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Probabilistic population projections for countries with generalized HIV/AIDS epidemics

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In 2015, the United Nations (UN) issued probabilistic population projections for all countries up to 2100, by simulating future levels of total fertility and life expectancy and combining the results using a standard cohort component projection method. For the 40 countries with generalized HIV/AIDS epidemics, the mortality projections used the Spectrum/Estimation and Projection Package (EPP) model, a complex, multistate model designed for short-term projections of policy-relevant quantities for the epidemic. We propose a simpler approach that is more compatible with existing UN projection methods for other countries. Changes in life expectancy are projected probabilistically using a simple time series regression and then converted to age- and sex-specific mortality rates using model life tables designed for countries with HIV/AIDS epidemics. These are then input to the cohort component method, as for other countries. The method performed well in an out-of-sample cross-validation experiment. It gives similar short-run projections to Spectrum/EPP, while being simpler and avoiding multistate modelling.

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Keywords: Bayesian hierarchical model; cohort component projection method; Estimation and Projection Package; Spectrum; UNAIDS; World Population Prospects

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Introduction

Population projections are used by governments at all levels, international organizations, social and health researchers, and the private sector. They are used for policy planning, monitoring development goals, and as inputs to economic and environmental models. The United Nations (UN) issues population projections by age and sex, updated every two years, for all the countries of the world to 2100 in 'World Population Prospects'. It is the only organization to do so, and its projections are the de facto standard at the global level (Lutz and KC 2010).

There has long been great interest in probabilistic population projections, to quantify uncertainty in projections and the risk of adverse demographic events. However, the dominant population projection methods are deterministic, and uncertainty has typically been conveyed by variant scenario projections (such as 'high' and 'low' projections), using different assumptions about future rates. This approach has been criticized as lacking validity, because it has no probabilistic basis and leads to possible contradictions (Lee and Tuljapurkar 1994; National Research Council 2000).

In a major step forward, the UN issued official probabilistic population projections for all countries for the first time in July 2015. This 'World Population Prospects: The 2015 Revision' is available at https://esa.un.org/unpd/wpp/Publications/ and is hereafter referred to as WPP 2015. These projections were developed using the method of Raftery et al. (2012). They take account of uncertainty about future levels of total fertility and life expectancy, using the Bayesian hierarchical models of Alkema et al. (2011) for fertility and Raftery et al. (2013) for life expectancy. Between-country correlation in fertility rates is accounted for by the method of Fosdick and Raftery (2014), and correlation between male and female life expectancy is modelled using the method of Raftery et al. (2014).

These statistical models allow a large number of trajectories of future fertility and mortality for all countries to be simulated from their predictive probability distributions. Each simulated trajectory of future life expectancy is converted to age-specific mortality rates using a modified Lee–Carter method (Li and Gerland 2011; Raftery et al. 2012; Li et al. 2013; Ševčíková, Li et al. 2016). Future age-specific fertility and mortality rates are then converted to future population by age and sex by the standard cohort component method (Whelpton 1936; Preston et al. 2001), using the bayesPop R package (Ševčíková, Raftery et al. 2016). The result is a sample of possible future trajectories of world population by country, age, and sex, to 2100.

The UN's probabilistic WPP currently treats countries with generalized HIV/AIDS epidemics (hereafter referred to as the 'AIDS countries') differently from others. These countries exhibit very different mortality patterns from countries without generalized HIV/AIDS epidemics; they tend to exhibit a large mortality hump in middle adulthood due to AIDS, and so cannot be modelled using, for example, standard model life tables.

The UN's current method for probabilistically projecting mortality for these countries starts with a deterministic projection derived from the Spectrum model (Stanecki et al. 2012; Stover et al. 2012; Avenir Health 2016), a complex, multistate model developed for UNAIDS that divides adults into 15 compartments according to their HIV status, and models transitions between these 15 compartments. In a second stage, the Bayesian hierarchical model of Raftery et al. (2013) for life expectancy and the modified Lee–Carter method are applied to all countries, including the AIDS countries, yielding simulated age- and sex-specific mortality rates. In a third and final stage, the predictive distribution of each future age- and sex-specific mortality rate is adjusted so that its median coincides with the deterministic projection from the first stage.

This method has several limitations. It relies on the Spectrum multistate model, which was developed primarily to answer short-term policy questions about the HIV/AIDS epidemic, such as the future need for antiretroviral therapy (ART) drugs or the future number of AIDS orphans. Because of its complexity and reliance on a large number of assumptions about transition rates between the many compartments, it was not designed for medium- and longer-term projections. Indeed, the UNAIDS Reference Group on Estimates, Modelling, and Projection notes that Spectrum projections more than five years into the future are unreliable (UNAIDS 2015, p. 9).

The needs of the UN Population Division (UNPD) are very different. The UNPD provides projections of population that are long term, to 2100, but that output only overall population and vital rates, and so do not need the level of detail in Spectrum. The need to use a different method for a subset of countries (about 20 per cent of the world's countries) is also a difficulty.

Here we propose an alternative method for probabilistic projection for the AIDS countries that is simpler than the current one, does not require any multistate modelling, and makes use of the bayesPop method used by the UNPD for other countries. It requires probabilistic projections of overall HIV prevalence, and these are obtained from the relatively simple non-age-structured Estimation and Projection Package (EPP) (Ghys et al. 2004, 2008; Brown et al. 2010; Ghys and Garnett 2010). Future life expectancy is modelled on HIV prevalence and ART coverage, and projected using a simple time series regression model (Godwin and Raftery 2017). The resulting simulated life expectancies and prevalences are converted to age-specific mortality rates using the HIV prevalence calibrated model life table method of Sharrow et al. (2014), which replicates the middle adulthood mortality hump characteristic of HIV/AIDS epidemics. The population projections are then obtained using the same bayesPop method as for other countries.

The resulting method fits observed age-specific mortality data well. An out-of-sample validation experiment showed that it is reasonably accurate and provides well-calibrated probabilistic projections of aggregate mortality and population quantities. It is simpler than the existing Spectrum method, but still matched its projections closely over the next 15 years.

The rest of the paper is organized as follows. In the next section, we describe our new methods and the data we use. In 'Results' we present results for four countries with generalized HIV/AIDS epidemics, chosen to represent a range of generalized HIV/AIDS epidemic experience: Botswana, Zimbabwe, Mozambique, and Sierra Leone. Following that, we show the results of an out-of-sample validation experiment to assess our method, and we also compare the resulting projections with those from Spectrum. We conclude with a discussion of the strengths and limitations of our proposed approach.

Methods and data

Population projection involves combining future values of age-specific fertility, age- and sex-specific

mortality, and international migration rates, in this case using the standard cohort component model. To make probabilistic projections for countries with high HIV prevalence, we follow the procedure described by Raftery et al. (2012) for making probabilistic projections of fertility in countries without generalized HIV/AIDS epidemics and use the UNPD assumptions about international migration (United Nations, Department of Economic and Social Affairs, Population Division 2015a, pp. 30–1), but we modify the mortality component to account for HIV/AIDS mortality.

