Incorporating Migration Into an Age-Structured Population Model With Variable Mortality Rate

G. Martinez, F. Nungaray, and L. Smith Chowdhury*

Abstract - We modify the McKendrick-von Foerster population model, an age-structured population model, by including a net migration term to model population dynamics when net migration is a significant contributor to population size. Net migration is treated as a continuous function of age and time. We consider the model's mortality rate as both a constant and as a function of age. By allowing the mortality rate to be a function of age, the model better captures more realistic death rates. We then apply this model to the United States population. When the mortality rate is considered as a constant, the model has 3.95% relative error. When the mortality rate is considered as a function of age, it yields a better approximation with a 2.33% relative error. This more accurate model of population dynamics can provide a framework for studying the effect of policy changes and major events on populations and sub-populations.

Keywords : mortality rate; migration; age-structure population model

Mathematics Subject Classification (2020) **:** 92D30; 35Q92

1 Introduction

Immigration and emigration have often become an important topic for countries with large numbers of migrants. In 2015, it was estimated that 244 million people were migrating into a foreign country seeking employment, refuge, and other incentives [8]. Over three million Venezuelans have emigrated to seek economic opportunity [6]. The civil war in Syria encouraged people to seek refuge in countries along the Mediterranean Sea [6]. Among all the countries in the world, the United States has become the country with the most immigrants [8]. Many population models focus on closed systems where individuals do not migrate in or out of the system. Since migration can greatly affect the size of a population, it will be necessary to include it in population models for countries where the net migration is significant, such as the United States.

Typically, a population model includes an initial population, birth rates, death rates, and other factors relevant to changes in the population. We modified a population model, known as the McKendrick-von Foerster age-structured population model, to include net migration [21]. An age-structured population model assumes individuals of the same age

---

*This work was supported by the Graduate Readiness and Access in Mathematics program, and funded by the National Science Foundation grant No. 1345012

will age together at the same rate and will die with the same death rate. Thus, these models use age and time as independent variables, resulting in a partial differential equation (PDE) model. An age-structured population model is appropriate for consideration since there is significant variability in both the age of migrants and the mortality rate for humans, which is highly dependent on age. For example, among U.S. children aged 1–4 years there were 28.6 deaths per 100,000 in 2007 [20], which is an extremely low death rate compared to older age groups, where there were 4,987.1 deaths per 100,000 for ages 75–84 [7]. Health problems such as heart disease and cancer remain as the top two causes of deaths for adults [7], giving a significantly higher death rate for the elderly. This leads us to include a mortality rate that depends on age in our age-structured population model. With this age-dependent mortality function and net migration, we are able to produce reasonable population estimates when applied to the United States population. We will show that our model yields a smaller error when age is incorporated as an independent variable than when it is omitted.

2 Literature Review

Age-structured and stage-structured population models are often used in the literature, since many aspects of population change depend on the age or stage of the individuals. Some models include independent variables such as age, size, or location. For example, the McKendrick model investigates the change in cell population relative to age and size [21]. In 1967, James W. Sinko and William Streifer proposed a size-structured population model that uses time, size, and age as independent variables [10]. The McKendrick-von Foerster model uses time and age as independent variables [21] and is a special case of the Sinko-Streifer model. In the 1970s, Gurtin and MacCamy also developed a similar nonlinear age-structured population models where the survival and maternity functions depended on both age and the current population size [28]. Since then, age-structured population models have been used in a variety of applications, such as in epidemiology [23, 24, 25, 26, 29], where disease latency or vaccinations are age-dependent. The McKendrick-von Foerster model has also been extended to a stochastic differential equation [19].

Age-structured population models are often in the form of differential equations. However, they may also be discrete models, such as the Leslie matrix. The Leslie model is used to track the succession of population groups over a selected interval of time [13]. Additionally, the Leslie model is one of the various ways to numerically approximate the McKendrick-von Foerster equation [13, 12]. The Leslie matrix has also been used in extensions that include stochasticity to allow for fluctuations due to demographic and environmental factors [15, 30].

The McKendrick-von Foerster model only considers population dynamics of a closed system, which does not allow for migration. By considering a continuous open system, a model would be able to better capture a population where migration is significant. One model modifies the McKendrick-von Foerster model with an immigration term, considering only the female population [27]. Another model that included immigration and emigration with similar modification was applied to the human population in Spain [14]. Here, the authors fit smooth curves to the birth, death, and migration data in order to make predictions about future population estimates. In a recent study, the authors consider immigration by modifying the McKendrick-von Foerster model into two separate equations, one for the resident population and the second for migrant population [18]. Another approach extends the McKendrick-von Foerster model in an environment divided into patches, allowing for migration between patches [17]. Instead of the McKendrick-von Foerster model, one approach was to add a non-negative age-dependent migration function to the similar Lotka-von Foerster system [11]. All of these models involve adding a term to the original model, and our approach is similar to that of [14, 18, 27]. We consider our base model to be the McKendrick-von Foerster model, since it is a first-order partial differential equation and can be solved using analytical methods.

3 U.S. Population Data

Data were collected for the following different categories: population, births, mortality, and migration. We include these categories in order to address the elements presented in the proposed model in Section 4.2.

3.1 Population Data

The population data were retrieved from the national intercensal datasets 2000–2010 and the annual estimates of the resident population 2010–2016 [1, 2]. The national intercensal datasets (estimates of the population between two official census dates) are estimates of resident population organized by single age per year, sex, race, and Hispanic origin from April 1, 2000 to July 1, 2010. The population data includes births and deaths of U.S. residents, domestic migration, international migration, and net movement of the U.S. armed forces [3]. Domestic migration and the net movement of the U.S. armed forces do not affect the model, since these populations do not migrate in or out of the U.S. population. The annual estimates of the resident population for the datasets from April 1, 2010 to July 1, 2016 were categorized by two criteria: age and sex of the individual. These estimates take into account the change in population from births, deaths, and migration. The national intercensal datasets and the annual estimates datasets are merged and organized by age for each year from 2004 to 2014 (see the Appendix for more detail). These are two separate datasets with two different methods of estimating population size, with the intercensal data providing population estimates up to age 85 and the remaining estimates are summed into age 999, an unrealistic age. The annual estimates provide data by age for each year up to age 100 with individuals over 100 grouped together. Due to this inconsistency in the data, our study utilizes only the data from ages 0 to 84 from the combined datasets.

3.2 Birth Data

The birth data were obtained for the years 2004 to 2014 from the Centers for Disease Control and Prevention (CDC) WONDER online data bank [5]. The datasets, natality for 2003–2006 and the natality for 2007–2016, were queried to extract the birth totals grouped by year. The data account for births in the United States from U.S. residents and non-residents (individuals not classified with resident status, such as people holding student visas) [5].

3.3 Mortality Data

The mortality data were obtained from the CDC WONDER online databases for underlying causes of death from 1999 to 2016. Data were available to download with grouped ages starting with "$<$ 1 year", "1–4 years", and then groups of 5 year intervals. The data do not include deaths of non-residents. The death counts are derived from death certificates from all fifty states, excluding Puerto Rico, Guam, the Virgin Islands, and other U.S. territories [5]. Death counts that are zero to nine are suppressed.

3.4 Immigration Data

Immigration data were retrieved from the U.S. Homeland Security Yearbook of Immigration Statistics [16]. The data are grouped by year, containing data on foreign nationals who were granted lawful permanent residence, admitted with a temporary status, or applied for asylum or refugee status [16]. Persons admitted with temporary status are considered "nonimmigrants" since their visit is short and without the intention of permanently residing in the U.S. territories. For the purposes of this study, legal permanent residents, refugees, and asylees are considered in the estimates of immigration data, as represented. To include temporary status individuals would require data on their departure, which is not recorded by any U.S. agency. Since their stay is considered temporary, primarily less than one year, we do not include them in the population count. Undocumented immigrants are not included in this dataset, and therefore, we do not include them in the model. The data are grouped by 5-year age groups up to age 64, followed by age groups 65–74 and over 75. We consider the immigration data to be estimates since the U.S. Homeland Security Yearbooks acknowledge that revisions occur to eliminate duplicates [16].

4 Model Description

This section describes our methodology for incorporating net migration into an age-structured population model. We first introduce size and age-structured population models and then provide the proposed model.

4.1 The Sinko-Streifer and the McKendrick-von Foerster Population Model

The Sinko-Streifer equation is a size-structured population model given as a partial differential equation with time and size as independent variables [9]. Here, size describes a characteristic such as height, weight, or age [9]. The Sinko-Streifer equation assumes individuals of the same size share some common traits [9]. The model defines $u(t,x)$ as the number of individuals of size x at time t. Individuals who increase in size can transition into other sizes as time progresses. It is also assumed that individuals of the same size have the same growth rate (rate of the individual's size increasing) and the same probability of death. Also, the size of the population is assumed to be sufficiently large, and the size x of an individual is within some size interval, $x_{min} \leq x \leq x_{max}$.

Sinko and Streifer proposed the model,

$$\frac{\partial}{\partial t}u(t,x) = -\frac{\partial}{\partial x}(g(t,x)u(t,x)) - \mu(t,x)u(t,x),$$

where the growth rate is denoted by $g(t,x)$ and the death rate as $\mu(t,x)$ for individuals of size x at time t. This PDE suggests that population change with respect to time is determined by the change of the growth of the population with respect to size and the number of individuals dying in the population. Births enter the population through a boundary condition, namely

$$R(t) = g(t,x_{min})u(t,x_{min}) = \int_{x_{min}}^{x_{max}} k(t,s)u(t,s)\ ds,$$

where $R(t)$ denotes the number of births at time t, and $k(t,x)$ is a function indicating the fertility rate of the population at a given time and size [9].

