

Sequential Monte Carlo Methods for United Kingdom Population Dynamics

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1 Abstract

2 Introduction

The study of population dynamics, particularly in the context of human populations, is a critical area of research with significant implications for policy and planning. Traditionally, deterministic models such as logistic growth, and time series of population counts, have been used to infer the demographic processes driving observed population fluctuations [2]. However, this approach presents certain challenges. Changes in observed population size reflect a combination of demographic variability and measurement error, making it difficult to accurately discern underlying demographic trends [3]. In this context, state space models (SSMs) have become increasingly popular for fitting population dynamics. These models offer a flexible framework for modeling time series data, accommodating (in this case) the intrinsic variability in population processes and the observation error inherent in population counts. The state space approach separates the true population state, which is often unobservable, (see Table 1) from the observation process, allowing for a more nuanced understanding of population dynamics. In the case of human population dynamics, this account for the complexity heightened by factors such as international migration, age structure, and spatial variation.

In this study, we apply three distinct state space models, delineating our analysis into two distinct inferential paradigms: frequentist statistical inference and Bayesian inference. The frequentist approach is exemplified by our first model, which employs Kalman Filters. Kalman Filter is a special case of linear SSMs with Gaussian errors and initial states, enabling an efficient recursive solution to the filtering problem [8]. Unlike Bayesian methods that integrate prior knowledge (of parameters and initial states) into analysis, the Kalman Filter adheres to the principles of Maximum Likelihood Estimation (MLE), focusing on estimate the hidden states of the model given a sequence of noisy observations. Although the two-stage predictive and updates steps can be linked to the posterior update of Bayesian inference, the Kalman Filter contrast the posterior density approach embodied by subsequent models. Our second and third models adopt a Bayesian approach, employing Sequential Monte Carlo (SMC) methods – namely, Particle Filtering – to approximate posterior distributions in non-linear models with non-Gaussian error structures [4]. These models allow for vague (or informative) prior distributions

Term	Definition
Filtering	$p(x_t y_{1:t})$ use observations to time t , $y_{1:t}$, to estimate x_t
Forecasting	$p(x_t y_{1:t-s})$ use observations s time steps before t to predict x_t
Observation	The observed measurements y_t at time t
Observation Equation	$g(y_t x_t)$, the probabilistic relationship between the hidden states and the observed measurements
Observation Error	The gap between the observed data and the true state, often modeled as noise in the observation equation.
Online Estimation	Continually estimate x_t based on information available at time t
Process Equation	$f(x_t x_{t-1})$ represents the probabilistic transition dynamics of the x_t in the system, capturing the temporal dependencies from one state to the next.
Process Error	The discrepancy between the predicted state and the actual hidden state, often modeled as noise in the process equation.
Smoothing	$p(x_t y_{1:T})$ use all T the observations to estimate the x_t
State	x_t represents the unobserved state (hidden states) of the system at time t , which is the quantity of interest
State Space Model	A statistical model to capture the system dynamics through a set of process equations for the state evolution over time and observation equations linking the hidden states to the observed data.

Table 1: Definitions of terms used in state-space models

on parameters like birth and death rates. The second model simulates population dynamics using a Bootstrap Filter through the `nimbleSMC` packages in R, capturing birth, death, and immigration processes. Our third model refines this approach, incorporating dynamic birth and death rates within a hard-coded particle filter algorithm. This model accounts for the stochasticity of demographic events, offering a nuanced understanding of population changes over time. These methods are crucial for accurately estimating measurement error, uncovering hidden demographic processes, and ultimately, determining population size with precision.

For the research presented in this dissertation, we have used extensive

data from the UK National Statistics, covering the period from 1839 to 2023. This data comprises detailed records of births, deaths, population estimates, and migration trends¹ in England and Wales. By employing state space models in conjunction with Kalman Filter and Particle Filtering techniques, our objective is to construct a robust model that effectively captures the nuances of population dynamics in the UK. This model aims to disentangle the complexities of demographic factors such as birth rates, death rates, and migration trends, to provide a clearer understanding of population fluctuations over the past 150 years.

3 Methods

3.1 Data Sources

3.1.1 Population Data

The data source comprises national and subnational population estimates for the UK and its constituent countries, the number of births and deaths, and the number of international and internal migrants. The data are collected and published by the Office for National Statistics (ONS) and the National Records of Scotland (NRS) and the Northern Ireland Statistics and Research Agency (NISRA). They include all usual residents regardless of nationality, incorporating international migrants, with specific historical adjustments [6].

3.1.2 Migration Data

The net migration was calculated as the difference between the inflow and outflow of international migrants. The migration data published by ONS, which only dates back to 1964 for England and Wales, was collected from various sources and only includes long-term migration due to the lack of a population registration system in the UK [5].

¹The migration data used in this study only includes the years 1964 to 2023.

3.2 Inference Methods for State-Space Models

In the context of State Space Models (SSMs), the unobserved states are denoted as x_t , which follow a Markov Process² initiated from x_0 and adhere to a process equation $p(x_t|x_{t-1})$ for $t \geq 1$ [8]. It can be written as:

$$x_t = f(x_{t-1}, \eta_t) \quad (1)$$

Where f is a function that describes the state transition, and η_t is the process noise.

Similarly, the observations y_t are conditionally independent given x_t with observation equation as $p(y_t|x_t)$ for $t \geq 1$, which can be written as:

$$y_t = g(x_t, \epsilon_t) \quad (2)$$

Where g is a function that describes how the state is observed, and ϵ_t is the observation noise. Together, they describe how the system evolves and how observations relate to the underlying state.