Raftery et al. (2012) simulate a large number of trajectories of the total fertility rate (TFR) using the Bayesian hierarchical model of Alkema et al. (2011). The projected TFRs are then converted to age-specific rates using model fertility patterns. For mortality, an equal number of trajectories of period life expectancy at birth (e_0) are simulated for women using the model of Raftery et al. (2013). Male life expectancies are conditional on the female e_0 and are derived from a model that predicts the gap in male and female e_0 (Raftery et al. 2014). These e_0 projections are converted to age-specific mortality rates using a variant of the Lee–Carter method (Li et al. 2013; Ševčíková, Li et al. 2016). Each trajectory of fertility, mortality, and migration is then converted to a future trajectory of age- and sex-specific population values using the cohort component method (Preston et al. 2001, chapter 6).

In our application, the projection of fertility remains the same—fertility is projected using the bayesTFR package (Ševčíková et al. 2011) in the statistical analysis software 'R'—as does the use of the UNPD assumptions about international migration and the cohort component method to combine these trajectories. While probabilistic methods for projecting international migration have been developed (Azose and Raftery 2015; Azose et al. 2016), in the interest of isolating any discrepancy between our results and WPP 2015 to our treatment of mortality, we do not incorporate those methods in this paper. In the following sections, we outline the methods of Godwin and Raftery (2017) for projecting e_0 accounting for HIV prevalence and Sharrow et al. (2013) for converting those quantities into age-specific mortality rates.

Projecting HIV prevalence

To make probabilistic projections of e_0 for countries with generalized HIV/AIDS epidemics and to convert those projections into age-specific mortality rates, we first need projections of HIV prevalence. We use the UNAIDS EPP (Alkema et al. 2007; Brown et al. 2010; Ghys and Garnett 2010; Raftery and Bao 2010), in its so-called EPP-Classic non-age-structured version for the statistical analysis software 'R' (R Core Team 2017), to make probabilistic projections of HIV prevalence up to 2100.

EPP works well to project HIV prevalence into the not too distant future, approximately five to ten years after the latest surveillance (UNAIDS 2015), but we imposed assumptions mirroring those made by UNPD in WPP 2015 on two of the EPP model parameters to make projections to 2100 (United Nations, Department of Economic and Social Affairs, Population Division 2011). For most countries, the model is fitted assuming that the relevant parameters have remained constant in the past. Beginning in the start year of the projection, the parameter ϕ, which reflects the rate at which new individuals enter the high-risk (or susceptible) group, is projected to decline by half every 20 years. The parameter r, which represents the force of infection, is projected to decline by half every 30 years. The reduction in r reflects the assumption that changes in behaviour among those subject to the risk of infection and increases in access to treatment for infected individuals will reduce the chances of HIV transmission.

For each country, we use a single UNAIDS deterministic trajectory of yearly HIV prevalence to 2100 as a baseline. We construct 1,000 trajectories of HIV prevalence using both this deterministic trajectory and multipliers created from the output from EPP. Let $z_{c,t}$ be the median of the trajectories of HIV prevalence from EPP for country c and year t. We use multipliers of the form $(z^k_{c,t}/z_{c,t})$ for $k = 1, \ldots,$ 1,000, where $z^k_{c,t}$ is the projected HIV prevalence for trajectory k. Combining these multipliers with the single deterministic trajectory yields a median determined by the UNAIDS trajectory and an uncertainty around that determined by the EPP projections. We generate uncertainty in this manner since Spectrum/EPP cannot be relied on over the long time frame of our forecasts. From these 1,000 yearly trajectories, we construct five-year time period estimates by taking five-year averages. A single trajectory of future ART coverage is then combined with the HIV projections to be used in the projection stage.

Projecting life expectancy at birth, e_0

Because a generalized HIV/AIDS epidemic can have a considerable depressing effect on life expectancy at

birth in a short time (Poit et al. 2001; Ngom and Clark 2003; Blacker 2004; Timæus and Jasseh 2004; Obermeyer et al. 2010; Bor et al. 2013; Sharrow et al. 2013; Reniers et al. 2014), a model that reflects the impact of HIV prevalence and ART coverage is necessary to make appropriate projections of e_0 in generalized epidemics. What follows is a brief description of such a model developed by Godwin and Raftery (2017).

Let $\text{HIV}_{c,t}$ and $\text{ART}_{c,t}$ be the HIV prevalence and adult ART coverage in country c at time t, respectively. We define $HnA_{c,t} = \text{HIV}_{c,t} \times (100 - \text{ART}_{c,t})$, so that $HnA_{c,t}$ represents the percentage of infected people not receiving ART in country c at time t. The model for projecting e_0, equation (1), predicts the five-year change in female life expectancy at birth from time $t-5$ to t as:

$$\Delta e_{0,c,(t-5:t)} = g(e_{0,c,t-5}|\theta^{(c)}) + \beta_{HnA}\Delta HnA_{c,t-5} + \varepsilon_{c,t-5} \quad (1)$$

where $\Delta e_{0,c,(t-5:t)}$ is the change in life expectancy for country c at time $t-5$ to t, $g(e_{0,c,t-5}|\theta^{(c)})$ is the double logistic fitted change in life expectancy at time $t-5$ to t, given life expectancy at time $t-5$, and $\varepsilon_{c,t-5}$ is the error term.

The double logistic term is the same as the model used for countries not substantially impacted by HIV/AIDS (Raftery et al. 2013) and reflects the transition from high to low mortality, which can be broken down into two processes, each represented by a single logistic function. The first process describes initial slow growth in e_0 with small improvements in mortality at low levels of e_0 resulting from gains in hygiene and nutrition, followed by a quicker pace of improvement. The second process represents continuing gains from combating noncommunicable diseases (Omran 2005; United Nations, Department of Economic and Social Affairs, Population Division 2015a).

The Bayesian hierarchical model (equation (1)) is constructed by placing priors on all country-specific parameters, which can be interpreted as world parameters. Proper and diffuse hyperpriors are placed on all world parameters, and the model is estimated via Markov chain Monte Carlo simulation. See Raftery et al. (2013) and Godwin and Raftery (2017) for further details.

The observed data are five-year female life expectancy estimates from 1950 to 2015 for all 201 countries with populations over 100,000 from WPP 2015 (United Nations, Department of Economic and Social Affairs, Population Division 2015b). We use the single UNAIDS trajectory of HIV prevalence to construct five-year averages for 1950–2015, and a single trajectory of ART coverage (percentage of seropositive individuals receiving ART) for five-year periods from 1950 to 2100 for each country, obtained from UNPD internal tabulations (United Nations, Department of Economic and Social Affairs, Population Division 2011). Note that *HnA* values for countries not experiencing a generalized epidemic are zero for all time periods.

To project female life expectancy to 2100, we input each trajectory of *HnA* and life expectancy into the model period by period starting from 2015, drawing random perturbations, $\varepsilon_{c,t}$, from a zero-mean Gaussian distribution whose variance is a function of life expectancy at time t for each five-year time period. Countries with a generalized HIV/AIDS epidemic have more intrinsic variability than those without. Therefore, AIDS countries draw random perturbations from a distribution with larger variance than those not experiencing an epidemic. The process for deriving sex- and age-specific mortality rates from the projected female e_0 is described in the following section.