The PDE represents the population dynamics of a closed system in which there are no external influences that affect the population. The model is equivalent to the McKendrick-von Foerster equation by considering size as the age α of individuals, giving the model the independent variable α. Since individuals age at the same rate that time passes, the change in age is the same as the change in time, giving $g(t,\alpha) = 1$. This gives the Mckendrick-von Foerster age-structured population model,

$$\frac{\partial}{\partial t}u(t,\alpha) = -\frac{\partial}{\partial \alpha}u(t,\alpha) - \mu(t,\alpha)u(t,\alpha). \tag{1}$$

Note that this model is also for a closed system with no movement in or out of the system except through birth or death.

4.2 Proposed Model

We consider an age-structured population model where individuals can enter and leave the system. We modify Equation 1 to include the net migration represented by the function $M(t,\alpha)$. The proposed model is

$$\frac{\partial}{\partial t}u(t,\alpha) = -\frac{\partial}{\partial \alpha}u(t,\alpha) - \mu(t,\alpha)u(t,\alpha) + M(t,\alpha). \tag{2}$$

The initial condition is given by

$$u(t_0, \alpha) = u_0(\alpha)$$

where $u_0(\alpha)$ is the initial age distribution. The boundary condition that incorporates the births, $R(t)$, into the population is given by

$$R(t) = g(t,0)u(t,0) = u(t,0) = \int_0^{\alpha_{max}} k(t,\alpha)u(t,\alpha)\ d\alpha,$$

where $k(t,\alpha)$ is the age-dependent fertility function and α_{max} is the maximum age.

The proposed model suggests that population change with respect to time is determined by the change in the population with respect to age, the number of individuals dying in the population, and the number of individuals migrating. Births are considered through a boundary condition of the PDE. Unlike Equation 1, the external influence affecting population change comes from the migration of individuals. To solve Equation 2, we require $M(t,\alpha)$ to be a continuous function that represents the rate of net migration. We model this $M(t,\alpha)$ in Section 5 for the U.S. population.

4.3 Process and Observation Errors

The data obtained have observation errors. For the intercensal years, the population data are estimated through models. Migrants might be double counted. Further, there is no record of individuals that emigrated out of the U.S. However, for the purpose of this study, we will assume that the observed data have no errors. An additional consideration for modeling is to include process errors [31]. For simplicity, we will assume our model to be deterministic. This approach may introduce bias in the parameter estimates. Treatment of these errors can be considered further using [32].

5 Modeling the Migration Function for the U.S. Population

The immigration data collected from the U.S. Homeland Security Yearbook of Immigration Statistics are an estimate of people entering the country [16]. Immigrants are counted by category (such as refugees, residents, non-residents), some of which may overlap, and thus, some are double counted. Since there is little to no record of U.S. citizens and residents departing or emigrating to other countries, we use the immigration data only to model a continuous function for $\hat{M}(t,\alpha)$. We then model the net migration $M(t,\alpha) = \delta\hat{M}(t,\alpha)$. This uses the assumption that the age distribution of those emigrating are similar to those immigrating. The variable δ represents the net proportion of $\hat{M}$ that are migrating into the country, which can be negative if more individuals are leaving the country than entering it.

For a fixed year the immigration data, plotted in Figure 1, have a bell curve behavior by age group where the largest population size is composed of middle-aged immigrants. This shape can be seen for each year from 2004 through 2014. As time increases, the peak decays. Based on these observations, we determined a reasonable model for the data is a Gaussian function for the bell curve behavior and an exponential function for time. The immigration data are approximated by,

$$\hat{M}(t,\alpha) \approx \gamma e^{-\beta(\alpha-\sigma)^2} e^{-\lambda(t-t_0)}. \tag{3}$$

Here, σ is approximately the median age, and t_0 is 2004. The γ estimates the maximum immigrant population size at age σ at time $t = t_0$. The parameters that give the least-squares fit to the migration data are,

$$\begin{aligned} \gamma &= 137464.1856 \; \textit{people}, \\ \beta &= 0.0019 \; yr^{-1}, \\ \sigma &= 34.7412 \; yr, \\ \lambda &= 0.0083 \; yr^{-1}. \end{aligned} \tag{4}$$

The immigration data and the migration model, $\hat{M}(t,\alpha)$, are shown in Figure 1. A superimposed comparison is shown in Figure 2. The relative error is 0.0827. Relative error indicates the accuracy of a measurement relative to the size of what is being measured, and it is calculated by

$$\text{Relative Error} = \frac{||\text{Actual} - \text{Estimated}||_2}{||\text{Actual}||_2}.$$

The net migration function is given by

$$M(t,\alpha) = \delta \hat{M}(t,\alpha), \tag{5}$$

where the δ is fit with the data using the entire model for the population.

In order to simplify the problem, a model for the migration needs to be chosen. Based on observing the data, the distribution of immigrants by age was similar to a Gaussian function. This choice has some issues, as we might not expect the data to be symmetric. Further, there is no reason to expect the immigration to decrease exponentially in the future, as this is highly dependent on the government's policies, the economy, political instability, and other factors. This model for the migration can be adjusted to include these factors or other model forms. Other functional forms for the model is left for future work. These could include non-symmetric distributions by age and perhaps linear or sinusoidal curves for time.

5.1 Comparison to Micó et al. Migration Model

To compare our migration model with previously proposed models, we examine the migration model from Micó et al. [14], given by

$$m(t,\alpha) = \left(a_1 e^{-\frac{\alpha}{b1}} + a_2 e^{-\frac{(\alpha-c_2)^2}{2b_2}} + a_3 e^{-\frac{(\alpha-c_3)^2}{2b_3}} + a_4 e^{-\frac{(\alpha-c_4)^2}{2b_4}} \right) \frac{\lambda \beta e^{-\lambda(t-t_0)}}{(1 + (\frac{\beta}{y_0} - 1) e^{-\lambda(t-t_0)})^2}.$$

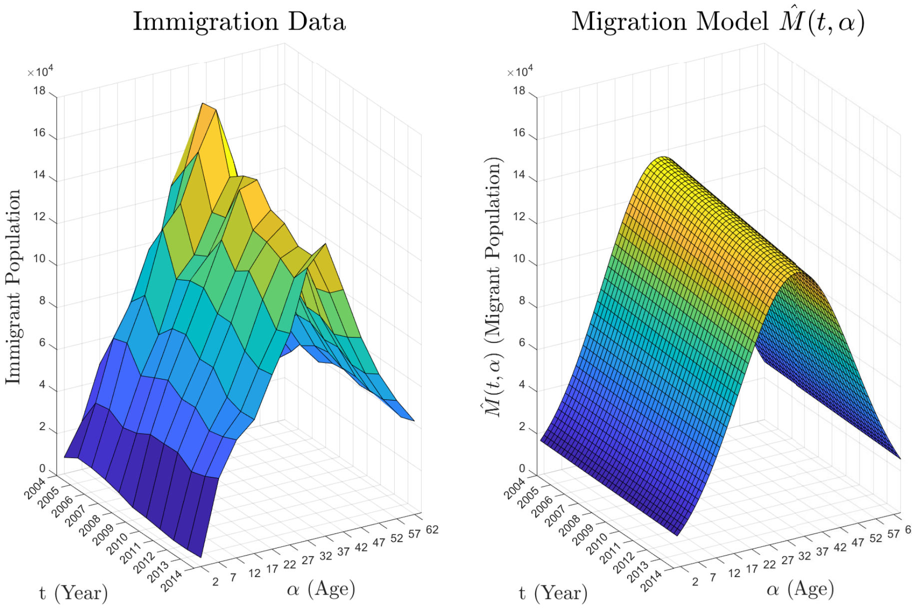

Figure 1: The surface graph on the left represents the data for the estimated immigrant population gathered from the U.S. Homeland Security Immigrant Yearbook Statistics. The surface graph on the right was created using Equation 3.

The parameters were found by a least-squares fit to the immigration data [14]. The Micó et al. model fits the 2004 – 2014 data with a 9.4% relative error, see Figure 3, which is larger than the 8.27% relative error from our model.

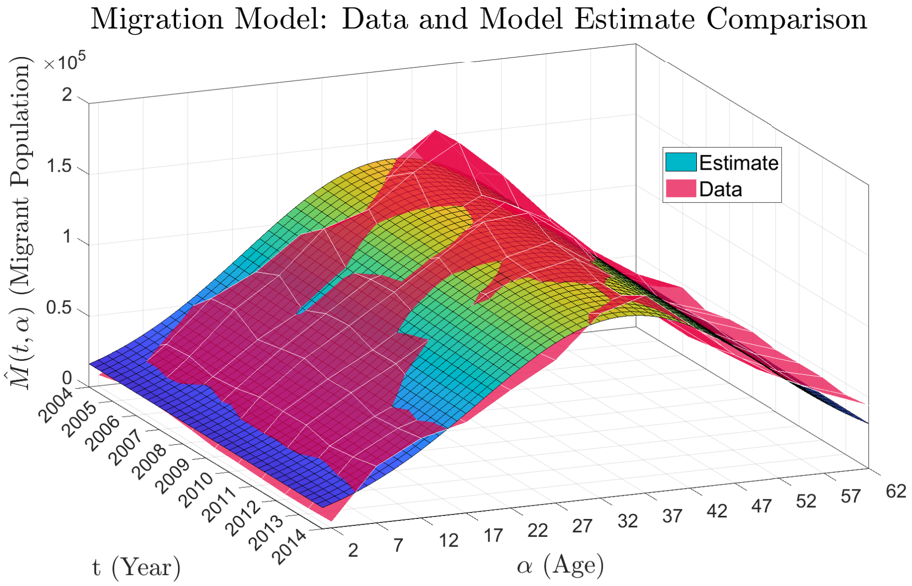

Figure 2: The migration data and the migration model $\hat{M}(t, \alpha)$ are overlaid for a better comparison. The migration model fits the data with a relative error of 8.27% and an AIC value of 2958.2.

