Probabilistic Projections of Mortality in Countries with Generalized HIV/AIDS Epidemics for Use in Total Population Projection*

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Abstract

The UN issued official probabilistic population projections for all countries to 2100 for the first time in July 2014. This was done by simulating future levels of total fertility and life expectancy from Bayesian hierarchical models, and combining the results using a standard cohort-component projection method. The 40 countries with generalized HIV/AIDS epidemics were treated differently from others, in that the projections used the highly multistate Spectrum/EPP model, a more complex 15-compartment model that was designed for short-term projections of quantities relevant to policy for the epidemic. Here we propose a simpler approach that is more compatible with the existing UN probabilistic projection methodology for other countries. Changes in life expectancy are projected probabilistically using a simple time series regression model on current life expectancy, HIV prevalence and ART coverage. These are then converted to age- and sex-specific mortality rates using a new family of model life tables designed for countries with HIV/AIDS epidemics that reproduces the characteristic hump in middle adult mortality. These are then input to the standard cohort-component method, as for other countries. The method performed well in an out-of-sample cross-validation experiment. It gives similar population projections to Spectrum/EPP, while being simpler and avoiding multistate modeling.

Keywords: *Bayesian hierarchical model, Cohort-component projection method, Estimation and Projection Package, Mortality, Multistate model, Model life table, Spectrum, UNAIDS, World Population Prospects*

1 Introduction

Population projections are used by governments at all levels and international organizations for policy planning, monitoring development goals and as inputs to economic and environmental models, by social and health researchers, and by the private sector. The United Nations (UN) issues population projections for all the countries of the world by age and sex to 2100, updated every two years, in the *World Population Prospects* (WPP). It is the only organization to do so, and its projections are the de facto standard at the global level (Lutz and Samir 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 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 on World Population Day (July 11), 2014, available at http://esa.un.org/unpd/ppp. These projections were developed using the methodology 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 modeled by 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 (Raftery et al. 2012). Each trajectory is then converted to future population by age and sex by the standard cohort-component method (Preston et al. 2001; Whelpton 1936), using the `bayesPop` R package (Ševčíková and Raftery 2012). The result is a sample of possible future trajectories of world population by country, age and sex, to 2100. It can be viewed as a large number of possible versions of the 2100 revision of the UN's *World Population Prospects* (which won't exist for another 85 years).

The UN's new Probabilistic Population Prospects currently treats countries with generalized HIV/AIDS epidemics (defined as having had HIV prevalence greater than 2% at any time since 1980, and hereafter referred to as the "AIDS countries") differently from others. This is because these countries have very different mortality patterns from others, with a large mortality hump in middle adulthood due to AIDS, and so they cannot be modeled using, for example, standard model life tables.

The UN's current method for probabilistically projecting mortality for these countries starts with the deterministic projection from the 2012 revision of the *World Population Prospects* (United Nations, Department of Economic and Social Affairs, Population Division 2013a). This uses the Spectrum model developed for UNAIDS (Futures Institute 2014; Stanecki et al. 2012; Stover et al. 2012), a complex multistate model that divides adults into 15 compartments according to their HIV status, and models transitions among these 15 compartments. In a second stage, the Bayesian hierarchical model of Raftery et al. (2013) 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 AIDS epidemic, such

as future need for antiretroviral therapy (ART) drugs, the number of AIDS orphans, and so on. 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 Estimation, Projection and Modelling recommends that it not be used for projections more than five years into the future.

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

Here we propose an alternative methodology for probabilistic projection for the AIDS countries that is simpler than the current one, does not require any multistate modeling, and makes use of the `bayesPop` methodology used by the UN 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) (Brown et al. 2010; Ghys et al. 2004; Ghys and Garnett 2010; Ghys et al. 2008), calibrated by the microsimulation model of Hontelez et al. (2012). Future life expectancy is projected using a simple time series regression model on HIV prevalence and ART coverage. The resulting simulated life expectancies and prevalences are converted to age-specific mortality rates using the HIV model life table method of Sharrow et al. (2014), which replicates the middle adult mortality hump characteristic of HIV epidemics. The population projections are then obtained with the same `bayesPop` methodology as for other countries.

The resulting method fits observed age-specific mortality data well. In an out-of-sample validation experiment it was reasonably accurate and provided well-calibrated probabilistic projections of aggregate mortality and population quantities. It is simpler than the extant Spectrum method, but still matched its projections closely over the next 15 years. This suggests that this method may be appropriate for probabilistic population projection for

AIDS countries.

The rest of the article is organized as follows. In Section 2 we describe our new methods and the data we use. In Section 3 we give results for four countries with generalized HIV/AIDS epidemics, chosen to represent the range of experience, namely Botswana, Lesotho, Mozambique and Ghana. Then in Section 4 we give the results of an out-of-sample validation experiment to assess our method, and we also compare the resulting projections with those of Spectrum/EPP. We conclude in Section 5 with a discussion of the strengths and limitations of our proposed approach.

2 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 high-HIV prevalence counties, we follow the procedure described by Raftery et al. (2012) for making probabilistic projections of fertility in countries and use the UNPD assumptions about international migration (United Nations, Department of Economic and Social Affairs, Population Division 2013b, p.36-38), 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, Raftery et al. (2012) simulate an equal number of trajectories of period life expectancy at birth (e_0) for females 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. The fertility, mortality, and migration trajectories

are then converted to a future trajectory of age- and sex-specific population values using the cohort component method (Preston et al. 2001, ch. 6).

In our application, the projection of fertility remains the same[1] along with the use of the UNPD assumptions about international migration and the cohort component method to combine these trajectories. However, HIV prevalence is now included as a predictor when modeling the future trajectory of e_0 and in converting the projected e_0 into age-specific mortality rates. A brief description of the methods for projecting e_0 and HIV prevalence as well as converting those quantities into age-specific mortality rates follows.

2.1 Projecting HIV Prevalence

To make probabilistic projections of e_0 for countries with generalized epidemics and to convert those projections into age-specific mortality rates, we first need projections of HIV prevalence. We use a version of the UNAIDS Estimation and Projection Package (EPP) (Alkema et al. 2007; Brown et al. 2010; Ghys and Garnett 2010; Raftery and Bao 2010) for the statistical analysis software `R` to make probabilistic projections of HIV prevalence up to 2100.

EPP works well to project HIV prevalence into the not too distant future, approximately 5-10 years after the latest surveillance (UNAIDS 2014, p. 9), but assumptions were imposed on two of the EPP model parameters to make projections to 2100. 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 of recruitment of new individuals into 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 behavior among those subject to the risk of infection and increases in access to treatment

[1]Fertility is projected using the `bayesTFR` package (Ševčíková et al. 2011) in the statistical analysis software, R.

for infected individuals will reduce the chances of HIV transmission.

The probabilistic trajectories from EPP were then calibrated by the HIV prevalence projections of Hontelez et al. (2012), who make projections up to 2040 using a microsimulation method (STDSIM). This method considered several relevant variables including background mortality, ART scale up as well as health care system capacity for future scale up, and HIV epidemic and sexual behavior profiles. We first took the probit transformation of the EPP median projection (ρ_t^{MED}) and of the Hontelez et al. results (ρ_t^H). We then recorded the difference between the probit-scaled EPP median and the Hontelez et al. projection in each year from 2011 to 2040 and imputed the probit level difference from 2041 to 2100 with the same value as the difference in 2040. Specifically, the difference λ_t is given by

$$\lambda_t = \begin{cases} \Phi^{-1}(\rho_t^{MED}) - \Phi^{-1}(\rho_t^H) & t = 2011, \cdots, 2040. \\ \lambda_{2040} & t = 2041, \cdots, 2100. \end{cases} \tag{1}$$

Finally, we subtracted the differences from the probit-scaled EPP trajectories and transformed them back to their original unit. We adjust each trajectory ρ_t to be

$$\rho_t^{adj} = \Phi(\Phi^{-1}(\rho_t) - \lambda_t). \tag{2}$$

2.2 Projecting Life Expectancy at Birth, e_0

Because a generalized HIV epidemic can have a considerable depressing effect on life expectancy at birth in a short time (Blacker 2004; Ngom and Clark 2003; Obermeyer et al. 2010; Poit et al. 2001; Sharrow et al. 2013; Timaeus and Jasseh 2004), a model that reflects the impact of HIV prevalence and antiretroviral therapy (ART) coverage is necessary to make appropriate projections of e_0 in generalized epidemics. The model for projecting e_0, Eq. 3,

predicts the five-year increase in total (non-sex-specific) life expectancy at birth from time $t-5$ to t as a function of two covariates: the double logistic fitted change in e_0 from the previous five-year period (described below) and HIV prevalence at time $t-5$ multiplied by the proportion of infected individuals not receiving ART:

$$\Delta e_{0,c,(t-5:t)} = \beta_0 + \beta_1 \Delta e^{DL}_{0,c,(t-5:t)} + \beta_2 \gamma_{c,t-5} + \delta_{c,t-5} \tag{3}$$

where $\Delta e_{0,c,(t-5:t)}$ is the change in life expectancy for country c at time $t-5$ to t, $\Delta e^{DL}_{0,c,(t-5:t)}$ is the double logistic fitted change in life expectancy at time $t-5$ to t acting on life expectancy at time $t-5$, $\gamma_{c,t-5}$ is HIV prevalence at time $t-5$ multiplied by the proportion of seropositive individuals not receiving ART at time $t-5$, and $\delta_{c,t-5}$ is the error term.