Converting e_0 and HIV prevalence projections to age-specific mortality rates

Once we have obtained probabilistic projections of female life expectancy and HIV prevalence, we need to map those quantities onto a set of sex- and age-specific mortality rates that can be combined with age-specific fertility rates and net migration using the cohort component method. In WPP 2015, for countries without high HIV prevalence, age-specific mortality rates are either extrapolated from recent data, if available, or obtained by converting e_0 projections to age-specific mortality rates using model mortality patterns (United Nations, Department of Economic and Social Affairs, Population Division 2015a, pp. 27–8). However, recent data are typically unavailable in parts of the world with high HIV prevalence and model mortality patterns are unable to replicate the particular age pattern of mortality resulting from large-scale HIV/AIDS epidemics (United Nations, Department of Economic and Social Affairs, Population Division 2015a, p. 28). Available model mortality patterns also have no relationship to HIV prevalence.

To convert the female life expectancy and HIV prevalence projections to sex- and age-specific mortality rates, we use the model of Sharrow et al. (2014) shown in equation (2). This model can reproduce the characteristic age pattern of mortality

associated with generalized epidemics, that is, an accentuated adult mortality hump concentrated between ages 30 and 45. The model represents the age pattern of mortality rates as a weighted sum of three age-varying components. The components, $b_{i,x}$, in equation (2) are derived from a singular value decomposition (SVD) of the matrix of observed historical mortality rates and the weights, $\omega_{i,l}$, are modelled as a function of HIV prevalence and female life expectancy at birth.

The SVD is performed on a matrix that keeps the mortality rates for men and women for a given country and period together, such that the $b_{i,x}$ are vectors of length 44 (twice the number of age groups). This step allows us to generate mortality rates for men and women simultaneously as a function of female e_0 and HIV prevalence. Because the age-varying components, $b_{i,x}$, are fixed, the component weights, $\omega_{i,l}$ (which are modelled as a function of HIV prevalence) and e_0 are the effective parameters in this model. We refer to this model as 'HIV MLT', which stands for 'HIV-calibrated model life table'. The model is defined as follows:

$$\ln(m_{x,l}) = c_l + \sum_{i=1}^{3} \omega_{i,l} b_{i,x} + \varepsilon_{x,l} \qquad (2)$$

where $m_{x,l}$ is the period age-specific mortality rate for age x in life table l; c is a constant specific to life table l; $b_{i,x}$ is the value of the ith component for age x; $\omega_{i,l}$ is the weight of the ith component for life table l; and $\varepsilon_{x,l}$ is the error term.

Figure 1(a) plots the fit from the HIV MLT model and four existing model life table systems to the WPP 2015 mortality rates for women in South Africa for 2010–15. HIV prevalence has remained high in South Africa and was roughly 17.5 per cent during this period, resulting in a large adult mortality hump. Figure 1(a) demonstrates how this pattern is well captured by the HIV MLT model. The other systems considered tended to produce patterns of mortality rates that matched the overall level of mortality as measured by period life expectancy at birth, but missed the age-specific rates that are critical for accurate population projection.

Note that as the epidemic matures and availability of ART increases, a paradox emerges where HIV prevalence stays elevated or even increases, while life expectancy also increases as greater numbers of infected individuals live to older ages. During this period in the epidemic, the 'hump' in middle age will eventually merge into the natural increase in mortality rates at older ages. HIV MLT is designed to handle this dynamic in mature epidemics with high life expectancy mitigating the effect of high prevalence, resulting in a flat pattern of mortality rates in middle age (Sharrow et al. 2014).

Our model takes e_0 and HIV prevalence as inputs, and produces a set of age-specific mortality rates that reflect those two inputs, that is, HIV MLT is designed to produce a set of age-specific mortality rates that yield an output life expectancy matching the input life expectancy. The HIV MLT model was originally calibrated with sex-specific e_0 (Sharrow et al. 2014), but for the present purpose we have recalibrated the model with the female e_0 only, since that is what is projected by the model described in the previous section.

To maintain the gap between male and female e_0, the recalibrated HIV MLT model produces complete sets of age-specific mortality rates for men and women simultaneously and matches the input e_0 to the female life expectancy derived from the output mortality rates for women by adjusting the intercept, c_l in equation (2). The rates for men are adjusted using the same adjusted intercept used to match female e_0. Figure 1(b) plots the sex-specific output e_0 from the HIV MLT model, while varying the two input parameters, female e_0 and HIV prevalence. The gap in life expectancy between men and women is maintained over all combinations of the two input parameters. For women, the output e_0 equals the input e_0, and the output e_0 for men is always below the output e_0 for women.

As described earlier, the HIV MLT model itself is deterministic (i.e., for a given e_0 and prevalence, HIV MLT will produce a specific set of mortality rates), but in validation experiments we found that prediction intervals derived from running the probabilistic e_0 and prevalence projections through HIV MLT with the deterministic form occasionally did not cover mortality rates at the oldest ages. To increase coverage, we added noise from the error term by randomly sampling from a normal distribution for each age with mean zero and standard deviation estimated from the distribution of residuals at each age.

The HIV MLT model is calibrated with five-year age-specific mortality rates for 1970–2015, obtained from WPP 2015 for the 40 countries experiencing a generalized epidemic. We define a generalized epidemic as having >1 per cent HIV prevalence at any time 1980–2015. HIV prevalence for calibrating this model is the same as for the model used for projecting e_0. To produce a draw from the predictive distribution of the vector of age-specific mortality rates, a sample from each of the predictive distributions of e_0 and prevalence projections is first produced. Then a sample vector of age-specific mortality rates is

