Forecasting US Mortality

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Modeling Mortality

Modeling human mortality has had a long history of attempts and revisions since Gompertz first made his claim of human mortality patterns in the 1880s. The ability to accurately model and describe rates of mortality can have numerous effects on how social institutions and policies can be structured in order to meet the needs of its populations. For example knowing the age pattern of mortality allows a society to build the medical infrastructure to cope with the needs of different aged individuals. Knowing the root causes of mortality allow for the change of policy in order to reduce specific drivers of mortality.

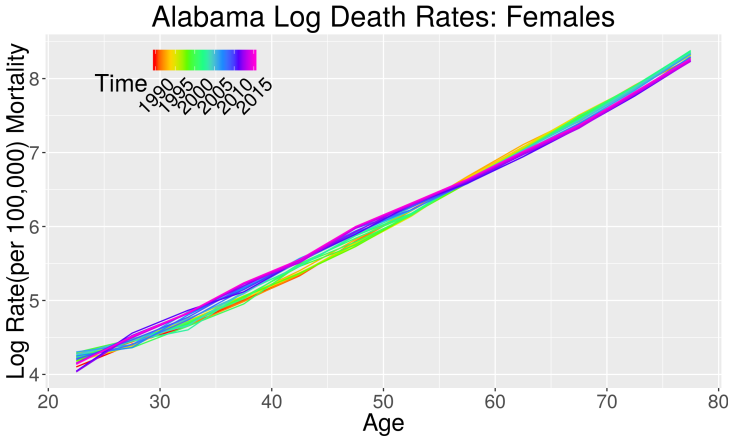
Another aspect of mortality that is often of concern is the future rates and how they differ from the past. Over the past century there has been dramatic declines in mortality across all locations and ages. While that progress has stagnated to some degree we still see dramatic decreases in mortality among developing countries where medical infrastructure is expanding and improving. As this happens we would expect there to be a direct effects on the population, production and needs of a society.

History of Descriptive Models

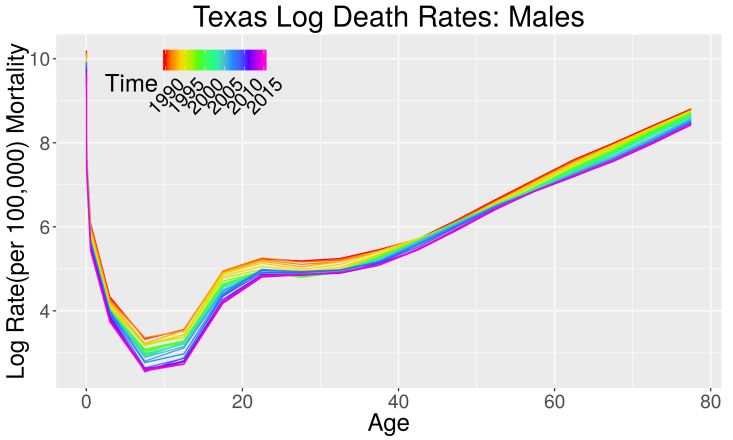
Descriptive models of mortality have an inherent age structure to them that allow for a simple descriptive explanation of how death effects individuals across their life-span. Gompertz first claim about human mortality was that there is a linear increase in log rate mortality as one aged. This model 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. Below is an example of this phenomenon where we graph the log rate mortality of women in Alabama between the ages of 22 and 77.



While this model holds well for older ages, henceforth referred to as the senescence group or period, younger individuals experience quiet different mortality patterns as they age. From birth the rate of mortality decreases exponentially until the senescence period is started at which time the mortality rates will then again increase. Below is the log rate mortality for males in Texas which shows this pattern that is visible not just within the United States but nearly all countries since written records of mortality have allowed for demographic analysis.



In order to capture this in 1983 Siler proposed a model to capture this switch in mortality patterns by decomposing rate of mortality into three terms, an infant mortality term, a constant risk term and a senescence term. Siler had originally formulated the model in terms of a survivorship $l(x)$, that is the equation estimated the percentage of the population that would live to some age x

$$l(x) = exp\bigg(-\frac{a_1}{b_1}\big(1 - exp(-b_1 x)\big)\bigg) exp(-a_2 x) exp\bigg(\frac{a_3}{b_3}\big(1 - exp(b_3 x)\big)\bigg)$$

If we assume that x represent discrete age groups then 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 than

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

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

$$m(x) = a_1 exp(-b_1 x) + a_2 + a_3 exp(b_3 x)$$

In this form the Siler model can be seen to have three independent components which 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 tuned by the parameters (a_1, b_1), the second is the constant mortality threat that is faced by individuals and most experienced in adulthood, parameter a_2, and last is the exponentially increasing rate of mortality that is experienced late in life, parameters (a_3, b_3).