The double logistic term mirrors 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 being 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 and the second represents continuing gains from combating non-communicable diseases (United Nations, Department of Economic and Social Affairs, Population Division 2013b, p. 28).

The model (Eq. 3) is estimated using five-year life expectancy estimates from 1985-2010 for the 40 countries experiencing a generalized HIV epidemic obtained from WPP 2012.[2] We use median HIV prevalence for 1985-2010 as estimated by the EPP program. We use estimates of ART coverage (percentage of seropositive individuals receiving ART) for the period 1985-2010 obtained from UNPD internal tabulations (United Nations, Department of Economic and Social Affairs, Population Division 2011). To make this model compatible with the model for countries without generalized epidemics, we set β_1, the coefficient for the

[2]These data are available in the `R` package `wpp2012` (Ševčíková et al. 2013).

double logistic curve, to 1 when we fit the model using regression. To project life expectancy to 2100, we input each trajectory of HIV prevalence and life expectancy period by period into the model starting from 2010.

2.3 Converting e_0 and HIV Prevalence Projections to Age-Specific Mortality Rates

Once we have obtained probabilistic projections of life expectancy and HIV prevalence, we need to map those quantities onto a set of age-specific mortality rates that can be combined with age-specific fertility rates and net migration using the cohort component method. In the WPP 2012 Revision, for countries without high HIV prevalence, e_0 projections are converted to age-specific mortality rates using model mortality patterns (United Nations, Department of Economic and Social Affairs, Population Division 2013b, p. 34), but these patterns are unable to replicate the particular age pattern of mortality resulting from large scale HIV epidemics (United Nations, Department of Economic and Social Affairs, Population Division 2013b, p. 35) and they have no relationship to HIV prevalence.

To convert the life expectancy and HIV prevalence projections to age-specific mortality rates we use a model by Sharrow et al. (2014), shown in Eq. 4. This model can reproduce the characteristic age pattern of mortality associated with generalized epidemics, i.e. an accentuated adult mortality hump concentrated at ages 30 to 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 Eq. 4, are derived from a Singular Value Decomposition of the matrix of observed mortality rates and the weights, $\omega_{i,\ell}$, are modeled as a function of HIV prevalence and life expectancy at birth.[3] We refer to this model as "HIV MLT," for "HIV-calibrated

[3]Although ART coverage is not directly included as a predictor with HIV prevalence and life expectancy, the model mimics the likely effect of future ART scale up on age-specific mortality rates, because at high levels of life expectancy (resulting from ART scale up), the model reduces the adult mortality hump even at very high prevalence (Sharrow et al. 2014).

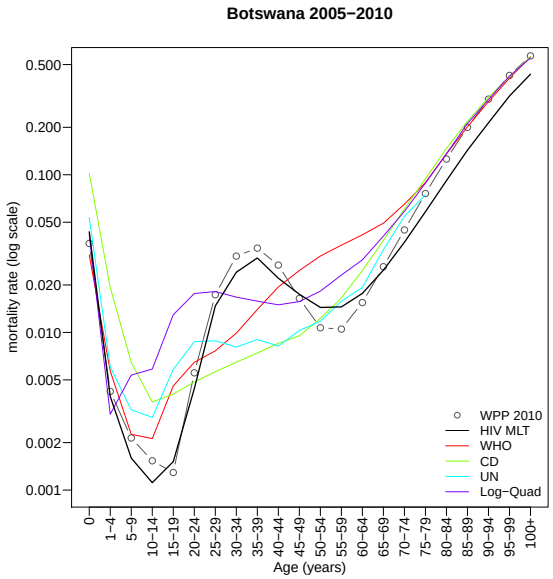
model life table." The model is defined as follows:

$$\ln(m_{x,\ell}) = c_\ell + \sum_{i=1}^{3} \omega_{i,\ell} b_{i,x} + \varepsilon_{x,\ell}, \tag{4}$$

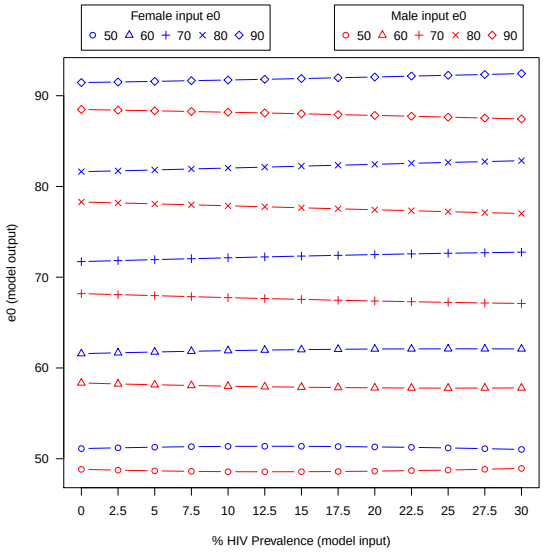
where $m_{x,\ell}$ is the period age-specific mortality rate for age x in life table ℓ, c_ℓ is a constant specific to life table ℓ, $b_{i,x}$ is the value of the ith component for age x, $\omega_{i,\ell}$ is the weight of the ith component for life table ℓ, and $\varepsilon_{x,\ell} \overset{\text{iid}}{\sim} N(0, \sigma^2)$ is the error term.

Figure 1 plots the fit from the HIV MLT model and four existing model life table systems for Botswana females 2005-2010. HIV prevalence has remained high in Botswana and was roughly 25 percent during this period, resulting in a large adult mortality hump. Figure 1 demonstrates how this pattern is fully captured only by the HIV MLT model. All other systems tend to produce high, flat patterns of mortality rates that match the overall level of mortality as measured by period life expectancy at birth but miss the age-specific rates, which are critical for accurate population projection.

This model takes e_0 and HIV prevalence as inputs and produces a set of age-specific mortality rates that reflect those two inputs. 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 re-calibrated the model with the total (non-sex-specific) e_0 because that is what is projected by the model described in section 2.2. To maintain the gap between male and female e_0, the re-calibrated model produces complete sets of male and female age-specific mortality rates simultaneously and matches the input e_0 to the combined life expectancy derived from the output male and female mortality rates by adjusting the intercept, c_ℓ in Eq. 4. Figure 1b plots the sex-specific output e_0 from the HIV MLT model while varying the two input parameters: non-sex-specific e_0 and HIV prevalence. The gap in life expectancy is maintained over all combinations of the two input parameters.



(a) Fit of HIV MLT model for Botswana females 2005-2010



(b) Sex-specific e_0 output for HIV MLT model at varying e_0 and prevalence inputs

Figure 1 Output from HIV MLT model. (a) Fit of HIV MLT model for Botswana females 2005-2010. HIV MLT model shown with black line. For comparison, fits from the WHO modified logit model (Murray et al. 2003) [red solid line], Coale and Demeny model life tables (Coale and Demeny 1966; Coale et al. 1983) [green solid line], UN model life tables for developing countries (United Nations. Department of International Economic and Social Affairs 1982) [teal solid line], and the Log-Quad model (Wilmoth et al. 2012) [purple solid line] are also shown. (b) Sex-specific output e_0, varying the two HIV MLT model inputs: non-sex-specific e_0 and HIV prevalence.

The HIV MLT model is calibrated with five-year age-specific mortality rates obtained from WPP 2012 from 1985-2010 for the 40 countries experiencing a generalized epidemic. HIV prevalence for calibrating this model is the same as for the model for projecting e_0 (see section 2.2). 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 produced conditionally on the simulated values of e_0 and HIV prevalence using Eq. 4.