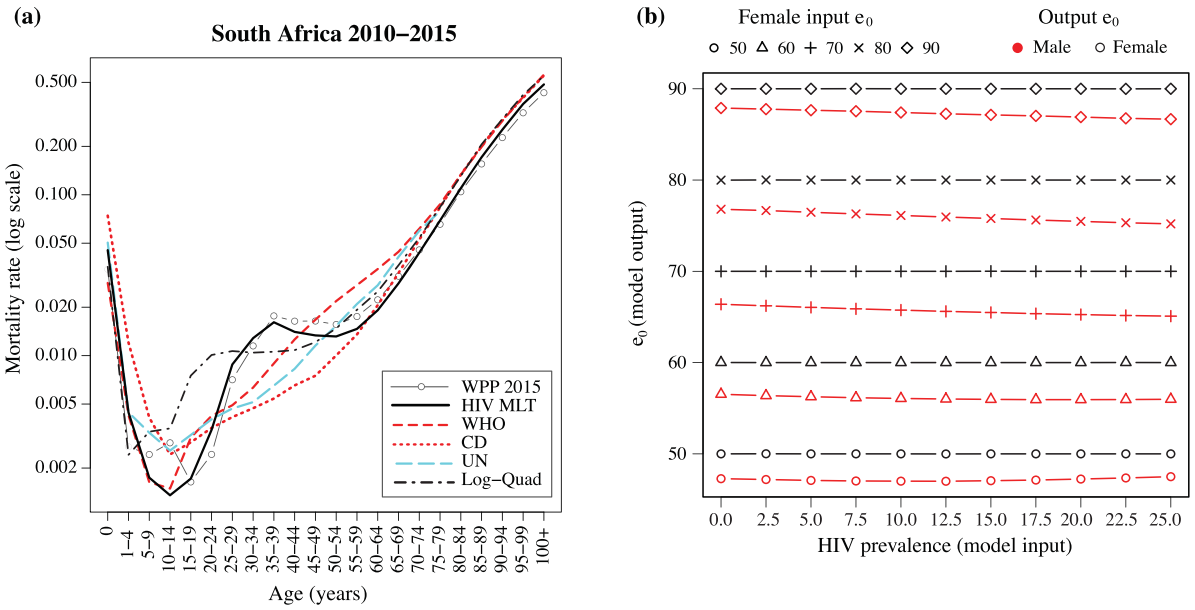

Figure 1 Output from HIV MLT model. (a) Fit of HIV MLT model to WPP 2015 mortality rates for women in South Africa, 2010–15. (b) Sex-specific output e_0, varying the two HIV MLT model inputs: female e_0 and HIV prevalence

Notes for (a): HIV MLT model (HIV-calibrated model life table) shown with solid line. For comparison, we also show fits from the WHO modified logit model: short-dash line; Coale and Demeny (CD) model life tables: short-dash-dot line; UN model life tables for developing countries: long-dash line; and the Log-Quad model: long-dash-dot line.

Source: Authors' own calculations; WHO modified logit model (Murray et al. 2003); Coale and Demeny model life tables (Coale and Demeny 1966; Coale et al. 1983); UN model life tables for developing countries (United Nations. Department of International Economic and Social Affairs 1982); the Log-Quad model (Wilmoth et al. 2012); and WPP 2015 (United Nations, Department of Economic and Social Affairs, Population Division 2015b).

produced conditionally on the simulated values of e_0 and HIV prevalence using equation (2).

Making full probabilistic population projections

To make full population projections, we modified the bayesPop software (Ševčíková, Raftery et al. 2016), which combines the fertility and mortality projections using the cohort component method. The software uses the method described by Raftery et al. (2012) to produce mortality projections, so the package functions were altered to include the mortality methods described earlier.

Results

In this paper, we mainly discuss results for four countries: Botswana, Zimbabwe, Mozambique, and Sierra Leone. These countries were chosen to represent different levels of current HIV prevalence. Botswana and Zimbabwe represent the largest historical epidemics, with peak HIV prevalences of over 25 per cent in 2000–05 and 1995–2000, respectively. Mozambique represents a smaller, but still substantial, epidemic (peak HIV prevalence $\approx$ 11 per cent in 2005–10), while Sierra Leone has a small generalized epidemic (peak HIV prevalence $\approx$ 1.6 per cent in 2010–15). Results for Botswana are shown in Figure 2, while results for the other three countries are in Figures S1–S3 in the supplementary material.

Figure 2(a) (top left panel) plots the total population projection for Botswana. We project an increase in total population until about 2065, when the total population begins to decline (median trajectory, shown by dash-dot line). Also in Figure 2(a), note the increasing width of the prediction intervals (PIs) as the projection reaches further into the future, reflecting the increase in uncertainty, a feature of the projection for all countries. WPP 2015 (solid line) also shows sustained population growth followed by a mild reversal in that trend towards the end of the projection period, but our median projection predicts fewer people in the total population over the entire projection horizon than WPP 2015.

The differences between the WPP 2015 projections and ours result from our treatment of mortality,

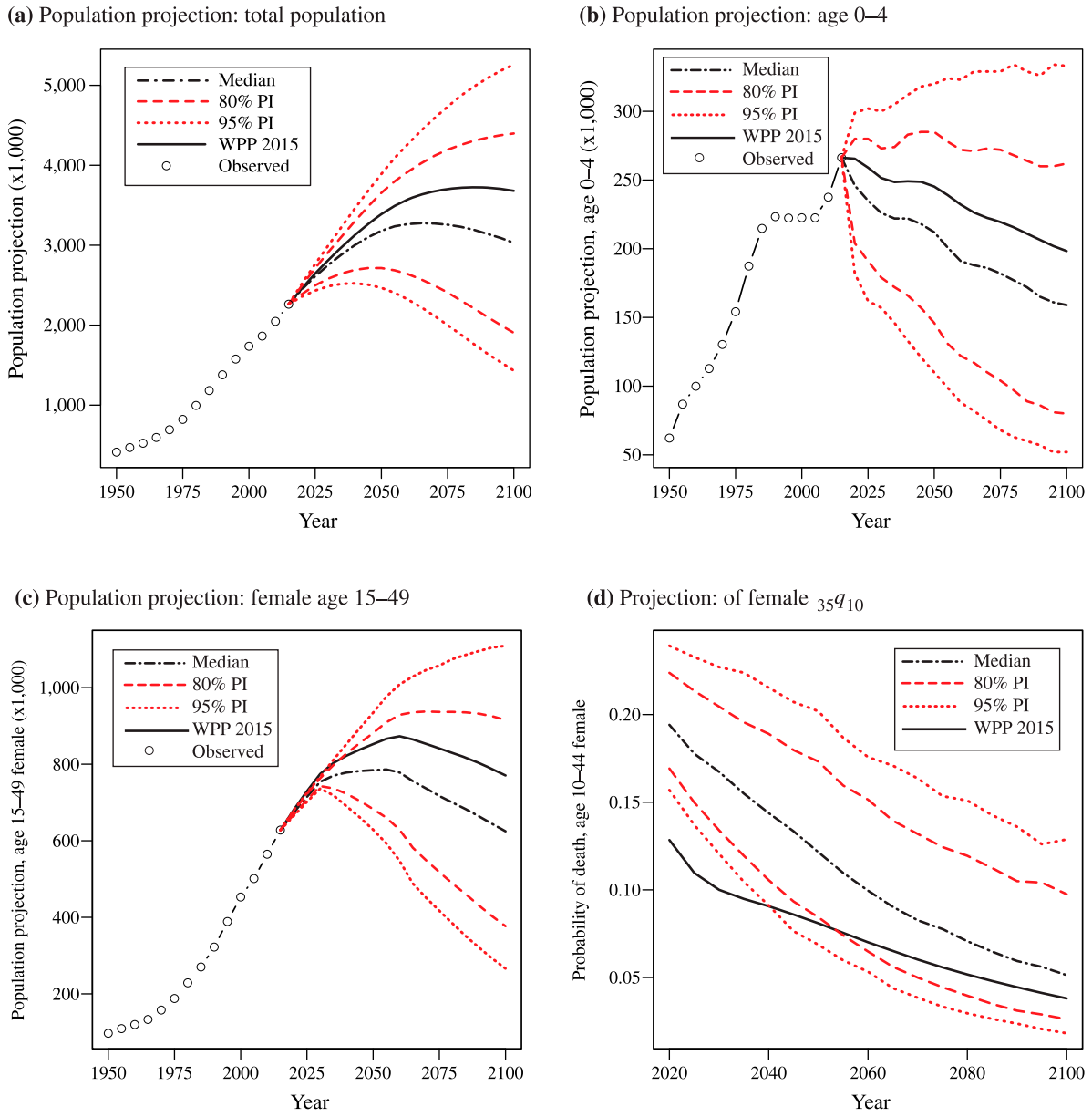

Figure 2 Probabilistic population projections for Botswana 2015–2100

Notes: Data: circles; median probabilistic projection: dash-dot line; 80 per cent predictive interval (PI): dashed lines; 95 per cent PI: dotted lines; WPP 2015 projection: solid line.

