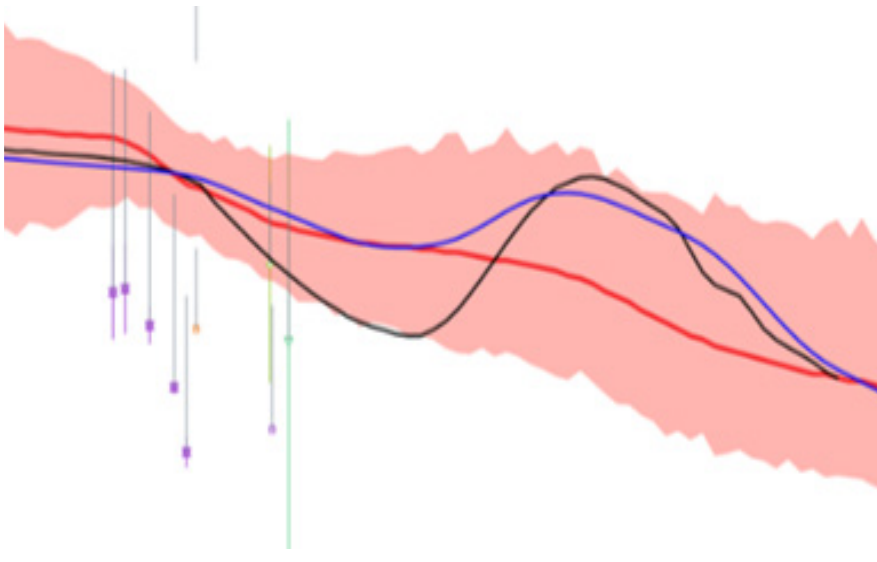
United Nations | Department of Economic and Social Affairs

Population Division
UN DESA/POP/2024/TP/No. 9
December 2024

Estimating age-sex-specific adult mortality in the *World Population Prospects*: A Bayesian modelling approach

Technical Paper

Fengqing Chao, Ivan Williams, Lubov Zeifman and Patrick Gerland



Population Division
Technical Paper
UN DESA/POP/2024/TP/No.9
December 2024

The Population Division of the Department of Economic and Social Affairs provides the international community with timely and accessible population data and analysis of population trends and development outcomes. The Division undertakes studies of population size and characteristics and of the three components of population change (fertility, mortality and migration).

The purpose of the **Technical Paper series** is to publish substantive and methodological research on population issues carried out by experts both within and outside the United Nations system. The series promotes a scientific understanding of population issues among Governments, national and international organizations, research institutions and individuals engaged in social and economic planning, research and training.

Suggested citation: Chao, Fengqing and others (2024). *Estimating age-sex-specific adult mortality in the World Population Prospects: A Bayesian modelling approach*. United Nations, Department of Economics and Social Affairs, Population Division, Technical Paper No. UN DESA/POP/2024/TP/No.9.

This technical paper is available in electronic format on the Division's website at www.unpopulation.org. For further information, please contact the Population Division, Department of Economic and Social Affairs, Two United Nations Plaza, DC2-1950, New York, 10017, USA; phone: +1 212-963-3209; e-mail: population@un.org.

Estimating age-sex-specific adult mortality in the *World Population Prospects*: A Bayesian modelling approach[*]

Fengqing Chao,[**] Ivan Williams,[***] Lubov Zeifman[***] and Patrick Gerland[***]

Abstract

As part of its efforts to revise population estimates and projections for the biennial *World Population Prospects* (WPP), the United Nations Population Division generates estimates of age- and sex-specific adult mortality for all countries and regions globally, spanning from 1950 to the present. These estimates draw upon diverse data sources, including civil registration and vital statistics systems, sample registration systems, surveys, national estimates, and population censuses, applying standard demographic techniques. Biases and inconsistencies inherent in the available data are rigorously evaluated and addressed to produce a consistent annual time series of age- and sex-specific mortality estimates.

This technical paper presents the Bayesian hierarchical model (BHM) developed by the Population Division to estimate trends and levels of adult mortality by age group and sex for all countries and regions since 1950. The model leverages an extensive database maintained by the Population Division, incorporating data from diverse sources and allowing for the sharing of information across countries and time periods. This approach addresses challenges related to sparse, biased, or unavailable data.

The resulting adult mortality estimates are critical for constructing life tables, particularly for approximately half of the world's countries, where detailed and accurate mortality data by age and sex are unavailable. For these countries, model-based approaches are employed to infer age-specific mortality rates based on annual series of under-five and adult mortality indicators.

The outputs of the *World Population Prospects* are widely utilized by the United Nations system, academic institutions, civil society, and other stakeholders. These estimates serve as key inputs for calculating various indicators, including nearly one fourth of those used to monitor the Sustainable Development Goals and for aggregating demographic quantities at regional and global levels.

Keywords: Adult mortality, estimation, Bayesian hierarchical model.

Sustainable Development Goals: 3.

[*] The authors gratefully acknowledge Helena Cruz Castanheira from United Nations, Economic Commission for Latin America and the Caribbean, Santiago de Chile, Chile, as well as Giulia Gonnella, Danan Gu, Sara Hertog, Yumiko Kamiya, Vladimira Kantorova, Joseph Molitoris, Thomas Spoorenberg, and Mark Wheldon from the United Nations Population Division for their insightful comments and useful inputs on the data, method development and results. Additionally, the authors are thankful to Karoline Schmid and Donna Culpepper for reviewing this report.
[**] Computational Social Science Division, School of Humanities and Social Science, The Chinese University of Hong Kong, CUHK-Shenzhen, Longgang District, Shenzhen, Guangdong, China.
[***] United Nations Department of Economic and Social Affairs, Population Division.