To facilitate inference, we define $x_{1:t} \equiv \{x_1, \dots, x_t\}$ and $y_{1:t} \equiv \{y_1, \dots, y_t\}$ respectively as a set of states and observations at time t . As mentioned earlier, we can fit the SSMs with both frequentist and Bayesian inference frameworks. For the frequentist approach, such as the Kalman Filter, we estimate the hidden states using the conditional distribution of the states given the observations and the fixed (or estimated) parameter values. The joint likelihood L_j for the states $x_{1:T}$ given a length T observations $y_{1:T}$ is defined as:

$$L_j(x_{1:T}|y_{1:T}) = \prod_{t=1}^T g(x_t, \epsilon_t) f(x_{t-1}, \eta_t), \quad (3)$$

For our online estimation setting, to estimate the state with a known parameter values $\hat{\theta}$, this (the probability distribution of states) can be represented as a filtering problem:

$$\hat{p}(x_{1:t}|y_{1:t}, \hat{\theta}) = \frac{L_j(x_{1:t}|y_{1:t}, \hat{\theta})}{\int L_j(x_{1:t}|y_{1:t}, \hat{\theta}) dx_{1:t}} \quad (4)$$

²A Markov process is a stochastic process where the future state depends solely on the present state, not the entire past history of the process.

Where the marginal likelihood, i.e. the integral in the denominator ensures that the probabilities sum to one.

In contrast to the frequentist approach, where parameters are treated as fixed but unknown values, the Bayesian framework considers both states and parameters as random variables [9]. In Bayesian inference, this involves specifying priors for demographic parameters of interest, such as birth and death rates, as well as the initial state if it is not assumed known [11]. Our goal is to recursively estimate the posterior distribution $p(x_{0:t}|y_{1:t})$. This is also known as the smoothing distribution, defined as $x_t|y_{1:T}$, the conditional probability of the state given all observations up to time T . We may also be interested in the filtering distribution defined as $p(x_t|y_{1:t})$ conditional only observation up to time t . Applying Bayes' theorem ³, the posterior distribution at time t is given by:

$$\begin{aligned} p(\theta, x_{1:t}|y_{1:t}) &= \frac{L_j(x_{1:t}, \hat{\theta}|y_{1:t})p(\theta)}{\int L_j(x_{1:t}, \hat{\theta}|y_{1:t})p(\theta) d\theta dx_{1:t}} \\ &= \frac{p(y_{1:t}|x_{1:t}, \theta)p(x_{1:t}|\theta)p(\theta)}{\int p(y_{1:t}|x_{1:t}, \theta)p(x_{1:t}|\theta)p(\theta) d\theta dx_{1:t}} \end{aligned} \quad (5)$$

Where θ represents the parameters, $p(\theta)$ is the prior distribution of parameters, $p(x_{1:t}|\theta)$ is the prior distribution of the states, and $p(y_{1:t}|x_{1:t}, \theta)$ is the likelihood of the data (joint likelihood) given the states & parameters, and the denominator integral is the marginal likelihood serves as a normalization factor, ensuring the posterior distribution sums up to 1 [10].

To simplify the estimation, we'll assume the parameters θ are known and

³The Bayes theorem $p(\theta|y) = \frac{p(y|\theta)p(\theta)}{p(y)}$ [9]

fixed, hence we can update the posterior recursively using the following steps:

$$\begin{aligned}
p(x_{0:t+1}|y_{1:t+1}) &= \frac{p(x_{0:t+1}, y_{1:t+1})}{p(y_{1:t+1})} \\
&= \frac{p(x_{t+1}, y_{t+1}|x_{0:t}, y_{0:t})p(x_{0:t}, y_{1:t})}{p(y_{t+1}|y_{1:t})p(y_{1:t})} \\
&= \frac{p(y_{t+1}|x_{t+1}, x_{0:t}, y_{0:t})p(x_{t+1}|x_{0:t}, y_{0:t})p(x_{0:t}, y_{1:t})}{p(y_{t+1}|y_{1:t})p(y_{1:t})} \\
&= \frac{p(y_{t+1}|x_{t+1})p(x_{t+1}|x_t)p(x_{0:t}|y_{1:t})}{p(y_{t+1}|y_{1:t})} \\
&= \frac{p(y_{t+1}|x_{t+1})p(x_{t+1}|x_t)}{p(y_{t+1}|y_{1:t})}p(x_{0:t}|y_{1:t})
\end{aligned}$$

We assume conditional independence such that y_{t+1} depends solely on the current state x_{t+1} and the Markov chain property on x , where the transition to the next state x_{t+1} relies only on the current state x_t . Hence, the posterior distribution $p(x_{0:t+1}|y_{1:t+1})$ can be expressed as the observation likelihood $p(y_{t+1}|x_{t+1})$ and the state transition probability $p(x_{t+1}|x_t)$ multiplied by the posterior distribution $p(x_{0:t}|y_{1:t})$ at time t .

Evaluating the marginal likelihood in (4) & (5) is challenging as it often involves a high-dimensional integration known proportionally to time t [4]. For example, for a SSM with a 1-dimensional state at each time step. If we want to evaluate the posterior distribution at time $t = 100$, we would need to compute a 100-dimensional integral. This is because the denominator in Bayes' theorem, as shown in (5), involves an integral over all possible values of $x_{0:t}$, which is a t -dimensional integral. As t increases, the dimensionality of this integral also increases, making it more difficult to compute. To address the problem, we can either assume a specific form of the state-space model, such as a linear Gaussian model (Model 3.3) by maximizing the likelihood, or use Monte Carlo (MC) methods (Model 3.4 and 3.5), sampling large number of states and parameters to approximate the posterior distribution [1].

3.3 Model 1 - Linear Gaussian with Kalman Filter

In this model, we assume that the population dynamics can be described by a linear Gaussian SSMs, suitable to be fit with a Kalman Filter using R packages `Fast Kalman filter`. The state-space model is defined by the

following process and observation equations:

$$x_t = c_t + T_t \cdot x_{t-1} + \eta_t, \quad (6)$$

where $\eta_t \sim \mathcal{N}(0, H_t)$. Deriving from $x_t = c_t + T_t \cdot x_{t-1} + Q_t \cdot \eta_t$ with d_t being a vector of annual net migration, η_t was assumed to be mean zero and variance H_t , and Q_t equals identity.