Source: Authors' own calculations; WPP 2015 (United Nations, Department of Economic and Social Affairs, Population Division 2015b).

which depends on projections of HIV prevalence and life expectancy. Botswana has one of the largest HIV/AIDS epidemics in the world in terms of prevalence. Figure 3 shows the probabilistic projections of HIV prevalence and female life expectancy at birth for Botswana in 2015–2100. HIV prevalence in Botswana is projected to remain high, dropping from a current level of about 24 per cent to roughly 14 per cent by 2050 in the median projection (Figure 3 (b)). Although declining, these high prevalences result in relatively low female life expectancies as modelled with equation (1), reaching just above 70 years by 2050, up from just under 50 years in 2005 (Figure 3(a)). Compared with the WPP 2015 projected life expectancy, our median projection shows sustained lower life expectancy, with an increasing gap over the entire projection period.

Figure 4 shows the difference between our median projection of the total population and the WPP 2015 projection of total population as a proportion of the WPP 2015 estimate for each of the 40 countries with generalized epidemics from 2015 to 2100. By

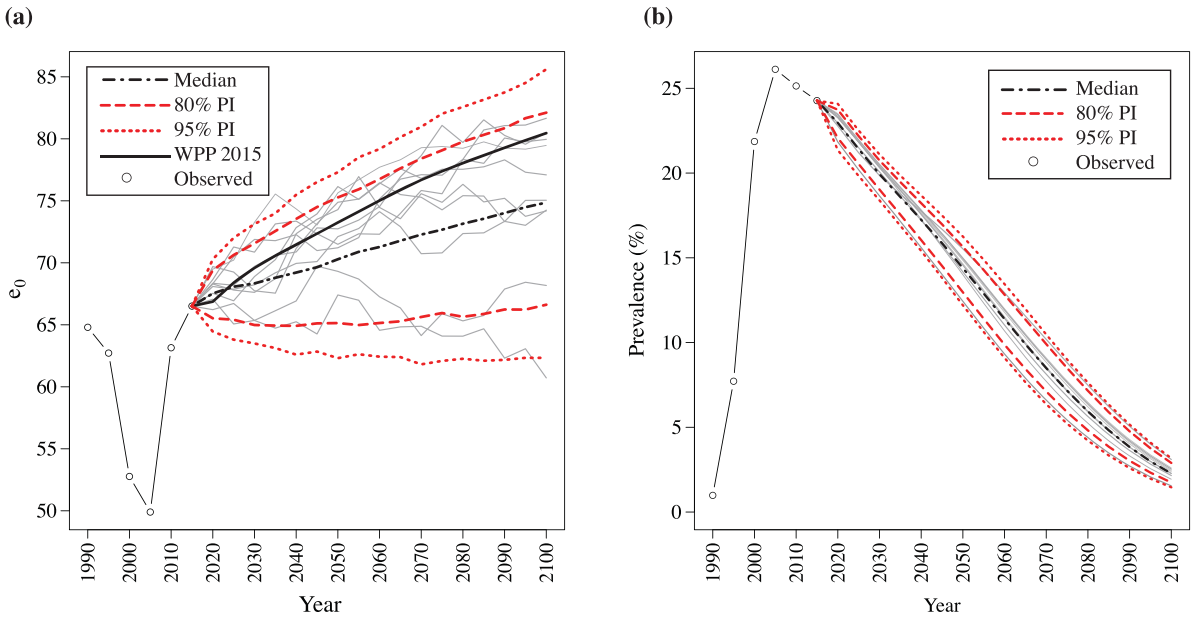

Figure 3 (a) Probabilistic female life expectancy and (b) HIV prevalence projections for Botswana 2015–2100
Notes: Median of probabilistic projection: dash-dot line; 80 per cent predictive interval (PI): dashed line; 95 per cent PI: dotted line; WPP 2015 projection: solid line; observed: circles. The grey lines in these figures are a random sample of ten trajectories from the final sample of 1,000 trajectories from the posterior distribution. HIV prevalence is not sex-specific.
Source: As for Figure 2.

2050, one of the largest differences from WPP 2015 is projected to be in Botswana, with about 7 per cent fewer people in the total population in our projections than in WPP 2015. In addition to projecting lower female life expectancy than WPP 2015 (see Figure 3(a)), our method also produces relatively high age-specific mortality rates at ages 25–45, consistent with the mortality generated under high HIV prevalence. This decline in projected total population is evidence of the crucial role age-specific mortality rates play in shaping future population structure in countries with generalized epidemics. Sustained high mortality for women during the reproductive years, compared with WPP 2015, results in fewer women alive during the reproductive years and thus fewer births than WPP 2015.

These effects can be seen in Figures 2(b)–(d). Figure 2(c) shows the probabilistic population projection for women aged 15–49 in Botswana. We project a decline in the number of women in this age category beginning around 2055, and Figure 2 (b) shows a shrinking population under age five throughout the entire projection period. The effect of high mortality in the reproductive adult years on future population size, especially for women (Figure 2(d)), reverberates for a number of years as smaller cohorts are born in each projected period, resulting in a smaller total population compared with WPP 2015. Combined with declining fertility, the effect of high adult mortality yields an eventual reversal in population growth for Botswana.

Similar conditions exist for some of the other countries with large negative proportional differences at 2050 shown in Figure 4 (e.g., Zimbabwe, Namibia, Central African Republic—all with negative differences greater than 5 per cent in 2050). These countries are typically experiencing large-scale HIV/AIDS epidemics (>10 per cent prevalence) and our median life expectancy projection is lower than that from WPP 2015, reducing the number of women of reproductive age and thus resulting in smaller birth cohorts. For example, Zimbabwe's total population in 2050 is projected to be about 12 per cent lower compared with WPP 2015. HIV prevalence is also projected to decline from about 14 to 10 per cent between 2015 and 2050. We project higher probabilities of death for women of reproductive age in Zimbabwe than WPP 2015 over the entire projection period (Figure S1(d)), likely resulting in a decreasing number of women of reproductive age past 2050 (Figure S1(c)) and consequently smaller birth cohorts over the projection horizon (Figure S1(b)).