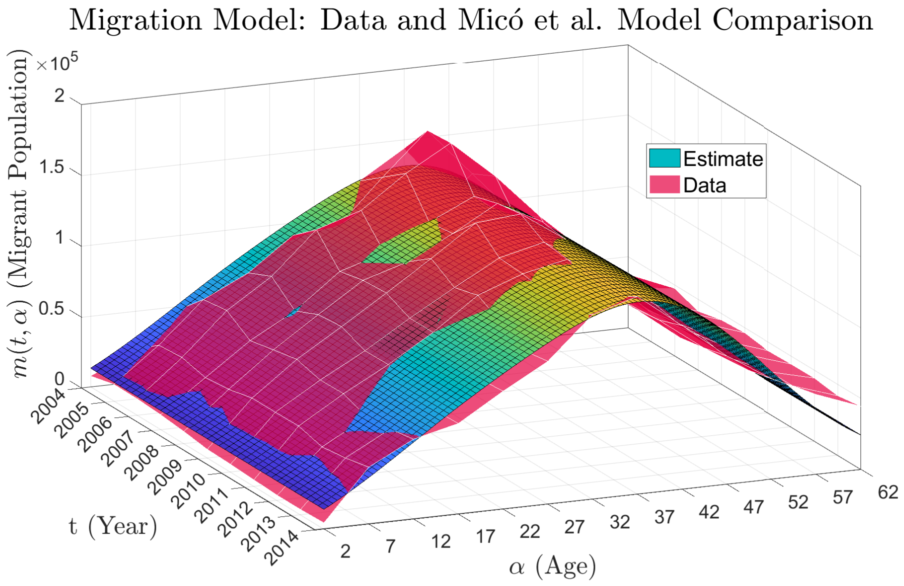

Figure 3: The migration data and the migration model proposed by Micó et al. are overlaid for comparison. The Micó et al. model and the migration data have a relative error of 9.4% and an AIC value of 3014.96.

A second measure used to compare the models is the Akaike Information Criterion

(AIC), where a lower value indicates a better quality model, taking into account the number of model parameters. Our model gave an AIC value of of 2958.2, which is lower than the 3014.96 AIC value of the Micó et al. model.

5.2 Sensitivity of the Model $\hat{M}(t, \alpha)$

Since the immigration data collected are only an estimate of the people entering the country, we wanted to test the sensitivity of the migration model $\hat{M}$ when noise (number of individuals) is added to the obtained data. To do this, for each data point we added noise sampled from a normal distribution at a given noise level. We then found the model parameters that had the least-squares fit of the model $\hat{M}$ to the perturbed data. We repeated this process 100 times for a given noise level and found the average and standard deviation of the model parameters. These average parameter values are included in the plots of Figure 4.

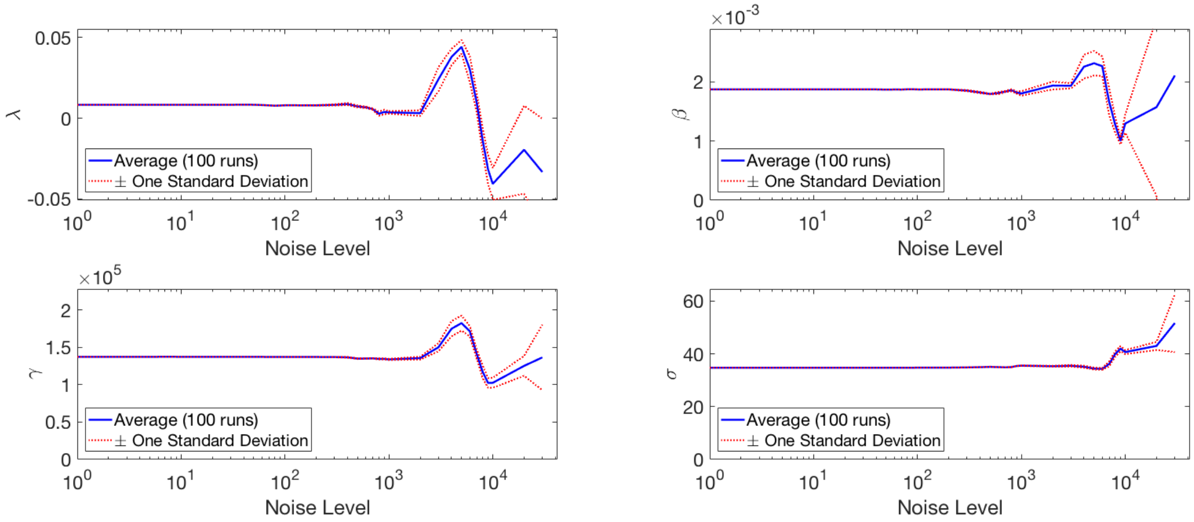

Figure 4: The sensitivity of $\hat{M}(t, \alpha)$ was examined by adding noise to each data point, sampled from a normal distribution with standard deviation given by the noise level. This was repeated 100 times for each noise level, and the resulting parameter values that gave the least-squares fit were obtained. The average for the runs at a given noise level are plotted with the solid curve. Note that the horizontal axis is on a logarithmic scale.

These plots indicate that the parameter values are not sensitive for noise levels from 1 up through approximately 1000 people. When the noise level increases beyond 2000 people, the parameter values begin to vary dramatically. The smallest data point is 3685 people, and so adding noise sampled from a distribution with standard deviation 3000 will often result in unrealistic negative values. Thus, the model $\hat{M}(t, \alpha)$ will not change greatly for data estimates that are slightly off of the true values.

6 Modeling the Mortality Function for the U.S. Population

The mortality data from the CDC WONDER databases are given in five year age groups along with the total population for each age group per year [3, 4]. With these two data categories, we obtain an approximate rate of the number of deaths per population size for each age group per year, visually represented in Figure 5. Since the data are provided with age groups in five-year blocks and not individual ages, we use the median age of each group for data fitting. Using this median we fit several functions using the least-squares criterion to these rates to approximate the $\mu(\alpha)$ function, including low-degree polynomials, an exponential model

$$\mu(\alpha) = Ae^{B(\alpha)},$$

and the mortality function from Micó et al. [14], given by

$$\hat{\mu}(\alpha) = a_1 e^{-\frac{\alpha}{b1}} + a_2 e^{-\frac{(\alpha - c_2)^2}{2b_2}} + a_3 e^{-\frac{(\alpha - c_3)}{b_3}}.$$

Many of the low-degree polynomials produced models with negative mortality rates, so we only include the constant function here. Higher degree polynomials (such as a seventh degree) were able to fit the data well, but had numerous parameters. Having fewer parameters will help us to not over-fit the model. We would like to use the function with the lowest AIC value, which balances fit and the number of parameters. The AIC values and the relative errors for these models are contained in Table 1.

Table 1: Relative Error and AIC Values of a Constant Rate Model, an Exponential Model, and the Micó et al. Model for $\mu(\alpha)$. Note the constant function and the Micó et al. models were fit to the respective age groups. The exponential model is fit for the 0–84 age group only. The relative error and AIC for the exponential model ages 0–74 calculates the error over these age groups using the model fit for 0–84.

Relative Error	**AIC**	**Age**
Constant Function Fit (Optimized for the respective age group)		
0.3428	-1234.2792	0–74
0.8305	-1091.6218	0–84
Micó et al. Function Fit (Optimized for the respective age group)		
0.0398	-1930.9609	0–74
0.1064	-1846.0554	0–84
Exponential Function Fit (Optimized for the 0–84 age group)		
0.0375	-1961.8593	0–74
0.2303	-1569.2769	0–84

The models fit to the 0–84 age range are displayed with the data in Figure 5. When comparing the models fit for the 0–84 age groups, the Micó et al. model has the lowest AIC of -1846.0554 and relative error of 10.64%. However, this model produces negative values for ages 10–34, and it grossly underestimates the rates for age groups below 65. The exponential model fit for the 0–84 age groups produced a relative error of 23.03% with an AIC value of -1569.2769 for ages 0–84, but performed with an outstanding 3.75% for ages 0–74. We note that this exponential function cannot yield a negative mortality rate unlike the Micó et al. function and the low-degree polynomials. Further, when the Micó et al. function is optimized for the 0–74 age groups, the AIC of -1930.9609 is greater than the exponential model's AIC for the restricted age range, -1961.8593. This is due to the exponential model having a better fit to the data for the lower age ranges and only deviates from the data for ages greater than 74. Moreover, the exponential function has only two parameters, making it a good choice for our mortality function model.

