Estimating levels and trends in adult mortality rates in countries with high HIV prevalence from 1950 to 2023

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Abstract

Accurate monitoring of adult mortality in countries with a high human immunodeficiency virus (HIV) prevalence is essential for disease measurement and population estimation. However, this is challenging because most countries experiencing high HIV prevalence lack good civil vital registration systems. The existing sets of mortality estimates are based on standard demographic techniques and partially deterministic approaches, especially in countries with high HIV prevalence. We developed Bayesian hierarchical models (BHM) to estimate the levels and trends in sex-specific adult mortality 45q15 from 1950 to 2023. The BHM make use of extensive databases and allow information sharing across country-periods. The effect of HIV prevalence on adult mortality was specifically modelled to capture the nonlinear pattern.

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The views expressed in this paper are those of the authors, and do not necessarily reflect the views of the United Nations.
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Contents

List of Tables

List of Figures

List of Abbreviations

ASMR	Age-Specific Mortality Rates
ART	Antiretroviral therapy
BHM	Bayesian hierarchical models
DHS	Demographic and Health Survey
HIV	human immunodeficiency virus
DRC	Death-reporting completeness2
INLA	integrated nested Laplace approximation
RW1	1st-order Random Walk
RW2	2nd-order Random Walk
PC	Penalized Complexity
SRS	Sample Registration System
VR	Vital Registration
WPP	World Population Prospects
GBD	Global Burden of Diseases
CRVS	Civil registration and vital statistics
U5MR	Under-5 mortality rate

1 Introduction

Accurate monitoring of adult mortality in countries with a high HIV prevalence is essential for disease measurement and population estimation. However, this is challenging because most countries experiencing high human immunodeficiency virus (HIV) prevalence lack good civil vital registration systems (Mathers et al. 2005). Hence, estimation of sex-specific mortality in these countries often relies on surveys that are subject to sampling errors and reporting bias. Furthermore, the model life table approaches are not able to estimate the mortality patterns in countries with high HIV prevalence since they are not designed to do so (Sharrow, Clark, and Raftery 2014).

Among the existing studies on sex-specific adult mortality with comparable global estimates, the *World Population Prospects* (WPP) released by the United Nations and the *Global Burden of Diseases* (GBD) produced by the Institute for Health Metrics and Evaluation are the most widely known. The most recent releases of WPP and GBD occurred in 2022 (United Nations 2022) and 2019 (Wang et al. 2020) respectively. However, these sets of estimates are based on standard demographic techniques and partially deterministic approaches (additional smoothing steps), especially in countries with high HIV prevalence.

In this full conference paper for EPC 2026, we developed Bayesian hierarchical models (BHM) to estimate the levels and trends in sex-specific adult mortality ${}_{45}q_{15}$ from 1950 to 2023, corresponding to mortality in age group 15–59 for countries with high HIV prevalence. These models make use of extensive databases for adult mortality from vital registration systems, censuses, surveys, and national reports. BHMs allow information sharing across data-rich country-periods with those where the data are sparse or without data entirely. The effect of HIV prevalence on adult mortality was specifically modelled to capture the nonlinear pattern. The model captures the mortality peaks due to high HIV prevalence and produces reasonable projections of mortality decline when HIV prevalence declines and antiretroviral therapy prevalence increases. Figure 1 summarizes the process for data preprocessing and Bayesian modeling.

2 Data Preparation

This section describes the preprocessing of the input dataset used in BHM, including the calculation of the stochastic error for CRVS data, the calculation of sampling error for non-CRVS data, the data adjustments for non-sampling biases.

2.1 Computation of Stochastic Error for CRVS Data

The first step in data preparation entails the computation of stochastic errors for the CRVS data. As previously stated, CRVS data were used only for combinations of country and year in which death reporting completeness was above 60 per cent. The number of deaths in a specific age group was computed as the product of the observed age-specific mortality rates (ASMR; also denoted as ${}_nm_x$, where x is the initial age and n is the length of the interval) by sex in that age group from the CRVS, and the number of persons in that age group (from WPP estimates of the population by age and sex)[1]. Generally, the number of deaths computed is smaller than the actual number because deaths are subject to under-reporting. Uncertainties from both under-reported and reported deaths were included in the calculation of stochastic errors of the CRVS data.

1. The mortality rates for broad age groups (${}_nm_x$) are obtained by converting the probability of dying between age x and $x+n$ (denoted ${}_nq_x$) using the following formula: ${}_nm_x = -2 \cdot {}_nq_x / ({}_nq_x \cdot n) - (2 \cdot n)$ based on Preston, Heuveline, and Guillot 2001, see p. 43.

