

# Forecasting US Mortality

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## Modeling Mortality

Modeling mortality has a long history of attempts and revisions since Gompertz first made his claim about human mortality patterns in the 1880s[1]. The ability to accurately model and describe rates of mortality have the potential to greatly inform how social institutions and policies should be structured in order to meet the needs of populations. For example, knowing the age pattern of mortality enables a society to build the medical infrastructure needed to cope with the demands of differently aged individuals. Understanding how mortality is likely to shift enables a population to plan ahead for its own needs.

Human mortality, however, is an evolving phenomenon that dramatically changes over time. Over the past century, there have been large declines in mortality across most locations due to medical, technological, and general standard of living improvements[1]. While that progress has stagnated to some degree in recent years[5], we are still observing decreases in mortality among developing countries where medical infrastructure is expanding and improving[1]. As a consequence of this drop in mortality, there are direct effects on the population structure and the production required to sustain the population. In order to prepare for these changing needs of a society it is vital that we explore how we can make accurate and informative forecasts of mortality patterns.

In this paper we will discuss three descriptive models of human mortality that describe how patterns of mortality change with age for a single snapshot in time. These models estimate mortality with parameters that are interpretable and comparable across analyses and are meant to be run on a single population for a single point in time. We then look at how a prominent model in forecasting mortality, the Lee-Carter model, largely abandoned this structure in favor of a functional form that can be trivially propagated into the future. Finally, we present a new innovative model that maintains the age structure of descriptive models while simultaneously incorporating data from different geographies and points in time to forecast rates of human mortality. We compare our model with the Lee-Carter model by testing the out-of-sample predictive validity of both models on mortality data from the United States. In addition, we offer future directions for improving upon the proposed model.

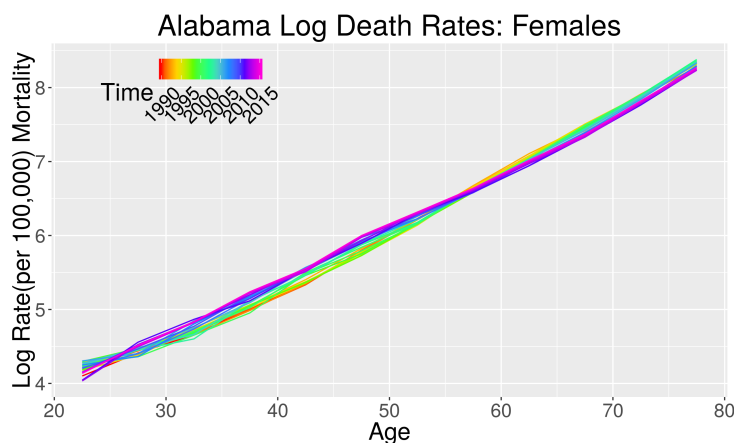
## History of Descriptive Models

Descriptive models of mortality are used to provide some modeling framework to the likelihood of mortality as a person ages. The parameters of the model often have an interpretable significance to the population that they describe, and have

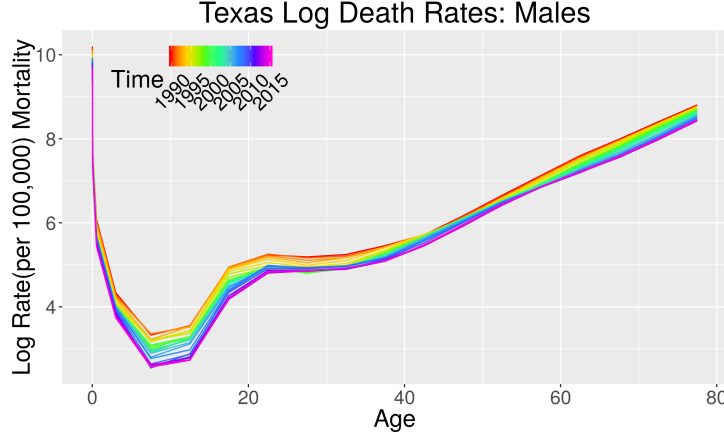
assumptions about the age structure of mortality embedded in the model. While a few mathematicians and epidemiologists had rough ideas about how mortality occurred, it was not until Benjamin Gompertz wrote out his model of decreasing protection against death with age that a model was widely accepted and used for planning. Gompertz's first claim about human mortality was that there is a linear increase in log rate mortality as one ages [1,3]. This model follows the form:

$$\ln(m(x)) = ax + b$$

where  $m_x$  is the mortality rate for an individual of age  $x$ ,  $a$  is the rate of increase in log rate mortality by increasing one unit of age, usually years, and  $b$  is the baseline mortality rate that you would expect to see at birth. The graph below is an example of this phenomenon, displaying the log rate mortality of women in Alabama between the ages of 22 and 77, where each line represents a different year in time.