The benefit of the Siler model of mortality is that it captures the change most of the phenomenon that we observe across age 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 tends to suffer and the amount of data needed to fit the model greatly increases. Even so, models that solely focus on the age structure of mortality are ill suited at making projections, either into the future or geographically, and do not take into account how these relationships can effect the estimates of the parameters in the model.

Forecasting and Lee Carter

These models all offer a descriptive frame work for mortality over age however they do not offer a good solution for mortality over time or across regions. In 2000 Lee & Carter developed a model that is still this day widely used for forecasting mortality at the all cause and cause specific level. Abandoning the traditional framework of looking at 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

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

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

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

$$m_{at} \sim \mathcal{N}(\mu_{at}, \sigma^2)$$
$$\mu_{at} = \beta a \gamma t$$
$$\gamma_t = \gamma_{t-1} + \theta + \epsilon_t$$
$$\epsilon_t \sim \mathcal{N}(0, \sigma_{rw}^2)$$

While this model has preformed well when tested on US mortality data from 1970 to 2005 within the US it has performed lackluster in other environments. Because of the lack of age structure th model produces nonsensical results where adjacent age groups have differing and sometimes opposite rates of change log rate mortality. In 2006 Girosi and King wrote a response to the model showing where the model works well and the many times that it doesnt and criticizing the approach for not pooling information across age and geography.

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

$$S_x = (N0exp(\lambda x) + c) \times (1 - pr_x) + pr_x \times (mx + b)$$

where

$$pr_x = 1/(1 + exp(3 * (\kappa - x)))$$

The first term in the first equation corresponds to infant mortality term in the Siler model and the second term is the senescence component. The model also has a temporal trend added to it which accounts for some technological innovation over time.

$$temporal = \beta \times time$$

This component has the ability incorporate within it the effects of covariates the mark medical and technological innovations that effect mortality however we will simply use time in this exercise as a proxy for their effect on mortality. That is to say that we expect that as time passes mortality will decrease as innovations happen.

The last component is the structured random error component which captures relatedness across three dimensions of error, age, space and time. The structure is as follows.

$$\phi \sim \mathcal{N}(0, Q^{-1})$$

Q acts as the precision matrix for this model which is composed of three independent portions.

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

The age and the time precision components follow an 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 will be using discrete units for bot age and time where the ages reflect Global Burden of Disease age Groups and years are single year groups. This allows for a trivial application for the AR1 precision matrix to be applied to each dimension.

The precision matrix for a the geospatial portion follows a conditional autoregressive form where elements are autoregressive if they are considered neighbors. Because we are using an areal approach 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 σ 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 ρ 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 seen as