2.4 Making Full Probabilistic Population Projections

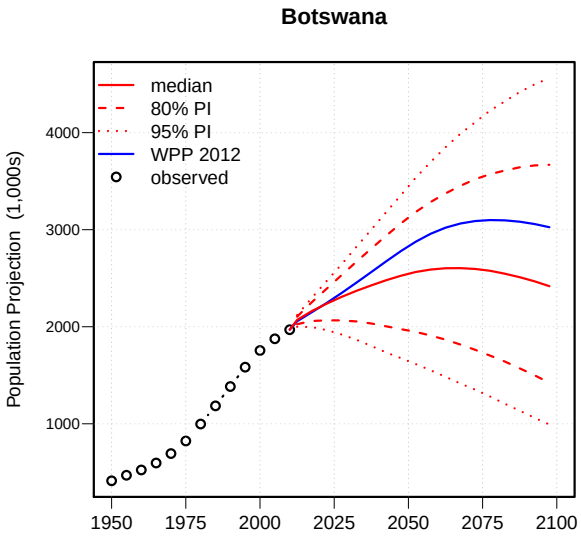
We modified the `bayesPop` software (Ševčíková and Raftery 2014), which combines the fertility and mortality projections using the cohort component method, to make full population projections. The software uses the method described by Raftery et al. (2012) to produce mortality projections, so the package functions were altered to include the mortality methodology described above.

3 Results

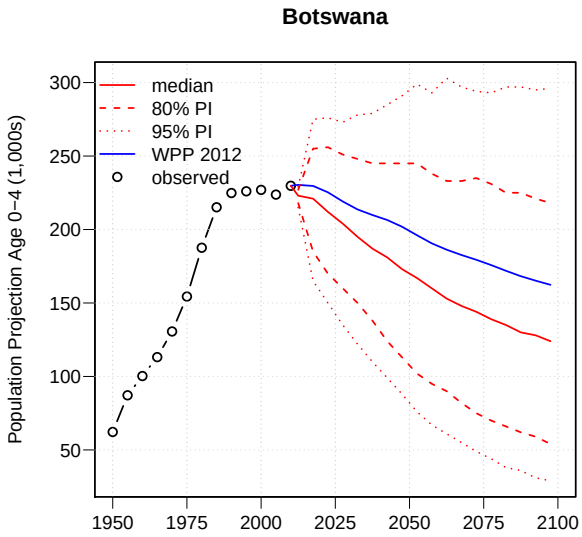
We discuss results here for four countries: Botswana, Lesotho, Mozambique and Ghana. These countries were chosen to represent different levels of current HIV prevalence. In 2010 Botswana and Lesotho represent the largest epidemics with HIV prevalences of roughly 25 percent; Mozambique represents a smaller but still substantial epidemic (HIV prevalence in 2010 $\approx$ 15 percent); while Ghana has a small generalized epidemic (HIV prevalence in 2010 $\approx$ 1.5 percent). Results for Botswana are shown in Figure 2, while results for the other three countries are in Figs. S1-S3 in Supplemental Materials.

Panel a (top left) of Figure 2 plots the total population projection for Botswana. We project an increase in population until about 2075 when the total population begins to decline. Also in Figure 2a note the increasing width of the prediction intervals as the projection reaches farther into the future reflecting the increase in uncertainty, a feature of the projection for all countries. WPP 2012 (solid blue line) also shows sustained population growth followed by a mild reversal in that trend around 2075, but our median projection predicts fewer people in the total population over the entire projection horizon.

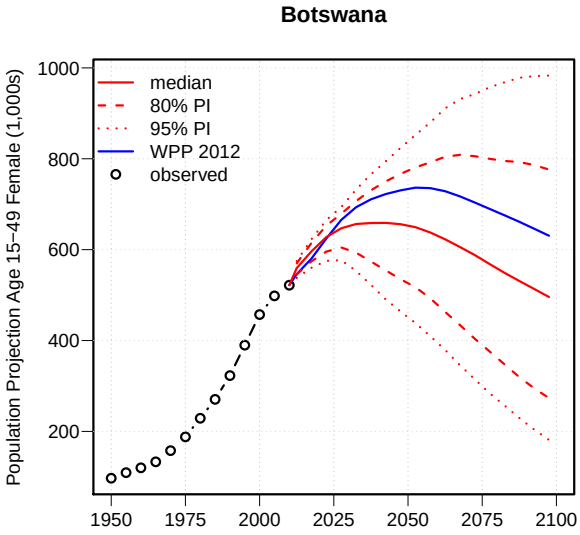
The differences from WPP result mainly from our treatment of mortality, which is dependent on projection of HIV prevalence and life expectancy. Botswana is experiencing one of the largest HIV epidemics in the world in terms of prevalence. Figure 3 shows the prob-



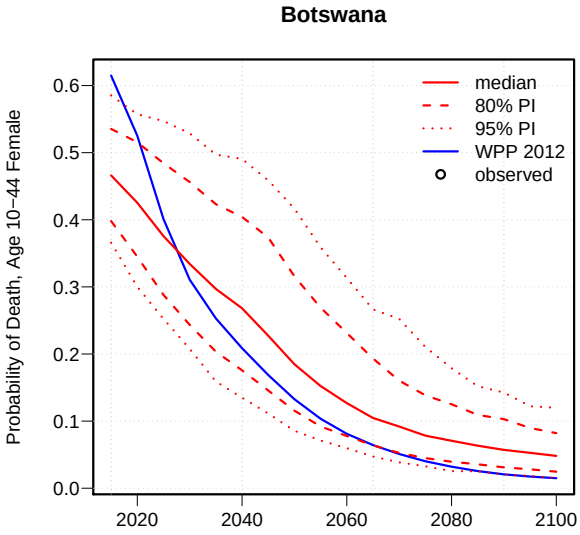
(a) Population Projection: total population



(b) Population Projection: age 0-4



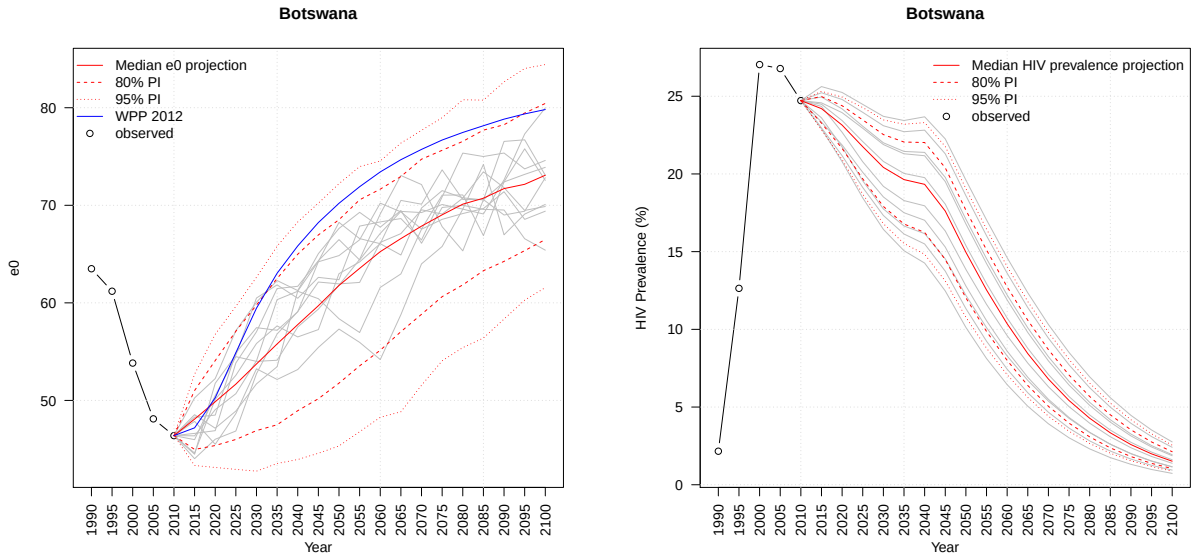
(c) Population Projection: female age 15-49



(d) Projection of female ${}_{35}q_{10}$

Figure 2 Probabilistic population projections for Botswana 2010-2100. Observed data: black circles; median probabilistic projection: solid red line, 80% predictive interval: dashed red lines; 95% predictive interval: dotted red lines; WPP 2012 projection: solid blue line.

abilistic projection of HIV prevalence and life expectancy at birth for Botswana 2010-2100. HIV prevalence in Botswana is projected to remain high, dropping from about 25 percent to roughly 13 percent by 2050. Although declining, these high prevalence rates result in low life expectancies as modeled with Eq. 3, reaching just above 60 years by 2050 from less than 50 years in 2010. Compared to the WPP 2012 projected life expectancies, our median projection shows sustained lower life expectancy of roughly 5-8 years over the entire projection period.



