A Bayesian cohort component projection model to estimate adult populations at the subnational level in data-sparse settings

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Abstract

Accurate estimates of subnational populations are important for policy formulation and monitoring population health indicators. For example, estimates of the number of women of reproductive age are important to understand the population at risk to maternal mortality and unmet need for contraception. However, in many low-income countries, data on population counts and components of population change are limited, and so levels and trends subnationally are unclear. We present a Bayesian constrained cohort component model for the estimation and projection of subnational populations. The model builds on a cohort component projection framework, incorporates census data and estimates from the United Nation’s World Population Prospects, and uses characteristic mortality schedules to obtain estimates of population counts and the components of population change, including internal migration. The data required as inputs to the model are minimal and available across a wide range of countries, including most low-income countries. The model is applied to estimate and project populations by county in Kenya for 1979-2019, and validated against the 2019 Kenyan census.

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1 Introduction

Reliable estimates of demographic and health indicators at the subnational level are essential for monitoring trends and inequalities over time. As part of monitoring progress towards global health targets such as the Sustainable Development Goals (SDGs), there has been increasing recognition of the substantial differences that can occur across regions within a country (World Health Organization (WHO) 2016b; Lim et al. 2016; He et al. 2017). As such, analysis of national-level trends is often inadequate, and subnational patterns should be considered in order to fully understand likely future trajectories. Indeed, estimates and projections of important indicators such as child mortality and contraceptive use are now being published at the subnational level (New et al. 2017; Wakefield et al. 2019).

To effectively measure health indicators of interest, we need to be able to accurately estimate the size of the population at risk. In order to convert the rate of incidence of a particular demographic or health outcome to the number of people affected by that outcome, we need a good estimate of the denominator of those rates. As such, population counts are essential knowledge for policy planning and resource allocation purposes. However, even something as seemingly simple as the number of people in an area of a certain age is relatively unknown in many countries, particularly low-income countries that do not have well-functioning vital registration systems. And as previously reported outcomes show, differences in estimates of the population at risk can have a large effect on the resulting estimates of key indicators. For example, in 2017 the United Nations Inter-agency Group for Child Mortality Estimation (UN-IGME) and the Institute for Health Metrics and Evaluation (IHME) both published estimates of under-five child mortality in countries worldwide (GBD 2016 Mortality Collaborators (IHME) 2017; UN-IGME 2017). However, estimates for 2016 differed markedly, with IHME’s estimate being 642,000 deaths lower than the UN-IGME estimate. The main reason for the discrepancy was the different sets of estimates of live births: IHME assumed there were 128.8 million live births in 2016, which was 12.2 million lower than the 141 million used by UN-IGME.

Data on population counts by age and sex at the subnational level vary substantially by country, and often data availability and quality is the worst in countries where outcomes are also relatively poor.
For example, many low-income countries may only have one or two historical censuses available, and very little data available on internal migration or mortality rates at the subnational level. This situation is in stark contrast to many high-income countries where multiple data sources on population counts, mortality and migration may exist. These varying data availability contexts both present challenges in estimates of population and the components of population change. In data-rich contexts, the challenge is to reconcile multiple data sources that may be measuring the same outcome. In data-sparse contexts, the challenge is to obtain reasonable estimates without many observations. In both cases traditional demographic models are often utilized, which often center around a cohort component projection framework and take advantage of the fact that patterns in populations often exhibit strong regularities across age and time. However, these classical methods do not give any indication of uncertainty around the estimates or projections, and incorporating information from different data sources often requires adhoc adjustments to ensure consistency. To overcome these limitations, we propose a method that builds on classical demographic estimation of populations by incorporating these techniques within a probabilistic framework.

In particular, we present a Bayesian constrained cohort component model to estimate subnational adult populations, focusing on women of reproductive age (WRA), i.e. women aged 15-49. This subgroup forms the population at risk for many important health indicators such as fertility rates, maternal mortality, and measures of contraceptive prevalence. The model presented embeds a cohort component projection setup in a Bayesian framework, allowing uncertainty in data and population processes to be taken into account. At a minimum, the model uses data on population and migration counts from censuses, as well as national-level information on mortality and population trends, taken from the UN World Population Prospects (UNPD 2019a). As data requirements are relatively small, the methodology is applicable across a wide range of countries, and overcomes limitations of previous subnational cohort component methods, which require relatively large amounts of data. Estimates and projections of population by age are produced, as well as estimates of subnational mortality schedules and in- and out- migration flows. As such, results from the model help to understand population at risk to demographic and health outcomes at the subnational level, but also to understand drivers of population change and how these may in turn affect trends in indicators of interest.
The remainder of this paper is structured as follows. The next section gives a brief overview of existing methods of subnational population estimation, and outlines the contributions of the model proposed here. We then describe the main data sources typically available for subnational population estimation in low-income countries, using counties in Kenya as an example, followed by detailed description of the proposed methodology. We then present results of fitting the model to data in Kenya and validate its out-of-sample projections against the 2019 census. Finally, possible extensions are discussed.

2 Existing methods of subnational population estimation

Methods to estimate population at the subnational level are similar to estimation methods at the national level. However, there are several notable challenges of subnational population estimation that do not exist at a country level. Firstly, migration flows are more important at the subnational level. While migration flows are often assumed to be negligible at the national level, they are usually larger as a proportion of total population size at the regional level. In addition, migration flows at the subnational level are also often more difficult to estimate. Any particular region could have net in- or out-migration, and flows to and from different regions can differ markedly in magnitude.

Secondly, when estimating subnational populations, it is important to ensure the sum of all regions agrees with national estimates produced elsewhere. In practice, this usually involves a process of calibration against a known national population so that they match the total. Lastly, data quality and availability is often poorer at the subnational level. Populations at the regional level are smaller and data are often more volatile, and data on key indicators of mortality and internal migration is often lacking or unreliable.

2.1 Traditional methods

Perhaps the simplest and least data-intensive methods of subnational population estimation involve interpolation and extrapolation of regional shares of the total population (Swanson and Tayman 2012). Given two (or more) censuses, one can calculate the relevant shares of the population by age, sex and region and see how they have changed over time. Intercensal estimations of populations assume constant increase (or decrease) over time. Projection of populations into the future can then
be made based on assumptions of constant levels or trends in shares. For example, the U.S. census Bureau produce subnational population estimates for the majority of countries worldwide (U.S. census Bureau 2017). The methods used to produce such estimates involve making assumptions such as constant or logistic growth, and iteratively calculating population proportions by age, sex and region such that they match the country’s total populations (Leddy 2017).

The most commonly used methods of population estimation and projection are cohort component methods. These center on the demographic accounting identity, which states that the population size \( P \) at time \( t \) is equal to the population size at \( t - 1 \), plus births \( B \) and in-migrants \( I \), minus deaths \( D \) and out-migrants \( O \) (Wachter 2014):

\[
P_t = P_{t-1} + B_{t-1} + I_{t-1} - D_{t-1} - O_{t-1}
\]

The above equation is for a total population, but the same accounting equation holds for each age group separately (where births only affect the first age group). The cohort component method of population projection (Leslie 1945) takes a baseline population with a certain age structure and survives it forward based on age-specific mortality, fertility and migration rates. Cohort component methods are important because they allow for overall population change to be related to the main components of that change. By estimating population size based on the components of fertility, mortality and migration, the method allows changes in these components to be taken into account. However, cohort component methods are more data-intensive than extrapolation methods, which is particularly an issue at the subnational level. For developing countries in particular, where well-functioning vital registration systems do not exist, sufficient data on mortality, fertility and migration is often lacking.