Contents

EXPLANATORY NOTES

The following symbols have been used in the tables throughout this report:

A full stop (.) is used to indicate decimals.

References to countries, territories and areas:

The designations employed in this publication and the material presented in it do not imply the expression of any opinion whatsoever on the part of the Secretariat of the United Nations concerning the legal status of any country, territory, city or area or of its authorities, or concerning the delimitation of its frontiers or boundaries. The term "country" as used in this publication also refers, as appropriate, to territories or areas.

The following abbreviations have been used:

AIDS	Acquired immunodeficiency syndrome
API	Application Programming Interface
ART	Antiretroviral therapy
ASMR	Age-specific mortality rate
BHM	Bayesian Hierarchical Model
CCM	Cohort Component Method
CDR	Crude Death Rate
CI	Credible Interval
COVID-19	Coronavirus Disease 2019
CRVS	Civil Registration and Vital Statistics
DHS	Demographic and Health Surveys
DRC	Death-reporting completeness
DYB	Demographic Yearbook
GBD	Global Burden of Disease
HLTD	Human Life Table Database
HMD	Human Mortality Database
HIV	Human immunodeficiency virus
IGME	Inter-agency Group for Child Mortality Estimation
IHME	Institute for Health Metrics and Evaluation, University of Washington
INLA	Integrated Nested Laplace Approximation
IPUMS	Integrated Public Use Microdata Series
LAMBdA	Latin American Mortality Database
M49	Standard Country or Area Codes for Statistical Use (Series M, No. 49)
MICS	Multiple Indicator Cluster Surveys
MLT	Model life table
NA	Not available
OECD	Organisation for Economic Co-operation and Development
PAPCHILD	Pan Arab Project for Child Development
PAPFAM	Pan Arab Project for Family Health
PC	Penalized Complex

PIs	Prediction Intervals
RHS	Reproductive Health Surveys
RW1	first-order random walk
RW2	second-order random walk
SDGs	Sustainable Development Goals
SQL	Structured Query Language
SRS	Sample Registration System
UNAIDS	Joint United Nations Programme on HIV/AIDS
UN DESA	United Nations Department of Economic and Social Affairs
UNFPA	United Nations Population Fund
UNICEF	United Nations Children's Fund
UNSD	United Nations Statistics Division
VR	Vital Registration
WFS	World Fertility Surveys
WHO	World Health Organization
WPP	World Population Prospects

I. Introduction

The Population Division of the United Nations Department of Economic and Social Affairs (UN DESA) releases a set of population estimates and projections every other year, known as the *World Population Prospects* (WPP). This comprehensive dataset is instrumental in analysing population trends at the global, regional and national levels. The WPP provides retrospective population reconstructions from 1950 to the present (population estimates) and includes various scenarios for future demographic development (population projections) (United Nations, 2024a).

The WPP employs the cohort component method (CCM) to estimate and project populations by age and sex. The CCM offers a consistent framework for reconciling historical population estimates with estimated levels and trends in fertility, mortality and net international migration. This method relies on the population balancing equation (Equation 1), whereby the national population can only increase or decrease between two points in time (e.g., t and $t + n$ where t is the initial date and n the time interval) as the result of births, deaths and movements of the population across national boundaries (i.e., emigration and immigration).

$$\mathrm{Pop(t+n)} = \mathrm{Pop(t)} + \mathrm{Births(t,t+n)} - \mathrm{Deaths(t,t+n)} + \mathrm{NetMigrants(t,t+n)} \quad (1)$$

As input for CCM, deaths within the time interval are compiled as the product of the estimates of age-specific mortality rates (ASMR) and the estimated number of persons in a given age group. Since the 2022 revision of the *World Population Prospects*, the time interval and age group on which CCM is applied are one-year periods and single years of age (1x1).

However, as explained in the methodological report for the *World Population Prospects* (see section I.C. Estimating Mortality Rates and Life Tables from United Nations, 2024a), the methods used to estimate mortality and life tables varied across countries depending on the type and quality of available empirical data. These methods can be described according to two main types of approaches: "empirical" and "model-based." The empirical approach was used for countries with reliable information to describe sex- and age-specific mortality rates from vital registration or estimates across a substantial part of the estimation period from 1950 to 2023. A model-based approach was used for countries that lacked sufficient information for the empirical approach. The metadata associated with the 2024 revision (available online), provides further details about the data and approach used to estimate mortality rates and life tables for each country.[1]

For 117 countries, empirical mortality rates by sex and age were too sparse or of insufficient quality to estimate the complete annual time series of mortality rates. Instead, model life tables were used to estimate the mortality rates by single year of age across the full age range from 0 to 130+ and for the years 1950 through 2023. These models require one or more mortality indicators as inputs to match the mortality level and the age pattern. Each model life table requires at least one parameter that describes the mortality rate among children (e.g., under-five mortality rate) or overall (e.g., life expectancy at birth). An additional parameter that describes mortality among adults is useful to further inform the choice of a model that best describes the true mortality age pattern in a given country and year, particularly when the levels and trends for children and adults change differently over time. In order to supply the parameters needed to identify appropriate model life table age patterns of mortality, complete annual time series of child and adult mortality from 1950 to 2023 were estimated for each country.

[1] Please see https://population.un.org/wpp/Download/Metadata/Documentation/

Monitoring adult mortality is particularly challenging in countries with high HIV prevalence, where civil registration systems are often incomplete or non-existent (Mathers and others, 2005). Estimates in these settings rely on survey data, which are subject to sampling errors and reporting biases. Standard model life tables also struggle to accurately capture mortality patterns in such contexts, as they are not designed to account for the non-linear impacts of HIV prevalence and antiretroviral therapy (ART) coverage.