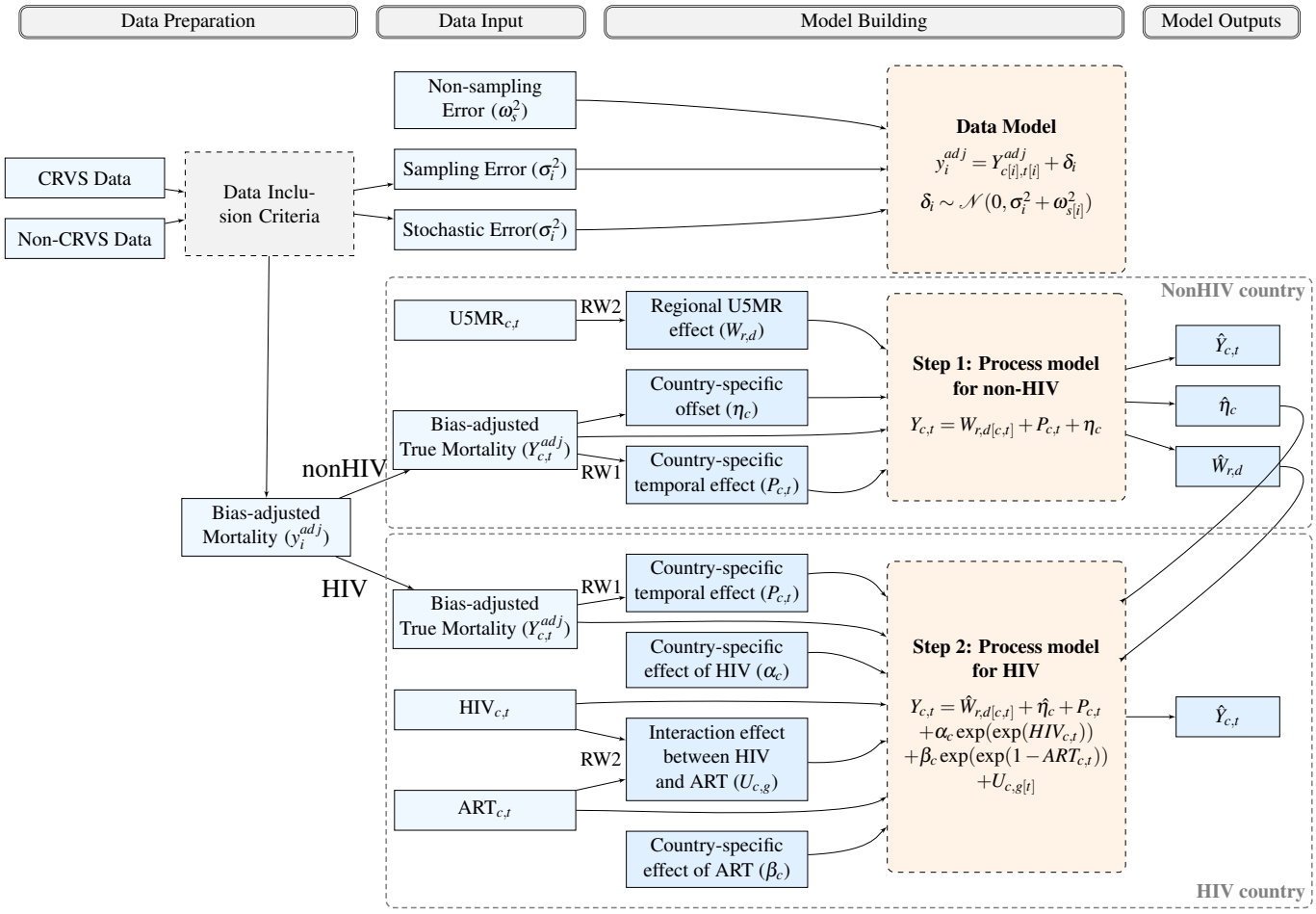

Figure 1: **Data and model process overview.** This flow chart summarizes the major steps of data pre-processing, input data, Bayesian models, and the model outputs.

First, the stated death-reporting completeness[2](DRC) for country c in year t, denoted as $z_{c,t}$, accounts for the uncertainty of under-reported deaths. The reported DRC $z_{c,t}$ was assumed to be uniformly distributed. The g-th simulated DRC $z^g_{c,t}$ is obtained by:

$$z^g_{c,t} \sim U\left(z_{c,t} - \delta(z)_{c,t},\ z_{c,t} + \delta(z)_{c,t}\right) \tag{1}$$

where $\delta(z)_{c,t}$ is the standard error of the reported DRC for country c in year t. $\delta(z)_{c,t}$ was assumed to decrease linearly from 0.25 to 0.05 when the reported DRC $z_{c,t}$ was within the interval [60%, 95%]. When $z_{c,t}$ further increased to 100%, $\delta(z)_{c,t}$ was assumed to decline linearly to zero. $\delta(z)_{c,t}$ was imputed as follows:

$$\delta(z)_{c,t} = 0.25 - \frac{0.25 - 0.05}{0.95 - 0.6}(z_{c,t} - 0.6) \qquad \text{if } 60\% \leq z_{c,t} < 95\% \tag{2}$$

$$\delta(z)_{c,t} = 0.05 - \frac{0.05}{1 - 0.95}(z_{c,t} - 0.95) \qquad \text{if } z_{c,t} \geq 95\% \tag{3}$$

It is worth noting that the assumptions made in simulating DRC are largely based on expert opinions. When additional information becomes available regarding the distribution of $z_{c,t}$, the simulation steps can be updated accordingly.