While this model holds well for the older age-group, henceforth referred to as the senescence group, younger individuals experience quite different mortality patterns as they age. From birth, the rate of mortality decreases exponentially until the senescence period begins, at which time mortality rates again increase. The graph below of log rate mortality demonstrates this pattern for males in Texas, though this pattern is visible not just within the United States but in nearly all countries since written records of mortality have allowed for demographic analysis.



In order to describe this phenomenon in 1983, Siler proposed a model to capture this change in mortality rate that occurs around five years of age[3] by decomposing rate of mortality into three terms: an infant mortality term, a constant risk term, and a senescence term. Siler originally formulated the model in terms of a survivorship model  $l(x)$ . In other words, the equation estimated the percentage of the population that would live to some age  $x$

$$l(x) = \exp\left(-\frac{a_1}{b_1}(1 - \exp(-b_1x))\right) \exp(-a_2x) \exp\left(\frac{a_3}{b_3}(1 - \exp(b_3x))\right)$$

If we assume that  $x$  represent discrete age groups, than, with  $l(x)$  we may calculate  $S(x)$ , which is the survival rate or the rate that individuals survive to age group  $x + 1$  given that they have lived to age group  $x$ , as well as  $m(x)$ , which is the mortality rate.

$$S(x) = \frac{l(x+1)}{l(x)}$$

if  $S(x)$  is per person then it is true that

$$S(x) = 1 - m(x)$$

and it can be found that  $m(x)$  is

$$m(x) = a_1 \exp(-b_1x) + a_2 + a_3 \exp(b_3x)$$

In this form, the Siler model can be thought to have three independent components that dictate the rate of mortality for three distinct stages in life. The first component dictates the rate of mortality that exponentially decreases from birth and is modeled by the parameters  $(a_1, b_1)$ . The second is the constant mortality

threat that is faced by all individuals and is highest in adulthood, parameter  $a_2$ . The last component is the exponentially increasing rate of mortality that is experienced throughout the senescence period, parameters  $(a_3, b_3)$ .

The benefit of the Siler model of mortality is that it captures most of the phenomenon that we observe across ages well, while still being a fairly straightforward and interpretable model. Others have proposed more complex models in order to catch other nuances observed in mortality, such as the higher than expected mortality rates for young adults; however, as more terms have been added, the generalizability of the model has suffered and the amount of data needed to fit the model has greatly increased[1,4]. Even so, models that solely focus on the age structure of mortality are ill-suited for making projections, either into the future or geographically, and do not take into account how these relationships can affect the estimates of the parameters in the model.

## Forecasting and Lee Carter

The previously mentioned models each offer a descriptive framework for mortality across age. They do not, however, offer a good solution for mortality over time or across regions. In 1992, Lee and Carter developed a model that is still widely used for forecasting mortality at the all-cause and cause-specific level[1,10]. Abandoning the traditional framework of examining age patterns, the model argues that better forecasts can be made by assuming that ages are largely independent in their level and only similar in their rate of change.

In this model we estimate  $m_{x,t}$  which is the rate of mortality for age  $x$  at time  $t$ .  $m_{x,t}$  is estimated using the following equation

$$\log(m_{x,t}) = a_x + b_x k_t + e_{x,t}$$

The model has terms that are both age group specific ( $a_x$  and  $b_x$ ), a set of terms that are specific to time ( $k_t$ ) and an error term that follows a normal iid distribution

$$e_{x,t} \sim \mathcal{N}(0, \sigma_e)$$

Lee and Carter outline a least squares estimate to these specifications in their original paper.  $a_x$  is calculated as the mean of age specific log mortality rates over time or