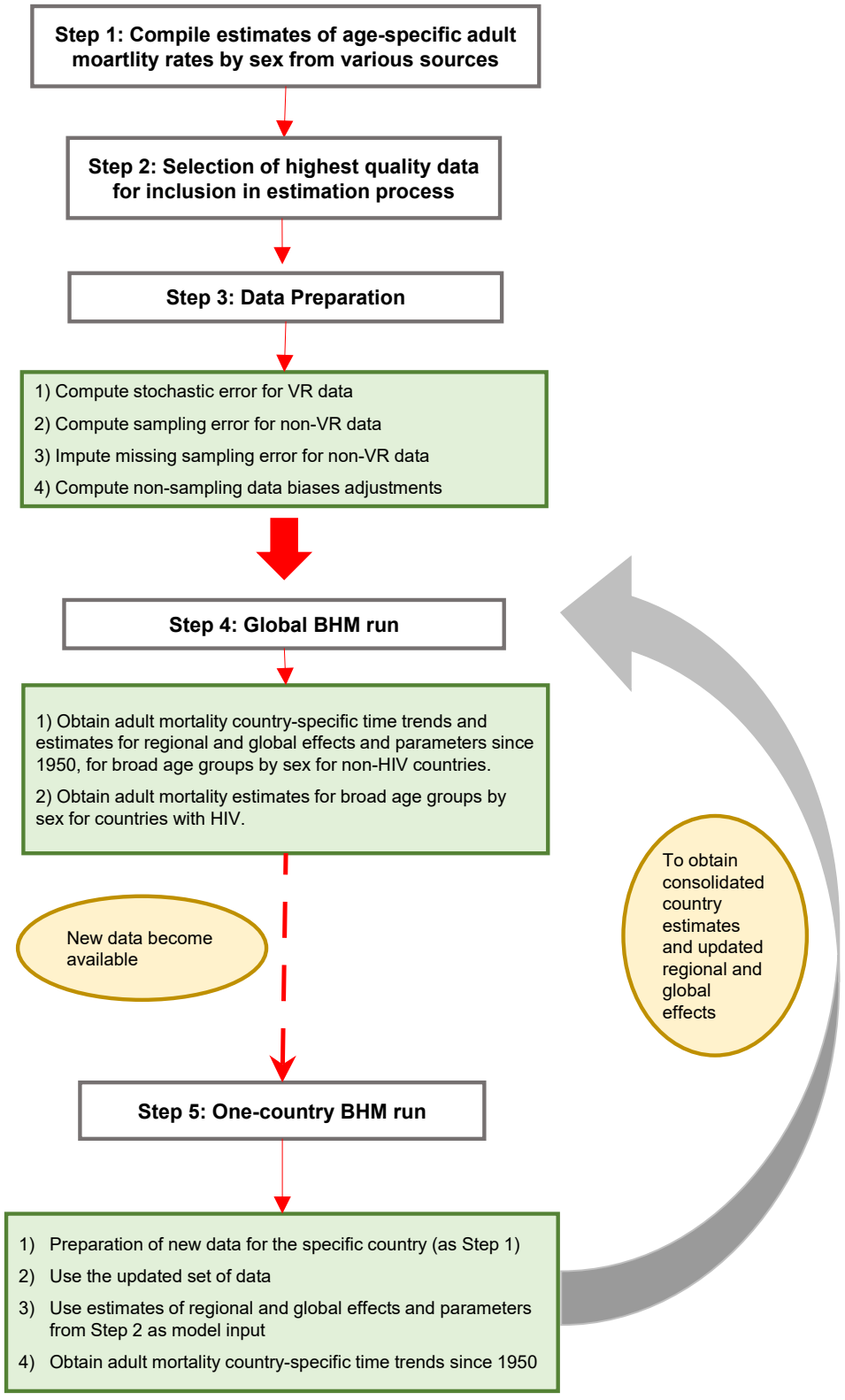
This technical report describes the Bayesian hierarchical model (BHM) developed to estimate annual age-sex-specific adult mortality, expressed, for example, as the probability of dying between ages 15 and 60 years, for all countries since 1950. The BHM leverages an extensive database of adult mortality estimates, including data from vital registration systems, censuses, surveys and national reports maintained by the Population Division. By sharing information across countries and time periods, the BHM addresses the challenges associated with sparse, biased or missing data.

The model estimates adult mortality on a logit scale to constrain probabilities between 0 and 1. It incorporates empirical observations alongside covariates, such as under-five mortality rates, prevalence of HIV infection and coverage of antiretroviral therapy (ART). The model accounts for non-linear regional effects linking under-five and adult mortality and specifically models the non-linear impacts of HIV on adult mortality. It effectively captures mortality peaks during periods of high HIV prevalence and projects declines as HIV prevalence decreases and antiretroviral therapy prevalence increases.

For countries with limited data, the model assumes associations between child and adult mortality similar to the patterns observed in neighbouring countries. In countries with vital registration data, observations with at least 60 per cent completeness were included and rates were adjusted for under-registration using the reciprocal of the proportion of registered deaths (Preston, 1984). Median estimates for each country were based on 10,000 trajectories of the model fitted to observed data, adjusting for biases and excluding periods of significant mortality crises (e.g., crude death rates exceeding five per 1,000). Crisis-related mortality was subsequently incorporated into the life table calculations by age and sex.

The model accounts for both sampling and non-sampling errors. Sampling errors arise from survey designs or stochastic variations in administrative records, whereas non-sampling errors stem from factors such as non-response, recall bias, or data entry inaccuracies. These sources of error were explicitly modelled to provide robust uncertainty estimates for mortality trends and levels. By employing this comprehensive approach, the WPP continues to refine estimates of adult mortality, providing critical inputs for demographic analyses and supporting evidence-based policymaking globally. The overall process is illustrated in figure 1.