For countries with smaller HIV/AIDS epidemics, the reduction in the number of women of reproductive age is less severe, and the difference between our projections and WPP 2015 tends to be smaller. Mozambique's HIV prevalence is projected to be

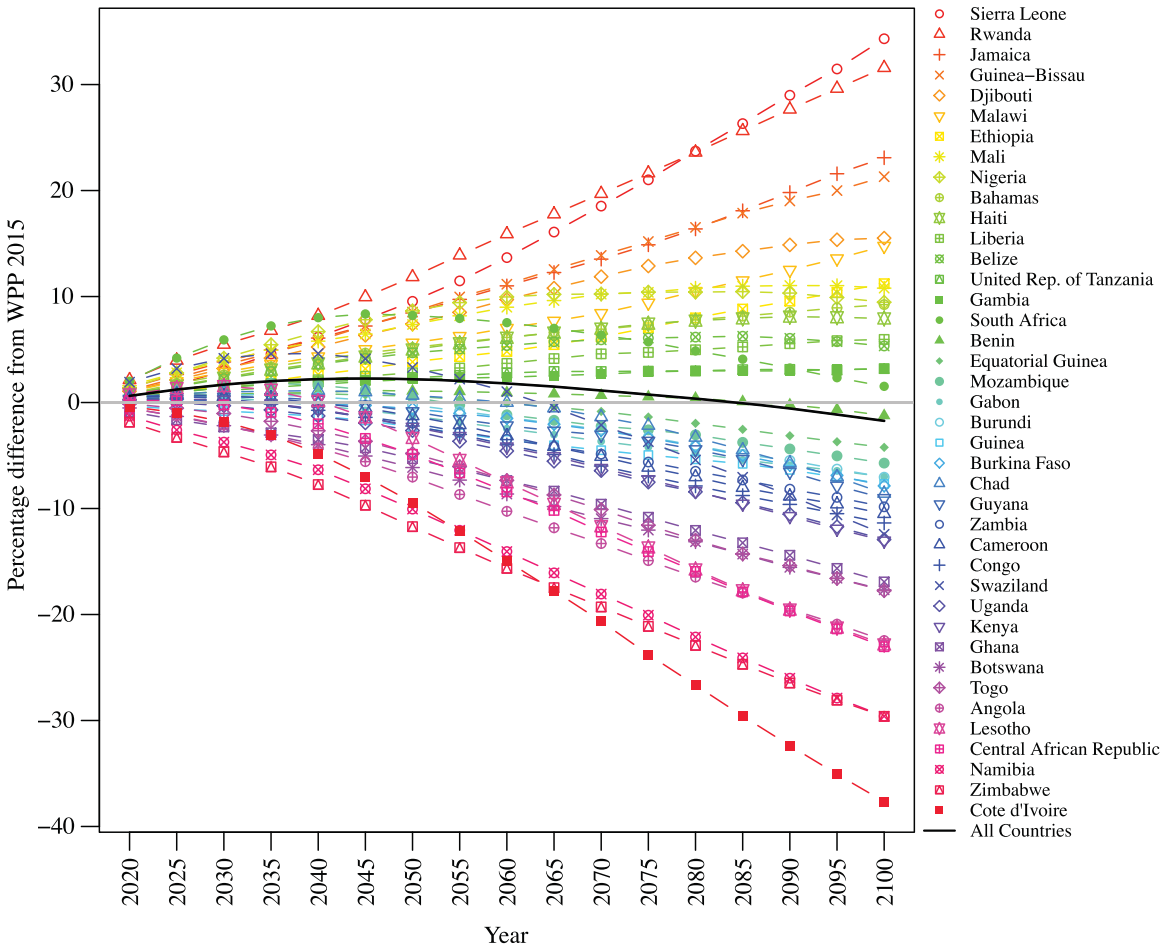

Figure 4 Comparison between our median total population projection and the equivalent WPP 2015 projection
Notes: Each line shows the percentage difference from the WPP 2015 total population estimate for each country and the solid line shows the difference at each period for all countries combined.
Source: As for Figure 2.

approximately 7 per cent (median projection) by 2050, down from around 10 per cent in 2015. Figure S2(a) shows that our median projection of the total population is similar to the WPP 2015 projection over the entire projection period. These smaller differences between our projections and the WPP 2015 projections can also be seen in Figures S2(b) and (c) showing the population projections for ages under five and for women aged 15–49, respectively.

Some countries see larger populations at 2050 in our projection compared with WPP 2015. For Sierra Leone, where HIV prevalence is projected to decrease from about 1.6 per cent in 2015 to less than 1 per cent by 2050, the difference from WPP 2015 is in the opposite direction (Figure S3(a)). We project about 10 per cent more people in the total population by 2050 than WPP 2015. Low HIV prevalence has a far less extreme depressing effect on total population in Sierra Leone in the long run as evidenced by Figures S3(b) and (c). In addition to relatively little effect from HIV on the age-specific mortality rates, compared with WPP 2015, we project consistently higher life expectancy over the projection period for Sierra Leone. This is consistent with the life expectancy projection for other countries for which our method projects higher populations than WPP 2015 (e.g., Djibouti, Ethiopia, Guinea Bissau, Jamaica, and Nigeria; see Figure 4).

Figure 5 plots the probabilistic projections of female life expectancy for six countries with positive differences in projected population at 2050 as shown in Figure 4. We also include the WPP 2015 female life expectancy projections for these countries in Figure 5. As this figure shows, a large portion of the difference between the WPP 2015 total population projections and our median projections for these countries arises from differences in the projections of life expectancy, since these countries have comparatively small HIV/AIDS epidemics, which limit the influence of HIV prevalence on the age pattern of mortality rates.