(a) Probabilistic Life Expectancy Projection **(b)** Probabilistic HIV Prevalence Projection

Figure 3 Probabilistic life expectancy and HIV prevalence projections for Botswana 2010-2100. median of probabilistic projection: solid, red line; 80% predictive interval: dashed, red line; 95% predictive interval: dotted, red line; WPP 2012 projection (a): solid, blue line; observed: black circles. The gray lines in these figures are a random sample of ten trajectories from the final sample of 1,000 trajectories from the posterior distribution.

Figure 4 shows the difference between our median projection of the total population and the WPP 2012 projection of total population as a proportion of the WPP 2012 estimate from 2015-2100 for each of the 40 countries under study here. In 2050, Botswana has one of the largest differences from WPP 2012 with about nine percent fewer people in the total population compared to the WPP 2012 Revision. In addition to projecting lower life

expectancy than WPP 2012 (see Figure 3a), 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 shows the big role age-specific mortality rates play in countries with generalized HIV epidemics. Sustained high mortality during the reproductive years for women (see Figure 2d) results in fewer women alive during the reproductive years and thus fewer births.

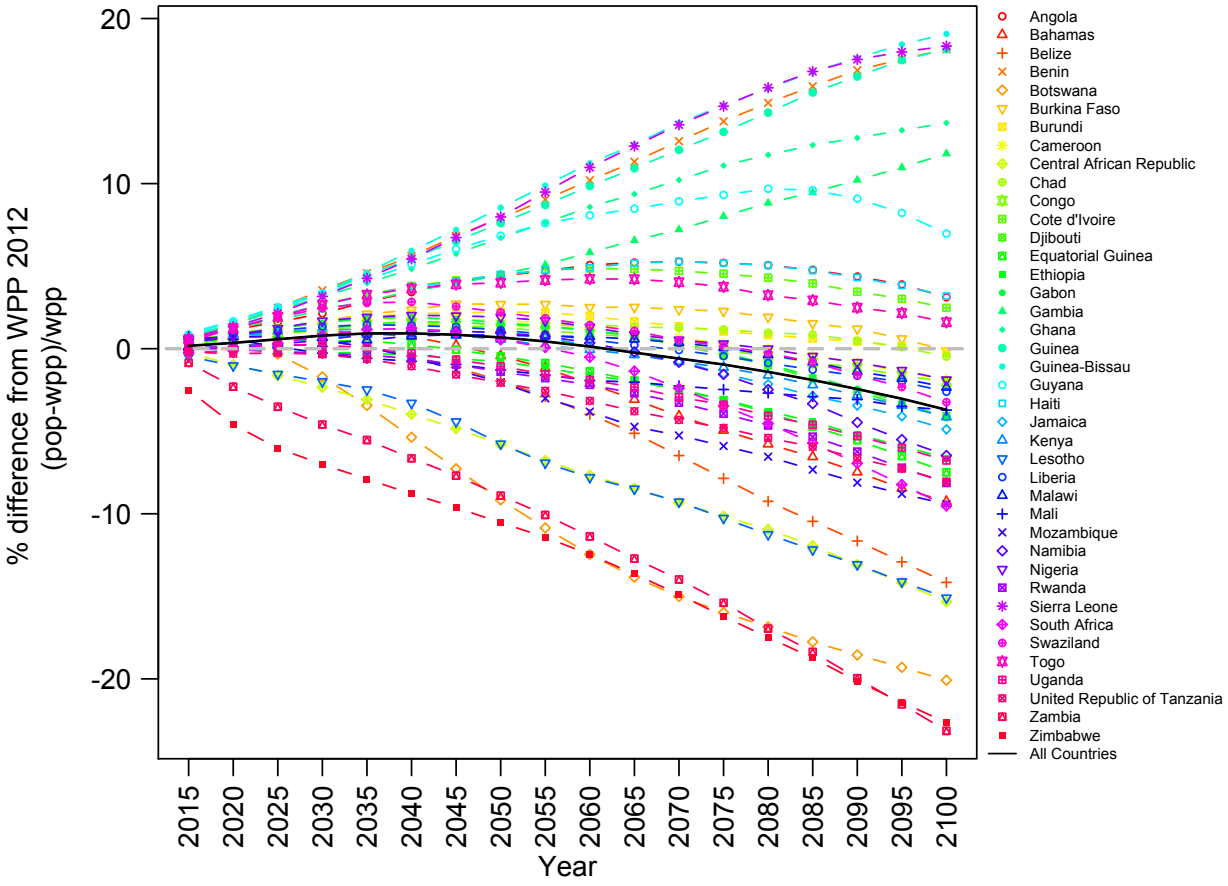


Figure 4 Comparison between our median total population projection and WPP 2012 median projection for total population. Each line shows the percentage difference from the WPP 2012 total population estimate for each country and the solid black line shows the difference at each period for all countries combined.

These effects can be seen in Figs. 2b-2d. Figure 2c shows the probabilistic population

projection for women aged 15-49. We project a decline in the number of women in this age category beginning around 2050, and Figure 2b shows a shrinking population under age five over the entire projection period. The effect of high mortality in the reproductive adult years on future population size, especially for women, reverberates for a number of years as smaller cohorts are born in each projected period, resulting in smaller total population compared to WPP 2012. Combined with declining fertility, the effect of high adult mortality yields an eventual reversal in population growth for Botswana.

Similar conditions exist for the other countries with the top five negative proportional differences at 2050 (Zimbabwe, Botswana, Zambia, Lesotho, and Central African Republic all with differences of greater than five percent) shown in Figure 4. All five of these countries have large scale HIV epidemics ($> 10\%$ prevalence), again reducing the number of women of reproductive age resulting in smaller birth cohorts. Lesotho is projected to have about 5.8 percent fewer people in the total population in 2050 compared to the WPP 2012 Revision. HIV prevalence is also projected to decline from about 24 percent to 18 percent between 2010 and 2050. We project higher probabilities of death for women of reproductive age compared to WPP 2012 (Figure S1d) over almost the entire projection period resulting in a likely decreasing number of women of reproductive age past 2050 (Figure S1c) and consequently smaller birth cohorts over the projection horizon (Figure S1b).

For countries with smaller HIV epidemics, the reduction in the number of women of reproductive age is less severe and thus the difference between our projections and WPP 2012 tends to be smaller. Mozambique is projected to have just under 10 percent prevalence (median projection) by 2050, down from around 15 percent in 2010. Figure S2a shows that our median projection of the total population is similar to the WPP 2012 projection, but we again project a smaller total population (2 percent fewer people in 2050, see Figure 4). The smaller differences from WPP 2012 can also be seen in Figs. S2b and S2c showing the population projections for under age five and women age 15-49 respectively.

For Ghana, where HIV prevalence is projected to decrease from about 1.5 percent in 2010 to under one percent by 2050, the difference from WPP 2012 is in the opposite direction. We project about 6.7 percent more people in the total population by 2050 compared to WPP 2012. The much lower rates of HIV prevalence have a far less extreme depressing effect on total population in Ghana in the long run as evidenced by Figs. S3b and S3c. In addition to relatively little effect from HIV on the age-specific mortality rates, compared to WPP 2012, we project consistently higher life expectancy over the projection period for Ghana along with the other top five positive difference countries compared to WPP 2012 (Guinea-Bissau, Sierra Leone, Benin, Guinea, and Guyana; see Figure 4).

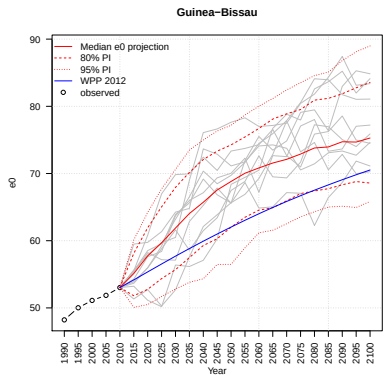
Figure 5 plots the probabilistic projections of life expectancy for the six countries with the largest positive proportional differences in projected population at 2050, as shown in Figure 4. Figure 5 also depicts the life expectancy derived from the WPP 2012 mortality projections for these countries As this figure shows, a large portion of the difference between the WPP 2012 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 epidemics, which will limit the influence of prevalence on the age pattern of mortality rates.