Other methods of subnational estimation involve building regression models which relate other variables of interest to changes in population over time. For example, one could regress the ratio of census populations (area of interest / total population) against the ratio of some other indicator e.g. births, deaths, voters, school enrollments (see Swanson and Tayman (2012) for a detailed review). However, given the lack of data available in many developing countries – on population counts, let alone other indicators of growth – these methods have limited use in our context.
These traditional methods of population estimation are deterministic and do not account for random variation in demographic processes and possible measurement errors that may exist in the data. In practice, the population data that are available in developing countries are often sparse and may suffer from various types of errors. When estimating and projecting population sizes through time, it is particularly important in developing country contexts to give some indication of the level of uncertainty around those estimates, based on stochastic error, measurement error and uncertainties in the underlying modeling process.

2.2 Bayesian methods

The use of Bayesian methods in demography has become increasingly common, as it provides a useful framework to incorporate different data sources in the same model, account for various types of uncertainty, and allow for information exchange across time and space (Bijak and Bryant 2016). Bayesian methods have been used to model and forecast national populations (Raftery et al. 2012; UNPD 2019a), fertility (Alkema et al. 2011), mortality (Alexander and Alkema 2018; Alkema and New 2014; Girosi and King 2008) and migration (Bijak 2008). In terms of estimating the full demographic accounting identity, Wheldon et al. (2013) propose a method for the reconstruction of past populations. The model embeds the demographic accounting equation within a Bayesian hierarchical framework, using information from available censuses to reconstruct historical populations via a cohort component projection framework. The authors show the method works well to estimate populations and quantify uncertainty in a wide range of countries with varying data availability (Wheldon et al. 2016). The method presented in Wheldon et al. (2013) is designed for population reconstruction at the national level, and as such, accounting for internal migration is not an issue. In addition, their method relies upon and calibrates to national population estimates produced as part of the UN World Population Prospects.

In the field of subnational estimation, Bayesian methods have also been used in many different contexts. For subnational mortality estimation, many researchers have used Bayesian hierarchical frameworks to share information about mortality trends across space and time, in contexts where the available data are both reliable (Congdon, Shouls, and Curtis 1997; Alexander, Zagheni, and Barbieri 2017) and sparse (Schmertmann and Gonzaga 2018). For subnational fertility estimation,
Sevcikova, Raftery, and Gerland (2018) propose a Bayesian model that produces estimates and projections of subnational total fertility rates (TFRs) that are consistent with national estimates of TFR produced by the UN. Building from the local level up, Schmertmann et al. (2013) propose a method which uses empirical Bayesian methods to smooth volatile fertility data at the regional level, before modeling using a Brass relational model variant.

In terms of population estimation at the subnational level, John Bryant and colleagues have shown how the demographic accounting equation can be placed within a Bayesian framework to account for and reconcile different data sources population counts and the components of population change (Bryant and Graham 2013; Bryant and Zhang 2018). Bryant and Zhang (2018) show how the underlying demographic processes can be captured through a process or system model, and different types of uncertainty around data inputs is captured through data models. The focus of Bryant and Graham (2013) is producing subnational population estimates for New Zealand, reconciling and incorporating information about the population from sources such as censuses, and school and voting enrollments. The approach that we take in this paper is similar to the Bryant et al. approach, in that we model population change with a process model, the components of which are described by system models, and different sources of information are combined through the use of data models. However, whereas Bryant et al. tries to overcome challenges of combining multiple data sources that may be measuring the same outcome, we are trying to overcome the challenges of estimating subnational populations in contexts where there is extremely limited amounts of data available.

There is an increasing amount of work using geo-located data and satellite imagery to estimate population sizes and flows in developing countries (Wardrop et al., 2019, Leasure et al. 2020). Led by the WorldPop project at the University of Southampton (WorldPop 2018), researchers have used information from satellite imagery to identify areas of settlements, and combined this information with census data to obtain highly granular population density estimates across Africa (Linard et al. 2012; Leasure et al. 2020). While this work contributes to information about subnational populations, the focus and goals of this estimation work are different to our goals in this paper. In particular, the goal of the WorldPop work is primarily to obtain estimates of total population and population density at a very granular level, rather than obtaining population estimates by age and sex. The results have then been combined with data on age- and sex-distributions from
censuses (or more recent surveys) to map the distribution of populations by age and sex. However, little attention is paid to how age distributions across regions change over time. But changes in age distributions are important in understanding broader population change and how this will impact global health indicators of interest. In addition, our approach is grounded in understanding the main components of demographic change – mortality and migration – over time and how they affect population sizes, rather than just estimating the population size as a single outcome.

The methodology proposed in this paper incorporates a cohort component projection model into a Bayesian hierarchical framework to understand changes in population structures over time. It allows estimates to be driven by available data and for uncertainty to be incorporated around estimates and projections. The approach has similarities with methodologies described in Wheldon et al. (2013) (but with a focus on subnational estimation) and in Bryant et al (2013; 2018) (but with a focus on data-sparse situations).

In particular, we introduce a framework to estimate subnational population counts and components of population change that relies on a minimal amount of data that is available for the vast majority of countries worldwide. Observations on subnational population counts an internal migration movements are taken from censuses, but no information on subnational mortality patterns is required. We instead use a mortality model approach based on principal components derived from national mortality schedules. Using principal components for demographic modeling and forecasting first gained popularity after Lee and Carter used the technique as a basis for forecasting US mortality rates (Lee and Carter 1992). More recently, principal components has become increasingly used in demographic modeling, in both fertility and mortality settings (Schmertmann et al. 2014; Clark 2016; Alexander, Zagheni, and Barbieri 2017).

While one strength of our approach is being able to estimate components of subnational population change with limited data, another strength of the proposed framework is that it can be readily extended to include other data or estimates. For example, gridded estimates produced as part of the WorldPop project could conceivably be treated as an additional data input to the model.
3 Data

We aim to estimate female population counts for ages 15-49 per 5-year age group for subnational areas that are the second administrative level down. This data description focuses on Kenya, for which the model is applied in later sections. However, the data and methods are more broadly applicable to other countries that have similar data available. Inputs used to obtain estimates come from two main sources: micro-level data from censuses, and national population and mortality estimates from the 2019 World Population Prospects. These data sources are outlined in the following sections.

3.1 Overview of Kenyan geography

In Kenya, the first administrative units are provinces, and the second administrative units are counties. There are eight provinces, including the capital Nairobi, and 47 counties. The county boundaries have changed over time, but have been stable since the 2009 census. We aim to produce estimates of populations of women of reproductive age at the county level based on county boundaries in 2009. Within the model, we also make use of harmonized district boundaries (see description below), which are slightly larger than counties. There are a total of 35 districts. Provinces and districts are illustrated below in Fig 1.