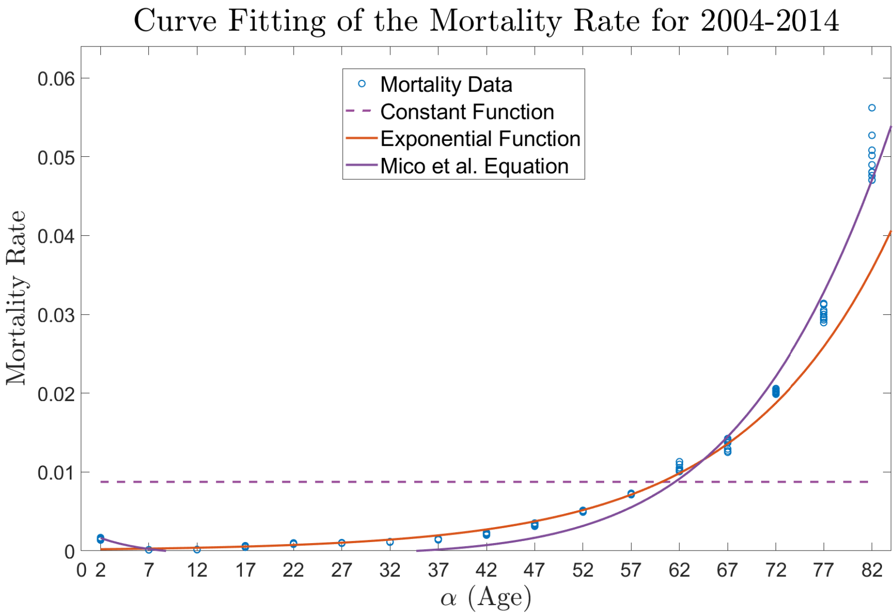

Figure 5: The approximate death rate for the median age of each age group was calculated for each year. An exponential function that represents the mortality rate function for the U.S. population from 2004–2014 is plotted with the data, along with the constant mortality rate ($\mu_0 = 0.00871703$), and the Micó et al. Equation for comparison.

Since the overall model that best fit the mortality data was the exponential function, we will use it as our $\mu(\alpha)$ for non-constant μ in the remainder of the paper. It is given by

$$\mu(\alpha) = l_1 \, e^{l_0 \alpha} \tag{6}$$

with the approximated coefficients $l_0 = 0.0644$ and $l_1 = 0.00018106$.

7 Implementation

This section gives the model implementation details. To find an approximation to the analytical solution with boundary and initial conditions coming from data, we apply the method of characteristics [9]. We consider two different cases regarding $\mu(t, \alpha)$, the mortality rate. We initially consider the mortality rate to be a constant, then consider the mortality rate as a function of age. The solution will be divided into two parts, the *initial condition driven solution* (the population presented initially at t_0) and the *recruitment driven solution* (those born into the population during the period of interest) [9].

7.1 The Method of Characteristics for Semilinear PDEs

Equation 2 is a first-order partial differential equation with variable coefficients. An estimate for Equation 2 is obtained through implementing a method to solve first order PDEs, known as the method of characteristics. Consider a first order homogeneous PDE with independent variables t and α. Values of the solution to the PDE are found by solving systems of ODEs along curves in the $t\alpha$-plane, known as characteristic curves [22]. These curves are parameterized by a new variable, s.

The method of characteristics transforms a semilinear PDE of the form

$$a(\alpha, t)u_\alpha + b(\alpha, t)u_t = c(\alpha, t, u)$$

into a system of ODEs given by

$$\begin{aligned} \frac{d\alpha}{ds}(s) &= a(\alpha, t) \\ \frac{dt}{ds}(s) &= b(\alpha, t) \\ \frac{du}{ds}(s) &= c(\alpha, t, u). \end{aligned}$$

The first two equations do not depend on u, giving a decoupled system. Solving these two equations with initial conditions $\alpha(0) = \alpha_0$ and $t(0) = t_0$ will give the characteristic curve projected into the $t\alpha-$plane, $\Gamma = (\alpha(s), t(s))$. Then, substituting the result for α and t in the third equation for $\frac{du}{ds}$ will give $u(\alpha, t)$ along Γ. Figure 6 shows an example of characteristic curves Γ projected onto the $t\alpha-$plane.

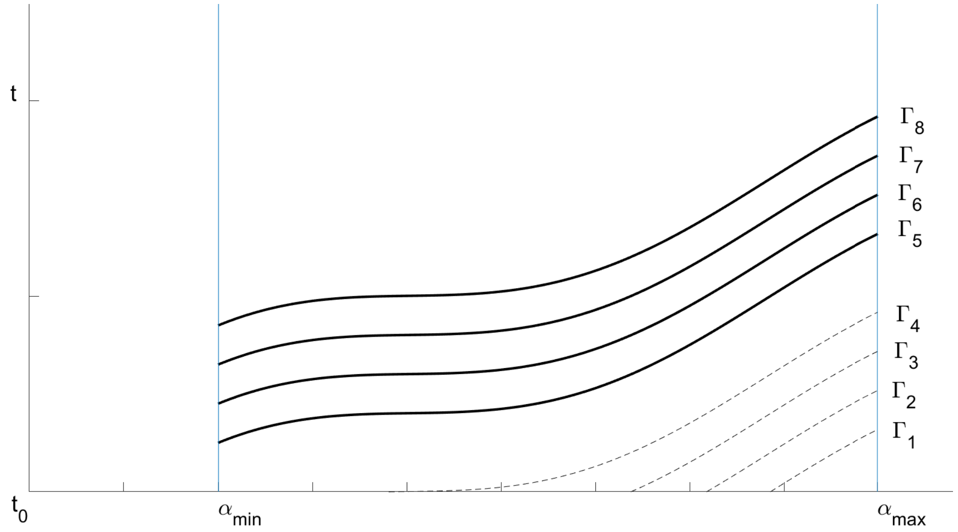

Figure 6: An example of characteristic curves. The curves Γ_1–Γ_4 (dashed lines) are curves where the initial conditions are specified at $t = t_0$. The curves Γ_5–Γ_8 (bold solid lines) are curves where the boundary conditions are specified at $\alpha = \alpha_{min}$.

7.2 Applying the Method of Characteristics

Using the method of characteristics, we take our PDE and convert it into three ordinary differential equations,

$$\begin{aligned}\frac{dt}{ds}(s) &= 1, \text{ and thus } t = s + t_0,\\ \frac{d\alpha}{ds}(s) &= 1, \text{ and thus } \alpha = s + \alpha_0,\\ \frac{du}{ds}(s) &= -\mu u + M.\end{aligned}$$

Solving for s yields the results,

$$s(t) = t - t_0 \text{ and } \alpha(t) = (t - t_0) + \alpha_0.$$

Next for $\frac{du}{ds}$, along with the explicit function $M = M(t, \alpha)$ from Equation 5, we get

$$\frac{du}{ds} + \mu(t(s), \alpha(s))u = \delta\gamma e^{-\beta(\alpha(s)-\sigma)^2-\lambda s}. \tag{7}$$

The solution to this ODE depends on the form of $\mu(t, \alpha)$, which we will consider by case.

7.2.1 Constant Mortality Rate $\mu(t, \alpha) = \mu_0$

We first consider $\mu(t, \alpha)$ as a constant rate. For $\mu(t, \alpha) = \mu_0$, Equation 7 becomes

$$\frac{du}{ds} + \mu_0 u = \delta\gamma e^{-\beta(s+\alpha_0-\sigma)^2-\lambda s}.$$

By applying an integrating factor we get

$$\frac{d}{ds}\left(e^{\mu_0 s}u\right) = \delta\gamma e^{-\beta(s+\alpha_0-\sigma)^2-\lambda s}e^{\mu_0 s}$$

with parameters γ, β, σ, and λ given by Equation 4. The parameter δ is fit using the population data.

We solve for $u(t, \alpha)$ by considering the initial condition for $u_0 = u(t_0, \alpha)$, the initial population at time t_0. This yields the initial condition driven solution for the constant mortality function with $t_0 = 0$,

$$u(t, \alpha) = \delta\gamma e^{-\mu_0 t}\int_0^t e^{-\beta(s+\alpha_0-\sigma)^2+(\mu_0-\lambda)s}ds + u(0, \alpha)e^{-\mu_0 t}. \tag{8}$$

Similarly, we find the recruitment driven solution. Let $R(t)$ be the total number of individuals born into the population at time t. Then the recruitment driven solution is given by

$$u(t, \alpha) = \delta\gamma e^{-\mu_0 t}\int_{t-\alpha}^t e^{-\beta(s+\alpha_0-\sigma)^2+(\mu_0-\lambda)s}ds + e^{-\alpha\mu_0}R(t-\alpha). \tag{9}$$

In solving for u, the integrals in Equations 8 and 9 cannot be determined analytically. We use the Composite Simpson's Rule to numerically estimate $u(t, \alpha)$.

7.2.2 Mortality Rate as a Function of Age, $\mu(t, \alpha) = \mu(\alpha)$

We use the best model from Section 6 for our $\mu(\alpha)$, given by Equation 6, which estimates the mortality rate according to age. We apply an integrating factor to Equation 7 with $\mu = \mu(\alpha)$ to get

$$\frac{d}{ds}\left(e^{L}u\right) = \delta\gamma e^{-\lambda s-\beta(s+\alpha_0-\sigma)^2+L},$$

where

$$L(s) = \frac{l_1}{l_0}e^{l_0(\alpha_0+s)}$$

obtained by integrating $\mu(\alpha)$. This results in the initial condition driven solution,

$$u(t, \alpha) = \delta\gamma e^{-L(t)}\int_0^t e^{-\lambda s-\beta(s+\alpha_0-\sigma)^2+L(t)}ds + e^{L(0)}u(0, \alpha)e^{-L(t)}, \tag{10}$$

and the recruitment driven solution

$$u(t, \alpha) = \delta\gamma e^{-L(t)}\int_{t-\alpha}^t e^{-\lambda s-\beta(s+\alpha_0-\sigma)^2+L(t)}ds + e^{L(t-\alpha)-L(t)}R(t-\alpha). \tag{11}$$

The integrals in Equations 10 and 11 cannot be solved analytically. We use the Composite Simpson's Rule to numerically estimate $u(t, \alpha)$.