Observations y_t are modeled as direct measurements of the state variable with added noise to account for the uncertainty and potential inaccuracies in population data. The observation noise ϵ_t was assumed normal with mean zero and variance G_t :

$$y_t = x_t + \epsilon_t, \quad (7)$$

where $\epsilon_t \sim \mathcal{N}(0, G_t)$. Deriving from $y_t = d_t + Z_t \cdot x_t + K_t \cdot \eta_t$ with d_t being a vector of annual net migration, Z_t equal 1 and η_t was assumed to be mean zero and variance G_t , and K_t equals identity.

- x_t is the state of the system at time t , with the starting value x_0 being the initial population count (in 1839).
- c_t is the number of net immigration count each year ⁴
- T_t is the state transition matrix, describing how the state evolves from time $t - 1$ to t , utilizing net effects of $\phi + \beta$ (mean death and birth rates) derived from the data. In the univariate case here, T_t is a scalar, representing the growth rate of the population.
- y_t is the observed population at time t .
- H_t and G_t are the process and observation noise variances, respectively. Both are assumed to be independent and identically distributed (i.i.d.) normal variables with a mean of zero [8]. The variance of H_t was estimated from the year-over-year population differences to capture stochasticity not explained by process equation (6). The variance of G_t was set based on 3% of the population count base on the 2021 ONS census report suggestion [7]. The implications of these assumptions will be discussed in 4.1.1.

⁴Available data from 1964 to 2023 and set to zero otherwise.

The Kalman filter output the analytical solutions recursively in two steps: prediction and update [8]. Given the initialization values x_0 and the covariance matrix P_0 , which, in this univariate case, simplifies to the variance of the estimation error. For each step at time $t - 1$:

1. Given state mean x_{t-1} and variance P_{t-1}

2. Prediction

- (a) we predict the state as $\hat{x}_t = T_t x_{t-1} + c_t$
- (b) with the variance as $\hat{P}_t = T_t P_{t-1} T_t^T + H_t$ where \hat{P}_t is the predicted variance at time t .

3. Update

- (a) We then calculate the Innovation (Prediction Error) as $e_t = y_t - \hat{x}_t = y_t - T_t \hat{x}_{t-1} - c_t$.
- (b) The Kalman Gain $K_t = \hat{P}_t + G_t$
- (c) We then update our estimation of x_t with a normal distribution of mean $x_t = \hat{x}_t + \hat{P}_t K_t^{-1} e_t$ and variance: $P_t = (I - \hat{P}_t K_t^{-1}) \hat{P}_t$ [8].

We iteratively apply the Kalman Filter to update our population estimates. The filtering distribution $p(x_t|y_{1:t})$ provide a refined view of the population size, by adjusting model's predictions with observed data. We also compute standard errors from the diagonal elements of the post-update variance P_t to construct 95% confidence intervals around the estimates.

3.3.1 Optimization for Estimating Standard Deviation

In the above example, we assume that the parameters (i.e. T_t) are known. In situations where the parameters vector θ - which may include H_t , G_t , among others - are unknown, a two-step approach is often employed. The first step involves the use of Maximum Likelihood Estimation (MLE) to estimate the values of θ that maximize the likelihood of the observed data, i.e. the marginal likelihood $L_m(\theta|y_{1:t})$ [13]. This is achieved by integrating out the hidden states $x_{1:t}$ from the joint likelihood L_j defined in Equation (3) [1]. Once the parameters are estimated, the second step involves using the

estimated $\hat{\theta}$ to perform state estimation using the conditional distribution defined in Equation 4. The marginal likelihood for θ is given by:

$$\begin{aligned} L_m(\theta|y_{1:t}) &= \int L_j(\theta, x_{1:t}|y_{1:t}) dx_{1:t} \\ &= \int [g(y_1|x_1, \epsilon_1; \theta) \dots g(y_t|x_t, \epsilon_t; \theta) \\ &\quad \times f(x_1|x_0, \eta_1; \theta) \dots f(x_t|x_{t-1}, \eta_t; \theta)] dx_{1:t} \end{aligned}$$

The log-likelihood function $\ell(\theta)$ for a vector of unknown parameters θ is then computed as⁵:

$$\ell(\theta) = \sum_{t=1}^T \log L_m(\theta|y_{1:t-1}), \quad (8)$$

While the Kalman Filter assumes zero mean white processes (observation) noise, real-world population dynamics rarely exhibit the constant birth and death rates and immigration flows implied by the process model. Process variance, H_t , addresses this uncertainty, allowing the Kalman Filter to prioritize recent measurements. A high H_t (relative to population) enables the model to closely track observations [8], deviating from the linear trajectory suggested by the process equation. Similarly, observation variance, G_t , accounts for errors in population data collection, such as non-response and double-counting in censuses [7]. For the parameter optimization, we fix the observation error G_t to be 3% of the population count. To further refine the process error H_t , we construct a function that takes G_t as its sole arguments. This function is based on the negative log-likelihood function detailed in 3.2. This optimization aims to minimize the negative log-likelihood of the Kalman Filter's output:⁶

$$\underset{H_t}{\text{minimize}} \quad -\mathcal{L}(H_t, \bar{G}_t, Y) \quad (9)$$

We employ the BFGS (Broyden-Fletcher-Goldfarb-Shanno) algorithm, a quasi-Newton method, to solve this optimization problem. BFGS builds upon the principles of Newton's method which uses the following update step:

$$x_{k+1} = x_k - [H_f(x_k)]^{-1} \nabla f(x_k) \quad (10)$$

where:

⁵Derivation of maximum likelihood estimation equation can be found in Appendix A

⁶ \bar{G}_t represents the default value of G_t

- x_k is the current estimate of the solution,
- $\nabla f(x_k)$ is the gradient of the function f at x_k ,
- $H_f(x_k)$ is the Hessian matrix of the function f at x_k .