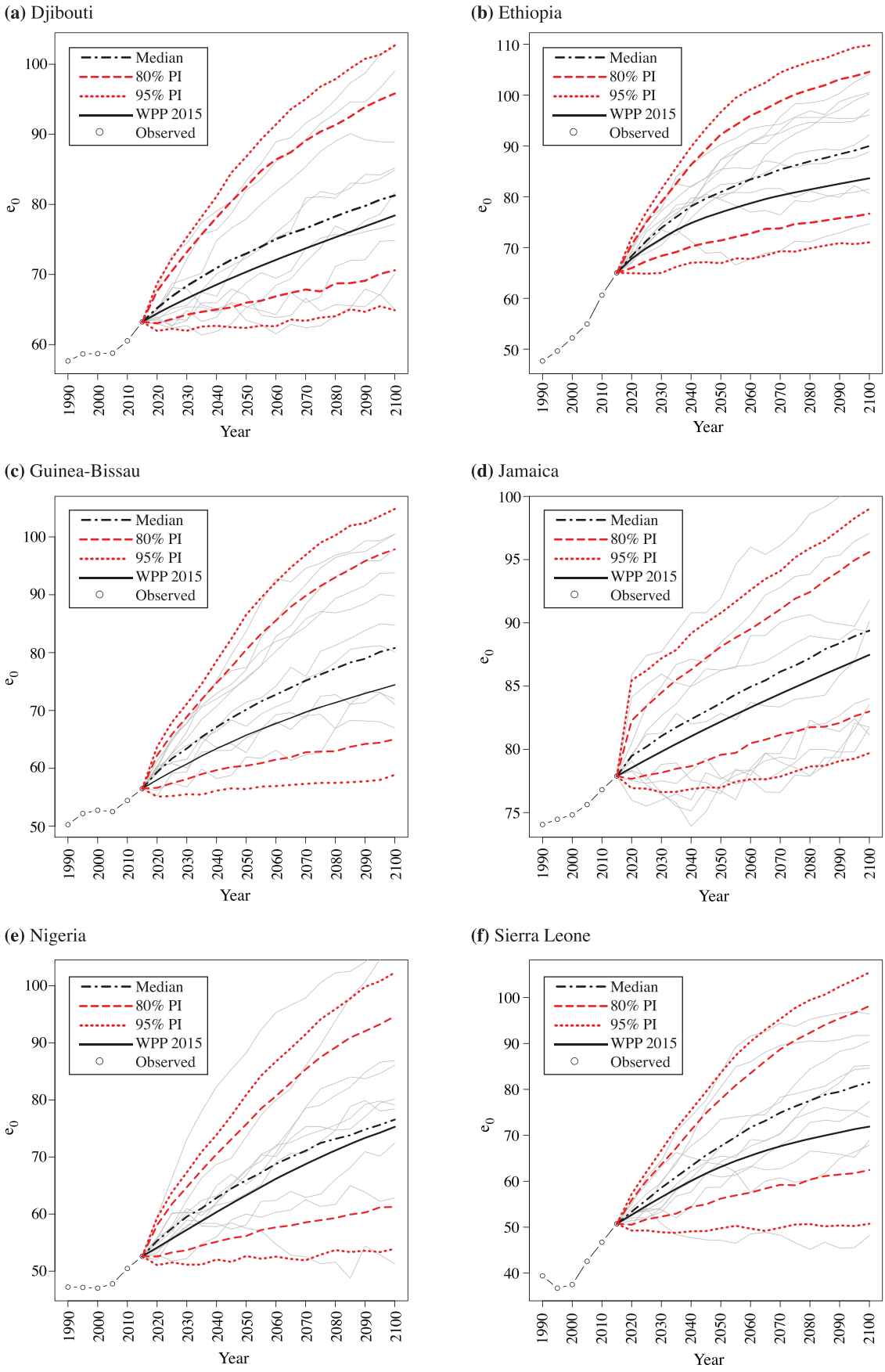

Figure 5 Probabilistic projections of female life expectancy for six countries 2015–2100

Notes: Median of probabilistic projection: dash-dot line; 80 per cent predictive interval (PI): dashed line; 95 per cent PI: dotted line; WPP 2015 projection: solid line; observed: circles. The grey lines in these figures are a random sample of ten trajectories from the final sample of 1,000 trajectories from the posterior distribution. *Source*: As for Figure 2.

Validation

Out-of-sample validation

To validate our method, we calibrated the e_0 projection and HIV MLT models with data for five-year periods in 1970–2010 from WPP 2015 and used those models to generate a population projection for the 2010–15 period for each of the 40 countries. We then compared the resulting mortality and population distributions with the observations from WPP 2015 for the 2010–15 period.

Because our method addresses the mortality component of the projection, we first assessed the accuracy of the mortality predictions for 2010–15 by calculating the mean absolute error (MAE) of our median projection for 2010–15, treating the WPP 2015 estimate as the observed value. We did this for four mortality indicators: e_0 (life expectancy at birth), ${}_5q_0$ (the probability a newborn will die before reaching age five), ${}_{45}q_{15}$ (the probability that a 15-year-old will die before reaching age 60), and ${}_{35}q_{10}$ (the probability that a ten-year-old will die before age 45). Table 1 presents the MAE by sex for the four mortality indicators. For men, the MAE for life expectancy is about 2.3 years, while the MAE for e_0 for women is slightly higher at 2.5 years, suggesting a good fit for the level of mortality. For the other three indicators, the MAE is less than 0.04 (in probability scale) for both men and women. Overall, our method predicts the WPP 2015 estimate for 2010–15 well for most countries (Figures S4–S9 plot the predicted distribution of these three mortality probabilities for men and women in 2010–15, along with the WPP 2015 estimate for the same period, for all 40 countries with generalized epidemics).

We assessed the accuracy of our method for projecting age-specific mortality rates further by calculating the proportion of age-specific mortality rates for 2010–15 (observed data that were left out of the calibration) that were captured within the 80, 90, and 95 per cent PIs for 2010–15 produced with our method. If the method is doing well, we should capture about the same percentage of the out-of-sample mortality rates as defines the PIs. The top two rows of Table 2 show the coverage (percentage of WPP 2015 mortality rates across all ages and all 40 countries captured by the various interval widths) for the 2010–15 period. For each PI, our method captures just under the expected proportion, indicating that the method provides reasonably well-calibrated projections for the out-of-sample period. The third row of Table 2 gives the coverage for the single quantity of female life expectancy in the out-of-sample period (i.e., the percentage of countries whose PIs captured the WPP 2015 estimate for female life expectancy). Coverage for female life expectancy is also good, with our method again capturing just under the expected proportion of predicted out-of-sample life expectancies.

Finally, we calculated coverage similar to that of mortality and life expectancy but for the total population prediction at 2010–15 (calculation of total population included running fertility projections for the out-of-sample period 2010–15 using the bayesTFR software). The bottom row of Table 2 shows the percentage of WPP 2015 total population estimates for 2010–15 captured in the 80, 90, and

Table 1 Mean absolute error for four mortality indicators for the 2010–15 out-of-sample period, using our method for projecting HIV prevalence and life expectancy, and using the HIV MLT model for converting to age-specific mortality rates

	Mean absolute error (MAE)			
	e_0	${}_5q_0$	${}_{45}q_{15}$	${}_{35}q_{10}$
Men	2.3	16.3	31.9	22.9
Women	2.5	13.9	33.4	30.6

Notes: HIV MLT stands for HIV-calibrated model life table. All models have been calibrated with data up to 2010 and used to predict values for the out-of-sample period 2010–15. The four mortality indicators are e_0 (life expectancy at birth in years), ${}_5q_0$ (probability a newborn will die before age five), ${}_{45}q_{15}$ (probability a 15-year-old will die before age 60), and ${}_{35}q_{10}$ (probability a ten-year-old will die before age 45). Probabilities are all ×1,000.
Source: Authors' own calculations, based on data from WPP 2015.

Table 2 Coverage of WPP 2015 sex- and age-specific mortality rates, female life expectancy at birth, and total population in the 80, 90, and 95 per cent predictive intervals (PIs) for the 2010–15 out-of-sample period, using our method for projecting HIV prevalence and life expectancy, and using the HIV MLT model for converting to age-specific mortality rates

	80 per cent PI	90 per cent PI	95 per cent PI
m_x, men	75	82	88
m_x, women	69	81	86
e_0, women	75	88	90
Total population	97	97	100

Notes: HIV MLT stands for HIV-calibrated model life table. Fertility was projected using the bayesTFR software. Data from 1970 to 2010 were used for calibration, and the resulting estimated model was used to predict values for the out-of-sample period 2010–15.
Source: As for Table 1.