Figure 1. Workflow to estimate age-sex-specific adult mortality rates



II. Data compilation and data preparation

A. Data compilation

Analysts from the Population Division collected available data from various reference data sources, such as population censuses, surveys, vital and population registers, analytical reports and other sources for a given country.[2] The preferred data source for adult mortality is counts of deaths by age and sex from a system of civil registration and vital statistics (CRVS) with national coverage and a high level of completeness (United Nations, 2014). In cases in which death registration is deficient or lacking, mortality estimates are typically obtained through household sample surveys or censuses. Demographic sample surveys may provide estimates of adult mortality by asking women (or men) detailed questions to obtain their complete sibling status. Current global survey programmes collecting detailed sibling histories include the Demographic and Health Surveys (DHS) and some recent Multiple Indicator Cluster Surveys (MICS). Separate from the global programmes, some countries field their national demographic surveys, and a few have established sample vital registration systems. Population censuses serve as additional sources of information on adult mortality through questions on the number of deaths of household members by age and sex that occurred in the last 12 (or 24) months before the census date. Moreover, some censuses and surveys have collected additional questions on the survival of parents and spouses, allowing the estimation of adult mortality. Finally, successive census age distributions can also be used to estimate intercensal adult or old-age survival based on various assumptions (United Nations, 2002, 2004; Moultrie and others, 2013; Li and Gerland, 2013).

From all compiled data in the empirical demographic database of the Population Division[3], when multiple sources of information were available, only the series that met the highest authoritative standards were selected for inclusion in the estimation model. For example, death registration data were used only for combinations of country and year, for which death registration completeness was higher than 60 per cent (Preston, 1984). Additionally, to avoid duplicates, when multiple sources of information existed, only one series of estimates and one series of vital registration were selected for each country and year combination. However, for the same time period, if results from multiple surveys, censuses, or vital registration were available, each of these different data sources (or estimation methods) were included.

Overall, 50.0 per cent for males and 52.2 per cent for females of the data selected for the estimation of adult mortality rates were from vital registration covering 175 countries or areas (table 1). Additional common data sources were surveys (17.3 per cent for males and 17.4 per cent for females of all observations, covering approximately 100 countries) and estimates (18.7 per cent for males and 19.5 per cent for females covering 107 countries). Other data sources providing a smaller percentage of selected data were censuses (13.4 per cent for males and 10.2 per cent for females of all observations covering approximately 150 countries) and sample registration systems (less than 1 per cent of all observations, but a particularly important source of data for 3 countries: Bangladesh, China and India).

[2] Traditionally, the data on number of deaths and mortality rates by age and sex are obtained from the United Nations Statistics Division (Demographic Yearbook), national statistical offices and regional ones (e.g., Eurostat, OECD), United Nations Regional Commissions, other United Nations entities (e.g., UNFPA, UNICEF, WHO), and complemented using international databases such as the Human Mortality Database (Max Planck Institute for Demographic Research (Germany) and others, 2023b), the Human Life Table Database (Max Planck Institute for Demographic Research (Germany) and others, 2023a), the Latin American Mortality Database–LAMBdA (Palloni and others, 2021), the Global Burden of Disease project (Institute for Health Metrics and Evaluation (IHME), 2020), and public use microdata archives (e.g., DHS, MICS, IPUMS-International).

[3] DemoData SQL database available at https://population.un.org/DemoData/web/.

TABLE 1. DATA AVAILABILITY BY TYPE OF DATA SOURCE

	Male adult mortality 15-59			Female adult mortality 15-59		
Source	Number of countries	Number of observations	Proportion of observations (percentage)	Number of countries	Number of observations	Proportion of observations (percentage)
Census	150	2,457	13.4	153	1,796	10.2
Survey	101	3,173	17.3	100	3,067	17.4
Estimate	107	3,435	18.7	107	3,434	19.5
CRVS	175	9,142	50.0	175	9,165	52.2
SRS	7	115	0.6	7	116	0.7
Total	237	18,322	100.0	237	17,578	100.0

Note: Observations were selected from the DemoData SQL database https://population.un.org/DemoData/web/) for analysis of age-specific mortality rates as of March 2024. CRVS: Civil Registration and Vital Statistics. SRS: Sample Registration System.

More than half of the observations from the surveys were obtained through DHS (more than 1,900 observations for males and 1,800 for females, 62.5 and 59.8 per cent of all survey observations, respectively) and MICS (more than 470 observations by sex, 14.9 per cent for males and 15.7 per cent for females) (table 2). Most of the observations from the demographic surveys were calculated using the full sibling histories (representing 51.4 per cent and 59.5 per cent of all observations from surveys for males and females, respectively), which reconstructed the list of siblings a woman had, including information on their living status and dates of birth and death (table 3). This type of data allows for the calculation of adult mortality rates by the sex of the siblings for the periods preceding the survey. In this context, the period between the interview and the event–death, in this case–can be classified into different intervals (4-year periods, or longer time intervals), and allows for over 150 surveys to go back for long periods preceding the survey.

TABLE 2. DATA AVAILABILITY BY TYPE OF SURVEY

	Male adult mortality 15-59			Female adult mortality 15-59		
Source	Number of countries	Number of observations	Proportion of observations (percentage)	Number of countries	Number of observations	Proportion of observations (percentage)
DHS	68	1,984	62.5	67	1,835	59.8
Other	46	529	16.7	48	495	16.1
MICS	64	474	14.9	64	480	15.7
WFS	9	84	2.6	8	68	2.2
PAPFAM/PAPCHILD	10	65	2.0	8	42	1.4
RHS	4	20	0.6	5	129	4.2
Panel				3	18	0.6
Total	204	3,173	100	203	3,067	100.0

Note: DHS: Demographic and Health Surveys. MICS: Multiple Indicator Cluster Surveys. WFS: World Fertility Surveys. RHS: Reproductive Health Surveys. PAPFAM: Pan Arab Project for Family Health. PAPCHILD: Pan Arab Project for Child Development.