BFGS avoids the computationally expensive task of directly calculating and inverting the Hessian matrix $[H_f(x_k)]$ at each iteration. Instead, it iteratively constructs an approximation of the inverse Hessian $[B_f(x_k)]^{-1}$ based on gradient information, guiding the search for optimal H_t [12]. We optimize the process errors H_t , with initial values set to the logarithm of their defaults to ensure positivity [1]. The inverse Hessian $[B_f(x_k)]^{-1}$ was initialized as the identity matrix I . The search direction d_k was calculated as:

$$d_k = -B_k^{-1} \nabla f(x_k) \quad (11)$$

The algorithm then finds a step size α_k that minimizes $f(x_k + \alpha_k d_k)$ as defined (4.9) above, and updates the positions $x_{k+1} = x_k + \alpha_k d_k$. We calculate change in parameter values x_k and gradient y_k as:

$$x_k = x_{k+1} - x_k = \alpha_k d_k, \quad y_k = \nabla f(x_{k+1}) - \nabla f(x_k) \quad (12)$$

Finally, we update the inverse Hessian B_{k+1}^{-1} using the BFGS formula:

$$B_{k+1} = B_k + \frac{y_k y_k^T}{y_k^T x_k} - \frac{B_k x_k x_k^T B_k}{x_k^T B_k x_k} \quad (13)$$

Final estimates for H_t was obtained by exponentiating the optimized results.

3.4 Model 2 - Sequential Monte Carlo with Bootstrap Filter

To address potential nonlinearities and non-gaussian in the population dynamics, we employ a Bayesian state-space model in conjunction with Sequential Monte Carlo (SMC) methods, specifically a bootstrap filter [4]. Population dynamics are shaped by the interplay of surviving population from the previous year, new births in the current year, and immigration count in the current year. [6]. The Birth, Survival, Immigration (BSI) model, derived from the BRS model in ecology [11], is a state-space model that represents the

dynamics of a population with two key stages: a survival process followed by a birth process. In this model, we assign a constant death rate ϕ and birth rate β throughout, establishing an 'uninformative' prior [9] with uniform distribution between 0 and 0.1 for both parameters. This upper bound is five times greater than the most extreme value observed in the birth and death data, regularizing variation in a reasonable range [4]. The model was formulated as follows with the process equation [11]:

$$x_t \sim \text{Poisson}(\lambda = x_{t-1} - d_t + b_t + I_t) \quad (14)$$

where x_t is the surviving population at time t , modeled as a Poisson process to account for 'overdispersion' and the variation in immigration data [11]. However, Poisson process might lead to 'overparameterization' of the model [9]. We will explore alternative model assumption in 4.1.2 to determine if a simpler model will be sufficient. b_t and d_t are the number of births and deaths at each year, as derived from the process below. The death process d_t was modeled as a binomial process [11] with death probability ϕ applied on the population size x_{t-1} from the previous year:

$$d_t \sim \text{Binomial}(x_{t-1}, \phi) \quad (\text{Binomial deaths}) \quad (15)$$

After the death process, the surviving population was updated as $x_t^1 = x_{t-1} - d_t$. A Poisson process is useful when modeling events that occur randomly and independently over time, such as births [11]. The birth process b_t was modeled as a Poisson process with rate $\beta \times x_t^1$, based on the updated surviving population.

$$b_t \sim \text{Poisson}(\beta \times x_t^1) \quad (\text{Poisson births}) \quad (16)$$

The net immigration, I_t , was incorporated as an exogenous input, directly augmenting the population size. In Summary, $f(x_t|x_{t-1})$, the state transition equation is summarized as:

$$x_t = \text{Poisson}(x_{t-1} - \text{Binomial}(x_{t-1}, \phi) + \text{Poisson}(x_t^1 \times \beta) + I_t) \quad (17)$$

The observed population Y_t is modeled as a Lognormal distribution to reflect the density dependent variance [11].

$$y_t \sim \text{Lognormal}(\log(x_t), \log(G_t)) \quad (18)$$

where G_t is the observation error variance.

To maintain consistency between the model's initial state x_1 representation and its process dynamics, the initial population x_1 was modeled with a Poisson distribution (rate parameter $\lambda = x_0$), while its corresponding observation was modeled as a log-normal distribution with mean equal to the log of x_1 and fixed observation error (3% of the 2021 population) [7]. The model was then fitted with a bootstrap filter to estimate state sequences, and equally weighted posterior samples of state variables are used to generate time series estimates of the population states. As we shall discuss in the result section ??, this hypothesis may be too simplistic, and we may need to incorporate stochasticity in error as elaborated in 3.5.

Algorithm at time step t each with M the number of particles [4]:

1. **Sample** (new particles from the state transition distribution): $\tilde{\mathbf{x}}_t^{(i)} \sim q(\mathbf{x}_t | \mathbf{x}_{t-1}^{(i)})$, $i = 1, \dots, M$ where $q(*)$ is the proposal distribution, which here is the process equation (17) defined above.
2. **Weighting** (Calculate importance weights for each particle): $w_t^{(i)} \propto p(\mathbf{y}_t | \tilde{\mathbf{x}}_t^{(i)})$, $i = 1, \dots, M$, which here is the observation equation (18). The weights reflect how well each propagated particle explains the current observation y_t . Normalized the weights.
3. **Resampling particles** (with replacement proportional to their previous step weights $w_{t-1}^{(i)}$): $\mathbf{x}_t^{(i)} \sim \tilde{\mathbf{x}}_t^{(i)}$, $i = 1, \dots, M$ promotional to $w_t^{(i)}$
4. **Approximates** the posterior $p(\mathbf{x}_t | \mathbf{y}_{1:t})$ with the new set of particles $\{\mathbf{x}_t^{(i)}\}_{i=1}^M$

The particle filtering enables us to estimate the posterior distribution of the population with a non-linear process equation in (17) which we cannot solve the likelihood analytically. However, in the result section, we may see that such model may suffer from 'particle degeneracy' issues [4] where only a few particles have significant weights, leading to a poor approximation of the posterior distribution.