The g-th simulated number of under-reported deaths $D^{\text{under}(g)}_{c,t}$ was calculated as the product of the number of deaths reported $D^{\text{report}}_{c,t}$ and the difference between 1 and the g-th simulated DRC $z^{(g)}_{c,t}$:

$$D^{\text{under}(g)}_{c,t} = D^{\text{report}}_{c,t}\left(1 - z^{(g)}_{c,t}\right). \tag{4}$$

The g-th simulated total number of deaths $D^{(g)}_{c,t}$ was obtained as the sum of reported deaths and g-th simulated under-reported deaths. The uncertainty in the estimates was included by assuming that the simulated number of deaths had a Poisson distribution:

$$D^{(g)}_{c,t} \sim \text{Poisson}\left(D^{\text{report}}_{c,t} + D^{\text{under}(g)}_{c,t}\right). \tag{5}$$

At this point, the g-th simulated number of total deaths $D^{(g)}_{c,t}$ was divided by the number of persons in the specific age-sex group $N^{\text{sex}}_{c,t}$ to obtain the g-th simulated $\text{ASMR}^{(g)}_{c,t}$:

$$\text{ASMR}^{(g)}_{c,t} = \frac{D^{(g)}_{c,t}}{N^{\text{sex}}_{c,t}} \tag{6}$$

The obtained age-specific mortality rate was finally converted back into the overall probability of dying based on Preston, Heuveline, and Guillot 2001, see p. 43:

$${}_nq^{(g)}_{x,c,t} = \frac{(2 \cdot n) \cdot \text{ASMR}^{(g)}_{c,t}}{2 + (n \cdot \text{ASMR}^{(g)}_{c,t})} \tag{7}$$

2. The completeness of death registration corresponds to the proportion of all deaths that occurred in a given year and were reported to civil registration authorities. The degree of completeness of death registration can be evaluated through various analytical methods, including aggregated analysis (comparing observed vital events with reference figures from an alternative source believed to represent the true potential value of expected events), individual-level analysis (comparing and linking individual records of vital events from multiple data sources to identify matched records and those present in one data source but not another), indirect demographic analysis (comparing reported deaths with those expected from intercensal survival or some statistical modelling based on covariates), or census or survey assessments (asking questions about whether vital events reported in the survey or census have been registered with local authorities) (Rao et al. 2020; Hill 2017).

The stochastic error is the standard deviation of the simulated $nq_{x,c,t}^{(g)}$:

$$\sigma_{c,t} = \sqrt{\frac{\sum_{g=1}^{G}\left({}_nq_{x,c,t}^{(g)} - \overline{{}_nq_{x,c,t}}\right)^2}{G-1}} \tag{8}$$

where

$$\overline{{}_nq_{x,c,t}} = \frac{\sum_{g=1}^{G} {}_nq_{x,c,t}^{(g)}}{G} \tag{9}$$

2.2 Computation of Sampling Errors for Non-CRVS Data

Whenever available, sampling errors were calculated from the micro-datasets. If sampling errors were missing, they were imputed as the median of the sampling errors within each combination of age groups and sex and the period between the interview and the event. The sampling errors were then calculated using a set of simulated normally distributed ${}_nq_x$ values, with a mean equal to the observed ${}_nq_x$ and a standard deviation equal to the sampling error computed from the microdata. The computed standard deviation of the simulated ${}_nq_x$ on the logit scale provided the sampling error of the non-CRVS data.

2.3 Data Inclusion Criteria

Additionally, observations with implausible extreme values were removed based on age-specific inclusion criteria: (1) exclude observations with extreme probabilities of dying equal either to zero or one in some age groups; (2) exclude observations below age-specific lower cut-off values based on the estimated lowest estimated probability of dying for all countries in 1950-2023 in the World Population Prospects (WPP) 2022 (United Nations 2022) equal to 0.2 between age 15 and 60, and 0.00001 for other broad ages to address issues with low mortality in small populations (even after grouping multiple consecutive years); (3) retrospective observations beyond 25 years before the survey (or census) were excluded due to excessively large sampling errors and concerns with recall biases; and (4) exclude observations for years with significant mortality crises to model the overall time trend for crisis-free adult mortality (i.e., with crude death rate attributable to mortality crises greater than or equal to 1 per 1000).