8 RESULTS

For our model, we first fit a mortality function ($\mu(\alpha) = \mu_0$ or $\mu(\alpha) = l_1 e^{l_0 \alpha}$) and the migration function ($\hat{M}(t, \alpha)$) using their respective data sets. Here, the mortality function is fit first, as described in Section 6, and then immigration function in Equation 3 is fit using the immigration data, as described in Section 5. The full model then only has one unknown parameter from Equation 5, δ, which is determined by using a least-squares error minimization method to find the best fit to the population data. In comparing the population models with the different mortality functions, we calculate their relative errors and AIC values, which are contained in Table 2 with their corresponding δ values. The relative error allows for evaluating the precision of the model, relative to the size of the data.

Table 2: Full Population Model Relative Error and AIC Values using a Constant Mortality Function, an Exponential Mortality Function, and the Micó et al. Mortality Function for $\mu(\alpha)$.

Model Fit

Function	**Rel. Error**	**AIC**	**δ Value**
Constant	3.9506e-02	24903.1	48.6622
Micó et al.	3.8958e-02	24910.9	2.6231
Exponential	2.3336e-02	23920.6	0.1380

We apply our model over the time period 2004–2014. Using the constant mortality function, $\mu_0 = 0.00871703$ deaths per population per year, we optimize δ. The δ value from this fit is $\delta = 48.6622$ with a 3.95% relative error and an AIC value of 24903.1, see Table 2. The estimate and the population data are superimposed in Figure 7 for a visual comparison. A figure of the difference between the data and the model is also plotted in Figure 8 to better show the error.

Next, using $\mu(\alpha)$ from Equation 6 (the exponential function) with the optimal parameters found in Section 6 gives the estimate for $u(t, \alpha)$ shown in Figure 9. We find the optimal δ using a least-square error minimization method with the population data to obtain $\delta = 0.1380$. We find that the model approximates the population data with a relative error of 2.33%. A figure of the difference between the data and the model is also plotted in Figure 10 to better show the error.

We include the Micó et al. model, which uses their migration function and mortality function. When fit to the U.S. population, the optimal $\delta = 2.6231$, giving a relative error of 3.9% and AIC 24910.9. This has the highest AIC of the three models, where a lower AIC indicates a better model choice.

If no migration had been incorporated into the model, $M(t, \alpha) \equiv 0$ in Equation 3, giving the McKendrick-von Foerster equation. If we were to fit this model to the population data for μ_0 without using the mortality data, this yields the optimal $\mu_0 = -0.00013$. This value is unrealistic since it is negative, indicating the need for migration to be included in the model.

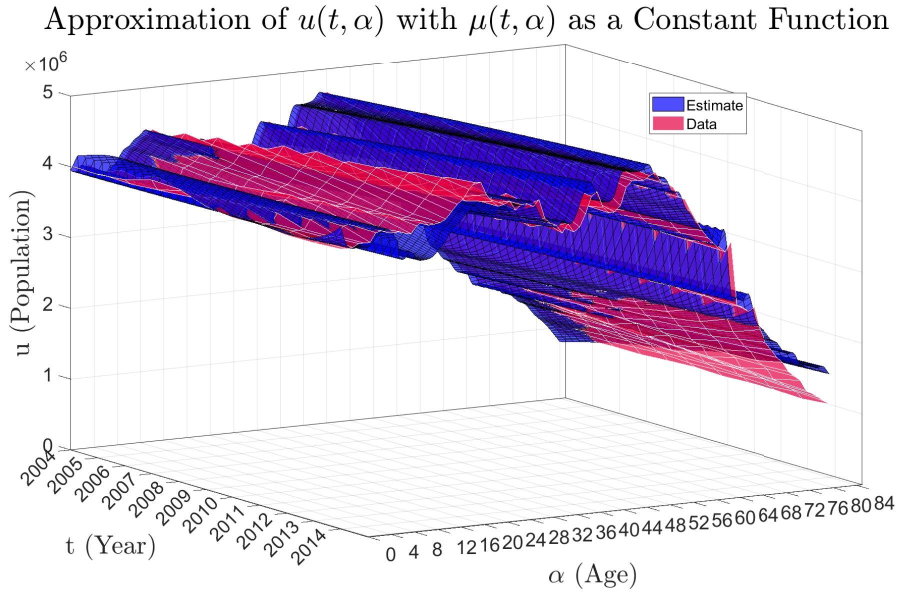

Figure 7: Population estimate for a constant mortality rate. The constant mortality rate is estimated to be $\mu_0 = 0.00871703$. Using the full model, δ is optimized to obtain $\delta = 48.6622$ with a relative error of 0.0395. The estimate and data are superimposed in this figure as a visual reference.

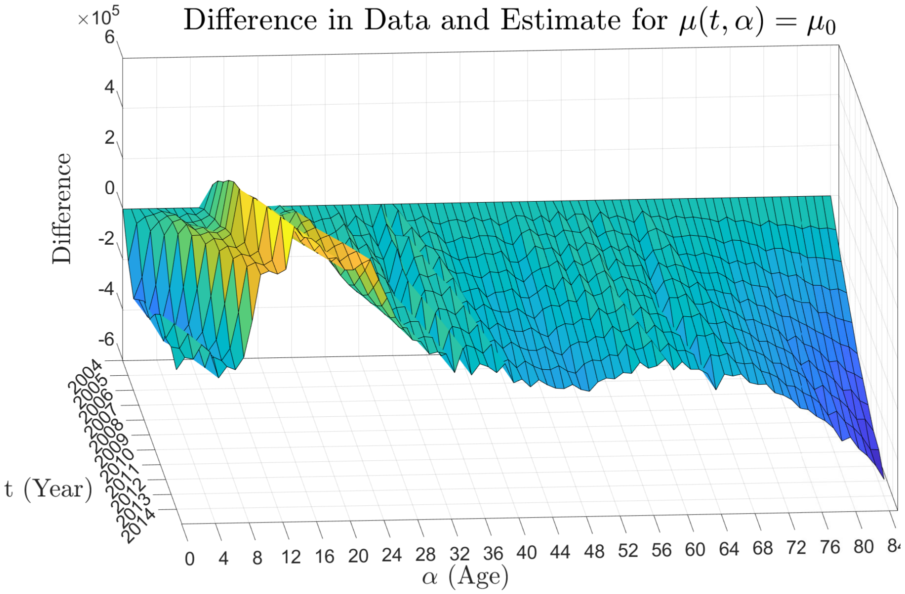

Figure 8: The difference between the population data and the model is plotted to distinguish the variability for each age per year for a constant mortality rate.

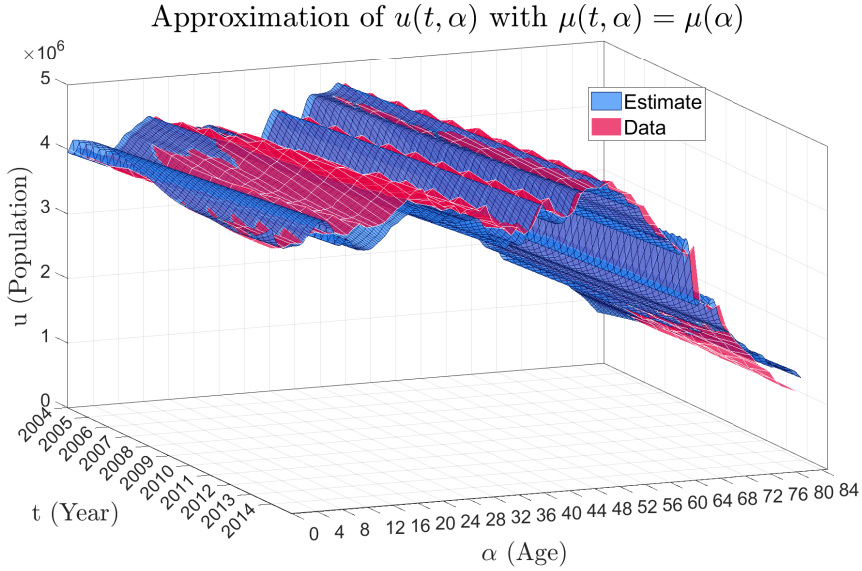

Figure 9: Population estimate using the exponential function $\mu(\alpha)$. The model was obtained by fitting $\hat{M}(t,\alpha)$ to the migration data and $\mu(\alpha)$ to the mortality data, and then included in Equations 10 and 11. Then the coefficient δ was optimized using the full model to produce a relative error of 0.0233 to the overall U.S. population and an AIC value of 23920.6.