3.4.1 Code Implementation Model 2 Bootstrap Filter

```
stateSpaceModelCode <- nimbleCode({
  # Priors
  phi ~ dunif(0, 0.1)    # phi (death rate)
```

```

beta ~ dunif(0, 0.1) # beta (birth rate)

# Initial state
S[1] ~ dpois(lambda = N_initial) # Initial population
Y[1] ~ dlnorm(meanlog = log(S[1]), sdlog = log(sdo)) # Initial state

# Process model
for (t in 2:T) {
  # Binomial death process
  d[t] ~ dbin(size = S[t-1], prob = phi)

  # Surviving population after deaths but before births
  S_post_death[t] <- S[t-1] - d[t]

  # Poisson birth process based on the updated surviving population
  b[t] ~ dpois(lambda = beta * S_post_death[t])

  # Update total surviving population including new births
  S[t] ~ dpois(lambda = S_post_death[t] + b[t] + I[t])

  # Observation process
  Y[t] ~ dlnorm(meanlog = log(S[t]), sdlog = log(sdo))
}
})

```

3.5 Model 3 - Particle Filter with Dynamic Birth and Death Rates

To address the limitations of deterministic birth and death rates in Model 2 (see Section 3.4), we enhance the bootstrap filter algorithm with additional stochasticity by introducing a birth and death rate process model.

The state space model at time t is defined with the process equations:

$$x_t = x_{t-1} - \text{Binomial}(x_{t-1}, \phi_{t-1}) + \text{Poisson}(x_{t-1} \cdot \beta_{t-1}) + I_t + \epsilon_{t,i}$$

where the observation model is:

$$y_t \sim \text{Lognormal}(\log(x_t), \log(G_{t,t})),$$

and the variance of the observation error at time t , $G_{t,t}$, is dynamically recalculated at each time step as 3% of the population of the previous year, y_{t-1} , similar to the Kalman Filter example in Section 3 [7].

Initialization: Birth and death rate particles i are initialized from a uniform distribution between 0 and 0.1:

$$\begin{aligned}\beta_{t,i} &\sim \text{Uniform}(0, 0.1), \\ \phi_{t,i} &\sim \text{Uniform}(0, 0.1).\end{aligned}$$

Simulation over time steps: Given the previous year’s population, x_{t-1} , and a death rate particle, $\phi_{t,i}$, deaths for year t are simulated using a binomial distribution. The surviving population then interacts with a birth rate particle, $\beta_{t,i}$, to simulate births using a Poisson distribution. The estimated population for year t , $\hat{x}_{t,i}$, is the sum of the surviving population, births, and immigration count i_t , with an added normal variation for process error, $\epsilon_{t,i} \sim \mathcal{N}(0, H_t)$, where H_t is set to the optimized process error of 1.61×10^{11} , indicating a constant process error variance across all time steps.

Weights Update: Particle weights are updated dynamically based on comparing the observed population y_t with a Lognormal distribution with a mean (in log scale) as the estimated population by each particle $\hat{x}_{t,i}$ and the annual variance $G_{t,i}$ as 3% of the preceding year population count [7]:

$$w_{t,i} = w_{t-1,i} \cdot p(y_t | \hat{x}_{t,i})$$

$p(y_t | \hat{x}_{t,i})$ returns the density of y_t under $\text{Lognormal}(\log(\hat{x}_{t,i}), \log(G_{t,i}))$.

Resample if ESS Low: The Effective Sample Size (ESS) is calculated, if it is below a threshold of 80% [10] (indicating particle degeneracy), particles are resampled based on their weights to ensure diversity in the particle set and prevent weight collapse. After resampling, weights are reset to uniform distribution, indicating equal confidence in all particles post-resampling.

To visualize the result, we employ the posterior mean as the point estimator, accompanied by the 95% posterior density distribution to capture the uncertainty in the population estimates.

3.5.1 Code Implementation Model 3

```
# Pseudocode
1. Initialize: Particles, weights, sdp = sqrt(1.6e11)
```


2. For each year:
 - Simulate deaths (Binomial) and births (Poisson) on prev_population
 - Update estimated_population =
 survived + births + immigration + Normal(0,sdp^2)
 - Update weights with Log-normal(observation, sd = log(sdo))
 - Normalize weights and calculate ESS
 - Resample if ESS < threshold (0.8): Resample
3. Estimate parameters: calculate mean birth and death rates
4. Calculate posterior density:
 - 2.5% and 97.5% quantiles for estimated_population

	Model 2: Sequential Monte Carlo with Bootstrap Filter	Model 3: Particle Filter with Dynamic Birth and Death Rates
Initialization	Constant ϕ and β with uniform priors between 0 and 0.1; initial population x_0 modeled as Poisson distribution	Initializes ϕ_t and β_t with the same uniform distribution; employs dynamic recalculation at each time
Process Model	Poisson process equation with 2 subprocess - Binomial deaths and Poisson births, incorporating immigration as an exogenous input	Normal process equation with a fixed variance derived from Section 3.3 result, subprocess similar to Model 2
Observation Model	Observations are modeled as Lognormal distributions with a fixed observation error variance H_t	Use the same Lognormal observation model but dynamically recalculates the variance of observation error $H_{t,t}$ at each time step
Resampling Strategy	Resampling at each time point proportional to particles' weights from the previous time step through <code>rankSample</code> [10] function from <code>NimbleSMC</code> packages	Resamples if ESS falls below a threshold (e.g., 80%), with post-resampling weights reset to uniform to ensure equal confidence across particles

Table 2: Comparison between SMC Model 2 and Model 3

4 Results

4.1 England & Wales

4.1.1 Model 1 - Kalman Filter

Starting with initial parameters $H_t = 1.61 \times 10^{11}$ and $G_t = 1.13 \times 10^6$, we achieved a close fit to the observations, as shown in Figure 4, with a log-likelihood of 2623.38. Optimization resulted in a slightly higher H_t estimate of 1.77×10^{11} and a new model likelihood of 2622.96. Regardless of the initial

uncertainty in P_0 , the filter converges to an optimal solution, as evidenced by the log-likelihood values for P_0 values of 10^3 and 10^6 .

As the process and observation error variances approach zero, the Kalman filter remains valid [8], but increasingly approximates a deterministic model with a near-fixed mean, as shown in Figure 3. When the process error was squared ($H_t = 4 \times 10^5$), the confidence interval significantly narrowed, resulting in more linear filtering and reduced responsiveness to new observations.