2.4 Adjustments for Non-sampling Biases

We performed a bias adjustment for the observations of adult mortality. We assume that previous WPP estimates of adult mortality are non-biased (Liu and Raftery 2020). Biases are computed only for observations that are not from the *civil registration and vital statistics* (CRVS/SRS).

We computed the bias for each record as the difference between the logit of observed mortality rate and corresponding logit estimate in the WPP (crisis-free with a certain level of smoothness). Then, for each country, we fitted the biases with a linear regression function using the following independent variables:

- Data source (categorical variable): census, Demographic and Health Survey (DHS) type, estimates, panel, CRVS/SRS, and other surveys and reports.
- The data collection method (categorical variable) included household death, intercensal survival, adjusted intercensal survival, life table, adjusted life table, orphanhood, widowhood, sibling survival, model-based estimates, and official figures.
- Under-5 mortality rate (U5MR; continuous variable): WPP 2022 revision, crisis-free.
- Recall lag (continuous variable).

We extracted the fitted biases from country-specific regression functions. We then adjusted each mortality observation by subtracting the fitted biases:

$$y_i^{\text{adj}} = y_i^{\text{obs}} - \hat{e}_i \tag{10}$$

where y_i^{adj} is the i-th bias-adjusted mortality observation on the logit scale used in the Bayesian estimation model, y_i^{obs} is the i-th observed mortality on the logit scale before bias adjustment, and $\hat{e}_i$ is the i-th fitted bias obtained from the country-specific regression functions.

3 Estimation Method: Bayesian Hierarchical Model

3.1 Process Model

This section provides a brief overview of the BHM developed for sex-specific adult mortality ${}_{45}q_{15}$. For simplicity, all terms in the rest of this section are sex-specific.

The adjusted mortality rate ${}_{45}q_{15}$ (see Section 2.4) for a certain country in a certain year is modelled on the logit scale to ensure that the mortality rate (a probability) falls within the bounds of 0 and 1. The logit of the adjusted mortality rate is assumed to be the sum of (1) the true underlying rate on the logit scale and (2) the measurement error.

We used a two-step modelling process to estimate mortality rates by separating country-years with high and low HIV prevalence:

- Step 1: Model for non-HIV countries based on adjusted data in all countries but excluding data in HIV countries after 1976, where the year 1976 was the earliest year in which the sex-specific HIV prevalence in any country-year was above 0.1%.
- Step 2: Model for HIV countries based on all data in HIV countries only.

3.1.1 Step 1: model for non-HIV countries

The true logit-scaled underlying sex-specific mortality $Y_{c,t}$ from country c in year t for all age groups is modelled as the sum of (i) the regional effect[3] from the crisis-free U5MR, $W_{r,d[c,t]}$, (ii) country-specific temporal effect, $P_{c,t}$, and (iii) country-specific offset, η_c. Specifically,

$$Y_{c,t} = W_{r,d[c,t]} + P_{c,t} + \eta_c \tag{11}$$

$W_{r,d[c,t]}$ modelled the regional nonlinear relationship between adult mortality and crisis-free U5MR for a country c and year t, where the index r refers to the SDG region r to which the country c belongs. Specifically, let $V_{c,t}$ denote the log of U5MR per 1000 for country c and year t, taken from the WPP 2022 revision (United Nations 2022). A grid of values κ_d is defined for $d \in \{1, \cdots, x\}$, x is the number of locations where $W_{r,d}$ is evaluated, and $\kappa_1 = \log(1)$ and κ_x are the maximum values of $V_{c,t}$ across all country-years with the data. We evaluated $W_{r,d}$ at every $\log(3)$ location, hence the total number of locations $x = 236$. Each $V_{c,t}$ is matched to the κ_d with the smallest absolute difference from $V_{c,t}$, denoting the dth index for country-year c,t as $d[c,t]$. A second-order random walk (RW2) process was used to model the relationship between $W_{r,d}$ and κ_d. $W_{r,d}$ is assumed to be constant outside the range of κ_1 and κ_x across all c and t. In particular:

$$\Delta^2(W_{r,d}) = W_{r,d} - 2W_{r,d+1} + W_{r,d+2} \tag{12}$$

$$\Delta^2(W_{r,d}) \sim \mathcal{N}\left(0, \frac{1}{\tau_r^w}\right), \quad \text{for } r \in \{1,\ldots,7\},\ d \in \{1,\ldots,x-2\} \tag{13}$$

3. The regional classification used are SDG regions. Further details about the classification used: https://population.un.org/wpp/DefinitionOfRegions.