TABLE 3. ESTIMATION METHODS USED TO CALCULATE AGE-SPECIFIC MORTALITY RATES FOR CENSUS AND SURVEY

		Male adult mortality 15-59		Female adult mortality 15-59	
Source	Method	Observations	Proportion of observations (percentage)	Observations	Proportion of observations (percentage)
Census	Household deaths	68	2.8	67	3.7
	Intercensal survival	522	21.2	525	29.2
	Orphanhood	486	19.8	791	44.0
	Widowhood	1,381	56.2	413	23.0
Survey	Household deaths	100	3.2	100	3.3
	Intercensal survival	51	1.6	51	1.7
	Orphanhood	574	18.1	1,001	32.6
	Sibling survival	1,632	51.4	1,826	59.5
	Widowhood	816	25.7	89	2.9

The years of the most recent observations of age-specific adult mortality rates from all available data sources and estimation methods vary greatly among countries. Among the 237 countries or areas, all but 55 had available adult mortality data collected in 2015 or later (table 4). The most recent available adult mortality data referred to 2019 or later for at least 124 countries, 2014 to 2018 for at least 66 countries, 2010 to 2013 for at least 20 countries, and at least 24 locations that had adult mortality data only up to the 2009 period. No empirical data on adult mortality were available for two locations (Bonaire, Sint Eustatius and Saba; Western Sahara). In terms of the differences in recent data availability across regions (figure 2), the majority of countries in Europe, Northern America, Australia and New Zealand had the latest data available between 2019 and 2021, whereas more than 55 per cent of countries in sub-Saharan Africa and more than 57 per cent in Oceania (excluding Australia and New Zealand) had the latest data available in 2016 or earlier. In the remaining regions, some countries had recent data between 2019 and 2021, whereas other countries had no recent data available.

The metadata associated with the 2024 revision of WPP, available online, provide further details about the age-specific mortality data used for each country[4] and for the development of BHM methods presented in this technical report. In many cases, the estimates derived from different data sources or methods vary significantly.