3.2 Census data

Data inputs on subnational population counts and internal migration flows come from national censuses. The census data are available through Integrated Public Use Microdata Series (IPUMS) International (Minnesota Population Center 2017). IPUMS-International contains samples of microdata for 305 censuses over 85 different countries. The majority of countries of interest have relatively recent censuses available through IPUMS-International. Kenya has decennial censuses available from 1979 to 2009. Micro-level data are not available for the 2019 Kenyan census, although population counts by sex and five-year age group and county are available through the national statistics office. The 2019 data are reserved for model evaluation, as detailed in the Model Evaluation section.

In the micro-level IPUMS data, location of residence is reported at the first (province) and second
(county) administrative levels, as well as a harmonized district level. For Kenya, the provinces are stable over time, but before 2009 the county boundaries changed. As such, we only have data at the county level for Kenya for 2009. However, we can make use of the harmonized districts for data in years prior to 2009. The districts represent slightly larger groups than the 47 Kenyan counties, which are harmonized and temporally stable (IPUMS 2018). In all cases, each 2009 county is completely contained in one unique district.

We used census data to obtain information on two different quantities: observed population counts; and observed patterns of in- and out-migration. Female population counts by five-year age groups for ages 15-49 and subnational administrative region are obtained directly from the IPUMS-International microdata. As these data are samples (most commonly 10%), the microdata are multiplied by the person weights to obtain counts by age and area.¹

Information on internal migration between counties and districts is also obtained from national censuses. This is based on questions about a migrant’s location of residence one year ago. We

¹The sampling error introduced by considering sampled microdata is accounted for in the data model, refer to the Methods section for details.
calculated in- and out-migration counts by age group, for each region and each census. For the 2009 census, the calculations were based on counties; for all earlier years the calculations were based on districts.

### 3.3 National estimates from WPP

The World Population Prospects (WPP) are the official population estimates and projections produced by the United Nations. WPP is revised every two years, with the latest revision being in 2019 (UNPD 2019a). WPP estimates are produced using a combination of census and survey data, and demographic and statistical methods. Both population counts and mortality estimates from WPP are used in the model.

We use estimates from WPP 2019 in two ways. Firstly, we would like to ensure that the sum of population estimates at the regional level agrees with published estimates at the national level. National population counts produced by WPP are used as a constraint in the model, subject to uncertainty. The WPP models populations of five-year age groups every five years from 1950-2100.

National mortality estimates produced by WPP are used as the basis of a mortality model for patterns at the regional level, capturing HIV/AIDS related patterns of mortality. WPP uses the relationship between infant mortality and the probability of dying between ages 15 and 60, i.e. $45q_{15}$, to estimate a life table based on Coale-Demeny Model Life Tables (UNPD 2019b). We use estimates of the probability of dying between ages $x$ and $x + 5$, $5q_x$.

### 3.4 Other potential data sources

We use census data and WPP estimates as inputs to the model. There are other available data sources that could be used as inputs. These sources and the reasons for not including them are discussed in Appendix A.
4 Model

4.1 Overview

In this section we describe the modeling framework to estimate female populations by five-year age group and county. The model is outlined for the situation where, like in the Kenyan case, we do not observe county-level information for every census, but we have information on larger, harmonized districts that fully encapsulate the counties. This situation is common for many low-income countries where geographic boundaries may vary over time but there exist some other stably-defined boundaries through the micro-data on IPUMS.

There are many components and several types of data going into the model at different stages. The overall model framework is summarized visually in Figure 2. We define $\eta_{a,t,c}$ to be the underlying ‘true’ population of women in age group $a$, year $t$ and county $c$. Our main modeling goal is to obtain estimates and projections of these quantities. The population counts follow a cohort component projection (CCP) model, which assumes population counts in the current time period are those from the previous period, after taking into account expected changes in mortality and migration. The CCP model also includes an additional age-time multiplier which captures any other variation not already captured by expected changes in mortality or migration. Our set-up allows for changes in mortality and migration to be projected forward even if there are no data on these components, and is useful in data-sparse contexts where there is limited information available on the individual components of population change.

As illustrated in Figure 2, the mortality, migration and additional age-time specific multipliers have additional ‘process models’ (shown on the third row), and data on population counts and migration are related to the underlying process through data models (shown in the top row).

The following sections broadly describe each component of the model. The full model specification and details can be found in Appendix B.

4.2 Population model

The model for population includes: the cohort component project model, the data model, which relates observations of population counts to the underlying quantities of interest; and the national-
Figure 2: Diagram showing the main components of the Bayesian cohort component projection model.
level constraint, which ensures the sum of the county-level populations is close to pre-published national estimates.

4.2.1 Cohort component projection model

The underlying population \( \eta_{a,t,c} \) can be expressed as

\[
\eta_{a,t,c} = (\eta_{a-1,t-1,c} \cdot (1 - \gamma_{a-1,t-1,c})) \cdot (1 + \phi_{a-1,t-1,c}) \cdot (\varepsilon_{a-1,t-1,c}),
\]

where \( \gamma_{a,t,c} \) is the expected conditional probability of death in age group \( a \), year \( t \) and county \( c \), \( \phi_{a,t,c} \) is expected net migration (that is, in- minus out-migration) as a proportion of population size, and \( \varepsilon_{a,t,c} \) is an additional age-year-county multiplier. Note that this is a form of a cohort component projection framework. As mentioned previously, our main modeling goal is to obtain estimates of the \( \eta_{a,t,c} \), but we are also interested in estimates of expected mortality \( (\gamma_{a,t,c}) \) and expected migration \( (\phi_{a,t,c}) \), and, if non-zero, the multipliers \( (\varepsilon_{a,t,c}) \).

4.2.2 Data model

Define \( y_i \) to be \( i \)th observed population count. Depending on the year of the census, \( y_i \) is either observed at the county \( c \) level or district \( d \) level. The data model is:

\[
\log y_i | \eta_{a,t,c} \sim \begin{cases} 
N \left( \log \eta_{a[i],t[i],c[i]}, s^2_y[i] \right) & \text{if } t = 2009, \\
N \left( \log \sum_{c \in d[i]} (\eta_{a[i],t[i],c[i]}), s^2_y[i] \right) & \text{if } t < 2009,
\end{cases}
\]

where \( s^2_y \) is the sampling error based on the fact that the micro-data in IPUMS is a 10% sample. The second case of the above equation dictates that if we have observations prior to 2009, we can only relate these to \( \eta_{a,t,c} \)'s that have been summed to the district level.

4.2.3 Constraints on national population

We would like to ensure the county-level populations \( \eta_{a,t,c} \) imply a national-level population that is consistent with previously-published estimates in WPP. To do this, we implement the following constraint in the model, which roughly corresponds to the sum of the subnational populations in
any age and year being within 90-110% of WPP. Further details on the constraint and priors in the population model are given in Appendix B.

4.3 Mortality model

Equation 2 requires estimates of the expected conditional probability of death in each age group, year and county. As discussed in the Data section and appendix, we do not have reliable information about mortality by age at the county level, and as such we use information about mortality trends at the national level as the basis for a mortality model at the subnational level. A semi-parametric model is used to capture the shape of national mortality through age and time, while allowing for differences by county. In particular, we model county mortality on the logit scale as

\[
\logit(\gamma_{a,t,c}) = \alpha_{0,c} + Y_{a,0} + \beta_{t,c,1} \cdot Y_{a,1} + \beta_{t,c,2} \cdot Y_{a,2},
\]

where \( Y_{a,0} \) is the mean age-specific logit mortality schedule of the national mortality curves and \( Y_{1} \) and \( Y_{2} \) are the first two principal components derived from national-level mortality schedules. Modeling on the logit scale ensures the death probabilities are between zero and one.