$P_{c,t}$ accounts for the within-country temporal fluctuations. We used a first-order random walk (RW1) to model $P_{c,t}$ as follows:

$$\Delta P_{c,t} = P_{c,t} - P_{c,t-1}, \tag{14}$$

$$\Delta P_{c,t} \sim \mathcal{N}\left(0, \frac{1}{\tau_c^p}\right), \quad \text{for } t \in \{1950, \ldots, 2023\},\ c \in \{1, \ldots, 236\} \tag{15}$$

Penalized Complex (PC) priors, which are vague priors, are assigned to the regional precision parameter τ_r^w for $r \in \{1, \ldots, 7\}$ and the country-specific precision parameter τ_c^p for $c \in \{1, \ldots, 236\}$.

$$\tau_r^w \sim \text{PC}(z, 0.01), \quad \text{for } r \in \{1, \ldots, 7\} \tag{16}$$

$$\tau_c^p \sim \text{PC}(1, 0.01), \quad \text{for } c \in \{1, \ldots, 236\} \tag{17}$$

where z represents the standard deviation of all observations. Detailed documentation of the PC prior specification can be found in Simpson et al. 2017.

3.1.2 Step 2: model for HIV countries

In the second modelling step, we focused on modelling adult mortality in HIV countries. We introduce the non-HIV effects from step 1 as model input in step 2 and add additional effects from HIV prevalence, antiretroviral therapy (ART), and their interaction. Specifically,

$$Y_{c,t} = \widehat{W}_{r,d[c,t]} + \hat{\eta}_c + P_{c,t} + \alpha_c \exp\left(\exp(HIV_{c,t})\right) + \beta_c \exp\left(\exp(1 - ART_{c,t})\right) + U_{c,g[t]} \tag{18}$$

The true logit-scaled underlying sex-specific mortality $Y_{c,t}$ from country c in year t is modelled as the sum of (i) $\hat{W}_{r,d[c,t]}$ the median estimates of regional effects from the crisis-free U5MR (obtained in step 1), (ii) $\hat{\eta}_c$ the median estimates of country-specific offset U5MR (obtained in step 1), (iii) $P_{c,t}$ country-specific temporal effect (estimated in step 2),(iv) α_c the country-specific effect of $\exp\left(\exp\left(HIV_{c,t}\right)\right)$, the double exponential for HIV prevalence, (v) β_c the country-specific effect of $\exp\left(\exp\left(ART_{c,t}\right)\right)$, the double exponential for ART prevalence, and (vi) $U_{c,g[t]}$ the country-specific interaction between HIV and ART. The choice of double exponential for $HIV_{c,t}$ and $ART_{c,t}$ allows for better fitting during the HIV endemic.

$P_{c,t}$ accounts for the within-country temporal fluctuations. We use a first-order random walk (RW1) to model $P_{c,t}$:

$$\Delta P_{c,t} = P_{c,t} - P_{c,t-1} \tag{19}$$

$$\Delta P_{c,t} \sim \mathcal{N}\left(0, \frac{1}{\tau_c^p}\right), \quad \text{for } t \in \{1950, \ldots, 2023\},\ c \in \{1, \ldots, 236\} \tag{20}$$

The country-specific regression coefficients for double exponential HIV prevalence $\exp\left(\exp(HIV_{c,t})\right)$ and double exponential ART prevalence $\exp\left(\exp(1 - ART_{c,t})\right)$ follow hierarchical normal distributions:

$$\alpha_c \sim \mathcal{N}\left(0, \frac{1}{\tau_\alpha}\right), \quad \text{for } c \in \{1, \ldots, 236\} \tag{21}$$

$$\beta_c \sim \mathcal{N}\left(0, \frac{1}{\tau_\beta}\right), \quad \text{for } c \in \{1, \ldots, 236\} \tag{22}$$

$U_{c,g[t]}$ models the country-specific nonlinear interaction between HIV prevalence and the ART prevalence for country c and year t. Specifically, let $M_{c,t}$ denote the $\text{HIV}_{c,t} \times (1 - \text{ART}_{c,t})$ per 1000 for the country c and year t. A grid of values λ_g is defined for $g \in \{1, \cdots, G\}$, G is the number of locations where $U_{c,g[t]}$ is evaluated, where $\lambda_1 = 1$ and κ_G as the maximum of $M_{c,t}$ across all country-years. We evaluated

locations for $U_{c,g[t]}$ that were 3 apart from each other, hence the total number of locations $G = 103$. Each $M_{c,t}$ is matched to λ_g with the smallest absolute difference from $M_{c,t}$, denoting the gth index for the year t as $g[t]$. A second-order random walk (RW2) process was used to model the relationship between $U_{c,g}$ and λ_g.$U_{c,g}$ is assumed to be constant outside the range of λ_1 and λ_G across all c and t. In particular:

$$\Delta^2(U_{c,g}) = U_{c,g} - 2U_{c,g+1} + U_{c,g+2} \tag{23}$$

$$\Delta^2(U_{c,g}) \sim \mathcal{N}\left(0, \frac{1}{\tau_c^U}\right), \quad \text{for } c \in \{1,\ldots,236\},\ g \in \{1,\ldots,G-2\} \tag{24}$$