As mentioned in 3.3, the assumption of constant observation error variance is questionable given the tripling of the population over 150 years. The variability in process noise is also likely changes over time due to factors such as advancements in census methods, suggesting the need for a time-dependent H_t (and G_t) model.

Lastly, the fitting results suggest an overestimation of the population from 2000, possibly due to the combined effects of immigration and constant birth and death rate assumptions, despite a likely decline in birth rates over time [6].

4.1.2 Model 2 - NimbleSMC Bootstrap Filter

The posterior samples' histogram for the final states, depicted in Figure 7, approximates a normal distribution, indicating stable state estimates and successful convergence of the bootstrap filter. The number of unique particles, shown in Figure 6, increases and stabilizes over time, further confirming convergence. However, the sharp increase may suggest over-stochasticity in the process model specification (as mentioned in Section 3.4), making the model overly sensitive to new data [8]. This could also indicate an excessively large process variance, inducing greater variability and necessitating more frequent resampling. The state estimations' time series, depicted in Figure 5, exhibits a narrow 95% posterior density interval, suggesting high confidence in the population estimates. However, the process model appears to systematically underestimate the population, as the posterior mean consistently falls below the observed population. This discrepancy may stem from the Poisson process assumption's potential unsuitability for modeling population dynamics or from incomplete immigration data. Incorporating immigration data from the 1960s enhanced the model's fit to the observed population. The estimate of log-likelihood for the model is 3828.82, higher than that of the Kalman Filter.

4.1.3 Model 3 - Hard-coded Bootstrap Filter

The analysis of the filtering result, as illustrated in Figure 8, reveals that the estimated population closely tracks the actual observed data, especially when net immigration is accounted for since 1960s. The 95% posterior density increases over time, caused by the proportional increase in the observation error variance, G_t , as the population grows. The evolution of Effective Sample Size (ESS) in Figure 9 shows indication of particle degeneracy, with ESS dropping below 80% each year, necessitating resampling. Finally, as the hard-coded model enable us to monitor the birth and death rates at each time step as in 10, we can see that the estimated death rate ϕ is consistently higher than the birth rate β . This contrast with the actual data, where in Figure 1, the birth rate is consistently higher. The discrepancy indicate missing covariates in the model, such as the effect of age structure on birth and death rates to be considered in future work.

5 Discussion

5.1 Implications of Findings

Implications of the findings

5.2 Limitations and Future Work

In our future work, we aim to extend our current model to separately analyze the population dynamics in England, Scotland, Wales, and Northern Ireland. We will leverage the datasets provided by the national Records of Scotland and the Northern Ireland Statistics and Research Agency (NISRA). These datasets include time series data on births, deaths, migration, and population estimates dating back to the mid-19th century.

In addition to the Sequential Monte Carlo and Kalman Filter methods used in this study, we also plan to explore the use of Markov Chain Monte Carlo (MCMC) methods for model fitting in our future work. This approach will provide us with another perspective and potentially enhance our ability to capture the unique demographic trends and influences in each of these regions.

5.3 Conclusion

Key findings and their significance.

A Proof of MLE for Kalman Filter

⁷ For the time series, a conditional probability density function is used to write the joint density function as

$$L(y_1, \dots, y_T; \theta) = \prod_{t=1}^T p(y_t | y_{1:t-1}) \quad (19)$$

Recall from Section 3.3 that, after the prediction step, we have the conditional distribution of y_t being normal with a mean $\hat{x}_t + e_t$ and variance P_t

$$e_t = y_t - \hat{x}_t - \epsilon_t$$

where the innovation covariance matrix P_t is given by:

$$P_t = \hat{P}_t + G_t \quad (20)$$

Assuming Gaussian noise, the PDF of the innovation at time t is:

$$p(e_t | y_1, \dots, y_{t-1}, \theta) = \frac{1}{\sqrt{(2\pi)^t \det(P_t)}} \cdot \exp\left(-\frac{1}{2} e_t^T P_t^{-1} e_t\right)$$

The joint likelihood function for all observations is the product of individual:

$$L(y_1, \dots, y_T; \theta) = \prod_{t=1}^T p(e_t | y_1, \dots, y_{t-1}, \theta) \quad (21)$$

We often work with the log-likelihood function for numerical stability:

$$\log L(y_1, \dots, y_T; \theta) = \sum_{t=1}^T \left[-\frac{1}{2} \log(\det(P_t)) - \frac{1}{2} e_t^T P_t^{-1} e_t - \frac{N}{2} \log(2\pi) \right]$$

We then able to use an optimization algorithm (Newton-Raphson or BFGS) to find the values of T_t, H_t, G_t that maximize the log-likelihood function.

⁷Adapted from *Forecasting, Structural Time Series Models and the Kalman Filter* Section 3.4 [8]

B Supplementary Code & Visualizations

B.1 Additional SMC Model

B.1.1 NimbleSMC Bootstrap Filter with Exact Rates

This model is expected to closely align the population estimation with a gap of net immigration, by employing the precise death rate ϕ and birth rate β , calculated as proportions of the annual total population corresponding to the number of deaths and births, respectively. See `Appendix BRS Other/BRS - Exact.R`.

B.1.2 NimbleSMC Bootstrap Filter with Dynamic Rates

We set up a dynamic death rate ϕ and birth rate β with uniform prior at each time t , and fit using the `NimbleSMC Bootstrap` function. The result fail to converge due to the over stochasticity in the model, encouraging us to use the hard-coded rates in Model 3. See `Appendix BRS Other/SMC Bin dynamic rate.R`.

B.1.3 NimbleSMC Bootstrap Filter with Binomial Process

Rather than assuming a Poisson birth process dependent on the surviving population, we employ two independent binomial processes for births and deaths, maintaining the same parameterization as in Model 2. The results mirror the trends observed in Model 2, albeit with marginally higher population estimates, while achieving a comparable log-likelihood of 3828.82. See `Appendix BRS Other/SMC - Bin.R`.