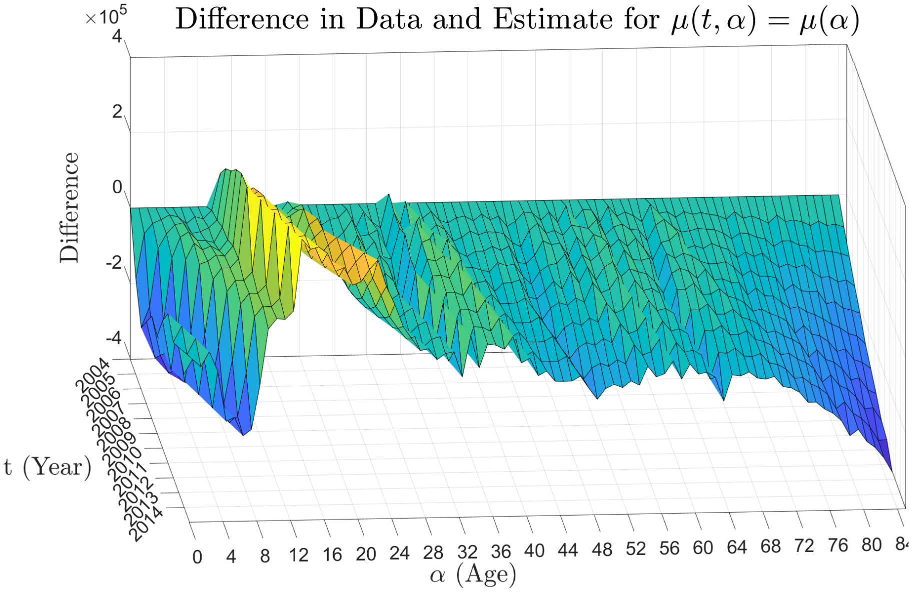

Figure 10: The difference between the population data and the model is plotted to distinguish the variability for each age per year for $\mu(t,\alpha)=\mu(\alpha)$.

8.1 Model Prediction

From the 2004–2014 data, we use our model to predict the population in 2015. In order to do this, we need to have a smooth curve for the initial and boundary conditions. This is done using cubic splines for both the birth data and the initial population. The prediction for the population is compared with the actual population data gathered from the Census data sets for 2015, see Figure 11.

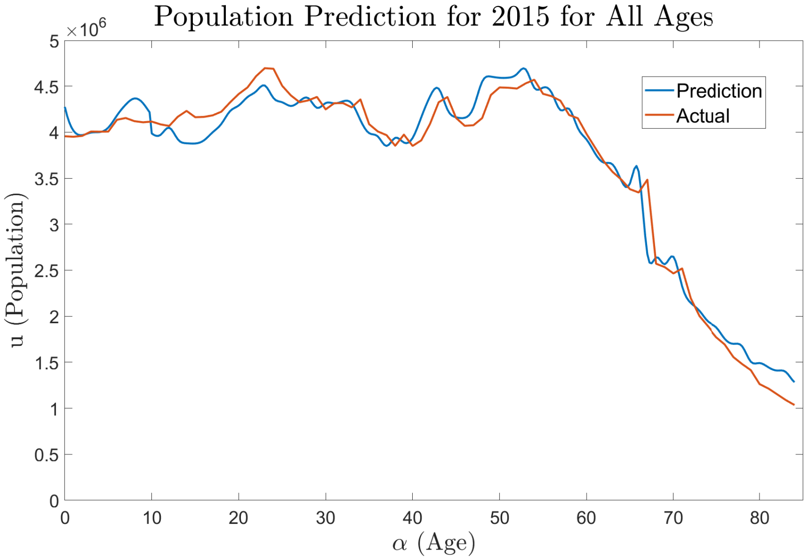

Figure 11: The population prediction of year 2015 for all ages is shown relative to the data provided by the US Census Bureau data bank.

9 Analysis

Our proposed model is able to capture the population dynamics of an open system. When we consider mortality rate to be a constant function, we find $\mu_0 = 0.00871703$ deaths per population per year. The result has a relative error of 3.95%. This indicates that the overall population would have the same death rate for all ages. However, teenagers have fewer chronic health problems, while seniors have a set of factors that significantly diminish their health due to their age. The gap in Figure 7 for the older age groups suggests that a model with a constant mortality rate does not fit the data well for all age groups.

By using a mortality rate function that depends on age, our model is able to closely match the data with relative error of 2.33%. For both the constant mortality rate and the exponential function mortality rate, the largest differences between the model and the data occur as ages increase from age 64. The difference could be caused by the estimating method used by the Census Bureau. The Census Bureau assumed a sum of zero for the net migration, which can be over counting emigrants who leave the country. Further, the immigration data is provided with different immigrant categories that might be overlapping, and so further investigation of those categories is required. We only use the datasets that have age as a subcategory up to age 64, so we are unable to count all immigrants. We are unable to obtain data for emigration estimates. To account for the missing emigration data, we use a multiple of the immigration estimates for the net migration, represented by the δ coefficient in Equation 3.

Of the three model fits, the only reasonable value for δ is given by the exponential model. A value of $\delta > 1$ indicates the net migration is more than the number of individuals immigrating into the country given by the data. A negative value would indicate more individuals are leaving than entering the country. A value $0 < \delta < 1$ would indicate that more individuals are entering the country than leaving the country. For $\delta = 0.1380$, this indicates the number of individuals emigrating out of the country is about 86.2% of the number of those immigrating into the country estimated by $\hat{M}$. This is a plausible estimate, given that we do not have the emigration data.

Due to the challenges with the migration data, we provide a sensitivity analysis on the migration model. With noise sampled from a normal distribution of standard deviation up to 1000 added to each point, the migration model parameters do not vary greatly. If we had more confidence in the data accuracy, then perhaps a different model should be used to better approximate the migration data, reducing the 8.27% relative error for the migration model.

We compare our migration model to that of Micó et al. Our model has a better relative error and AIC, indicating a better fit to the migration data. We then compare our mortality function with that of an optimized Micó et al. Even though the Micó et al. mortality function has a 10.64% relative error for all age groups, it does not produce an adequate result for the overall population estimate. This is due to the negative mortality rates it produces for the age groups 10 to 34. We also compare our mortality function to several other models, including low degree polynomials. While some of these models have better fits to the mortality data, they unfortunately give negative mortality rates for some age groups and are therefore not considered. The exponential function provides a better fit to the mortality data for age groups 0 to 74. However, the data for the older age groups deviate from the model, which accounts for a large difference in the population and estimate as seen in Figure 9.

With the data for 2004–2014, we project our model forward to 2015 and compare our prediction with the 2015 data. Our prediction closely follows the actual data. We slightly underestimate the population for ages approximately 10–27, and overestimate ages 40–53.

10 Conclusion

We proposed an age-structured population model that allowed for migration in and out of the system. We modified the McKendrick-Von Foerster model and applied it to the United States data, creating models for both migration and mortality. We required birth, death, population, and migration data to accomplish this goal. Without the inclusion of migration into the model, the mortality rate yields an invalid negative rate. By including a migration term into the PDE model, the results significantly improved with a 3.95% relative error when the mortality rate was considered to be constant for all ages. This error was substantially improved to 2.33% when the mortality rate was allowed to vary by age. The model we used for the mortality function was an exponential function. This was chosen to be the best since it did not produce negative values for mortality rates and the AIC and relative error values were adequate.

With a small relative error, this model closely captures the U.S. population over time. The model can be used to predict how the population is affected if migration, birth, or death patterns change. For example, different migration models could be used to test for a surge or drop in migration, both overall and for different age groups. Alternatively, if there is a wide-spread epidemic that affects certain age groups more than others, the mortality function could be adjusted to understand this outcome. With the decrease in the U.S. fertility rate, the birth rates could be projected to take this into consideration to see the long-term implications on the total population and the different age groups.

Appendix

The appendix contains additional information regarding the data used for the study. It also contains the main MATLAB code used.

Population Data

The national intercensal datasets (estimates of the population between two official census dates) are estimates of resident population organized by single age per year, sex, race, and Hispanic origin from April 1, 2000 to July 1, 2010. The estimates were calculated by the Census Bureau using a population base and the result of the population size from the year 2000 from the previous decennial census (occurring every ten years), and then updated using the Das Gupta method, which assumes that the ratio from the intercensal estimate follows a geometric progression [3]. Terms in a geometric progression are found by multiplying the previous term by a constant common ratio. The annual estimates of the resident population for the datasets from April 1, 2010 to July 1, 2016 are categorized by two criteria: age and sex of the individual. These estimates take into account the change in population from births, deaths, and migration. The annual population estimates are calculated by the Census Bureau using a cohort component method derived from a demographic balancing equation using a population base from the previous decennial census estimate [4]. Here, the next population estimate takes the previous population estimate, adds new births and migrants, and subtracts deaths. The population estimate from the intercensal dataset for age 85 ranges from 4,545,883 to 5,367,301 individuals from 2004 to 2009, while the annual estimates mark the population size for age 85 to fall between 915,071 to 914,112 individuals. This presents an unexplained jump for this particular age.

Main Code

In this section, we provide some of the main code used for the model fitting and model solution.