4 Validation

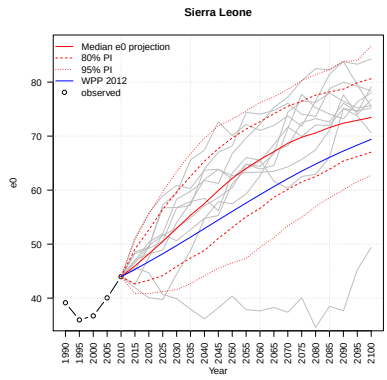
4.1 Out-of-Sample Validation

To validate our method, we calibrated the e_0 projection and HIV MLT models with 5-year data from the WPP 2012 revision 1985-2005 and used those models to generate a population projection for the 2005-2010 period for 38 countries.[4] We then compare the

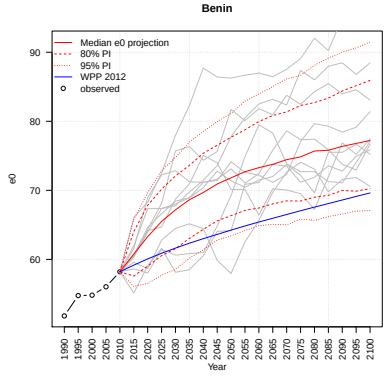
[4]Sierra Leone and Liberia were excluded from this validation experiment because they do not have ante-natal clinic or national population based survey data before 2005 so we cannot make prevalence projections.



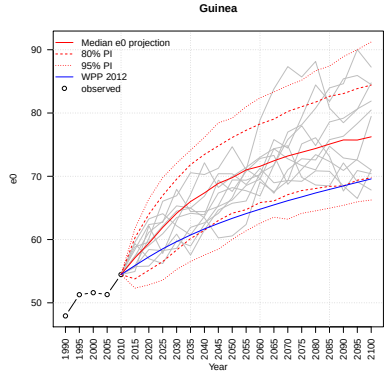
(a) Guinea-Bissau



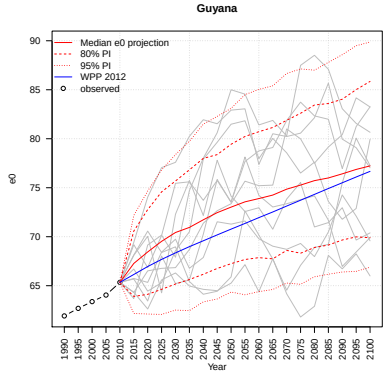
(b) Sierra Leone



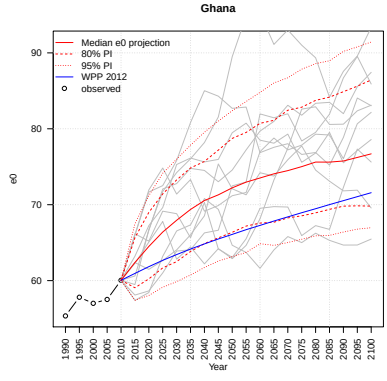
(c) Benin



(d) Guinea



(e) Guyana



(f) Ghana

Figure 5 Probabilistic life expectancy projections for six countries 2010-2100. median of probabilistic projection: solid, red line; 80% predictive interval: dashed, red line; 95% predictive interval: dotted, red line; WPP 2012 projection: solid, blue line; observed: black circles. The gray lines in these figures are a random sample of ten trajectories from the final sample of 1,000 trajectories from the posterior distribution.

resulting mortality and population distributions with the observations from WPP 2012 for 2005-2010.

Because our method addresses the mortality component of the projection, we first assess the accuracy of the mortality predictions for 2005-2010 by calculating the mean absolute error (MAE) of our median projection for 2005-2010, treating the WPP 2012 estimate as the observed value, for four mortality indicators: e_0 (life expectancy at birth), ${}_5q_0$ (the probability a new born will die before reaching age five), ${}_{45}q_{15}$ (the probability a 15-year-old will die before reaching age 60), and ${}_{35}q_{10}$ (the probability a 10-year-old will die before age 45). Table 1 presents the MAE by sex for the four mortality indicators. For males, the mean absolute error for life expectancy among the 38 countries considered for validation is about two years, while the MAE for e_0 for females is slightly less at 1.7 years, suggesting a good fit for the level of mortality. For the other three indicators, the MAE is less than four per 1000 for both sexes.[5] Overall, our method predicted the WPP 2012 estimate for 2005-2010 well for most countries.

Table 1 Mean absolute error for four mortality indicators for the 2005-2010 out-of-sample period (${}_5q_0$, ${}_{45}q_{15}$ and ${}_{35}q_{10}$, all per thousand) using our method for projecting HIV prevalence and life expectancy and using the HIV MLT model for converting to age-specific mortality rates. All models have been calibrated with data from 1985-2005 and used to predict the out-of-sample period 2005-2010.

	Mean Absolute Error			
	e_0	${}_5q_0$	${}_{45}q_{15}$	${}_{35}q_{10}$
Male	2.0	24.4	37.7	32.3
Female	1.7	22.9	39.5	39.3

We further assess the accuracy of our method for projecting age-specific mortality rates by calculating the observed proportions of age-specific mortality rates for 2005-2010 (observed data that were left out for calibration) captured in the 80%, 90%, and 95% predictive intervals

[5]Figure S4 plots the predicted distribution of these three indicators for 2005-2010 along with the WPP 2012 estimate for 2005-2010. This figure lends context to the magnitude of the MAEs in table 1.

(PI) for 2005-2010 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 our predictive intervals. The top two rows of Table 2 show the coverage (percentage of WPP 2012 mortality rates across all ages and all 38 countries captured by the various interval widths) for the 2005-2010 period. For each PI, our method captures just under the expected proportion, indicating that the method provides reasonably well calibrated projections for the left out period, even with just four periods for calibration.

Table 2 Coverage of WPP 2012 sex-age-specific mortality rates and total population in the 80%, 90%, and 95% PIs for the 2005-2010 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. Fertility and migration were projected using the `bayesPop` software. Data from 1985–2005 were used for calibration, and the resulting estimated model was used to predict the out-of-sample period 2005-2010.

	80% PI	90% PI	95% PI
m_x			
Male	76	86	92
Female	74	87	92
Total Population	71	79	84

Finally, we calculate coverage similar to that of mortality but for the total population prediction at 2005-2010.[6] The bottom row of Table 2 shows the percentage of WPP 2012 total population estimates for 2005-2010 captured in the 80%, 90%, and 95% predictive intervals. The coverages for the mortality rates are not significantly different from the nominal coverages of the PIs. For total population, the coverages are slightly below the nominal values.

4.2 Comparison to Spectrum/EPP

Spectrum/EPP provides useful information to UNAIDS about high-HIV prevalence countries including estimates of HIV prevalence, total population, life expectancy, and a host of other

[6]Calculation of total population includes running fertility projections for the out-of-sample period 2005-2010 with the `bayesTFR` software.

demographic and epidemiological variables in the short term (five years). However, it is, of necessity, quite complex. We propose a simpler method to project over a longer projection horizon.

Table 3 shows the mean difference (MD) between our median projection using the full dataset for calibration (i.e. no out-of-sample period was removed) and Spectrum among all 40 countries for prevalence and life expectancy at birth for the first three projection periods.[7] For prevalence, our projections were lower than those of Spectrum by about one percentage point on average during the first three projection periods, which is substantially less than the prediction margin of error. The mean differences for life expectancy show that on average across the 40 countries we differ from Spectrum by less than a third of a year in either direction. Thus, overall our projections are similar to those of Spectrum, but using a much simpler model.

Table 3 Mean difference (MD) for 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. All our models were calibrated with data from 1985-2010. All results for Spectrum derived from the Spectrum software version 5.06.

	MD[a]		MPD[b]		
	Prevalence	e_0	Total Pop.	Total Pop 0-4	Female Pop. 15-49
2010-2015	-0.9	-0.1	-12.5	-8.4	-12.7
2015-2020	-0.9	0.3	-11.9	-6.1	-12.2
2020-2025	-1.0	0.1	-11.2	-5.1	-11.6

[a] Mean Difference between our estimate and that of the Spectrum software for all 40 countries. These numbers are on the scale of prevalence (percentage points) and life expectancy (years).

[b] Mean Proportional Difference is the difference between our median estimate and the Spectrum estimate as a proportion of the Spectrum estimate. Varying absolute population sizes among the 40 countries necessitate taking the proportional error.

[7] All Spectrum results were obtained with Spectrum version 5.06 downloaded June 2014 (Futures Institute 2014).

The right three columns of Table 3 show the mean proportional difference (MPD) between our median projection and Spectrum 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 but it should approximate Spectrum at least in the short run. For total population, our median estimates of total population were about 12.5% lower than the Spectrum estimate for the most recent projection period, 2005-2010. The mean proportional difference declines for each of the next two periods. Our projections of the population aged 0-4 are also lower than the Spectrum result but by smaller proportional differences than for total population with average proportional differences of less than 10% for all three periods. Finally, our short term projection results for the female reproductive age population are also close to the Spectrum result with just 11-13% average proportional difference over all three periods. In sum, results from table 3 suggest our less complex method reasonably approximates the short-term projections of Spectrum.