$$a_x = \sum_{t=1}^T \log(m_{x,t}) / T$$

where  $T$  is the ordinal time points in the analysis indexed from 1, such as years.  $b_x$  and  $k_t$  are calculated simultaneously by taking the singular value decomposition of the matrix  $\log(m_{x,t}) - a_x$  such that the equation follows  $\log(m_{x,t}) - a_x = USV^\top$  from which  $b_x$  and  $k_t$  can be obtained from  $U[, 1]$  and  $V[, 1]$  respectively. These values then can generate estimates for any in sample time point. In order to forecast Lee Carter states that the  $k_t$  parameters can be forecasted forward using a forecasting method from the ARIMA family. In their paper they use a Random Walk model that follows the specification

$$k_t = k_{t-1} + d + \epsilon_t$$

$$\epsilon_t \sim \mathcal{N}(0, \sigma_\epsilon)$$

This model produces sensible results in terms of short term forecasts and has performed well in datasets in the US from 1970 to 2005[1,10]. Furthermore, the Social Security Administration and the US Census Bureau have reported using variants of the Lee-Carter model for their projections and social security planning[1].

While this model has performed well when tested on US mortality data, it has performed lackluster in other environments. Because of the lack of age structure, the model produces nonsensical results where adjacent age groups have differing and sometimes opposite rates of change in log rate mortality. This is seldom a problem for short-term forecasting, such as 5 years, but with more long-term forecasting, it can create patterns of mortality that do not resemble the standard age curve that Siler captured in his descriptive model. In 2006, Girosi and King wrote a response to the Lee-Carter model showing where the model works well, the times that it does not, and criticizing the approach for not pooling information across age and geography[2].

## Modified GeoTemporal Siler

In order to fit all the dimensions of concern while still maintaining a coherent age structure this project attempts to use a modification of the Siler model which accounts for deviations away from the expected value due to relatedness across multiple dimensions while also including temporal change. The model can be broken down into three familiar components. The first component is a modification of the Siler model specified above and follows the form

$$S_a = (N0exp(\lambda a) + c) \times (1 - pr_a) + pr_a \times (ma + b)$$

where

$$pr_a = 1/(1 + exp((\kappa - a)))$$

The first term in the first equation corresponds to the infant mortality term in the Siler model and the second term is the senescence component. The terms  $N0$

and  $c$  dictate the drop in infant mortality from birth as the rate and intercept in log space. The terms  $m$  and  $b$  account for the linear growth in log space in older ages of mortality. The  $pr_a$  term accounts for the transition from experiencing mortality at child levels to adult levels which begins to transition at some age  $k$ . This component uses a logit transfer to model the parameters scaled from 0 to 1 as age increases such that, as one gets older, one experiences less and less of the infant mortality effects.

The second component in the equation is a temporal term, which accounts for technological innovation over time.

$$temporal = \beta \times time$$

This component has the ability to incorporate within it the effects of covariates relating to medical and technological innovations that affect mortality. For this analysis, we simply used time as a proxy for innovations and their effect on mortality. That is to say that we expect that, as time passes and innovations happen, mortality will decrease.

The first two components constitute what we consider the deterministic skeleton. The deterministic skeleton is how we perceive that mortality changes over age and how we believe it progresses over time, independent of any observations. Observations that we do see are assumed to be centered around this deterministic skeleton with some error.

The last component is the structured random error term, which captures relatedness across three dimensions: age, space, and time. In this way, we acknowledge that the deterministic skeleton captures the baseline estimate, and that our errors are not independent but, rather, are correlated across the dimensions as stated above. In order to capture the relatedness of these errors, we use the following specification

$$\phi_{l,a,t} \sim \mathcal{N}(0, Q^{-1})$$

$\phi$  can either be thought of as a vector of random variables, which follow the distribution as shown above on the right, or a 3-dimensional array for the dimensions location, age, and time, which we show above on the left for the convenience of notation.

$Q$  acts as the precision matrix, which is the inverse of the variance-covariance matrix. This matrix is a square and of length equal to the product of the numbers of locations, ages, and times and is composed of three structured precision matrices corresponding to our dimensions of concern. These precision matrices can be combined for joint precision by using the Kronecker product as shown below.

$$Q = Q_{loc} \otimes Q_{age} \otimes Q_{time}$$

The age and the time precision components follow a first order autoregressive (AR1) process where the precision matrix is as follows

$$Q_{i,j}^{AR} = \begin{cases} \frac{1}{\sigma^2}, & \text{if } i = j = 0 | i = j = \max(i) \\ \frac{1+\rho^2}{\sigma^2}, & \text{else if } i = j \\ \frac{-\rho}{\sigma^2}, & \text{else if } i \sim j \\ 0, & \text{otherwise} \end{cases}$$

For modeling purposes, we used discrete units for both age and time where the ages reflect binned age groups, described in detail later, and years are single year groups. This method allows for a trivial application for the AR1 precision matrix to be applied to each dimension.