Fitting Polynomial Function

This code fits a polynomial function of n-degrees to the deaths per population per year data.

```
t_i = 2004:2014;
age_j = 2:5:84;

% Data Setup
load('..\deathsAdj.mat')
load('..\usPopMatrix.mat')
popAdj = [[popmatrix(1,:)+popmatrix(2,:)];[popmatrix([3:18],:)]];
muPop=deathsAdj(1:17,:);   %deathsAdj matrix up to age group 80-84;
muPopNorm=muPop./popAdj;    % num of deaths per age group / pop of age group

% Residuals of muPopNorm per age per year
mupopAll = muPopNorm(:);
agegroupAll = [];

for year=1:11
    agegroupAll = [agegroupAll; age_j'];
end

Ndeg(1:11,1:11)=zeros;
for n=0:8
    p_All=polyfit(agegroupAll,mupopAll,n)';
    [p,S]=polyfit(agegroupAll,mupopAll,n);
    for i=1:n+1
       Ndeg(n+1,i)=p(i);
    end
end
nDEG_nonOpt=Ndeg';
```

Fitting Exponential Function

The code fits an exponential function to the deaths per population per year data.

```
% Fitting the Mortality Function - exponential function
t_i = 2004:2014;
age_j = 2:5:84;

% Retrieve data
load('..\deathsAdj.mat')
load('..\usPopMatrix.mat')
popAdj = [[popmatrix(1,:) + popmatrix(2,:)]; popmatrix([3:18],:)];
```

```
muPop = deathsAdj(1:17,:);   %deathsAdj matrix up to age group 80-84;
muPopNorm = muPop./popAdj;    % num of deaths per age group / pop of age group

% Residuals of muPopNorm per age per year
mupopAll = muPopNorm(:);
agegroupAll = [];
for year=1:11
    agegroupAll = [agegroupAll; age_j'];
end

%fitting of unknown coefficients
p = polyfit(agegroupAll, log(mupopAll),1);
beta = p(1)
lambda = exp(p(2))
```

Fitting Migration Model

This code finds the least-squares approximation for the migration data to the migration model, $\hat{M}(t, \alpha)$.

```
% Fitting the Migration Data
t_i = 2004:2014;
age_j = 2:5:64;
[T,Age] = meshgrid(t_i,age_j);

% Retrieve Data
load('..\refugeeResidentMatrix.mat')
M=refRes_immigrants(1:13,:);

% Fit the parameters
parameter_guess = [1/11*log(8.237/3.941),0.01, 1.678e05, 37];

J = @(params) sum(sum((migration_model(params, t_i, age_j) - M).^2));

% Least-squares approximation
[parameter_estimate,Jval] = fminsearch(J, parameter_guess);
```

Migration Model Function

This function gives the migration model with input of parameters, time, and age.

```
function [migration_est] = migration_model(params, t_i, age_j)

%Parameters
lambda = params(1);
```

```
beta = params(2);
gamma = params(3);
sigma = params(4);

[T,Age] = meshgrid(t_i,age_j);

migration_est = gamma*exp(-beta*(Age-sigma).^2).*exp(-lambda*(T-2004));
```

Finding Optimal δ Coefficient using a Constant Mortality Rate $\mu(t, \alpha) = \mu_0$

```
t_i = 2004:2014;
age_j = 0:84;
[T,Age] = meshgrid(t_i,age_j);


% Get data
load('usPopMatrix_age.mat')
POP=popmatrix((1:85),1:11);

%==== Fit the parameters.
parameter_guess = 40;

J = @(params) sum(sum((fitDeltap0(params, t_i, age_j) - POP).^2));

[parameter_estimate,Jval] = fminsearch(J, parameter_guess);
deltaValue = parameter_estimate
model_estimate = fitDeltap0(parameter_estimate, t_i, age_j);
```

Function for the Population Model with Constant Mortality Rate $\mu(t, \alpha) = \mu_0$

This function gives the population model for an inputted constant mortality rate for an unknown δ value.

```
function [param_est] = fitDeltap0(vars,t_i, age_j)
%Function optimizes delta using full model and pop data for a polynomial of n-degrees.
%The constant function is given by n=1 within the for loop.

load('nDEG.mat') %load polynomial coefficient matrix

delta = vars;

n = 1; %Deg of polynomial is n-1
params(1,:) = nDEG((11:-1:1),n)';
```

```
%INITIALIZE variables
gamma=137464.185474326;
beta=0.001871913;
sigma=34.741176748;
lambda=0.008333126;

%Polynomial coefficients are assigned to variables.
%If empty the value is 0.
l_0 = params(1);
l_1 = params(2);
l_2 = params(3);
l_3 = params(4);
l_4 = params(5);
l_5 = params(6);
l_6 = params(7);
l_7 = params(8);
l_8 = params(9);

[T,Age] = meshgrid(t_i,age_j); %time and age matrix

% Restriction of the Recruitement Driven Solution
X = T>Age+2004;

%LOAD POPULATION DATA
load('usPopMatrix_age.mat')
POP=popmatrix(1:85,1:11);
load('..\births.mat')
iniPop = POP(:,1); %defining initial population


%DEFINE s for each portion of the characteristic curve
s = T-2004;
s_r = (s-Age).*X; %s for recruitement driven
s_i = s.*(1-X); %s for intial driven

%SETUP DATA: recruitement driven solution
R = zeros(size(T));
%LOAD Infant Population in Migration Model
InfantMigration= migration_model([lambda, beta, gamma, sigma], t_i, 0);
Rb=births(:,2)+InfantMigration; %Include Infant migration into Birth data

for i=1:size(R,1)
    for j=1:size(R,2)
```

```
        if X(i,j)>0
            R(i,j) = Rb(T(i,j)-2004+1-Age(i,j));
        end
    end
end

%SETUP DATA: initial driven solution

IP = zeros(size(T));
for i=1:size(IP,1)
    for j=1:size(IP,2)
        if X(i,j)==0
            IP(i,j) = iniPop(Age(i,j)-(T(i,j)-2004)+1);
        end
    end
end

mainPOP = zeros(size(T));

for i=1:85
    for j=1:11
        if X(i,j)==1 %Recruitment Driven Solution
            ageNot=(s_r(i,j));
            [ lamBarVal ] = lamBar_n( l_0, l_1, l_2, l_3, l_4, l_5,...
            l_6, l_7, l_8, s_r(i,j), ageNot, n-1 );
            f = @(ss) exp(lambda*ss-beta*( ss + ageNot - sigma )^2 + ( l_8/9*...
            ( ss + ageNot )^9 + l_7/8*( ss + ageNot )^8 + l_6/7*( ss +...
            ageNot )^7 + l_5/6*( ss + ageNot )^6 + l_4/5*(ss + ageNot )^5...
            + l_3/4*( ss + ageNot )^4 + l_2/3*( ss + ageNot )^3 + l_1/2*...
            ( ss + ageNot )^2 + l_0*ss));
            [integVal] = csr( f, T(i,j)-Age(i,j)-2004 , T(i,j)-2004 ,10 );
            mainPOP(i,j) = delta * gamma*(lambda)*exp(-lamBarVal)*integVal+...
            exp(lamBar_n(l_0, l_1, l_2, l_3, l_4,...
            l_5, l_6, l_7, l_8, T(i,j)-...
            Age(i,j)-2004, ageNot, n-1))*R(i,j)*exp(-lamBar_n(l_0, l_1, l_2,...
            l_3, l_4, l_5, l_6, l_7,l_8, T(i,j)-2004, ageNot, n-1));
        else %Initial Driven Solution
            ageNot=Age(i,j)-s_i(i,j);
            [ lamBarVal ] = lamBar_n( l_0, l_1, l_2, l_3, l_4, l_5, l_6,...
            l_7, l_8,s_i(i,j), ageNot, n-1 );
            f = @(ss) exp(lambda*ss-beta*( ss + ageNot - sigma )^2 + ( l_8/9*...
            ( ss + ageNot )^9 + l_7/8*( ss + ageNot )^8 + l_6/7*...
            ( ss + ageNot )^7 + l_5/6*( ss + ageNot )^6 + l_4/5*(ss...
```

```
            + ageNot )^5 + l_3/4*( ss + ageNot )^4 + l_2/3*( ss +...
            ageNot )^3 + l_1/2*( ss + ageNot )^2 + l_0*ss));
            [integVal] = csr( f, 0 , T(i,j)-2004 ,10 );
            mainPOP(i,j) = delta * gamma*(lambda)*exp(-lamBarVal)*integVal+...
            exp( lamBar_n( l_0, l_1, l_2, l_3, l_4, l_5, l_6, l_7, l_8,...
            0, ageNot, n-1 ))*IP(i,j)*exp(-lamBarVal);

        end
    end
end
param_est = mainPOP;
```

Function for Optimizing Delta using the Population Model with Non-Constant Mortality Rate $\mu(t,\alpha) = \mu(\alpha)$