5 Discussion

We have presented a method for making probabilistic population projections for countries with generalized HIV 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 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 UN's assumptions about future migration are combined using the cohort component method of projection. These projections

are potentially useful to researchers and policy makers 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 UN's current method for projecting mortality in high-HIV prevalence settings and better captures the age pattern of mortality rates during a generalized HIV epidemic.

Results from the projections described here show that by 2050 and beyond, we project smaller total populations for 15 of the 40 countries under study here compared to WPP 2012. Many of the countries with the largest negative differences in projected total population compared to WPP 2012 have large scale HIV 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 compared to WPP 2012. 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 -3.7% difference in total population amongst all 40 countries by 2100 compared to WPP 2012, a difference of approximately 114 million people.

Although the method presented here for mortality and elsewhere for fertility takes into account uncertainty about future levels of fertility and mortality, it does not include uncertainty about international migration in the future, which can be an important source of forecast errors. 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 2012, some of which are themselves modeled, so they reproduce only the variability in the quantities of

interest contained in the WPP results. To the extent that the WPP 2012 data and results used to calibrate these models reflect the empirical reality, the models we present here should as well. Finally, as in Raftery et al. (2012), this method does not take into account random variation in the number of birth or deaths, given the fertility and mortality rates.

References

Alkema, L., Raftery, A. E., and Clark, S. J. (2007). Probabilistic projections of HIV prevalence using Bayesian melding. *The Annals of Applied Statistics*, 1(1):229–248.

Alkema, L., Raftery, A. E., Gerland, P., Clark, S. J., and Pelletier, F. (2011). Probabilistic projections of the total fertility rate for all countries. *Demography*, 48(3):815–839.

Blacker, J. (2004). The impact of AIDS on adult mortality: Evidence from national and regional statistics. *AIDS*, 18(suppl. 2):S19–S26.

Brown, T., Bao, L., Raftery, A. E., Salomon, J. A., Baggaley, R. F., Stover, J., and Gerland, P. (2010). Modeling HIV epidemics in the antiretroviral era: the UNAIDS Estimation and Projection Package 2009. *Sexually Transmitted Infections*, 86:3–10.

Coale, A. J. and Demeny, P. (1966). *Regional Model Life Tables and Stable Populations*. Princeton University Press.

Coale, A. J., Demeny, P., and Vaughan, B. (1983). *Regional Model Life Tables and Stable Populations*. Academic Press New York, 2nd edition.

Fosdick, B. K. and Raftery, A. E. (2014). Regional probabilistic fertility forecasting by modeling between-country correlations. *Demographic Research*, 30:1011–1034.

Futures Institute (2014). Spectrum/EPP 2014 version 5.06. (downloaded June 2014). http://www.futuresinstitute.org/spectrum.aspx.

Ghys, P. D., Brown, T., Grassly, N. C., Garnett, G., Stanecki, K. A., Stover, J., and Walker, N. (2004). The UNAIDS estimation and projection package: A software package to estimate and project national HIV epidemics. *Sexual Transmitted Infections*, 80:i5–i9.

Ghys, P. D. and Garnett, G. P. (2010). The 2009 HIV and AIDS estimates and projections: methods, tools and analyses. *Sexually Transmitted Infections*, 86(Suppl. 2):ii1–ii2.

Ghys, P. D., Walker, N., McFarland, W., Miller, R., and Garnett, G. P. (2008). Improved data, methods and tools for the 2007 HIV and AIDS estimates and projections. *Sexually Transmitted Infections*, 84:i1–i4.

Hontelez, J. A., de Vlas, S. J., Baltussen, R., Newell, M. L., Bakker, R., Tanser, F., Lurie, M., and Bärnighausen, T. (2012). The impact of antiretroviral treatment on the age composition of the HIV epidemic in Sub-Saharan Africa. *AIDS (London, England)*, 26:19–30.

Lee, R. D. and Tuljapurkar, S. (1994). Stochastic population forecasts for the United States: Beyond high, medium, and low. *Journal of the American Statistical Association*, 89:1175–1189.

Lutz, W. and Samir, K. C. (2010). Dimensions of global population projections: what do we know about future population trends and structures? *Philosophical Transactions of the Royal Society B*, 365:2779–2791.

Murray, C. J. L., Ferguson, B. D., Lopez, A. D., Guillot, M., Salomon, J. A., and Ahmad, O. (2003). Modified logit life table system: Principles, empirical validation, and application. *Population Studies*, 57:165–182.

National Research Council (2000). *Beyond Six Billion: Forecasting the World's Population*. National Academy Press, Washington, D.C.

Ngom, P. and Clark, S. J. (2003). Adult mortality in the era of HIV/AIDS: Sub-Saharan Africa. Technical report, Population Division, United Nations, New York.

Obermeyer, Z., Rajaratnam, J. K., Park, C. H., Gakidou, E., Hogan, M. C., Lopez, A. D., Murray, C. J. L., and Timaeus, I. (2010). Measuring adult mortality using sibling survival: A new analytical method and new results for 44 countries, 1974-2006. *PLoS Medicine*, 7(4).

Poit, P., Bartos, M., Ghys, P. D., Walker, N., and Schwartländer, B. (2001). The global impact of HIV/AIDS. *Nature*, 410:968–973.

Preston, S. H., Heuveline, P., and Guillot, M. (2001). *Demography: Measuring and Modeling Population Processes*. Blackwell, Malden, MA.

Raftery, A. E. and Bao, L. (2010). Estimating and projecting trends in HIV/AIDS generalized epidemics using incremental mixture importance sampling. *Biometrics*, 66(4):1162–1173.

Raftery, A. E., Chunn, J. L., Gerland, P., and Ševčíková, H. (2013). Bayesian probabilistic projections of life expectancy for all countries. *Demography*, 50(3):777–801.

Raftery, A. E., Lalic, N., and Gerland, P. (2014). Joint probabilistic projection of female and male life expectancy. *Demographic Research*, 30(4):795–822.

Raftery, A. E., Li, N., Ševčíková, H., Gerland, P., and Heilig, G. K. (2012). Bayesian probabilistic population projections for all countries. *Proceedings of the National Academy of Sciences*.

Ševčíková, H., Alkema, L., and Raftery, A. E. (2011). bayesTFR: An R package for probabilistic projections of the total fertility rate. *Journal of Statistical Software*, 43(1):1–29.

Ševčíková, H., Gerland, P., Andreev, K., Li, N., Gu, D., and Spoorenberg, T. (2013). *wpp2012: World Population Prospects 2012*. R package version 2.0-0.

Ševčíková, H. and Raftery, A. (2014). *bayesPop: Probabilistic Population Projection*. R package version 5.0-0.

Sharrow, D. J., Clark, S. J., Collinson, M., Kahn, K., and Tollman, S. (2013). The age pattern of increases in mortality affected by HIV: Bayesian fit of the Heligman-Pollard model to data from the Agincourt HDSS field site in rural northeast South Africa. *Demographic Research*, 29(39):1039–1096.

Sharrow, D. J., Clark, S. J., and Raftery, A. E. (2014). Modeling age-specific mortality for countries with generalized HIV epidemics. *PLoS ONE*, 9(5).

Stanecki, K., Garnett, G. P., and Ghys, P. D. (2012). Developments in the field of HIV estimates: methods, parameters and trends. *Sexually Transmitted Infections*, Supplement (December).

Stover, J., Brown, T., and Marston, M. (2012). Updates to the Spectrum/Estimation and Projection Package (EPP) model to estimate HIV trends for adults and children. *Sexually Transmitted Infections*, 88:11–6.

Timaeus, I. M. and Jasseh, M. (2004). Adult mortality in Sub-Saharan Africa: Evidence from Demographic and Health Surveys. *Demography*, 41(4):757–772.

UNAIDS (2014). *Quick Start Guide for Spectrum*. UNAIDS.

United Nations, Department of Economic and Social Affairs, Population Division (2011). World Population Prospects: The 2010 Revision, Special Tabulations.

United Nations, Department of Economic and Social Affairs, Population Division (2013a). *World Population Prospects: The 2012 Revision*. New York: United Nations.

United Nations, Department of Economic and Social Affairs, Population Division (2013b). *World Population Prospects: The 2012 Revision, Methodology of the United Nations Estimation and Projections*. New York: United Nations.

United Nations. Department of International Economic and Social Affairs (1982). *Model life tables for developing countries*. United Nations, New York.