The precision matrix for the geospatial portion follows a conditional autoregressive (CAR) form where elements are autoregressive if they are considered neighbors. Because we are using an areal approach, using two dimensional units in space rather than a single point in space, we determine neighbors as those geographical units that share a border with one another. The matrix is defined as follows

$$Q_{i,j}^{CAR} = \begin{cases} \frac{1}{\sigma^2}, & \text{if } i = j \\ \frac{-\rho}{\sigma}, & \text{else if } i \sim j \\ 0, & \text{otherwise} \end{cases}$$

Restrictions to this precision matrix require that  $\sigma$  be greater than zero and the matrix be diagonal dominant. That is that any diagonal element for any row must be greater than the sum of the absolute values of the off diagonal for that row. This may be achieved, by making the maximum value of  $\rho$  be slightly less than 1 over the maximum numbers of neighbors any one location has. This may be achieved by a logit transform with a scale.

The full model is then described as

$$\log(\mu_{lat}) = S_a + temporal_t + \phi_{lat}$$

with a probability distribution

$$\log(m_{lat}) \sim \mathcal{N}(\mu_{lat}, \sigma_{obs})$$

where  $m_{lat}$  is the observed data and  $\mu_{lat}$  is the predicted.

In structuring the model in this way, the deterministic skeleton ensures that estimates will follow a coherent age structure that fits with our past observations regarding the way that mortality operates.

Forecasting using this model is rather trivial, as no parameters in the deterministic skeleton change over time and the random effects can be propagated into the future with uncertainty by using the precision structure defined above.

## **Fitting the model**

### **Data**

We evaluated the model as fitted on US state mortality data between the years of 1990 and 2015. US data affords the luxury of being from a near complete and comprehensive vital registration system that tracks most deaths at the state level for any given year, while documenting age. This data also provides the benefit of being used for testing many times such that comprehensive benchmarks already exist for forecasting. Data was collected from the Institute for Health Metrics and Evaluation (IHME) reporting values for the Global Burden of Disease (GBD) Project 2015. Data was obtained for all states within the United States, including the District of Columbia but excluding Hawaii and Alaska because of their geographic isolation, for every year between 1990-2015, and for the age groups reported in the GBD. Data on the number of deaths that occur in a state along with the population for each year and age group were used to calculate an observed rate of death for each state.

The model uses discrete age groups in line with what IHME has produced for the GBD projects. The age groups used are 0-7 days, 8-28 days, 28-365 days, 1 year to 5 years, and then 5 year age groups up to 80 years of age, for a total of 19 mutually exclusive age groups.

### **Evaluation**

To evaluate the model performance, the model was fit on the years spanning between 1990 and 2005, and error metrics were calculated using various holdout data from 2006 to 2015. Afterwards, full forecasts were made out to 2030 using the entire data set. Separate models were run for males and females.

In order to benchmark our model, we compared our results against the Lee-Carter model described above. Comparisons were made by taking the out-of-sample root mean squared error (RMSE) for the holdout fitted model in two time points, 2009 to 2011, and 2013 to 2015. These time points were chosen to test how changes deeper in forecasting periods can reflect differences in model performance. Results were reported separately for males and females.