This code gives the population model for an inputted non-constant mortality rate, represented by an exponential function for an unknown δ value.

```
function [param_est] = fittingDelta(vars)
%This function fits coefficient 'delta' from Mhat exponential function using the
%overall population model
%INITIALIZE variables
gamma=137464.186103456;%M^ coefficients
beta=0.001871913;
sigma=34.741176825;
lambda=-0.008333126;

delta = vars;

params = [1.8106e-04, 0.0644]; %Exponential Fun coefficients

l_0 = params(1);
l_1 = params(2);

t_i = 2004:2014;
age_j = 0:84;

[T,Age] = meshgrid(t_i,age_j); %time and age matrix

% Restriction of the Recruitement Driven Solution
X = T>Age+2004;

%LOAD POPULATION DATA
load('usPopMatrix_age.mat')
```

```
POP=popmatrix(1:85,1:11);
load('..\births.mat')
iniPop = POP(:,1); %defining initial population


%DEFINE s for each portion of the characteristic curve
s=T-2004;
s_r = (s-Age).*X; %s for recruitement driven
s_i = s.*(1-X); %s for intial driven

ageNot=Age-s_i; %defining ageNot

%SETUP DATA: recruitement driven solution
R = zeros(size(T));
%LOAD Infant Population in Migration Model
InfantMigration= migration_model([lambda, beta, gamma, sigma], t_i, 0);
Rb=births(:,2)+InfantMigration; %Include Infant migration into Birth data

for i=1:size(R,1)
    for j=1:size(R,2)
        if X(i,j)>0
            R(i,j) = Rb(T(i,j)-2004+1-Age(i,j));
        end
    end
end

%SETUP DATA: initial driven solution

IP = zeros(size(T));
for i=1:size(IP,1)
    for j=1:size(IP,2)
        if X(i,j)==0
            IP(i,j) = iniPop(Age(i,j)-(T(i,j)-2004)+1);
        end
    end
end


mainPOP = zeros(size(T));

for i=1:85 %1:85
    for j=1:11
        if X(i,j)==1 %Recruitment Driven Solution
```

```
            ageNot=(s_r(i,j));
            [ lamBarVal ] = lamBarExp( l_0, l_1, s_r(i,j), ageNot );
            f = @(ss) exp(-lambda*ss-beta*( ss + ageNot - sigma )^2 + l_0 *...
            exp( l_1*(ss + ageNot)));
            [integVal] = csr( f, T(i,j)-Age(i,j)-2004 , T(i,j)-2004 ,10 );
            mainPOP(i,j) = delta*gamma*exp(-lamBarVal)*integVal+exp(...
            lamBarExp( l_0, l_1, T(i,j)-Age(i,j)-2004, ageNot ) )*R(i,j)*...
            exp( -lamBarExp( l_0, l_1, T(i,j)-2004, ageNot) );
        else %Initial Driven Solution
            ageNot=Age(i,j)-s_i(i,j);
            [ lamBarVal ] = lamBarExp( l_0, l_1, s_i(i,j), ageNot );
            f = @(ss) exp(-lambda*ss-beta*( ss + ageNot - sigma )^2 + l_0 *...
            exp( l_1*(ss + ageNot)));
            [integVal] = csr( f, 0 , T(i,j)-2004 ,10 );
            mainPOP(i,j) = delta*gamma*exp(-lamBarVal)*integVal+exp( lamBarExp(...
            l_0, l_1, 0, ageNot ) )*IP(i,j)*exp(-lamBarVal);
        end
    end
end
param_est = mainPOP;
```

Composite Simpson's Rule

This function approximates a definite integral using Composite Simpson's Rule.

```
function [XX] = csr(f,lowlim,uplim,n)
% lowlim and uplim give the bounds of integration
% n is the number of subintervals

h = (uplim - lowlim)/n;
x10 = f(lowlim) + f(uplim);
x11 = 0; x12 = 0;
for i = 1:n-1
    X = lowlim + i*h;
    if mod(i,2) == 0
        x12 = x12 + f(X);
    else
        x11 = x11 + f(X);
    end
end
XX = h*(x10 + 2*x12 + 4*x11)/3;
```

Acknowledgments

We are immensely grateful for all the time Dr. Laura Smith Chowdhury has given us in helping our understanding in mathematics. Every moment during this research was a challenge that contributed to our own professional growth thanks to Dr. Chowdhury as well as our advisors Dr. Anael Verdugo and Dr. Scott Annin. We would also like to thank the referees and editors for their constructive and detailed feedback.

References

[1] Population Division U.S. Census Bureau, available online at the URL: `https://www.census.gov/data/datasets/time-series/demo/popest/intercensal-2000-2010-national.html`

[2] Population Division U.S. Bureau, available online at the URL: `https://factfinder.census.gov/faces/tableservices/jsf/pages/productview.xhtml?pid=PEP_2016_PEPSYASEXN&prodType=table`

[3] Population Division U.S. Census Bureau, available online at the URL: `https://www2.census.gov/programs-surveys/popest/technical-documentation/methodology/intercensal/2000-2010-intercensal-estimates-methodology.pdf`

[4] Population Division U.S. Census Bureau, available online at the URL: `https://www2.census.gov/programs-surveys/popest/technical-documentation/methodology/2010-2016/2016-natstcopr-meth.pdf`

[5] Center for Disease Control and Prevention, available online at the URL: `http://wonder.cdc.go/ucd-icd10.html`

[6] Central Intelligence Agency World Factbook, available online at the URL: `https://www.cia.gov/library/publications/the-world-factbook/geos/ve.html`

[7] J. Xu, S.L. Murphy, K.D. Kochanek, B. Bastian, E. Arias, Deaths: Final Data for 2016, *Natl. Vital Stat. Rep.*, **67** (2018), 1–76.

[8] US News Washington D.C., *10 Countries That Take the Most Immigrants*, (2018), available online at the URL: `https://www.usnews.com/news/slideshows/10-countries-that-take-the-most-immigrants?slide=11`

[9] H.T. Banks, H.T. Tran, *Mathematical and Experimental Modeling of Physical and Biological Processes*, pages 245–274. Chapman & Hall/CRC, 2009.

[10] J.W. Sinko, W. Streifer, A New Model for Age-Size Structure of a Population, *Ecol.*, **48** (1967), 910–918.

[11] H. Inaba, Asymptotic Properties of the Inhomogeneous Lotka-Von Foerster System, *Math. Popul. Stud.*, **1** (1988), 247–264.

[12] B.L. Keyfitz, N. Keyfitz, The McKendrick Partial Differential Equation and the Uses in Epidemiology and Population Study, *Math. Comput. Modelling*, **26** (1997), 1–9.

[13] P.H. Leslie, On the Use of Matrices in Certain Population Mathematics, *Biometrika*, **33** (1945), 183–212.

[14] J.C. Micó, D. Soler, A. Caselles, Age-Structured Human Population Dynamics, *J. Math. Sociol.*, **30** (2006), 1–31.

[15] S. Engen, R. Lande, B. Saether, Effective Size of a Fluctuating Age-Structured Population, *Genet. Soc. Amer.*, **170** (2005), 941–954.

[16] Department of Homeland Security, avialable online at the URL: `https://www.dhs.gov/immigration-statistics/yearbook`

[17] O. Arino, E. Sánchez, R. Bravo de la Parra, A Model of an Age-Structured Population in a Muiltipatch Environment, *Math. Comput. Modelling*, **27** (1998), 137–150.

[18] A. Zincenko, S. Petrovskii, Dynamics of a Two Subpopulations System Including Immigration, *Math. Model. Nat. Phenom.*, **12** (2017), 46–57.

[19] M. Chowdhury, E.J. Allen, A Stochastic Continuous-Time Age-Structured Population Model, *Nonlinear Anal.*, **47** (2001), 1477–1488.

[20] G.K. Singh, P.C. van Dyck, Infant Mortality in the United States, 1935–2007: Over Seven Decades of Progress and Disparities, *U.S. Dept. HHS*, (2010), 1–8.

[21] A.G, McKendrick. Applications of Mathematics to Medical Problems, *PEMS*, **44** (1925), 94–130.

[22] S.J. Farlow, *Partial Differential Equations for Scientists and Engineers*, John Wiley & Sons, 1982.

[23] P. Magal, Compact attractors for time periodic age-structured population model, *Electron. J. Differential Equations*, **65** (2001), 1–35.

[24] G. Huang, X. Liu, Y. Takeuchi, Lyapunov functions and global stability for age-structured HIV infection model, *SIAM J. Appl. Math.*, **72** (2012), 25–38.

[25] C.C. McCluskey, Global stability for an SEI epidemiological model with continuous age-structure in the exposed and infectious classes, *Math. Biosci. Eng.*, **9** (2012), 819–841.

[26] J. Wang, R. Zhang, T. Kuniya, Global dynamics for a class of age-infection HIV models with nonlinear infection rate., *Nonlinear Anal. Real World Appl.*, **432** (2015), 289–313.

[27] H.L. Langhaar, General population theory in the age-time continuum, *J. Franklin Inst.*, **293** (1972), 199–214.

[28] M.E. Gurtin, R.C. MacCamy, Some Simple Models for Nonlinear Age-Dependent Population Dynamics, *Math. Biosci.*, **43** (1979), 199–211.

[29] L. Liu, X. Ren, Z. Jin, Threshold dynamical analysis on a class of age-structured tuberculosis model with immigration of population, *Adv. Difference Equ.*, (2017), 1–21.

[30] S. Engen, R. Lande, B. Saether, H. Weimerskirch, Extinction in relation to demographic and environmental stochasticity in age-structured models, *Math. Biosci.*, **195** (2005), 210–227.

[31] R. Hilborn, M. Mangel, *The Ecological Detective: Confronting Models with Data*, pages 59–62. Princeton University Press, 1997.

[32] P. De Valpine, A. Hastings, Fitting population models incorporating process noise and observation error, *Ecol. Monographs*, **72** (2002), 57–76.

Freddy Nungaray
California State University, Fullerton
800 N State College Blvd Fullerton, CA 92831
E-mail: `nungarayf1@csu.fullerton.edu`

Gabriel Martinez
California State University, Fullerton
800 N State College Blvd Fullerton, CA 92831
E-mail: `lazvertiigo@csu.fullerton.edu`

Laura Smith Chowdhury
California State University, Fullerton
800 N State College Blvd Fullerton, CA 92831
E-mail: `lausmith@fullerton.edu`

Received: March 28, 2019 **Accepted**: July 22, 2020
Communicated by Alex Chen