Vague priors are assigned to country-specific precision parameters τ_c^U for $c \in \{1,\ldots,236\}$, τ_c^p for $c \in \{1,\ldots,236\}$, the global precision parameters $\tau_\alpha = 1/\sigma_\alpha^2$, and $\tau_\beta = 1/\sigma_\beta^2$ as follows.

$$\tau_c^U \sim \text{PC}(1, 0.01), \quad \text{for } c \in \{1,\ldots,236\} \tag{25}$$

$$\tau_c^p \sim \text{PC}(1, 0.01), \quad \text{for } c \in \{1,\ldots,236\} \tag{26}$$

$$\tau_\alpha \sim Gamma(1, 0.00005) \tag{27}$$

$$\tau_\beta \sim Gamma(1, 0.00005) \tag{28}$$

3.2 Data Model

The i-th adjusted mortality observation on the logit scale, y_i^{adj}, is modelled as shown in 29. The logit of the observed mortality rate is assumed to be the sum of (1) the true underlying rate on the logit scale $Y_{c[i],t[i]}^{adj}$ for country $c[i]$ in year $t[i]$, and (2) the measurement error δ_i for the i-th adjusted observation y_i^{adj}. The indices $c[i]$ and $t[i]$ are used to distinguish multiple observations from the same country-year c and t. The i indexes observations across all country-years.

$$y_i^{adj} = Y_{c[i],t[i]}^{adj} + \delta_i \tag{29}$$

As shown in 30, the measurement error δ_i is modelled as the sum of (i) the sampling/stochastic error σ_i^2 and (ii) the non-sampling error $\omega_{s[i]}^2$ for the data source type s to which the i-th observation y_i^{adj} belongs:

$$\delta_i \sim \mathcal{N}\left(0, \sigma_i^2 + \omega_{s[i]}^2\right) \tag{30}$$

The sampling/stochastic errors σ_i^2 were precalculated for each observation as described in the Section 2.1 and Section 2.2. They reflect the uncertainty resulting from the survey sampling design for data from surveys and censuses and stochastic uncertainty from administrative records for vital registration data. Non-sampling errors ω_s^2, for $s \in \{1,\ldots,5\}$ are usually unknown, but are inevitable during data collection and processing. They represent uncertainty from non-responses, recall bias, and data input errors, among others. Therefore, we modeled non-sampling errors as data-source-specific parameters by assigning vague priors to $1/\omega_s^2$, for $s \in \{1,\ldots,5\}$ as follows, and z represents the standard deviation of all observations..

$$\frac{1}{\omega_s^2} \sim \text{PC}(z, 0.01), \quad \text{for } s \in \{1,\ldots,5\} \tag{31}$$

Table 1 summarizes the distribution of number of observations across data source types.

Data source	Female	Male
DHS Direct	4,593	4,651
DHS Indirect	7,989	7,419
other DHS Direct	1,280	1,001
Others Direct	606	575
VR/SRS	37,432	37,364
Total	**49,200**	**51,010**

Table 1: **Observation distribution by data source type and age group for adult mortality.** "Direct" refers to data obtained from full sibling histories . "Indirect" refers to indirect demographic analysis, such as comparing reported deaths with those expected from intercensal survival or some statistical modelling based on covariates. DHS: Demographic and Health Surveys. SRS: Sample Registration System. VR: Vital Registration.

4 Model Validation

4.1 Validation Methods

Out-of-sample validation is the mostly used method to test the model performance. Given the retrospective nature of adult mortality and the occurrence of data in series, the training set was constructed not merely by leaving out observations at random, but by reserving all available data series before certain year. And the left-out observation is usually around 20% of the total.

We leave out data after survey year 2010 as test set, which occupy around 20.7% of total observations, then we fit the model to the training set and obtain point estimates and uncertainty intervals that would have been constructed in 2010 based on available data set in the survey year selected.

Various validation measures (mean or median errors, coverage) are calculated to assess the performance (1) based on the left-out observations, (2) and based on the estimates obtained from the full dataset and the estimates obtained from the training dataset.