## Statistical Approach

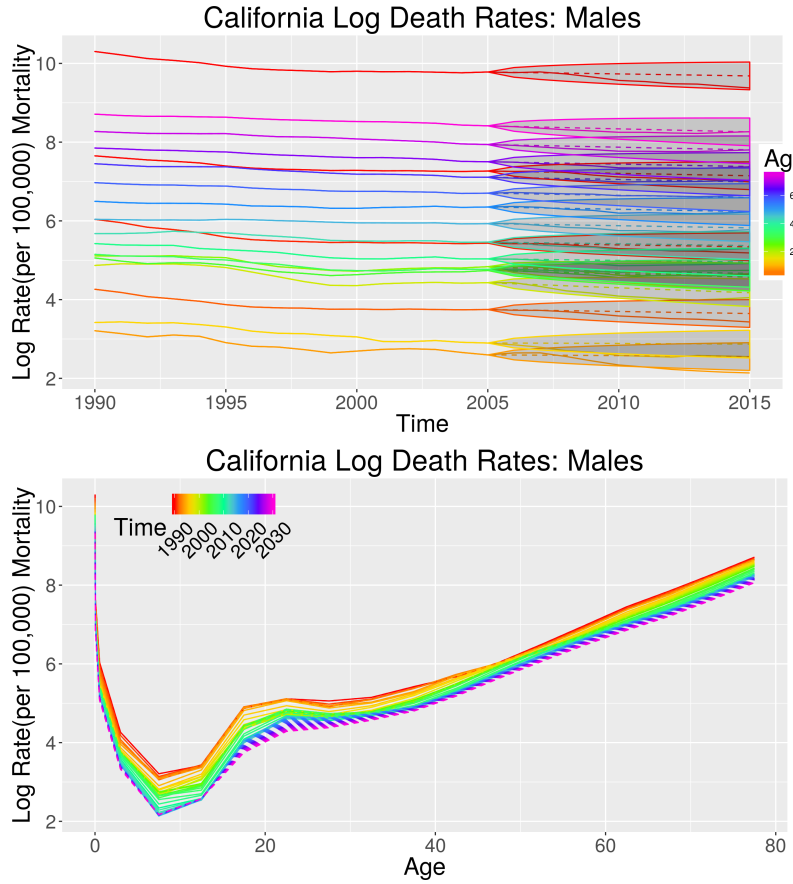
Both models were fit using R version 3.3.2 on a unix operating system. The modified Siler model used the package Template Model Builder (TMB) which uses a C++ template file to obtain the maximum likelihood estimate of a model's parameters given a set of observed data. TMB allows users to specify which parameters to be considered as fixed effects vs. random effects, dictating which part of the optimization process, inner or outer, the parameter is part of. All parameters in the deterministic skeleton were considered fixed effects for this analysis, while all others were considered random effects. The likelihood of the model is determined by the probability distribution specified above. The model is fit using a maximum likelihood estimate to minimize the negative log likelihood of the data, given the random effects structure of our  $\phi$  parameter.

The full set of code used to run the analysis can be found here:

[https://github.com/nmmarquez/2016\\_Spatio-temporal\\_models/tree/master/mort\\_project](https://github.com/nmmarquez/2016_Spatio-temporal_models/tree/master/mort_project)

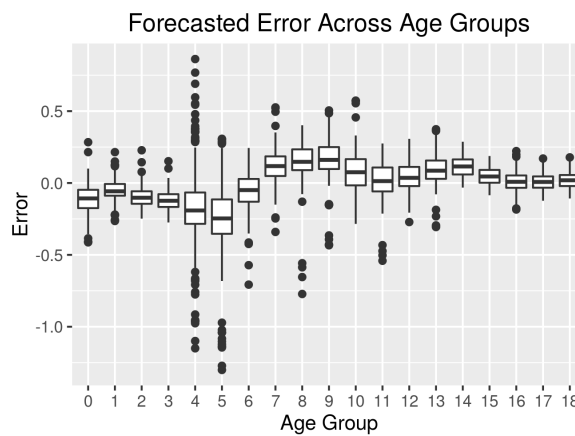
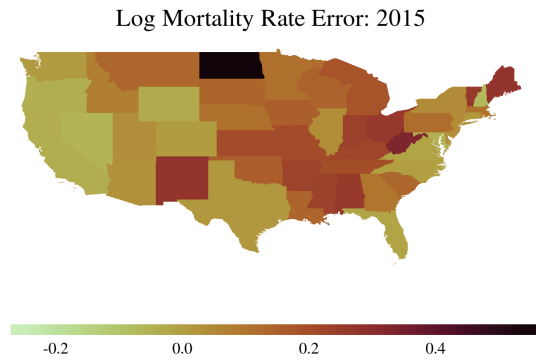
## Results

Below is the fit of data between the years 1990 and 2005, predicting forward to 2015 for the state of California. The second plot switches the age and time dimensions to show that, as the model forecasts, it maintains the Gompertz age structure. The second plot is fitted using the full data set and forecasted out to 2030.



