Liu and Li (2015) by introducing a vanishing effect J_t controlled by the parameter a

$$\ln(m_{x,t}) = \alpha_x + \beta_x \kappa_t + J_t + e_{x,t} \quad (2)$$

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$$\begin{aligned}\ln(m_{x,t}) &= \alpha_x + \beta_x \kappa_t + \beta_x^{(J)} J_t + e_{x,t} \\ J_t &= aJ_{t-1} + N_t Y_t,\end{aligned}\tag{2}$$

where $a \in [0, 1)$ controls the rate of decay.

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where $a \in [0, 1)$ controls the rate of decay.

- Own model is a generalization of Eq. (1) that is recovered if $a = 0$.
- The time effect κ_t is assumed to be a random walk with drift

$$\kappa_t = \kappa_{t-1} + d + \xi_t, \quad \xi_t \stackrel{iid}{\sim} \mathcal{N}(0, \sigma_\xi^2).$$

- Two common routes of estimation called Route I and Route II in the terminology of Haberman and Renshaw (2012).
- The traditional approach (Route I) estimates mortality rates directly.
- Route II models the first differences of log mortality rates, called mortality improvements.
- Mortality improvements are given by

$$Z_{x,t} := \ln(m_{x,t+1}) - \ln(m_{x,t}).$$

- Own model specification of Eq. (2) is then

$$\begin{aligned} Z_{x,t} &= \beta_x (\kappa_{t+1} - \kappa_t) + \beta_x^{(J)} (J_{t+1} - J_t) + \varepsilon_{x,t} \\ Z_{x,t} &= \beta_x (d + \xi_{t+1}) + \beta_x^{(J)} \Delta J_t + \varepsilon_{x,t}, \end{aligned} \tag{3}$$

where $\varepsilon_{x,t} = e_{x,t+1} - e_{x,t}$ with $\varepsilon_{x,t} \stackrel{iid}{\sim} \mathcal{N}(0, 2\sigma_e^2)$.

Identifiability Constraints I

- The Lee Carter model suffers from non-identifiability.
- Own approach of Eq. (3) can be thought an extension of the Lee Carter model.
- According to Hunt and Blake (2020, Theorem 1.) the typical Lee Carter transformations can be generalized into higher dimensions.
- Let $\mathbf{b}_x = (\beta_x, \beta_x^J)^\top$ and $\mathbf{v}_t = (\Delta\kappa_t, \Delta J_t)^\top$, then Eq. (2) can be written as

$$Z_{x,t} = \mathbf{b}_x^\top \mathbf{v}_t + \varepsilon_{x,t}.$$

- Let there be a (2×2) invertible matrix $\mathbf{A}$, then the parameters can be transformed using

$$\{\tilde{\mathbf{b}}_x, \tilde{\mathbf{v}}_t\} = \{\mathbf{b}_x \mathbf{A}^{-1}, \mathbf{A} \mathbf{v}_t\}.$$

- Since $\mathbf{A} \in \mathbb{R}^{2 \times 2}$ there are a total of four free parameters
→ we need to impose four identifiability constraints !

- To make the model identifiable we impose the standard sum-to-one constraints

$$\sum_{x=1}^A \beta_x = 1 \quad \text{and} \quad \sum_{x=1}^A \beta_x^{(J)} = 1.$$

- Other constraints are possible, i.e. like using the Euclidean norm.
- In addition, we apply a corner constraint and set $\Delta J_{t_1} = 0$ as well as $\Delta k_{t_1} = d$.
- Constraints on the age parameters are the same as Liu and Li (2015).

- Parameter estimation done in a Bayesian setting.
- NIMBLE (Numerical Inference for statistical Models for Bayesian and Likelihood Estimation) (de Valpine et al., 2017)
- NIMBLE is a framework for writing statistical models and algorithms.
- Can be accessed in R via the *nimble* package (de Valpine et al., 2023)
- Allows to sample discrete parameters and lets you choose which sampler to select for each parameter.

Prior Overview

Parameter	Prior Distribution	Hyperprior 1	Hyperprior 2
Age Parameter			
$(\beta_1, \dots, \beta_A)$	Dirichlet(1, ..., 1)	-	-
$(\beta_1^{(J)}, \dots, \beta_A^{(J)})$	Dirichlet(1, ..., 1)	-	-
Time Parameter			
$\Delta\kappa_t$	$\Delta\kappa_t \stackrel{iid}{\sim} \mathcal{N}(d, \sigma_\xi^2)$	$d \sim \mathcal{N}(0, 5)$	$\sigma_\xi \sim \mathcal{N}_+(0, 2)$
N_t	$N_t \stackrel{iid}{\sim} \text{Bern}(p)$	$p \sim \text{Beta}(1, 20)$	-
Y_t	$Y_t \stackrel{iid}{\sim} \mathcal{N}(\mu_Y, \sigma_Y^2)$	$\mu_Y \sim \mathcal{N}_+(0, 5)$	$\sigma_Y \sim \mathcal{N}_+(0, 2)$
a	$a \sim \text{Beta}(1, 5)$	-	-
Other Parameters			
σ_ε	$\sigma_\varepsilon \sim \mathcal{N}_+(0, 2)$	-	-