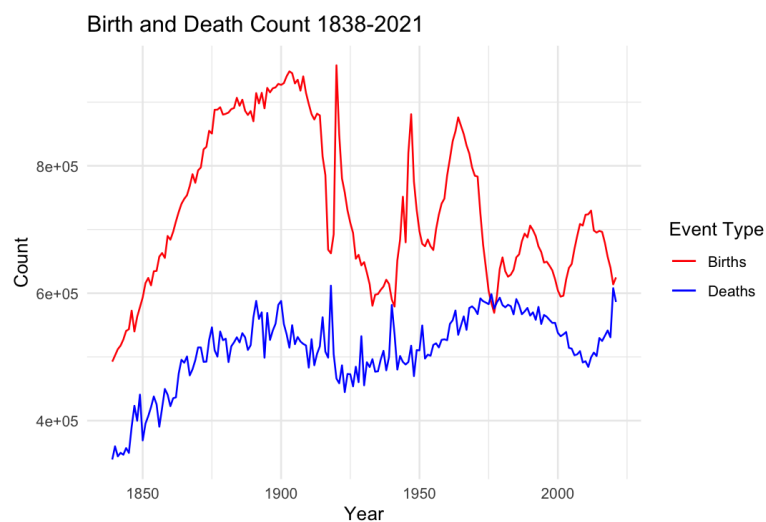


Figure 1: Birth and Death - England & Wales - 1838-2021

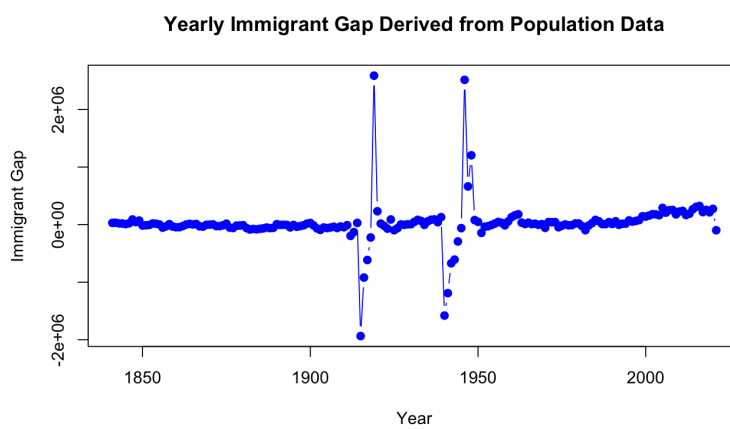


Figure 2: Immigration Gap - England & Wales - 1838-2021

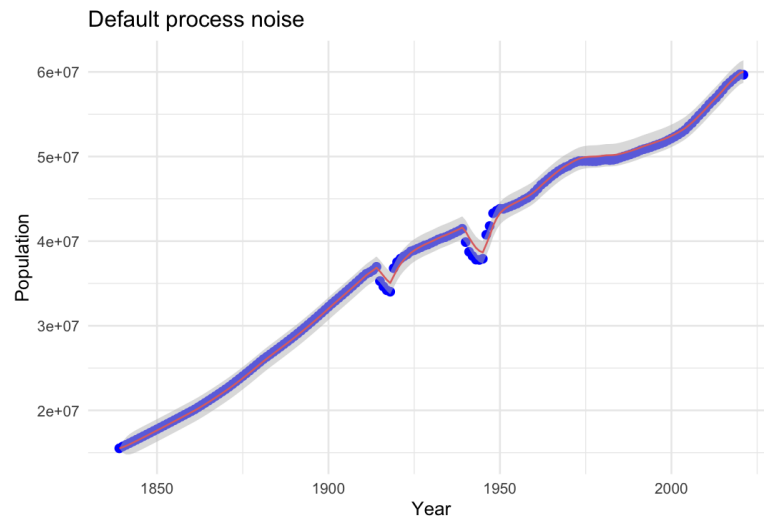


Figure 3: Model 1 - Kalman Filter Default Error- England & Wales

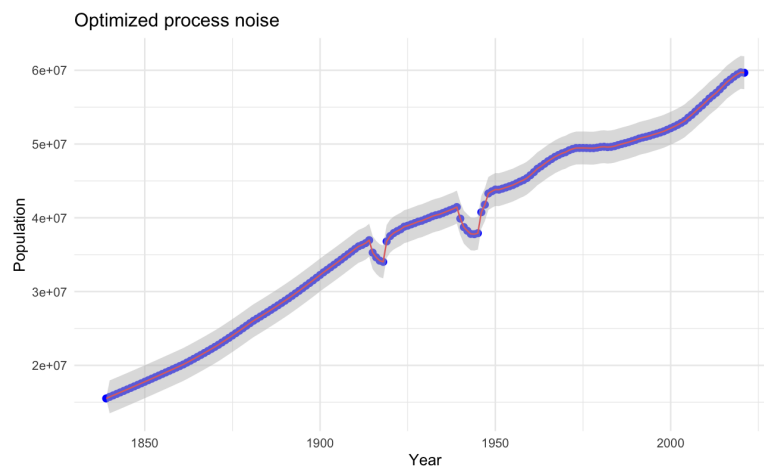


Figure 4: Model 1 - Kalman Filter Optim Error- England & Wales

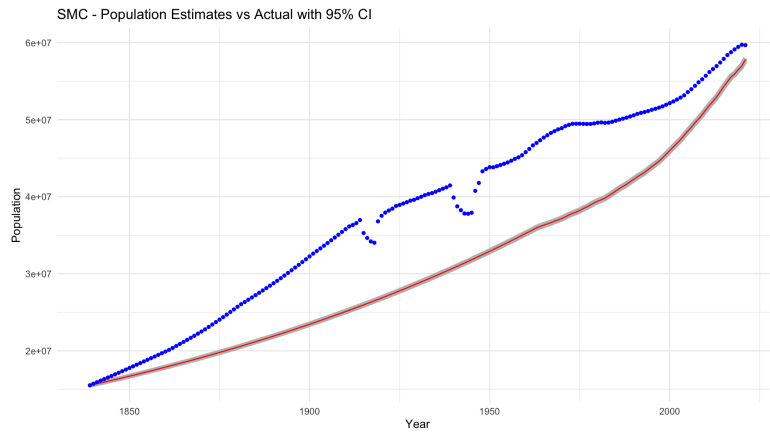


Figure 5: Model 2 - SMC Bootstrap Filter - England & Wales

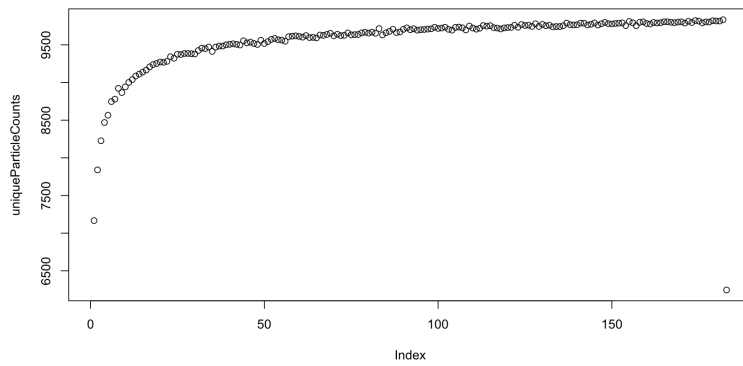