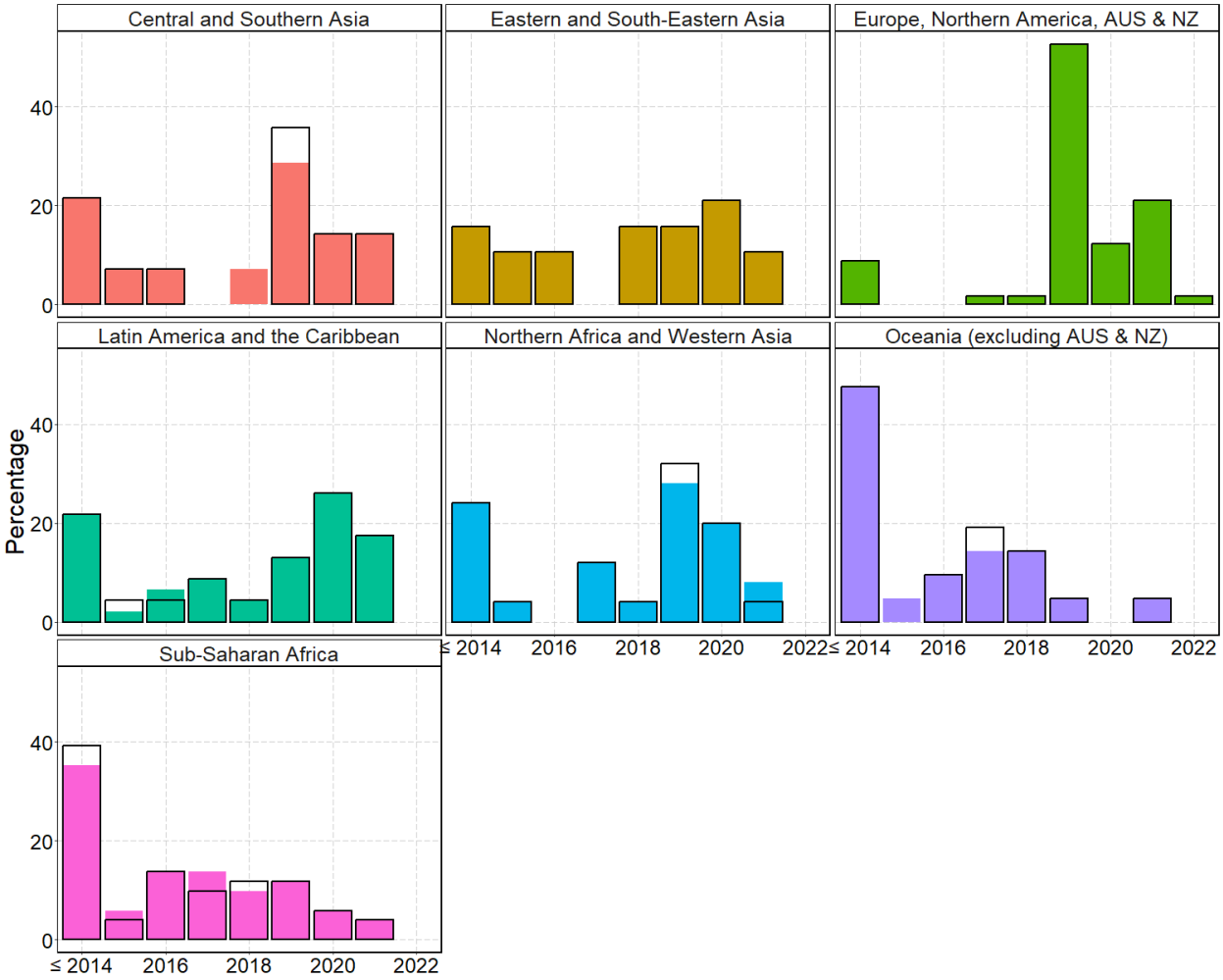
TABLE 4. NUMBER OF COUNTRIES BY THE LATEST YEAR WITH DATA AVAILABLE BY SEX

	Male adult mortality 15-59	Female adult mortality 15-59
Year	Countries	Countries
2009 and earlier	24	26
2010	7	9
2011	5	3
2012	3	2
2013	6	6
2014	10	11
2015	9	8

[4] Please see https://population.un.org/wpp/Download/Metadata/Documentation/ and https://population.un.org/wpp/DataSources/.

	Male adult mortality 15-59	Female adult mortality 15-59
Year	Countries	Countries
2016	15	14
2017	18	17
2018	16	16
2019	57	59
2020	35	35
2021	30	29
2022	2	2

Figure 2. Proportion of countries by latest year of available data by SDG regions (percentage)



Note: Solid coloured bars refer to the percentage distribution for males and black outline bars refer to the percentage distribution for females.

B. Data preparation

This section describes the preparation 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, and the non-sampling data biases adjustments.

1. Stochastic error of 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)[5]. 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.

First, the stated death-reporting completeness[6] (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 $z_{c,t}^{g}$ is obtained by:

$$z_{c,t}^{g} \sim U\left(z_{c,t} - \delta(z)_{c,t}, z_{c,t} + \delta(z)_{c,t}\right) \tag{2}$$

where $\delta(z)_{c,t}$ is the standard error of the reported DRC for country c in year t. 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:

$$\begin{aligned} \delta(z)_{c,t} &= 0.25 - \frac{0.25 - 0.05}{0.95 - 0.6}\left(z_{c,t} - 0.6\right) && if\ 60\% \le z_{c,t} < 95\% \\ \delta(z)_{c,t} &= 0.05 - \frac{0.05}{1 - 0.95}\left(z_{c,t} - 0.95\right) && if\ z_{c,t} \ge 95\% \end{aligned} \tag{3}$$

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.

---

[5] 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: ${}_nm_x = (-2 * {}_nq_x) / (({}_nq_x * n) - (2 * n))$ based on Preston and others (2001, page 43).

[6] 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 and others, 2020; Hill, 2017).

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

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

The g-th simulated total number of deaths $D_{c,t}^{(g)}$ 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:

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

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

$$\text{ASMR}_{c,t}^{(g)} = D_{c,t}^{(g)} / N_{c,t}^{\text{sex}} \tag{6}$$

The obtained age-specific mortality rate was finally converted back into the overall probability of dying based on Preston and others (2001, page 43):

$${}_nq_{x_{c,t}}^{(g)} = \left((2 * n) * \text{ASMR}_{c,t}^{(g)}\right) / \left(2 + \left(n * \text{ASMR}_{c,t}^{(g)}\right)\right) \tag{7}$$

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. 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.

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).

4. Non-sampling data biases adjustments

A bias adjustment was applied to the observations of adult mortality, assuming that previous WPP estimates of adult mortality were unbiased (Liu and Raftery, 2020; Liu and others, 2023). Biases are computed exclusively for census and survey observations and not for data from CRVS/SRS. Mortality estimates from the previous WPP revision (United Nations, 2022) were treated as unbiased and used as a baseline reference.

The bias for each record was calculated as the difference between the observed mortality rate and corresponding crisis-free smoothed WPP estimate. For each country, the biases were modelled using a linear regression function with the following independent variables:

- data source (categorical variable): including census, Demographic and Health Survey (DHS) type, estimates, panel, CRVS /SRS, and other surveys and reports.
- data collection method (categorical variable): including household deaths, intercensal survival, adjusted intercensal survival, life table, adjusted life table, orphanhood, widowhood, sibling survival, model-based estimates, and official figures.
- under-five mortality rate (U5MR; continuous variable): from WPP 2022 revision (United Nations, 2022), crisis-free.
- recall lag (continuous variable in years).

The fitted biases were extracted from country-specific regression functions, and each mortality observation was adjusted by subtracting the fitted biases, as follows:

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

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

III. Bayesian hierarchical model for estimating age-sex-specific adult mortality

Bayesian hierarchical models (BHM) in the context of demographic analysis allow the use of data from different sources, while accounting for uncertainty and potential biases (Bijak and Bryant, 2016). This section provides the technical details of the BHM used to estimate the age-sex-specific adult mortality by sex and broad age groups; first, explaining the process models (section III A), which are theoretical models used to describe the levels and trends in the true underlying adult mortality, and second, the data models (section III B), which are models that describe patterns and uncertainties in the adult mortality observations, given the process models. The process and data models were applied to each sex and broad age group (e.g., 15-59. 15-49, 60-74) because different parameters are used.

A. Process model

This section provides a brief overview of the Bayesian hierarchical model (BHM) developed for WPP adult mortality estimates and applied to each age-sex-specific adult mortality summary indicator (35q15, 45q15, and 15q60). For simplicity, all terms discussed here are age- and sex-specific.

The adjusted mortality rate (see section II for pre-model adjustment) for a given country in a given year is modelled on the logit scale to ensure that the mortality rate, as a probability, remains within the 0 to 1 range. The logit of the adjusted mortality rate is represented as the sum of (1) the true underlying rate on the logit scale and (2) measurement error.