Principal components create an underlying structure of the model in which regularities in age patterns of human mortality can be expressed. Many different kinds of shapes of mortality curves can be expressed as a combination of the components. Incorporating more than one principal component allows for greater flexibility in the underlying shape of the mortality age schedule.

Principal components were obtained from a decomposition on a matrix which contains a set of standard mortality curves. As discussed in the Data section, we used national Kenyan life tables published in the World Population Prospects 2019. In particular, let \( X \) be a \( N \times G \) matrix of logit mortality rates, where \( N \) is the number of years and \( G \) is the number of age-groups. In this case, we had \( N = 16 \) years (estimates every 5 years from 1950 to 2025) of \( G = 7 \) age-groups (15–19, 20–24, . . . , 45–49). The SVD of \( X \) is

\[
X = UDV',
\]

where \( U \) is a \( N \times N \) matrix, \( D \) is a \( N \times G \) matrix and \( V \) is a \( G \times G \) matrix. The first two columns
of $V$ (the first two right-singular values of $X$) are $Y_{1:1,1}$ and $Y_{1:1,2}$.

The mean mortality schedule and the first two principal components for Kenyan national mortality curves between ages 15-49 from 1950–2020 are shown in Fig. 3. The mean logit mortality schedule shows a standard age-specific mortality curve, with mortality increasing over age. The first two principal components have demographic interpretations. The first shows the average contribution of each age to mortality improvement over time. This interpretation is similar to the $b_x$ term in a Lee-Carter model (Lee and Carter 1992). For the case of Kenya, the second principal component most likely represents the relative effect of HIV/AIDS mortality by age.

![Figure 3: Mean logit mortality schedule and first two principal components.](image)

The county-specific mortality intercepts are modeled using a Normal distribution centered at zero:

$$\alpha_{0,c} | \sigma_\alpha^2 \sim N(0, \sigma_\alpha^2).$$

(6)

The county-specific coefficients $\beta_{t,c,k}$ are modeled as fluctuations around a national mean:

$$\beta_{t,c,k} = B_{t,k}^{nat} + \delta_{t,c,k},$$

(7)

$$\delta_{t,c,k} | \delta_{t-1,c,k}, \sigma_\delta^2 \sim N(\delta_{t-1,c,k}, \sigma_\delta^2),$$

(8)

where $B_{t,k}^{nat}$ are the national coefficients on principal components, derived from WPP data. The county-specific fluctuations are modeled as a random walk.
4.4 Migration model

The second population change component of Equation 2 refers to the net-migration rate in a particular age group, year and county. Specifically, define the net-migration rate as

\[
\phi_{a,t,c} = \frac{\psi_{in}^{a,t,c} - \psi_{out}^{a,t,c}}{\eta_{a-1,t-1,c}},
\]

(9)

where \( \psi_{in}^{a,t,c} \) is the number of in-migrants and \( \psi_{out}^{a,t,c} \) is the number of out-migrants.

For the migration component, we use observed data from the census. As such, in a similar way to the population model, we have a process model, which defines the underlying migration process for the ‘true’ migrant parameters, and a data model, which relates observations from the census to the underlying truth.

4.4.1 Process model

The model form for the number of in-migrants and out-migrants is informed by patterns observed in the raw census data. In particular, looking at the age distribution of both in- and out-migration (i.e. the proportion of total migrants who are in age group \( a \)) suggests that, while the overall magnitude of migration changes over time, the age patterns in migration are fairly constant (see figures in Appendix C). This observation allowed us to simplify the expression for the number of in-migrants and out-migrants, which are modeled as

\[
\phi_{a,t,c} = \frac{\psi_{in}^{a,t,c} - \psi_{out}^{a,t,c}}{\eta_{a-1,t-1,c}},
\]

(10)

\[
\psi_{in}^{a,t,c} = \Psi_{in}^{t,c} \cdot \Pi_{in}^{a,c},
\]

(11)

\[
\psi_{out}^{a,t,c} = \Psi_{out}^{t,c} \cdot \Pi_{out}^{a,c},
\]

(12)

where \( \Psi_{in}^{t,c} \) and \( \Psi_{out}^{t,c} \) are the total number of in- and out-migrants, respectively, and \( \Pi_{in}^{a,c} \) and \( \Pi_{out}^{a,c} \) are the relevant age distributions. In this way the age distributions are assumed to be constant over time while the total counts vary. We model the total counts as a second order random walk to impose a certain level of smoothness in the counts over time. As the model is meant to capture internal migration flows in and out of each county, it must be the case that the sum of all in-migration flows
must equal the sum of all out-migration flows. As such, we also constrain the difference between the sum of all estimated in- and out-migration flows to be close to zero. See Appendix B for further details.

### 4.4.2 Data model

Finally, we relate the observed age-specific in- and out-migration counts in the censuses, denoted $M_{i}^{in}$ and $M_{i}^{out}$, respectively, to the underlying true counts $\psi_{a,t,c}^{in}$ and $\psi_{a,t,c}^{out}$ through the following data model:

\[
\log M_{i}^{in} | \psi_{a,t,c}^{in} \sim \begin{cases} 
N \left( \log \psi_{a[i],t[i],c[i]}^{in}, s_{in}^{2} \right) & \text{if } t[i] = 2009 \\
N \left( \log \sum_{c \in d[i]} (\psi_{a[i],t[i],c[i]}^{in}), s_{in}^{2} \right) & \text{if } t[i] < 2009
\end{cases}
\] (13)

\[
\log M_{i}^{out} | \psi_{a,t,c}^{out} \sim \begin{cases} 
N \left( \log \psi_{a[i],t[i],c[i]}^{out}, s_{out}^{2} \right) & \text{if } t[i] = 2009, \\
N \left( \log \sum_{c \in d[i]} (\psi_{a[i],t[i],c[i]}^{out}), s_{out}^{2} \right) & \text{if } t[i] < 2009.
\end{cases}
\] (14)

In a similar fashion to the data model for population, data observed prior to 2009 can only be related to the migration counts that have been summed to the district level. In addition, the $s_{in}^{2}$ and $s_{out}^{2}$ are the sampling errors based on the fact that the micro-data in IPUMS is a 10% sample.

### 4.5 Additional age-time multiplier $\varepsilon_{a,t,c}$

In both the models for expected mortality and migration discussed above, constraints are imposed on the age-specific effects. In particular, the use of the SVD approach to model mortality results in mortality age patterns that are linear combinations of the mean schedule and the components of change (the Y’s). Additionally, the migration model assumes a constant age pattern of migration over time with varying magnitudes of in- and out-migration. We assume these forms in order to greatly reduce the number of parameters that need to be estimated in each model, such that reasonable estimates of mortality and migration rates can still be obtained in data-sparse settings.