For each left-out observation on logit scale $y_j = logit(q_j)$, we simulate its predictive probability distribution (PPD) $\{y_j^{(l)} \mid l = 1, ..., L\}$. Let $y_j^{(l)}$ be the l-th simulated PPD for y_j, it is simulated as:

$$y_j^{(l)} \sim \mathcal{N}\Big(Y_{c[j],t[j]}^{(l)},\, \sigma_j^2 + (\omega^{(l)})^2\Big) \tag{32}$$

where $Y_{c[j],t[j]}^{(l)}$ denotes the true underlying mortality on the logit scale for country c and reference year t. σ_j^2 refers to the known sampling error variance. $(\omega^{(l)})^2$ is the unknown non-sampling error variance. Let $\tilde{q}_j$ denote the posterior median of the PPD for $logit^{-1}(y_j)$:

$$\tilde{q}_j = median\{logit^{-1}(y_j^{(l)}) \mid l = 1, ..., L\} \tag{33}$$

Median errors and median absolute errors for the j-th left-out observations, where error is defined as:

$$e_j = q_j - \tilde{q}_j \tag{34}$$

Coverage is given by:

$$\frac{1}{J}\sum_{j=1}^{J} \mathbb{I}_j\big(q_j \geq l_j\big)\, \mathbb{I}_j\big(q_j \leq u_j\big), \tag{35}$$

where J refers to the total number of left-out data, l_j and u_j refers to the lower and upper bounds of 90% prediction interval for the left-out observation q_j.

For the median estimates based on full data set and training data set, error is calculated as:

$$e_{c,t} = \hat{Q}_{c,t} - \tilde{Q}_{c,t}, \tag{36}$$

where $\hat{Q}_{c,t}$ is the posterior median for country c in year t based on the full data set, and $\tilde{Q}_{c,t}$ is the posterior median for the same country-year based on the training data set. Coverage is computed in similar way as for the left-out observations, based on the lower bounds and upper bounds of the 90% uncertainty interval for $\tilde{Q}_{c,t}$ from the training data set.

4.2 Validation Results

We left out all observations that were collected after the year 2010. For age group 15-59, 6804 observations in total were left out, corresponding to 19.9% of all observations. Table 2 summarizes the results related to the left-out observations for the validation exercise. Median errors were close to zero for left-out observations in both sex groups. In general, coverage of 90% prediction intervals (PI) are 90.73% and 88.93% for male and female groups respectively, which aligns with the expectations. We will further investigate the details of these coverage results.

Sex Group	**Male**	**Female**
Median error	-0.01	-0.01
Absolute median error	0.02	0.01
% of left-out observations below 90% prediction interval	7.98	10.01
% of left-out observations above 90% prediction interval	1.29	1.06
Expected proportions(%)	**5.00**	**5**

Table 2: **Validation results for left-out observations by sex group.** Errors are defined as the difference between a left-out observation and the posterior median of its predictive distribution.

Table 3 shows the results for the comparison between estimates based on the full data set, and estimates based on the training set. Median errors and the median absolute errors were close to zero and the proportion of updated estimates that fell outside the uncertainty intervals constructed based on the training set was small.

Sex group	**Male**		**Female**	
Year	2000	2005	2000	2005
Median error	-0.00	-0.00	-0.00	-0.00
Median absolute error	0.00	0.00	0.00	0.00
Below 95% uncertainty interval (%)	0.4	1.2	0.4	0.8
Above 95% uncertainty interval (%)	0.0	0.4	0.0	0.0
Expected proportions (%)	**$\leq$2.5**	**$\leq$2.5**	**$\leq$2.5**	**$\leq$2.5**

Table 3: **Summary of differences in adult mortality 45q15 estimates in observation years 2000 and 2005 based on training set and full data set.** Errors are defined as the differences between estimates based on the full dataset and the training set. The proportions refer to the proportions (%) of countries in which the median adult mortality estimates based on the full data set fall below or above their corresponding 95% uncertainty intervals based on the training dataset. The results are broken down by sex groups and observation years.

5 Preliminary Results

In this section, we present the BHM estimates of adult mortality from selected countries with high HIV prevalence. Figure 2 presents the adult mortality rate ${}_{45}q_{15}$ BHM estimates from Côte d'Ivoire, Eswatini, and South Africa. The three selected countries had high HIV prevalence. Côte d'Ivoire and South Africa have reasonably good coverage of data in recent decades, but Eswatini lacks data near the end of the HIV endemic. Most of the data in these countries are from surveys and censuses. Since the 1990s, the HIV prevalence in these countries has started to increase, which is reflected in the mortality data collected during this period. With the additional effects related to HIV and ART prevalence modelled in the second step of estimation, the BHM can capture the unique hump pattern in mortality rate primarily due to HIV prevalence since the 1980s. When HIV prevalence decreased, and ART receipt proportion increased, the BHM was able to estimate a downward trend in the mortality rate, largely due to the inclusion of the HIV and ART interaction effect.