An important take away from these results is the difference in the rate of declining mortality for all age groups. Because the temporal component of the model varies by age group, much of the explanation of temporal change is attributed to the correlation in the error, with only a minimal portion attributed to the temporal trend component of the model. Because of this, we see big drops in mortality in the future at the age groups around 20 year olds and smaller drops in mortality in other age groups.

Below is the average difference between the predicted value and observed value for every age group by state for both males and females between 2013 and 2015. This geographic error shows that there is still systematic bias overestimating mortality in the Midwest states compared to states on the west coast, suggesting that we may not be capturing all of the geographic trend with our parameter  $\phi$ .



Above is the average difference between the predicted value and observed value for each age group by state for both males and females between 2013 and 2015. Younger age groups tend to have an underestimated prediction, shown by the negative error in the age plot, while the age groups in the middle ages tend to have a systematic overestimation in the mortality rate. In addition, looking at age group 4, which is the age group of individuals from 5 years to 10 years old, there is a large amount of variation in the residuals when compared to the adjacent age groups. This suggests that our model may not be successful at capturing the transition from declining mortality rates at young ages to increasing rates at older ages.

## Comparison to Lee Carter Model

### Model RMSE Results for Males

YEARS EVALUATED	SILER	LEE CARTER
2009-2011	.1329	.1470
2013-2015	.1822	.1844

### Model RMSE Results for Females

YEARS EVALUATED	SILER	LEE CARTER
2009-2011	.1629	.1627
2013-2015	.1910	.1875

Despite the faults described, comparisons to the Lee-Carter model via out-of-sample RMSE show comparable results. The modified Siler model performs better in measures of RMSE for both sets of years evaluated for males, while the reverse is true for females. This result indicates that the Siler model is more robust to the shifts in mortality for males than for females. Both models had a higher out-of-sample RMSE for the female model, indicating that there is more variation in females that is difficult to capture with either model. Case and Deaton have highlighted in a recent study that there has been a recent reversal of mortality trends over time for middle-aged females within the United States[5]. Perhaps both models have struggled to capture this phenomenon, however, this has not been tested in this analysis.

## Discussion

In this test case scenario using data from the US, our Siler model performed at least as well as the Lee-Carter in the demographic breakdowns that we analyzed. As is, the model could be considered for use in other endeavors of demographic forecasting, given that it performs well in out-of-sample validity tests.

### Potential Alterations to the Deterministic Skeleton

While the modified Siler model presented performed well in predicting data that was held out from the model building process, further adjustments could improve model process or at least offer a diagnostic for model fit. The backbone of the modified Siler model is in the deterministic skeleton, which closely resembles the original Siler model with an added component for temporal technological advancement. The advantage of this model is that it constrains estimates to be centered around a pattern of mortality relating to age that we have empirically

observed to be true. This being said, there have been several descriptive models used in the field of descriptive demography that could have been used as the basis for our model. Testing how this model performs as the age governing portion of the deterministic skeleton changes could lead to a better fit of the data. Two potential candidates for replacement of the Siler model are the Heligman-Pollard model and the multi-exponential model, both of which are outlined in a review of mortality models and forecasting by Boothe and Tickle[1,4].

In addition to replacing the deterministic skeleton with a similar model for mortality, which largely imposes our assumptions about how mortality operates over age, we could also use a less-structured model and allow the data to govern the shape of the base model. One way that this could be done is by the use of a spline model. Spline models have the advantage of being well-studied outside of the context of demographic studies, while still having a history of use in mortality modeling. Both Currie and Shyamalkumar[7,8] outline how they have used P-splines and cubic splines respectively in order to make estimates for mortality, with Currie detailing methods for making projections. One advantage of using a spline model is that formulations exist that reduce the amount of correlation among parameters, such as a basis spline. This is a peril that most of the descriptive models of mortality face as outliers have an extreme effect on parameters due to the high correlated nature of those parameters.