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

with a probability distribution

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

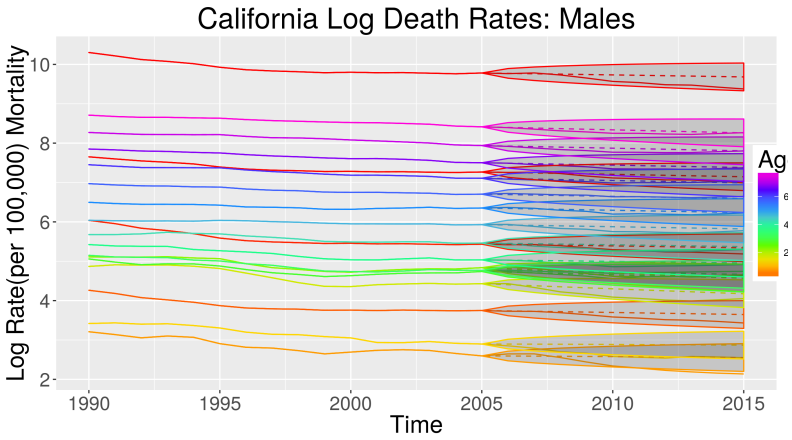
Fitting the model

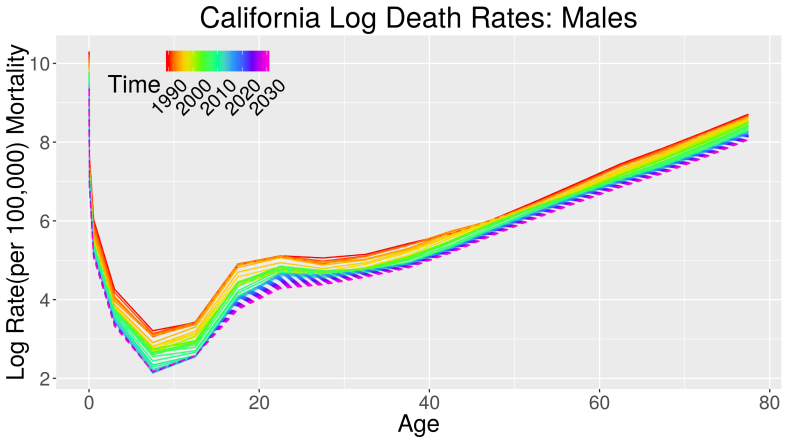
In order to test the model we will evaluate the model as fitted on US state mortality data between the years of 1990 to 2015. US data has the luxury of being from a near complete and comprehensive vital registration system that tracks most deaths at the state level for any given year well while documenting age. This data also has the benefit of being tested on many times such that comprehensive benchmarks exist for forecasting.

To evaluate the model performance the model will be fit on the years spanning between 1990 and 2005 and then error metrics will be calculated using holdout data from 2012 to 2015. After this full forecasts will be made out to 2030 using the entire data set. Separate models will be run for males and females.

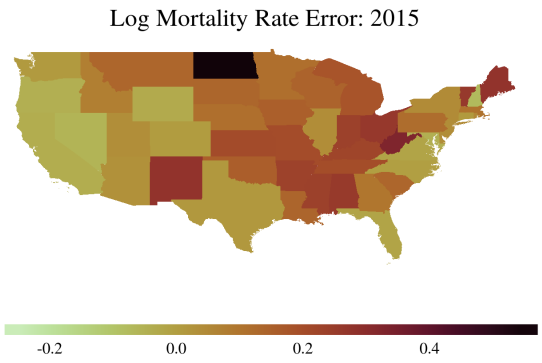
Results

Below is the fit of data between the years 1990 and 2005 predicting from then on forward 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.

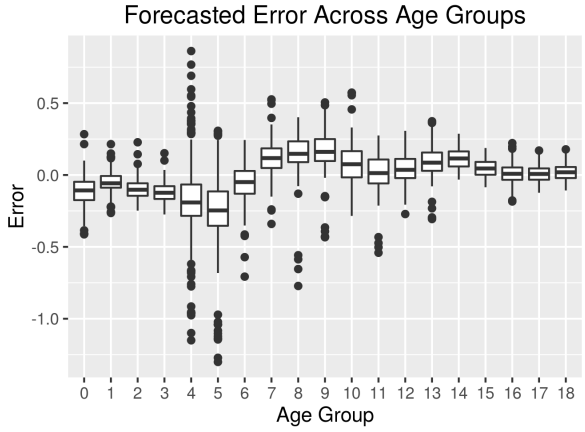




Below is the error map shown with model for out of sample results between 2013 and 2015.



And below is the difference in out of sample error within age groups.



Discussion

While the model fits the data relatively well future changes to the exact parameterizations of the model will need to be done to account for the current biases in the model. Currently the model systematically is biased upwards for young age groups relative to old age groups. This can be seen in the error by age group graph above for out of sample data. This could mean that changes to log rate mortality are changing more rapidly for young ages compared to older ages.

In addition the map above shows that there may be some regional effects that are not captured well in this model. In order to alleviate this a random effect that just captures geography effect could be added.

While this model was unable to come to the level of predictive validity of either the Girosi-King model or the Lee-Carter model, it retention of age pattern offers hope that it can be used in the future. In these runs of US data the temporal trend for the model was shown to be relatively weak however the US is a relatively stagnant country when it comes to decreases in log rate mortality over time and testing on other countries is a must to get the full scope of the generalizability of this model.

References

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[2] Girosi, F., King, G. (2006). Demographic Forecasting. Cambridge University Press, Cambridge.

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