In order to allow for county-specific age- and time- variation that may not have already been captured by other components, we introduced an additional age-time multiplier $\varepsilon_{a,t,c}$ in the population cohort component model (see Equation 2). We model these multipliers on the log scale, and to ensure
identifiability we assume the mean of the sum of the log multipliers over all age groups is zero. This constraint is implemented through the re-parameterization:

$$\log \varepsilon_{1:a,t,c} = D(DD')^{-1} \zeta_{1:(A-1),t,c},$$  \hspace{1cm} (15)

$$\zeta_{a,t,c} \sim N(0, \sigma_\zeta^2),$$  \hspace{1cm} (16)

where $D$ is first-order difference matrix (with $D_{i,i} = -1$, $D_{i,i+1} = 1$, and $D_{i,j} = 0$ otherwise) such that $\zeta_{a,t,c} = \log \varepsilon_{a,t,c} - \log \varepsilon_{a-1,t,c}$.

4.6 Computation

The model was fitted in a Bayesian framework using the statistical software R. Samples were taken from the posterior distributions of the parameters via a Markov Chain Monte Carlo (MCMC) algorithm. This was performed using JAGS software (Plummer 2003). Standard diagnostic checks using trace plots and the $\hat{R}$ diagnostic (Gelman et al. 2020) were used to check convergence.

Best estimates of all parameters of interest were taken to be the median of the relevant posterior samples. The 95% Bayesian credible intervals were calculated by finding the 2.5% and 97.5% quantiles of the posterior samples.

5 Results

In this section we illustrate some key results of population counts, mortality and migration. Additional results are presented in Appendix D.

5.1 Population estimates and projections

Figure 4 shows the WRA population by province in 1979-2019. The black line and associated shaded area are the model estimates and associated 95% credible intervals. The red dots are the data from decennial censuses. Populations of WRA are increasing in every province, with the two largest provinces being Nairobi and Rift Valley. While Northeastern is the smallest province by population size, the growth rate is relatively rapid. This is likely due to the relatively high fertility rates in this province (Westoff and Cross 2006; Kenya National Bureau of Statistics 2015), whereas
rapid population increases in Nairobi are driven by in-migration.

Figure 4: Estimates of female population aged 15-49 by province, Kenya, 1979-2020.

Figure 5 illustrates populations over age and time for 3 different counties. Note the different y-axis scales for each county. For Nairobi, populations are much larger and the presence of net in-migration far surpasses the effects of mortality, leading to an inverted-U shaped age distribution. For Wajir, a relatively rural county in the northeast, population growth seems rapid over time. For Baringo, populations are relatively small and decline regularly over age due to mortality.

Figure 5: Estimates of female population aged 15-49 (‘000) by age and year for three counties.

5.2 Mortality

In addition to getting estimates of population counts, we also obtain estimates of the components of population change, namely mortality and migration. In terms of mortality, there is evidence of
variation across the counties. Focusing on the three counties as above, mortality profiles are quite different, with Baringo’s estimates being similar to the national mean (Figure 6).

Figure 6: Estimates of mortality by age and year for three counties.

5.3 Migration

In addition to mortality, there is substantial variation in patterns in migration across Kenyan counties. Figure 7 shows estimates of all migration components in the three case study counties. For total in-migration and out-migration estimates (Figure 7a), flows into and out of Nairobi are much larger, with net in migration reaching almost 400,000 people per year. Flows into Wajir are much smaller (<10,000 people), and in 2019 Baringo had net out-migration of around 10,000. The estimated age patterns of migration for the three counties are also shown in Figure 7b. Some differences exist, with Nairobi’s immigrants much more concentrated around age 20.
Figure 7: Estimates and 95% credible intervals of migration components for three counties.

5.4 Age-time multiplier

Figure 8 shows the age-time multipliers $\varepsilon$ for the three example counties. For Baringo, the multipliers are essentially always zero on the log scale. This observation is true for the majority of counties (see Appendix D for plots for additional counties), which suggests that most of the patterns over age and time are captured well by the mortality and migration components. For county-years where multipliers do deviate from zero, estimates are at most around 10% of the total population magnitude, and usually between 0-0.05%. For example for Nairobi, the estimated multiplier suggests that, after accounting for the expected mortality and migration components, in 1989, we see an additional increase around age 20 (of around 10%) and an additional decrease of around 10% at the oldest age group.
Figure 8: Age-time specific multipliers for three counties.
5.5 Model evaluation

A national census was run in Kenya in 2019. While the microlevel data are not yet publicly available (for example, via IPUMS), the resulting population counts by age, sex and county have been published by the Kenya National Bureau of Statistics (Kenya National Bureau of Statistics 2019). We can therefore evaluate the 2019 projections from our model with the actual counts from the 2019 census.

We extracted census population counts by age, sex and county from a PDF file containing the results following code provided by Alexander (2020). We compared the 2019 projections from the Bayesian cohort component projection model with these counts and calculated several summary metrics. We define the relative error \(e_g\) for a particular group \(g\) as

\[
e_g = \frac{y_{g,2019} - \hat{\eta}_{g,2019}}{y_{g,2019}},
\]

where \(y_{g,2019}\) refers to the census-based population count for that population and \(\hat{\eta}_{g,2019}\) to the model-based projection. A group \(g\) can refer to an age-county or age-district group, for example.

Based on the errors, we calculate mean, median, and root mean squared errors by age group and for the total population. We compared these results to the results of a similar linear extrapolation model, where the population in 2019 was estimated based on applying the same proportion change seen between the 1999-2009 censuses. Errors are summarized over districts, as estimates by county are not possible with the linear extrapolation method (as we only have one previous set of census observations by county).

Error summaries by age group and for the total population are shown in Table 1. In general, the Bayesian model projections are within ~1% of the census populations. The magnitudes of the RMSEs for the simple linear interpolation is 3-10 times higher than that of the Bayes CCP. The bias results suggest that the point estimate from the Bayes CCP is often slightly lower than the census observation, whereas linear interpolation substantially over-estimates population counts.

We also calculated the coverage of the 95% prediction intervals of the Bayesian cohort component projection model estimates for 2019, compared to the observed 2019 census counts, and the proportion
Table 1: Summary of errors in district population sizes by age group comparing 2019 census counts with two methods, linear interpolation and the Bayesian cohort component projection model (Bayes CPP).

Table 2: Proportion of 2019 census county counts falling within, above, and below the 90% prediction intervals as estimated by the Bayesian CPP model.

We also calculated the probability integral transform (PIT) to assess the consistency between the 2019 projections and observed counts. Results are presented in Appendix E.
6 Discussion

In this paper we proposed a Bayesian cohort component projection framework to estimate adult subnational populations with limited amounts of data available. The model uses information on population and migration counts from censuses, as well as mortality patterns from national schedules, to reconstruct populations based on cohorts moving through time. The modeling framework also naturally extends to allow projection of populations. In addition, the model ensures the national populations implied by the sum of subnational areas agree with national pre-published UN WPP estimates.

The model was used to estimate and project populations of women of reproductive ages (WRA) for counties in Kenya over the period 1979-2019. Results suggested continued growth of WRA populations in all districts, and accelerated growth in particular in areas such as Nairobi and Northeastern. The mortality component of the modeling framework highlighted the stagnating progress through the 1990s and 2000s, largely due to HIV/AIDS, but more recent mortality declines. The estimates from the Kenyan example also highlighted substantial differences in internal migration patterns across the nation.

The model requires only inputs from national censuses and WPP estimates, which are available for the majority of countries. Thus, while the model was tested on estimation in Kenya, the methodology is applicable to a wide range of countries with very little alterations. For example, there is currently census microdata available for almost 100 counties on the IPUMS-International website.