A two-step modelling process estimates mortality rates by separating country-years with high and low human immunodeficiency virus (HIV) prevalence:

- Step 1: model for non-HIV countries using adjusted data in all countries but including data from HIV countries before 1976. This cutoff corresponds to the earliest year in which the sex-specific HIV prevalence in any country exceeded 1per cent for generalized epidemics.
- Step 2: model for HIV countries, based solely on data from these countries.

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 was modelled as the sum of (i) a regional effect[7] derived from the crisis-free under-five mortality rate (U5MR), $W_{r,d[c,t]}$, (ii) a country-specific temporal effect, $P_{c,t}$, and (iii) a country-specific offset, η_c. Formally,

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

Here, $W_{r,d[c,t]}$ models the regional non-linear relationship between adult mortality and crisis-free U5MR for the country c year t. The index r refers to the SDG region to which the country c belongs. The log of U5MR per 1000 ($V_{c,t}$) for country c year t, obtained from the WPP 2022 revision (United Nations, 2022), was used to define a grid of values κ_d for $d \in (1, \cdots, x)$, and x is the number of locations where

[7] The regional classification used are SDG regions. For further details about the classification used please see https://population.un.org/wpp/DefinitionOfRegions/.

$W_{r,d}$ is evaluated. The range of κ_d extends from $\kappa_1 = \log(1/1000)$ to κ_x as the maximum of $V_{c,t}$ across all country-years with data, evaluated at increments of $\log(3/1000)$, resulting in 160 locations ($x = 160$).

Each $V_{c,t}$ is matched to the κ_d with the smallest absolute difference from $V_{c,t}$, assigning the dth index for country-year c, t as $d[c, t]$. The relationship between $W_{r,d}$ and κ_d is modelled using a second-order random walk (RW2) process:

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

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

where τ_r^w denotes the regional precision parameter. This process is assumed to hold for $r \in (1, \dots, 7)$ and $d \in (1, \cdots, x-2)$ with $W_{r,d}$ constant outside the range of κ_1 and κ_x across all c and t.

The within-country temporal effect $P_{c,t}$ accounts for fluctuations over time and is modelled as a first-order random walk (RW1):

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

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

where τ_c^p is the country-specific precision parameter, applied for $t \in (1950, \dots, 2023)$ and $c \in (1, \dots, 236)$.

Penalized Complex (PC) priors are assigned to the regional precision parameter τ_r^w for $r \in (1, \dots, 7)$, and country-specific precision parameter τ_c^p for $c \in (1, \dots, 236)$ to regularize the estimates:

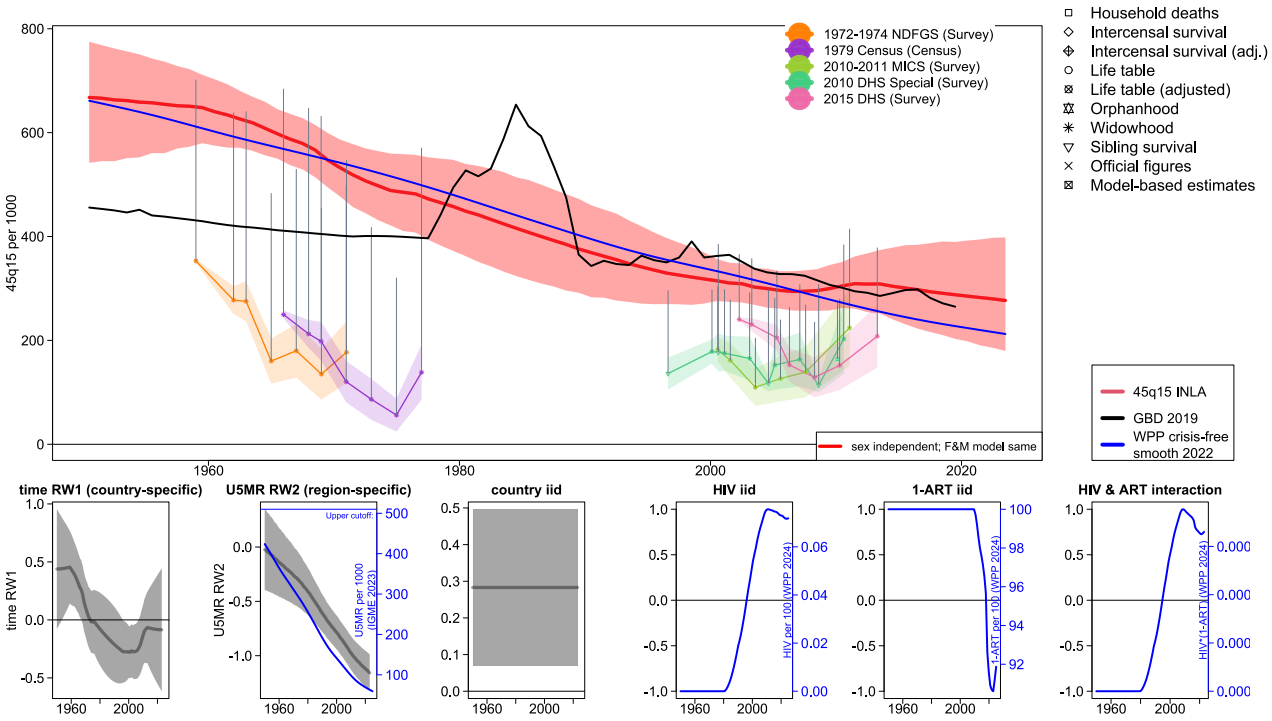
$$\tau_r^w \sim \text{PC}(z, 0.01), \quad \text{for } r \in (1, \dots, 7), \tag{16}$$

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

where z represents the standard deviation of all observations. The PC prior is a vague prior. Detailed documentation of the PC prior specification can be found in Simpson and others (2017).