Table: Selection of Priors

- We obtained death rates for countries which were heavily affected by the COVID-19 Pandemic, according to deaths per 100 K people (<https://coronavirus.jhu.edu/data/mortality>).
- Data from two sources: Human Mortality Database (HMD) and Eurostat.

Country	Year	Source
Italy	1980 - 2021	Eurostat (demo_magec)
	2022	Eurostat (demo_r_mkw_05)
Spain	1980 - 2021	Eurostat (demo_magec)
	2022	Eurostat (demo_r_mkw_05)
United States	1980 - 2021	HMD

Table: Sources of Data

- Total of $A = 10$ age groups with $x \in [0, 10), [10, 20), \dots, [90, \infty)$.
- $T = 41$ years, respectively $T = 42$ (for european countries)

- Compare own modelling approach with that of Liu and Li (2015) for all three countries.
- Classical out-of-sample evaluation not feasible due to pandemic's recent occurrence.
- Comparison of in-sample fit only, via widely applicable or Watanabe-Akaike information criterion (WAIC; Watanabe, 2010) as well as the leave-one-out cross validated predictive density (LOO-CV).
- The LOO-CV gets multiplied by -2 to be on the deviance scale (lower is better).

Model	Italy	Spain	US
<i>WAIC</i>			
Own	-1568.39	-1534.34	-1898.16
Liu-Li	-1569.27	-1526.26	-1896.61
<i>LOO-CV</i>			
Own	-1563.38	-1527.30	-1890.85
Liu-Li	-1564.92	-1517.83	-1889.60

Table: In-Sample Fit comparison.

Results II

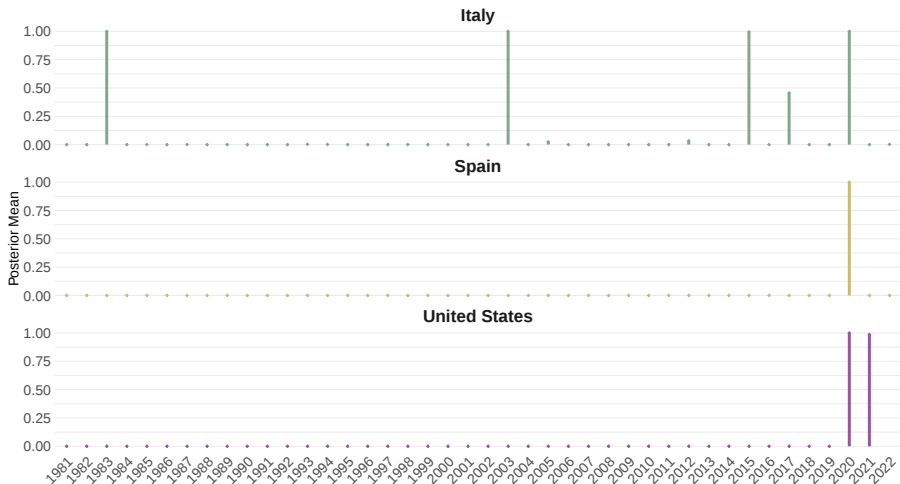


Figure: Posterior mean estimate of N_t (Jump occurrence) for each country.

Results III

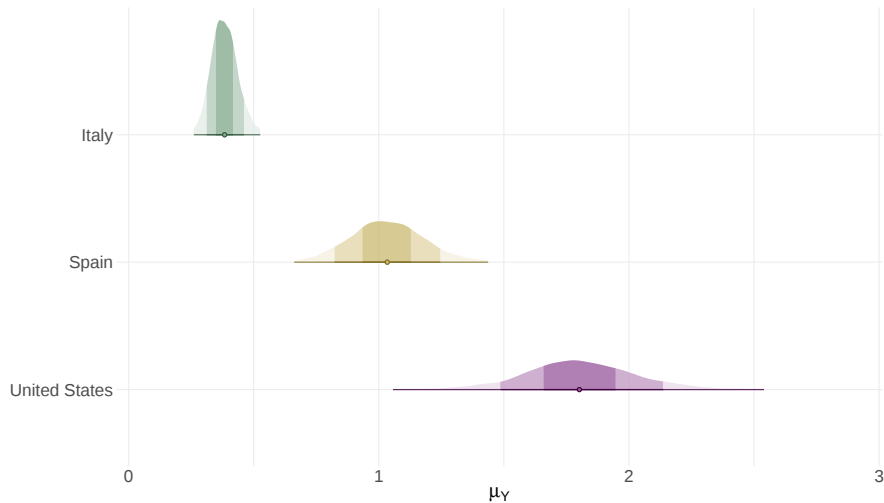


Figure: Posterior estimate of μ_Y (mean of jump effect) for each country.