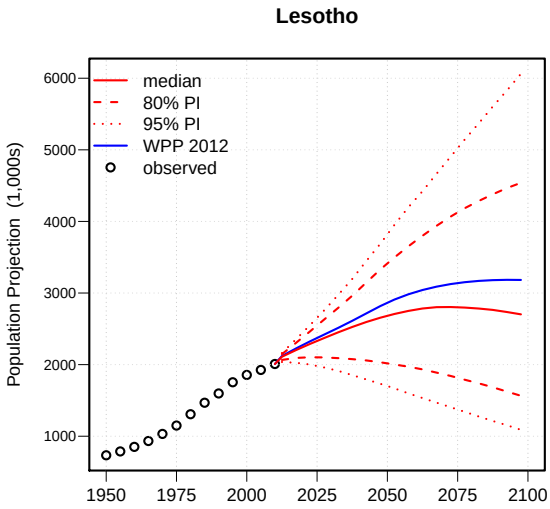
Ševčíková, H. and Raftery, A. E. (2012). *bayesPop: Probabilistic Population Projection*. R package version 1.0-3.

Whelpton, P. K. (1936). An empirical method of calculating future population. *Journal of the American Statistical Association*, 31(195):457–473.

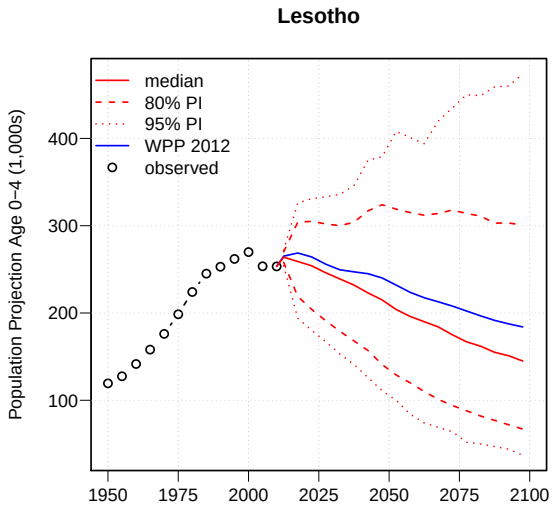
Wilmoth, J., Zureick, S., Canudas-Romo, V., Inoue, M., and Sawyer, C. (2012). A flexible two-dimensional mortality model for use in indirect estimation. *Population Studies*, 66(1):1–28.

Supplemental Material

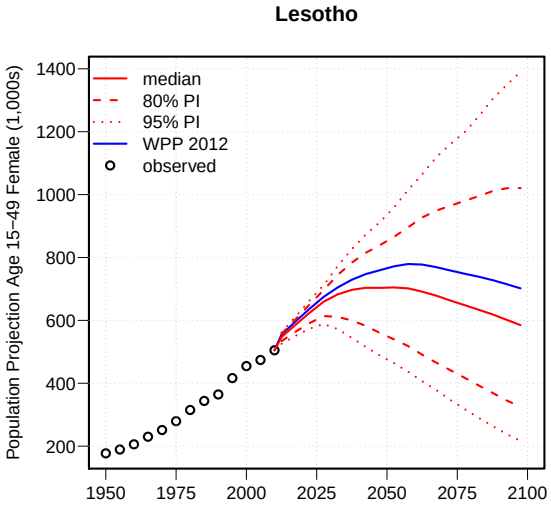
Probabilistic Population Projections for selected countries



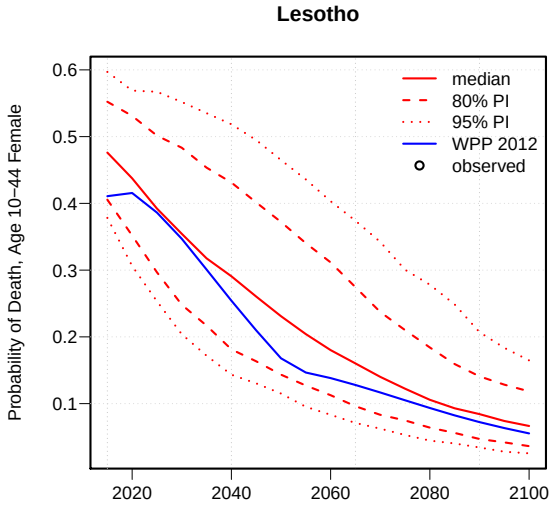
(a) Population Projection: total population



(b) Population Projection: age 0-4

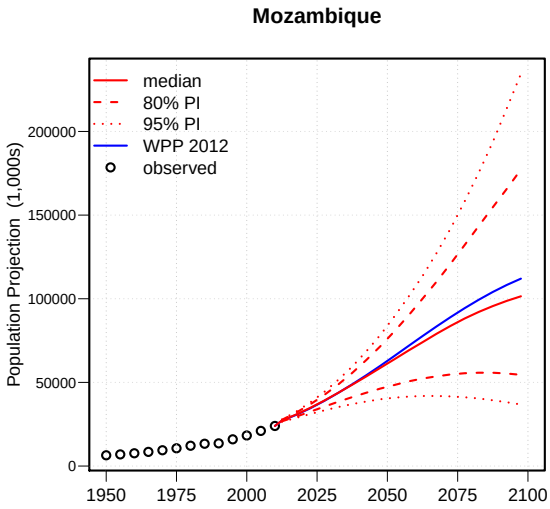


(c) Population Projection: female age 15-49

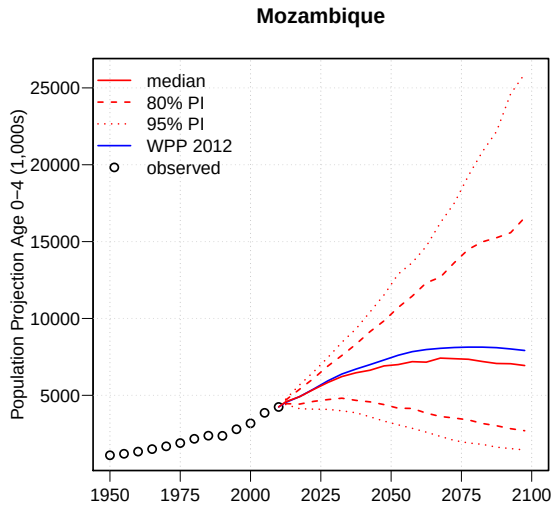


(d) Projection of female ${}_{35}q_{10}$

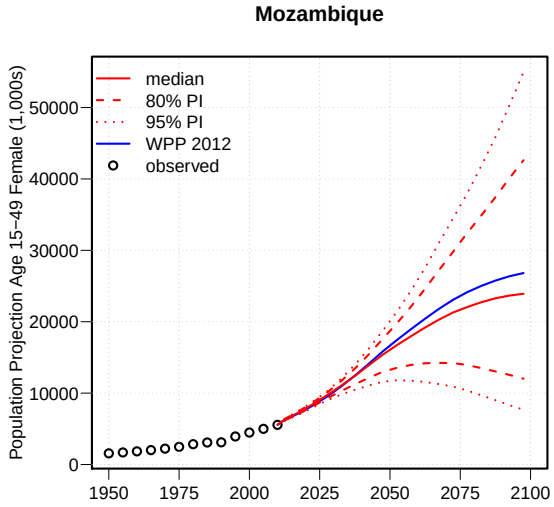
Figure S 1 Probabilistic population projections for Lesotho 2010-2100. Observed data: black circles; median probabilistic projection: solid red line, 80% predictive interval: dashed red lines; 95% predictive interval: dotted red lines; WPP 2012 projection: solid blue line.



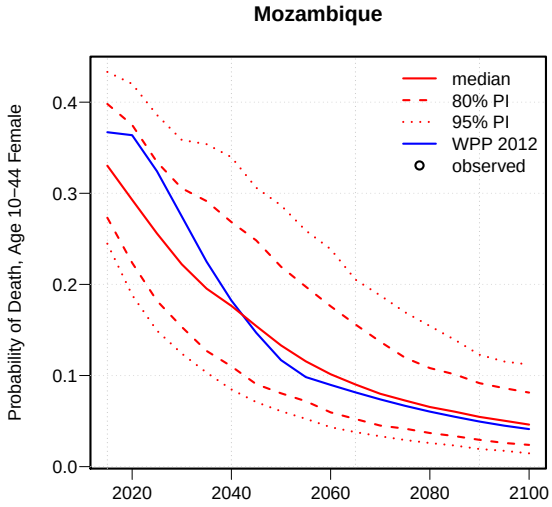
(a) Population Projection: total population