One other component of the model that may be changed that is not directly related to the deterministic skeleton is the likelihood evaluation portion of the model. Currently, the likelihood of the model is assessed in log rate space with a normal distribution centered around our estimate. The data generation process, however, is observed in counts and thus may not reflect a normal distribution in log space. Rather than evaluate the model's likelihood in this fashion with a normal distribution

$$\log(m_{lat}) \sim \mathcal{N}(\mu_{lat}, \sigma_{obs})$$

we could alternatively evaluate the models counts using a Poisson distribution.

$$deaths_{lat} \sim Poiss(\mu_{lat} * pop_{lat})$$

where  $pop_{lat}$  is the population for a particular observed location, age, and time,  $\mu_{lat}$  is our predicted rate from the model and  $deaths_{lat}$  is the actual observed counts of death in that demographic. While this model was not feasible for our case due to the unit size of our location, this model could act as an alternative with smaller areas of estimation, such as at the county or zip code level.

## Alterations to the Random Effects Structure

Another area of potential improvement comes from the structure of the random effects. To review, each location, age, year for a modeled sex had its own random effect that was correlated in each dimension by using either a CAR or AR1 precision structure from which the Kronecker product was taken to get the joint change across these demographic dimensions, captured in our parameter  $\phi$ . This structure captures the joint correlation in the residuals of these dimensions; however, it can be argued that each of these dimensions has an independent effect as well.

To highlight how additional random effects alter the model, we will describe three hypothetical parameters that may be included, what including them means for our estimates, and how their inclusion can be used as a diagnostic tool for the model. Each of these vectors of parameters will be described as marginal effects, as they pertain to the effect of correlation across a single dimension and can be conceptualized as the partial derivative with respect to that dimension. Each marginal effect will have the same covariance structure as the corresponding precision matrix in the parameter  $\phi$ . That is to say that the marginal time, age, and location parameters will have a covariance structure of AR, AR, and CAR respectively.

The first marginal effect we will examine is the age marginal effect. This is potentially the most interesting because our model is strongly based on defining a sensible age structure. Nonetheless, the inclusion of a marginal age effect would reduce the variation in age that is placed on the joint parameter  $\phi$  while individually highlighting the amount of variation explained only by changes in age. This effect serves as a diagnostic tool for the age structure of our deterministic skeleton, because we would expect that, as the skeleton more accurately describes the general pattern of mortality across age, the amount of variability explained by the age marginal effect would decrease.

A marginal effect on time serves a different theoretical purpose than the marginal effect on age. Rather than acting as an indicator of the goodness of fit for the deterministic skeleton, the time marginal effect acts as a safeguard to shocks that affect a single year across all geographies. Perhaps the most exemplary example of this kind of temporal shock in the US is the flu epidemic that occurred in 1918. What is often considered to be one of the deadliest natural disasters in recent human history, the 1918 influenza epidemic caused life expectancy to drop in males from 49.6 to 36.6 years of life and 54.3 and 42.2 years of life in females in the US[6]. While the time series that we covered in this analysis did not cover any mortality epidemics of the magnitude of this incident, the effects that the 2008 financial fallout had on mortality rates could be a temporal factor affecting mortality patterns that is not currently modeled appropriately.

A marginal geographic effect would offer the same kind of protection to consistent geographic outliers in our data set, independent of age and time. An example

of this is the low life expectancy and conversely high mortality rates, that have been observed in the southern states of the US[9].

## Conclusion

In this analysis we presented an alternative model for forecasting mortality, which uses a structured age component based off the Siler model of mortality, a temporal component for development as a deterministic skeleton, and structured random effects to allow pooling data across regions and time. Additionally, the model contains an explicit method for forecasting mortality results for separate locations and ages. This model differs from other models in that it incorporates the age structure that is inherent in descriptive models of mortality, while simultaneously leveraging relationships in other dimensions of concern, namely time and space, in order to make estimates. In doing so, the model is able to take into account rates of change observed in the past for a particular age group, as in the Lee-Carter model, while keeping a coherent age structure, a criticism that was posited by Girosi-King in their critique of the Lee-Carter model.

In addition to addressing the theoretical concerns that are often addressed when modeling mortality, this model was shown to produce comparable results in terms of out-of-sample RMSE when compared to the Lee-Carter model, a model that is used heavily in demographic forecasting for mortality. The benefit of the modified Siler model over the Lee-Carter model is that it maintains the age structure of observed results well into the future. While this model is not meant to take the place of any existing models for forecasting mortality, it has proven in this analysis to provide comparable results to well-established models such as the Lee-Carter model, and should be considered when modeling mortality and pooling data across geographies and time.

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