6 Discussion

The BHMs presented in this extended abstract produce estimates of adult mortality from 1950 to 2023 for countries with high HIV prevalence. The estimates were based on extensive databases from all available data sources at the national level. The Bayesian model can produce reliable estimates that are data-driven, flexible to reflect the hump pattern in adult mortality due to HIV prevalence, and smooth enough to reduce the artifact fluctuation in survey data due to sampling errors and biases. Estimates in countries with limited or no data or good coverage of low-quality data are particularly improved by borrowing information from other countries in the region or countries around the world in a reproducible fashion.

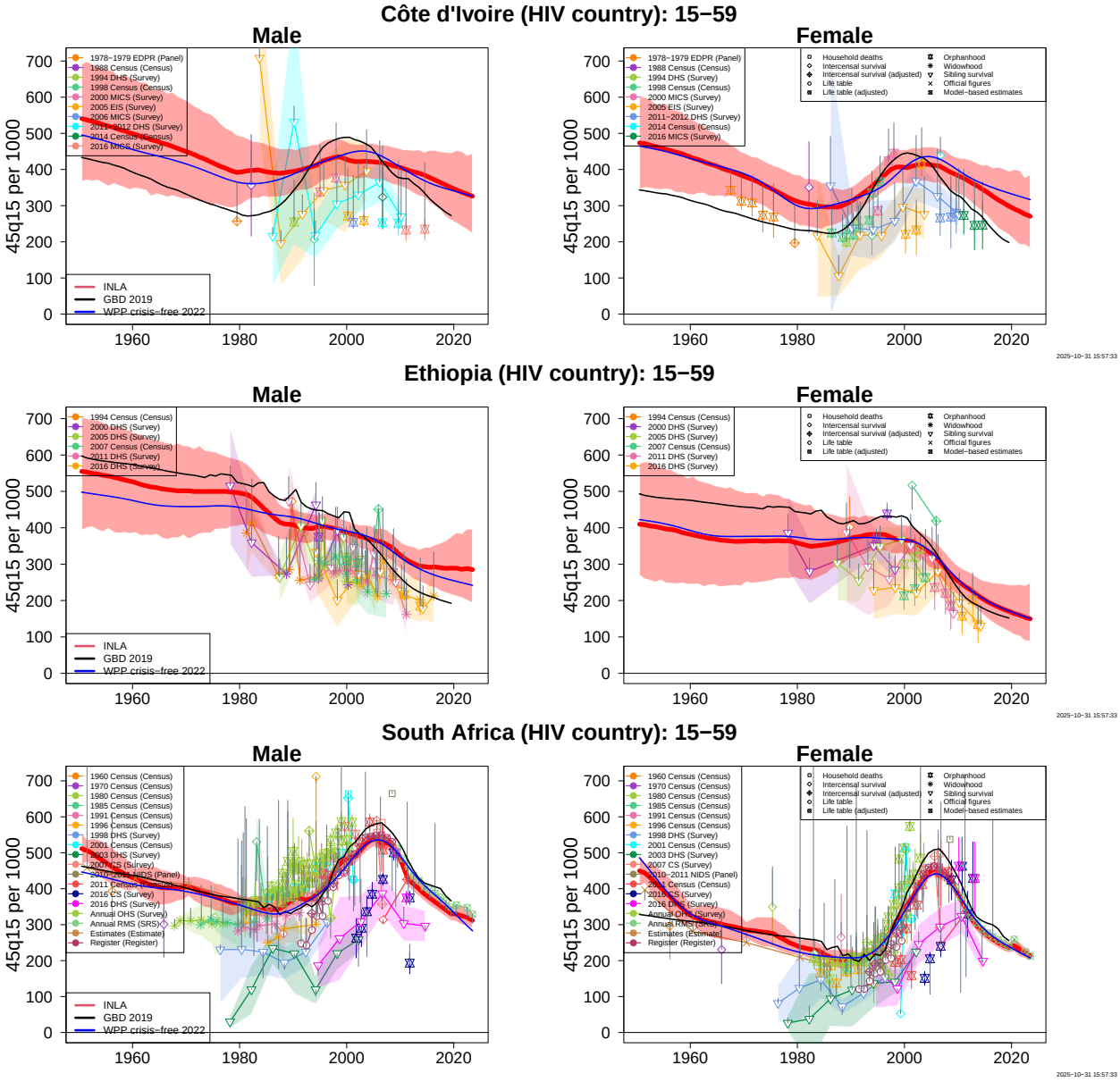

Figure 2: **Adult mortality $_{45}q_{15}$ model estimates from 1950 to 2023 in Côte d'Ivoire, Eswatini and South Africa.** Note: United Nations 2022 in blue, Wang et al. 2020 in black and median estimates of own calculations in red curves. The curves show the posterior medians. The shades show the 95% uncertainty bounds. Dots are observations used for modelling. Shades and vertical lines around dots are sampling errors (if available). The vertical grey bars at dots shows the bias adjustment done before BMH model fitting. Grey bars are absent for observations if bias adjustment is zero.

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