(b) Population Projection: age 0-4

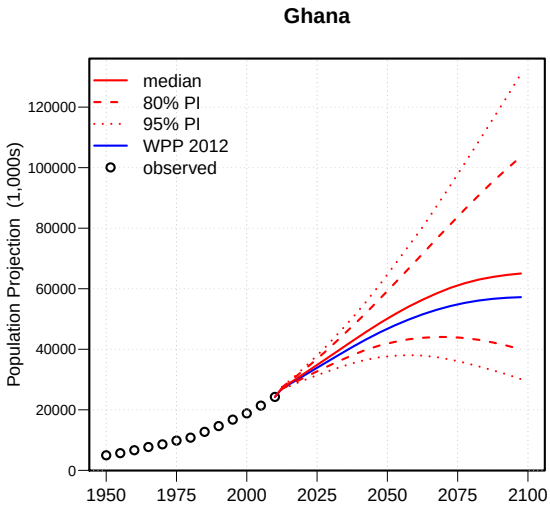


(c) Population Projection: female age 15-49

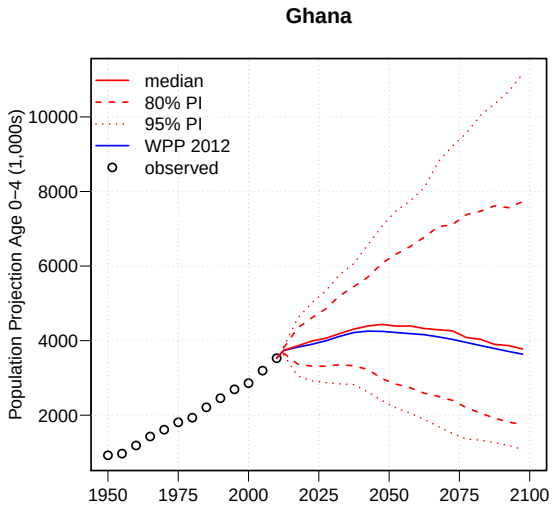


(d) Projection of female ${}_{35}q_{10}$

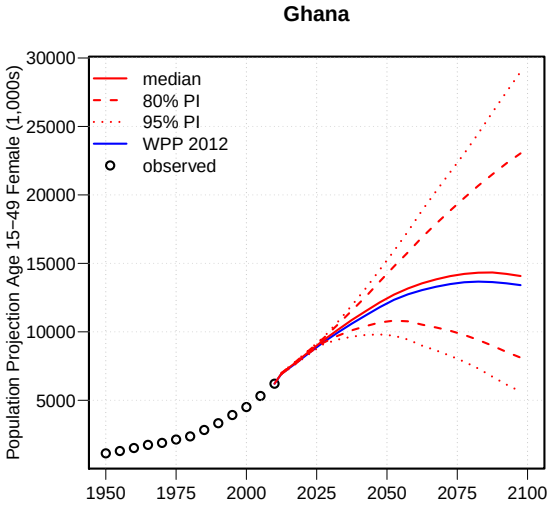
Figure S 2 Probabilistic population projections for Mozambique 2010-2100. Observed data: black circles; median probabilistic projection: solid red line, 80% predictive interval: dashed red lines; 95% predictive interval: dotted red lines; WPP 2012 projection: solid blue line.



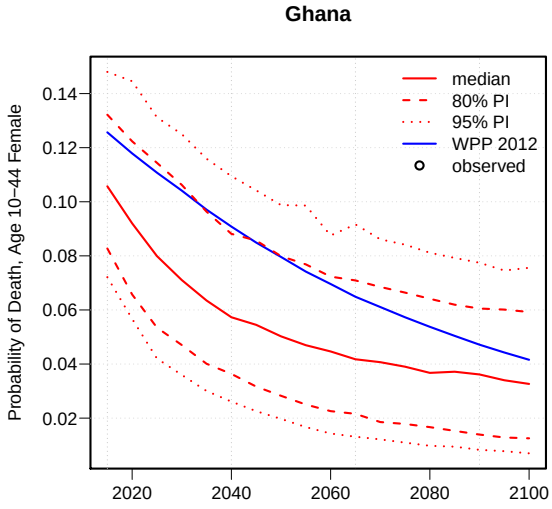
(a) Population Projection: total population



(b) Population Projection: age 0-4

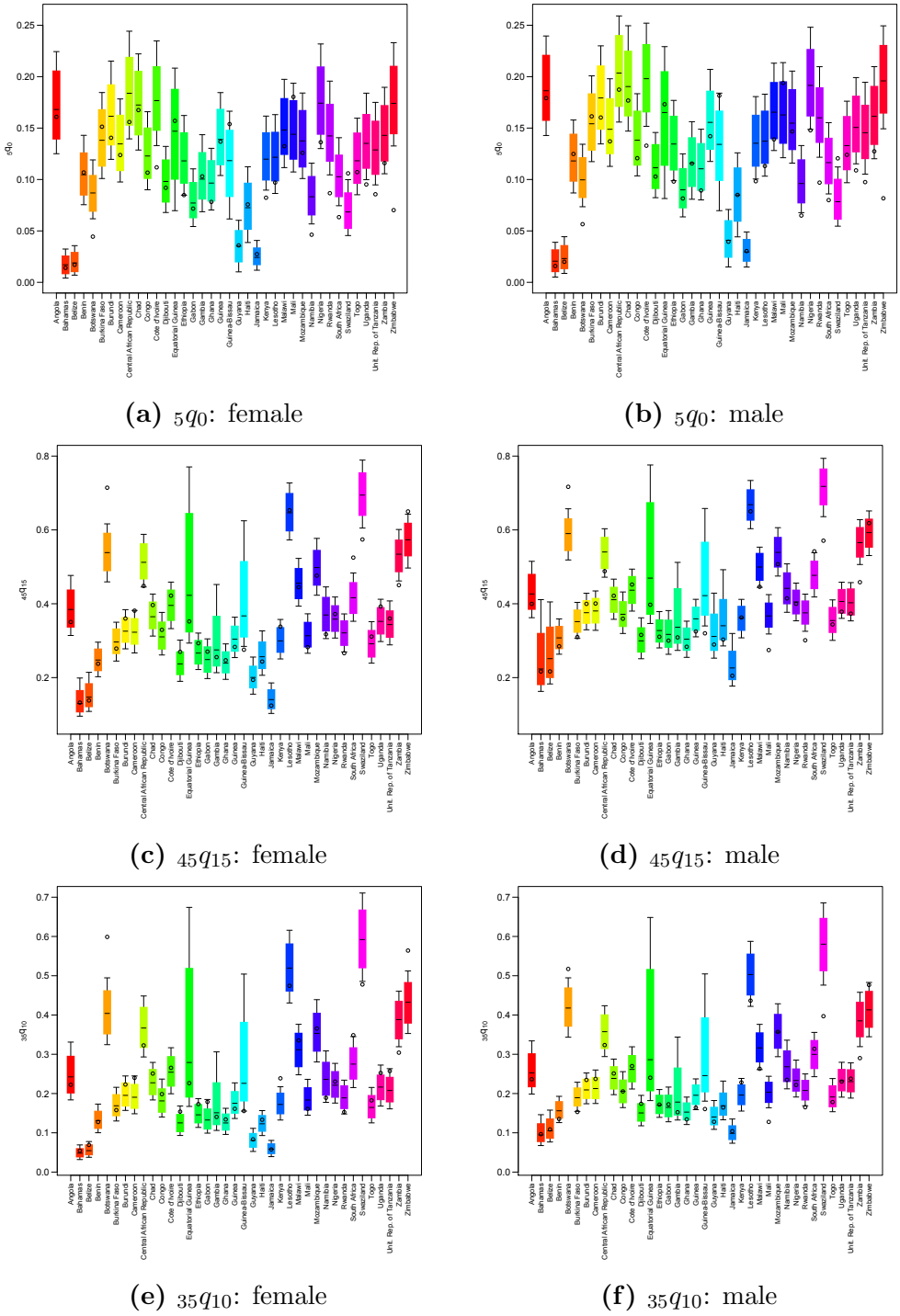


(c) Population Projection: female age 15-49



(d) Projection of female ${}_{35}q_{10}$

Figure S 3 Probabilistic population projections for Ghana 2010-2100. Observed data: black circles; median probabilistic projection: solid red line, 80% predictive interval: dashed red lines; 95% predictive interval: dotted red lines; WPP 2012 projection: solid blue line.



(a) $_5q_0$: female **(b)** $_5q_0$: male

(c) $_{45}q_{15}$: female **(d)** $_{45}q_{15}$: male

(e) $_{35}q_{10}$: female **(f)** $_{35}q_{10}$: male

Figure S 4 Distribution of predicted $_5q_0$, $_{45}q_{15}$, and $_{35}q_{10}$ by country for out-of-sample validation period 2005-2010. In these figures the ends of the "whiskers" are the 95% PI, the ends of the box are the 80% PI, and the horizontal black line in the center of each box is the median. The WPP 2012 estimate for 2005-2010 is shown with a black circle for comparison.