Results IV

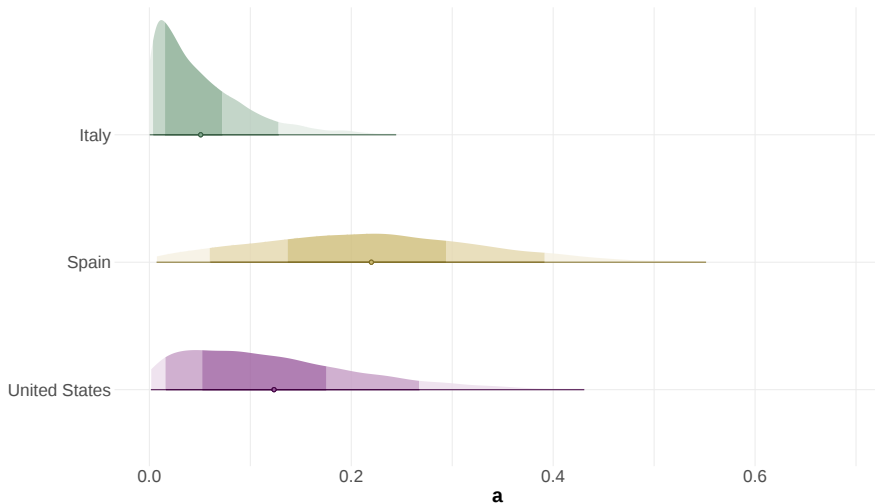


Figure: Posterior estimate of the vanishing parameter a for each country.

Results V

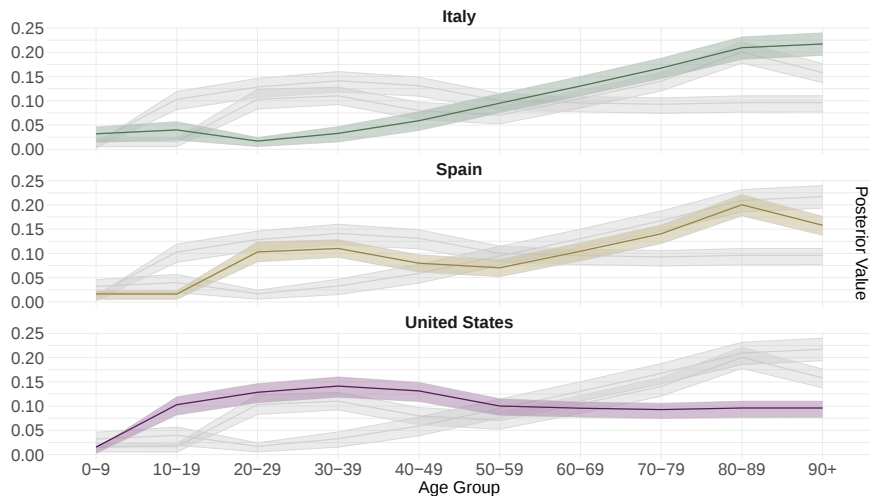


Figure: Age Pattern of $\beta_x^{(J)}$. Thick line denotes posterior mean, colored shades denote 50%- posterior intervals. Light gray shades show posterior estimates of the other countries.

- Analyse how jump models affect forecasts of mortality rates
- Use a hierarchical structure to estimate the vanishing parameter a as well as jump parameters μ_Y and σ_Y for multiple countries jointly.
- Use some regularization on the vanishing parameter a , e.g. the horseshoe prior.

Thank you for your attention!

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- The WAIC is based on the log pointwise predictive density (lppd) defined as

$$\text{lppd} = \sum_{i=1}^N \ln \int p(y_i|\theta)p(\theta|y_i)d\theta,$$

where $y_1, \dots, y_N$ denotes the data at hand.

- The above quantity is computed using draws from the posterior where $\theta^{(s)}$ denote the usual simulations with $s = 1, \dots, S$, then

$$\widehat{\text{lppd}} = \sum_{i=1}^N \ln \left(\frac{1}{S} \sum_{s=1}^S p(y_i|\theta^{(s)}) \right)$$

- The WAIC is given by

$$\text{WAIC} = -2\text{lppd} + 2p_{waic}$$

$$p_{waic} = \sum_{i=1}^N V_{s=1}^S \left(\ln p(y_i | \theta^{(s)}) \right),$$

where $V_{s=1}^S$ denotes the sample variance over all s posterior draws.