Based on a series of validation measures, the proposed model outperformed a benchmark model of linear interpolation. In addition to having lower performance than Bayes CCP, note that with the simple interpolation method, it is not possible to get estimates by county easily, because 2009 is the first year which the counties as they are today were recorded. In addition, another advantage of the Bayesian model is that the population estimates also have an associated uncertainty level, and that estimating not only population counts but also mortality and migration rates allows us to better understand the drivers of population change by county.

There are several other advantages and contributions of this modeling framework to the estimation of subnational populations. The model is governed by a cohort component projection model, tracking
cohorts as they move through time. This has advantages over more aggregate techniques such as interpolation and extrapolation, because it allows us to understand trends in overall population as a process governed by separate components that add or remove population. In addition, this process takes into account intercensal events such as trends in HIV/AIDS mortality and produces estimates and projections with uncertainty.

Secondly, the modeling framework proposes a parsimonious model for internal net-migration across subnational areas. In cohort component models, it is often the case that migration components are assumed to be negligible or considered to just be the residual once mortality has been taken into account. Very little data usually exists on migration patterns, and estimation of all migration components by age, region and year becomes very intensive. After observing key patterns in the data, we proposed a net-migration model which separates migration patterns into independent age and time components. The result is an age-specific net migration model with parameters that are easier to estimate when data are limited.

More broadly, one of the contributions of our proposed framework over existing work in this area is the use of mortality and migration models that have relatively strong functional forms, which allow plausible estimates to be produced even in the absence of good-quality data. Our approach to modeling mortality through the use of characteristic age patterns is inspired by the long demographic tradition of using model life tables where information on mortality are sparse.

While we have illustrated the utility of this approach in data-limited contexts, the framework can naturally be extended to include additional sources of data. For example, if there exist observations of age-specific mortality rates at the subnational level (even at some ages), these data could be used as inputs to the mortality model. If more reliable data on internal migration flows were available, the existing migration process model — which assumes a fixed age schedule with varying magnitude over time — could be reformulated to be more flexible. In general, to be able to handle population projection in a low data availability context, the model proposed here includes mortality and mortality process models that separate age- and time-trends into independent effects. Additional age-time specific effects were then captured by the multiplier \( \varepsilon \). If more data are available, the underlying process models could be extended to better understand these age-time specific effects and how they relate to either mortality or migration.
Another possible extension of this framework is to include other total population estimates such as those from WorldPop as additional “data” that could be used to inform estimates. As such, we view this methodology and subnational population estimates produced from it as complementary to estimates produced by other efforts such as the WorldPop project. As mentioned in Section 2, the primary goal of the WorldPop estimates is to produce extremely fine-grained estimates of total population, whereas we are more interested in understanding population patterns by age and sex and the underlying components of population change within larger subnational areas.

The incorporation of a cohort component projection model into a probabilistic setting allows for different sources of uncertainty, such as sampling and non-sampling error, to be included into the modeling process. The Bayesian hierarchical framework allows information from different data sources to be consolidated without the need for post-estimation redistribution changes as is often the case with subnational population estimation (Swanson and Tayman 2012). In addition, it allows for increased flexibility in modeling population processes compared to traditional deterministic techniques, while still keeping the basis of an underlying demographic process.
A Other potential data sources

We use census data and WPP estimates as inputs to the model. There are other available data sources that could be used as inputs. These sources and the reasons for not including them are discussed below.

A.1 Mortality

Mortality is estimated at the subnational level based on national patterns of mortality from WPP, as well as changes in subnational population counts over time. Thus, no explicit information on subnational mortality levels is used; mortality is estimated based on likely patterns at the national level and intercensal changes in population. There are two main sources for subnational mortality data in Kenya that are not included as data inputs.

Firstly, the Demographic and Health Survey (DHS) collects information about sibling mortality histories. Adult mortality can be calculated from these data using the sibling history method, where cohorts of siblings are constructed and age-specific mortality rates are calculated based on when they died. Previous research has illustrated sibling data produces relatively reliable estimates at the national level (Masquelier, 2013). However, the DHS does not ask the location of residents of the siblings who died, thus the data cannot be used to inform differentials in subnational mortality.

A second source of information on subnational mortality comes from a question about household deaths, that was collected in the most recent census (2009). This can be used to obtain death probabilities by age. However, previous research has found that the value of $45q_{15}$ implied by household deaths is often much lower or higher than other mortality sources (Masquelier et al. 2017). Indeed, mortality information from census household deaths is excluded from other mortality analyses due to its unreliable nature (e.g. child mortality, see UN-IGME (2017)). As such, we chose to omit this information for now. Future work will investigate this data source to see if it can be used to inform age patterns of mortality by subnational region.
A.2 Migration

There are two other potential sources of information on internal migration in Kenya that are not included as data inputs. Firstly, the census also includes a question about how many years the person has resided in their current locality of residence, referring to the district level. The question is asked in the 1999 and 2009 censuses. Based on the year of the census and the age of the respondent, as well as how many years they indicated they had lived in the current locality, the implied year and age of in-migration can be calculated. However, this method gave much lower numbers of in-migration compared to those implied by the ‘location one year ago’ question. As such this information was not used in the model.

Secondly, the DHS contains some information about migration.\(^2\) For Kenya, it is possible to obtain information about the proportion of the population who moved to a particular province in the year before the survey. However, when compared to corresponding data from the census, there were large discrepancies, and trends in DHS proportions were erratic over time.

\(^2\)Note that questions about migration in the DHS differ by country. The migration questions in the Kenya DHS are quite minimal; however for other countries there may be more useful data available.
B Full Model Specification

The full model specification is described below.

B.1 Population

B.1.1 Cohort component projection model

The underlying population by age group, year and county \( \eta_{a,t,c} \) is

\[
\eta_{a,t,c} = (\eta_{a-1,t-1,c} \cdot (1 - \gamma_{a-1,t-1,c})) \cdot (1 + \phi_{a-1,t-1,c}) \cdot (\varepsilon_{a-1,t-1,c}),
\]

where \( \gamma_{a,t,c} \) is the conditional probability of death in age group \( a \), year \( t \) and county \( c \), \( \phi_{a,t,c} \) is net migration (that is, in- minus out-migration) as a proportion of population size and \( \varepsilon_{a,t,c} \) is an additional age-year-county multiplier.