Figure 6: Model 2 - Unique Particles Numbers - England & Wales

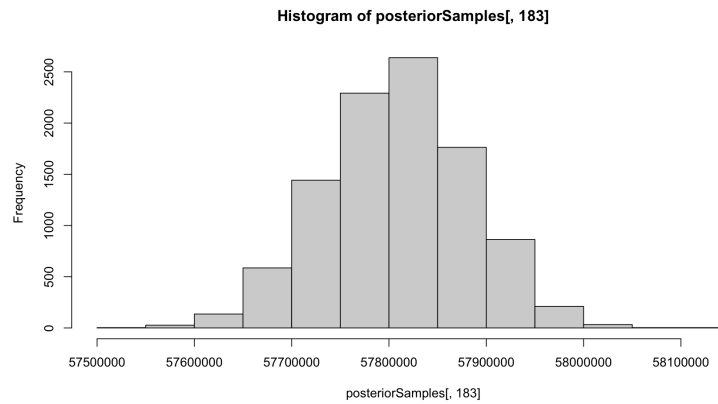


Figure 7: Model 2 - Posterior Density of Final State - England & Wales

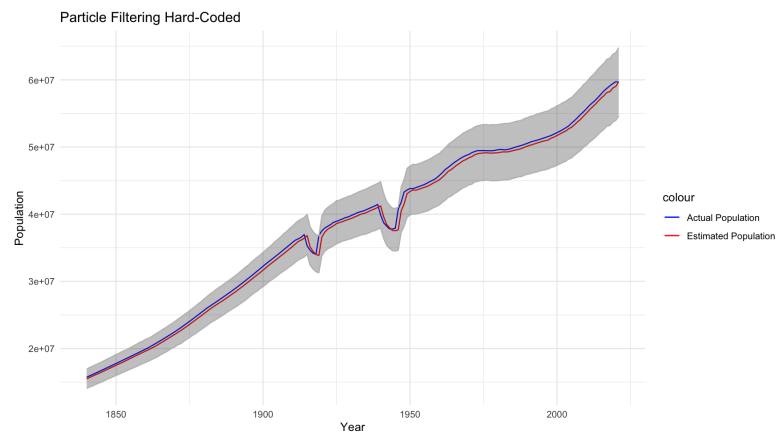


Figure 8: Model 3 - SMC Hard-Coded - England & Wales

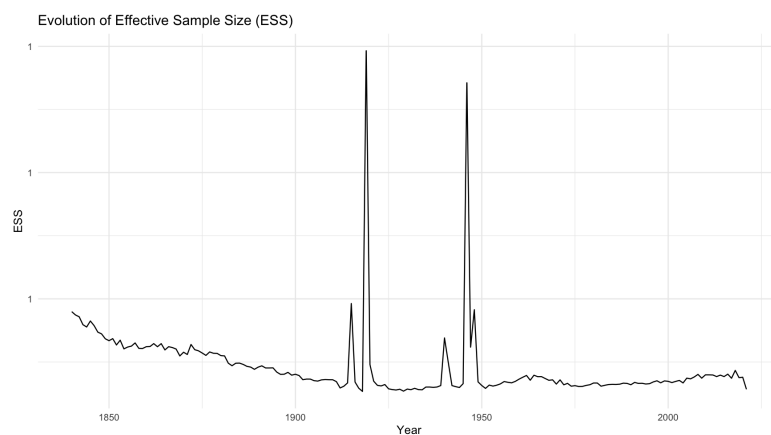


Figure 9: Model 3 - SMC Hard-Coded ESS- England & Wales

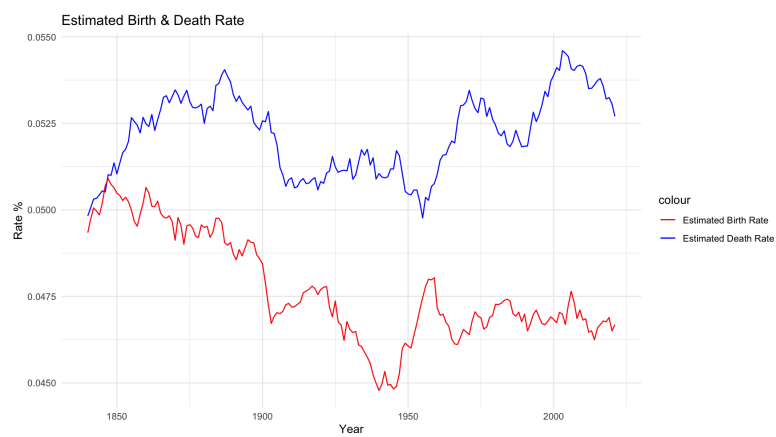


Figure 10: Model 3 - SMC Hard-Coded Birth & Death Rates - England & Wales

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