- The leave-one-out predictive density (lppd_{loo}) in a Bayesian setting is calculated by

$$\text{lppd}_{\text{loo}} = \sum_{i=1}^N \ln p(y_i | y_{-i}),$$

where

$$p(y_i | y_{-i}) = \int p(y_i | \theta) p(\theta | y_{-i}) d\theta$$

- Instead of estimating the posterior $p(\theta | y_{-i})$ for each of the N cross validation points, the density can be approximated using importance sampling (Vehtari et al., 2017).
- For the lppd_{loo} to be on the deviance scale we calculate $\text{loo-cv} = -2\text{lppd}_{\text{loo}}$

Sampler Overview

Sampler	Parameter
AF Slice Sampler	$(\beta_1, \dots, \beta_A)$ $(\beta_1^{(J)}, \dots, \beta_A^{(J)})$
Binary Sampler	$N_t \quad \forall t \in \{1, \dots, T\}$
Gibbs	d p
Random Walk Metropolis	σ_ε σ_ξ
Slice Sampler	$\Delta\kappa_t \quad \forall t \in \{1, \dots, T\}$ μ_ξ σ_Y

Table: Overview of Samplers

Death Rates Italy I

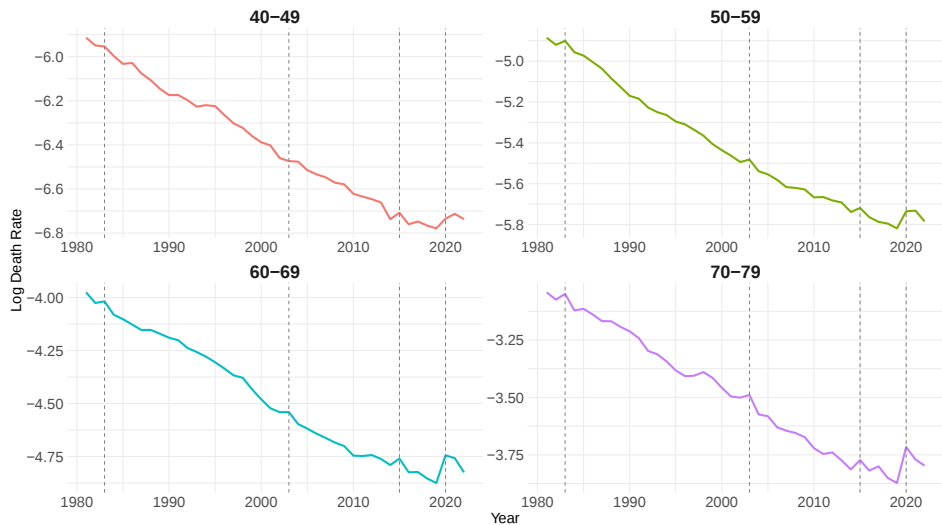


Figure: Log Death Rates for Italy

Death Rates Italy II

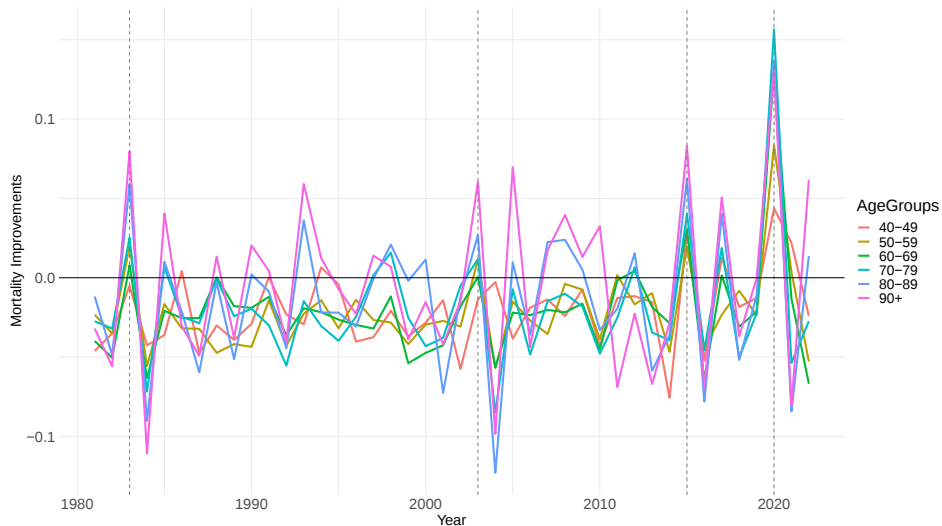


Figure: Mortality Improvements Italy