B.1.2 Data model

The data model is:

\[
\log y_i | \eta_{a,t,c} \sim \begin{cases} 
N \left( \log \eta_{a[i],t[i],c[i]}, s^2_y[i] \right) & \text{if } t = 2009, \\
N \left( \log \sum_{c \in d[i]} \eta_{a[i],t[i],c[i]}, s^2_y[i] \right) & \text{if } t < 2009,
\end{cases}
\]

where \( y_i \) is \( i \)th observed population count, \( s^2_y \) is the sampling error based on the fact that the micro-data in IPUMS is a 10% sample. The second case of the above equation dictates that if we have observations prior to 2009, we can only relate these to \( \eta_{a,t,c} \)'s that have been summed to the district level.
B.1.3 National constraints

We constrain the sum of the county populations by age and year to be within approximately 10% of the national estimates produced by WPP:

\[
\Lambda_{a,t} < \sum_c \log \eta_{a,t,c} \leq \Omega_{a,t},
\]

\[
\log \Lambda_{a,t} \sim N(\log 0.9 WPP_{a,t}, 0.1^2) T(\log WPP_{a,t}),
\]

\[
\log \Omega_{a,t} \sim N(\log 1.1 WPP_{a,t}, 0.1^2) T(\log WPP_{a,t}).
\]

B.1.4 Priors on first year and age group

The cohort component projection framework requires priors to be placed on populations in the first year and age group. We use the following priors:

\[
\log \eta_{1,t,c} \sim N(\log WPP_{1,t} + \log prop_{1,t,c}, 0.01^2),
\]

\[
\log \eta_{a,1,c} \sim N(\log WPP_{a,1} + \log prop_{a,1,c}, 0.01^2),
\]

where \(WPP_{a,t}\) is the national-level population count from WPP in the relevant age group and year, and \(prop_{a,t,c}\) is the proportion of the total population in the relevant age, year and county, which was calculated based on interpolating census year proportions and assuming the proportion of a district’s population in each county was constant at a level equal to 2009.

B.2 Mortality

The model for mortality is as

\[
\logit \gamma_{a,t,c} = \alpha_{0,c} + Y_{a,0} + \beta_{1,c} \cdot Y_{a,1} + \beta_{2,c} \cdot Y_{a,2},
\]

where \(Y_{a,0}\) is the mean age-specific logit mortality schedule of the national mortality curves and \(Y_{1}\) and \(Y_{2}\) are the first two principal components derived from national-level mortality schedules. Modeling on the logit scale ensures the death probabilities are between zero and one.

The county-specific mortality intercepts are modeled using a Normal distribution centered at zero:
\[ \alpha_0, c | \sigma^2_\alpha \sim N(0, \sigma^2_\alpha), \]

The county-specific coefficients \( \beta_{t, c, k} \) are modeled as fluctuations around a national mean:

\[ \beta_{t, c, k} = B_{t, k}^{nat} + \delta_{t, c, k}, \quad (26) \]

\[ \delta_{t, c, k} | \delta_{t-1, c, k}, \sigma^2_\delta \sim N(\delta_{t-1, c, k}, \sigma^2_\delta), \quad (27) \]

where \( B_{a, t, k}^{nat} \) are the national coefficient on principal components, derived from WPP data. The county-specific fluctuations are modeled as a random walk.

### B.3 Migration

#### B.3.1 Process model

The process model for the net-migration is:

\[ \phi_{a, t, c} = \frac{\psi_{in}^{a, t, c} - \psi_{out}^{a, t, c}}{\eta_{a-1, t-1, c}}, \quad (28) \]

\[ \psi_{in}^{a, t, c} = \Psi_{in}^{t, c} \cdot \Pi_{in}^{a, c}, \quad (29) \]

\[ \psi_{out}^{a, t, c} = \Psi_{out}^{t, c} \cdot \Pi_{out}^{a, c}, \quad (30) \]

where \( \Psi_{in}^{t, c} \) and \( \Psi_{out}^{t, c} \) are the total number of in- and out-migrants, respectively, and \( \Pi_{in}^{a, c} \) and \( \Pi_{out}^{a, c} \) are the relevant age distributions. We model the total counts as a second order random walk to impose a certain level of smoothness in the counts over time:

\[ \Psi_{in}^{1, c} \sim U(0, y_c), \quad (31) \]

\[ \log \Psi_{in}^{2, c} | \Psi_{in}^{1, c}, \sigma^2_{in} \sim N(\log \Psi_{in}^{1, c}, \sigma^2_{in}), \quad (32) \]

\[ \log \Psi_{t, c}^{in} | \Psi_{(t-2):(t-1), c}^{in}, \sigma^2_{in} \sim N(2 \log \Psi_{t-1, c}^{in} - \log \Psi_{t-2, c}^{in}, \sigma^2_{in}), \quad (33) \]

\[ \Psi_{out}^{1, c} \sim U(0, y_k[c]), \quad (34) \]

\[ \log \Psi_{out}^{2, c} | \Psi_{out}^{1, c}, \sigma^2_{out} \sim N(\log \Psi_{out}^{1, c}, \sigma^2_{out}), \quad (35) \]

\[ \log \Psi_{t, c}^{out} | \Psi_{(t-2):(t-1), c}^{out}, \sigma^2_{out} \sim N(2 \log \Psi_{t-1, c}^{out} - \log \Psi_{t-2, c}^{out}, \sigma^2_{out}). \quad (36) \]
where $y_c$ refers to the observed total population for county $c$ based on the census in the first observation period.

We place Uniform priors on the non-normalized age distributions of in- and out-migration, with equal prior probability on each age group:

$$
\Pi_{a,c}^{in*} \sim \text{Uniform}(0, 1), \quad \Pi_{a,c}^{out*} \sim \text{Uniform}(0, 1).
$$

We then normalize the age distributions as

$$
\Pi_{a,c}^{in} = \frac{\Pi_{a,c}^{in*}}{\sum_a \Pi_{a,c}^{in*}},
$$

$$
\Pi_{a,c}^{out} = \frac{\Pi_{a,c}^{out*}}{\sum_a \Pi_{a,c}^{out*}}.
$$

### B.3.2 Data model

We relate the observed age-specific in- and out-migration counts in the censuses, denoted $M_{i}^{in}$ and $M_{i}^{out}$, respectively, to the underlying true counts $\psi_{a,t,c}^{in}$ and $\psi_{a,t,c}^{out}$ through the following data model:

$$
\log M_{i}^{in} | \psi_{a,t,c}^{in} \sim \begin{cases} 
N \left( \log \psi_{a[i],t[i],c[i]}^{in}, s_{in}^{2} \right) & \text{if } t[i] = 2009, \\
N \left( \log \sum_{c \in d[i]} (\psi_{a[i],t[i],c[i]}^{in}), s_{in}^{2} \right) & \text{if } t[i] < 2009,
\end{cases}
$$

$$
\log M_{i}^{out} | \psi_{a,t,c}^{out} \sim \begin{cases} 
N \left( \log \psi_{a[i],t[i],c[i]}^{out}, s_{out}^{2} \right) & \text{if } t[i] = 2009, \\
N \left( \log \sum_{c \in d[i]} (\psi_{a[i],t[i],c[i]}^{out}), s_{out}^{2} \right) & \text{if } t[i] < 2009.
\end{cases}
$$

### B.3.3 Constraint

Using the fact that the sum of all internal migration for a particular age group and year should be around zero, we implement the following constraint:

$$
\sum_c -0.1 \eta_{a,t,c} < \sum_c \psi_{a,t,c}^{in} - \sum_c \psi_{a,t,c}^{out} \leq \sum_c 0.1 \eta_{a,t,c}.
$$
The constrain states that the difference between the sum of all in- and out-migration flows across all counties cannot be more than ±10% of the total estimated national population for that particular age group and year.