95 per cent PIs. While the coverages for the mortality rates are not markedly different from the nominal coverages of the PIs, coverage of the single total population estimate is near universal (i.e., the observed total population estimate for the out-of-sample period 2010–15 is within the 80 and 90 per cent PI for all but one country, Swaziland, and within the 95 per cent PI for all countries). This near universal coverage of the total population estimate is not surprising since total population is unlikely to be greatly impacted by the changes we make to the mortality component of the projection in only one five-year period. The change in mortality from the method used in WPP 2015 markedly affects only certain ages and, even then, may not show those effects for some time on total population. Further mitigating the short-term effect of mortality change is the treatment of fertility, which remains the same in our projections as in WPP 2015.

Comparison with Spectrum/EPP

Spectrum/EPP (Stanecki et al. 2012; Stover et al. 2012; Avenir Health 2016) provides useful information to UNAIDS about countries with high HIV prevalence, including estimates of HIV prevalence, total population, life expectancy, and a host of other demographic and epidemiological variables in the short term (five years). However, the method for deriving these quantities is, by necessity, quite complex. We propose a simpler method to project over a longer projection horizon, but it is instructive to compare our projection results with those obtained from Spectrum in the short term.

Table 3 shows the mean difference (MD) between our median projection using the full data set for calibration (i.e., no out-of-sample period was removed) and the equivalent Spectrum projection, among all 40 countries for both HIV prevalence and life expectancy at birth, for the first three projection periods (2015–20, 2020–25, and 2025–30). All Spectrum results were obtained with Spectrum version 5.441, downloaded July 2016 (Avenir Health 2016). For prevalence, our projections differ from Spectrum by less than one percentage point on average across the 40 countries during each of the first three projection periods, which is substantially less than the prediction margin of error. The MDs for life expectancy show that on average across the 40 countries our projection is between one and two years lower than the Spectrum projection in the very short term. Thus, overall our projections are similar to those of Spectrum for these quantities, despite using a much simpler model.

The three right-hand columns of Table 3 show the mean proportional difference (MPD) between our median projection and Spectrum's equivalent projection for three population quantities: the total population across all ages, the total population aged 0–4, and the female population aged 15–49. The MPD is the average difference between our median estimate and Spectrum as a proportion of the Spectrum estimate for a given population indicator. Again, we present a simpler method for long-term projection, but it should approximate Spectrum at least in the short run. For total population, our median estimates of total population are about 1 per cent lower than the Spectrum estimate for the most recent projection period, 2015–20. The MPD is between 1 and 2 per cent for each of the next two periods. Our projections of the population aged 0–4 are also lower than the Spectrum result by roughly 1 per cent. Finally, our short-term projection results for the female population of reproductive age are also close to the Spectrum result with less than 0.5 per cent average proportional difference over all three periods. In

Table 3 Mean difference (MD) for HIV prevalence and life expectancy and mean proportional difference (MPD) for total population, population aged 0–4, and female population aged 15–49, between our method and the Spectrum/EPP software for the first three projection periods

	MD[1]		MPD[2]		
	HIV prevalence	e_0	Total population	Population aged 0–4	Female population aged 15–49
2015–20	0.7	−1.76	−0.9	−0.8	−0.2
2020–25	0.8	−1.10	−1.3	−1.0	−0.3
2025–30	0.9	−0.97	−1.6	−1.2	−0.3

[1]Mean difference between our estimate and that of the Spectrum software for all 40 countries. HIV prevalence is in percentage points and life expectancy in years.
[2]Mean proportional difference between our median estimate and the Spectrum estimate as a proportion of the Spectrum estimate (shown as a percentage). Varying absolute population sizes among the 40 countries necessitate using the proportional error.
Notes: All results for Spectrum derived from the Spectrum software version 5.441.
Source: As for Table 1.

sum, results from Table 3 suggest that our less complex method approximates the short-term projections of Spectrum for these demographic quantities reasonably closely.

Discussion

In this paper, we have presented a method for making probabilistic population projections for countries with generalized HIV/AIDS epidemics. We accomplish this by following the Bayesian probabilistic projection method described by Raftery et al. (2012) for fertility and the international migration assumptions of the UNPD, but because of the singular nature of mortality in generalized HIV/AIDS epidemics, we modify the mortality component of the projection to incorporate the future trajectory of the epidemic in terms of HIV prevalence and ART coverage. The probabilistic fertility and mortality projections and the UNPD's assumptions about future migration are combined using the cohort component method of projection.

These projections are potentially useful to researchers and policymakers, as this method provides a predictive distribution for population quantities of interest such as total population, life expectancy, and support ratios into the future. Our method takes into account uncertainty about future levels of mortality and fertility, the major drivers of population change, as well as uncertainty about the trajectory of HIV prevalence. Our approach is less complex than the UNPD's current method for projecting mortality in settings with high HIV prevalence and better captures the age pattern of mortality rates during a generalized HIV/AIDS epidemic.

Results from the projections described here show that by 2050 and beyond we project smaller total populations than WPP 2015 for about half of the 40 countries under study here. Many of the countries with the largest negative differences in projected total population compared with WPP 2015 are experiencing large-scale HIV/AIDS epidemics. For these countries, we tend to project lower total life expectancy over the course of the projection period. Combined with projected high HIV prevalence, the lower life expectancies result in high age-specific mortality rates during the younger adult years, and thus fewer women of reproductive age and consequently smaller birth cohorts. Projected into the future, these trends lead to smaller total population projections than WPP 2015. Coupled with declining fertility, high mortality rates resulting from HIV/AIDS-related deaths produce a reversal in population growth by 2100 for some countries with very large epidemics. Overall, these trends amount to a −1.7 per cent difference in total population among all 40 countries by 2100 compared with WPP 2015, a difference of approximately 52.5 million fewer people.

Although the method presented here for mortality, and elsewhere for fertility (Alkema et al. 2011; Ševčíková et al. 2011; Raftery et al. 2012), takes into account uncertainty about future levels of mortality and fertility, it does not include uncertainty about international migration in the future, which can be an important source of forecast errors. While this paper focuses on the treatment of mortality in population forecasting for countries with generalized HIV/AIDS epidemics, future projections should incorporate recent advances in probabilistic forecasting of migration (Azose and Raftery 2015; Azose et al. 2016) to address this potential source of forecast error. Likewise, the life expectancy projection model and the model used to convert e_0 projections to age-specific mortality rates are calibrated with results from WPP 2015, some of which are themselves modelled, so they reproduce only the variability in the quantities of interest contained in the WPP 2015 results. To the extent that the WPP 2015 data and results used to calibrate these models reflect the empirical reality, the models we present here should do as well. Finally, as in Raftery et al. (2012), this method does not take into account random variation in the numbers of births or deaths, given the fertility and mortality rates.

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