B.4 Age-time multiplier

We model multipliers on the log scale, and to ensure identifiability we assume the mean of the sum of the log multipliers is zero. This constraint is implemented through the re-parameterization:

\[
\log \varepsilon_{1:A,t,c} = D(DD')^{-1}\zeta_{1:(A-1),t,c},
\]

\[
\zeta_{a,t,c} \sim N(0,\sigma^2) ,
\]

where \(D\) is first-order difference matrix (with \(D_{i,i} = -1, D_{i,i+1} = 1, \text{and } D_{i,j} = 0\) otherwise) such that \(\zeta_{a,t,c} = \log \varepsilon_{a,t,c} - \log \varepsilon_{a-1,t,c}\).

B.5 Priors on variance parameters

All variance parameters that are estimated (\(\sigma^2_\alpha, \sigma^2_\delta, \sigma^2_\psi, \sigma^2_{in}\) and \(\sigma^2_{out}\)) have half-Normal standard priors placed on them, i.e.

\[
\sigma \sim N^+(0,1).
\]
C Age patterns in migration data

In the Bayesian cohort component model, specifically in the migration process model, we assume the age distribution of in- and out-migrants by count is constant over time (see Equations 13 and 14). This is a somewhat strong assumption and was made to ensure identifiability of all parameters in the model in cases where we do not have very much data. While the assumption is relatively strong, it was motivated by age patterns observed in census data. Figures 9 and 10 show the proportion of all in- and out-migrants by age group for each year and district, and illustrate that the age patterns remain remarkably constant over time. For reference, the broad areas covered by the IPUMS districts are listed in Table 3.

Figure 9: Observed age patterns of in-migration from Kenyan censuses, 1979-2009.
Figure 10: Observed age patterns of out-migration from Kenyan censuses, 1979-2009.
| District   | Areas                                                                                                                                 |
|-----------|---------------------------------------------------------------------------------------------------------------------------------------|
| 404001001 | Nairobi East, Nairobi North, Nairobi West, Westlands                                                                                  |
| 404002001 | Gatanga, Gatundu, Githunguri, Kiambu (Kiambaa), Kikuyu, Lari, Muranga, Nyandarua, Ruiru, Thika, Maragua                             |
| 404004001 | Chalbi, Laisamis, Marsabit, Moyale                                                                                                   |
| 404004002 | Garba Tulla, Igembe, Inenti, Isiolo, Maara, Meru, Tharaka, Tigania, Meru                                                               |
| 404004003 | Embu, Kangundo, Kibwezi, Machakos, Makueni, Mbeere, Mbooni, Mwala, Nzaui, Yatta                                                        |
| 404004004 | Kitui North, Kitui South (Mutomo), Kyuso, Mwingi                                                                                     |
| 404005001 | Fafi, Garissa, Igara, Lagdera                                                                                                       |
| 404005002 | Wajir East, Wajir North, Wajir South, Wajir West                                                                                     |
| 404005003 | Mandera Central, Mandera East, Mandera West                                                                                          |
| 404006001 | Bondo, Rarieda, Siaya                                                                                                                 |
| 404006002 | Kisumu East, Kisumu West, Nyando                                                                                                     |
| 404006003 | Homa Bay, Kuria East, Kuria West, Migori, Rachuonyo, Rongo, Suba                                                                     |
| 404002002 | Nyeri North, Nyeri South                                                                                                             |
| 404007001 | Turkana Central, Turkana North, Turkana South                                                                                         |
| 404007002 | Pokot Central, Pokot North, West Pokot                                                                                               |
| 404007003 | Samburu Central, Samburu East, Samburu North                                                                                          |
| 404007004 | Kwanza, Trans Nzoia East, Trans Nzoia West                                                                                           |
| 404007005 | Baringo, Baringo North, East Pokot, Koibatek, Laikipia East, Laikipia North, Laikipia West                                             |
| 404007006 | Eldoret East, Eldoret West, Warend, Uasin Gishu                                                                                       |
| 404007007 | Keiyo, Marakwet, Elgeyo Markwet                                                                                                      |
| 404007008 | Nandi Central, Nandi East, Nandi North, Nandi South, Tinderet                                                                          |
| 404007009 | Kajiado Central, Kajiado North, Loitokitok, Molo, Naivasha, Nakuru, Nakuru North, Kajiado                                             |
| 404002003 | Kirinyaga                                                                                                                             |
| 404007010 | Narok North, Narok South, Trans Mara                                                                                                 |
| 404007011 | Bomet, Buret, Kericho, Kipkelion, Sotik                                                                                               |
| 404008001 | Butere, Emuhaya, Hamisi, Kakamega, Lugari, Mumias, Vihiga, Butere/Mumias                                                             |
| 404008002 | Bungoma East, Bungoma North, Bungoma South, Bungoma West, Mt. Elgon                                                                    |
| 404008003 | Bunyala, Busia, Samia, Teso North, Teso South                                                                                         |
| 404888001 | Waterbodies                                                                                                                           |
| 404003001 | Kilindini, Kilindini, Mombasa                                                                                                       |
| 404003002 | Kinango, Kwale, Msambweni                                                                                                             |
| 404003003 | Kaloleni, Kilifi, Malindi                                                                                                             |
| 404003004 | Tana Delta, Tana River                                                                                                                |
| 404003005 | Lamu                                                                                                                                   |
| 404003006 | Taita, Taveta, Taita Taveta                                                                                                          |

Table 3: IPUMS district codes and areas covered
D Additional results

In this section we highlight several other components that are estimated within the model; specifically the coefficients on the first and second principal components. Results are illustrated on three example counties: Nairobi, Wajir and Baringo. Additionally, we show estimates for the age-time multiplier for all counties.

Figure 11 shows estimates over time of the coefficient of the first and second principal component within the mortality model (i.e. $\beta_{tc,1}$ and $\beta_{tc,2}$). Broadly, the first principal component relates to overall mortality improvement, and the second relates to the effect of the HIV/AIDS epidemic. Coefficients on the first component suggest mortality improvement is relatively slow in Nairobi, and better than the national average in Wajir. Based on patterns on the second principal component, there is evidence to suggest that the effect of HIV/AIDS epidemic was relatively small in Wajir (Figure 11). In both cases, estimates for Baringo are not significantly different from the national mean.

Figure 12 shows the estimated age-time specific multiplier for all counties. As can be seen, the estimates on the log scale are very close to zero for the majority of age groups, years and counties.
Figure 11: County-specific deviations from national-level mortality improvements (first component) and HIV/AIDS mortality (second component) for three counties.
Figure 12: Age-time specific multipliers for all counties.
E PIT histogram

A Probability Integral Transform (PIT) histogram is a tool for evaluating the similarity between model projections and left out observations. The predictive distributions of the projections are compared with the actual observations.

For each observation $j$ for 2019 (i.e. each population count by age group and county) we have observation $y_j$ from the 2019 census, and sample $\eta_j^{(S)}$ from the corresponding posterior distribution (with a total of $S$ samples). The PIT for observation $j$ was calculated as

$$PIT_j = \frac{\sum_{s=1}^{S} \eta_j^{(s)} \leq y_j}{S}.$$  \hspace{1cm} (46)

If the predictive distribution is well calibrated, the result should be a uniform distribution of PIT values. Figure 13 shows the PIT histogram for 2019. The relatively high density in the middle of the distribution suggests the model is somewhat over-dispersed, and the low density towards 1 suggests the upper bound of population projections is in general too conservative.

![Figure 13: PIT histogram comparing projected 2019 population counts with observed 2019 census counts.](image-url)
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