Figure 3 presents an overview of the BHM used for 45q15 for Afghanistan. Since Afghanistan is considered a non-HIV country, all mortality observations were included in the model fitting. In part (i), the main assumption is that the levels and trends in crisis-free U5MR have similar effects on adult mortality across countries within the same region. Since crisis-free U5MR patterns are usually non-linear, their effect on the patterns of adult mortality is assumed to be non-linear across regions. Part (ii) models the correlation over time for each country, while part (iii) offsets the discrepancy between the logit-scaled true level of mortality and all other effects at the country level.

Figure 3. Age-sex-specific adult mortality model illustration for male age group 15–59 from Afghanistan

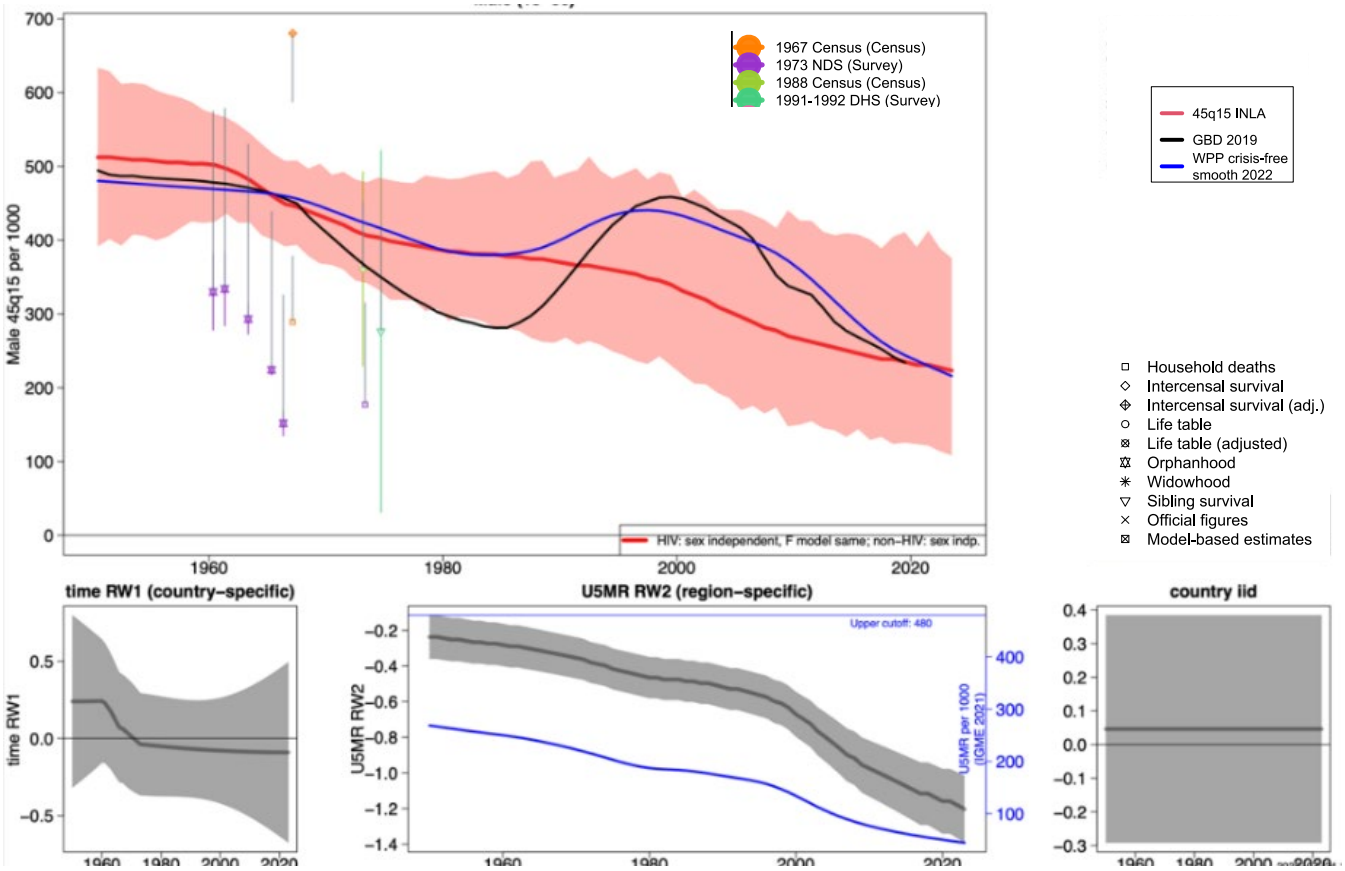


Source: United Nations (2024b), IHME (2020) and calculations by authors.

Note: The curves show the posterior medians. The shades show the 95 per cent 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 show the bias adjustment done before the BMH model fitting. Grey bars are absent for observations if the bias adjustment is zero. The scale of the y-axis in the second-row plots is an inverse-logit numerical value for each effect.

Figure 4 presents an overview of the BHM used for 45q15 for the United Republic of Tanzania. Since the United Republic of Tanzania is considered an HIV country, all observations before 1976 are included in the model fitting in step 1 of the modelling process.

Figure 4. Age-sex-specific adult mortality model illustration for male age group 15–59 from the United Republic of Tanzania



Source: United Nations (2024b), IHME (2020) and calculations by authors.

Note: The curves show the posterior medians. The shades show the 95 per cent 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 show the bias adjustment done before the BMH model fitting. Grey bars are absent for observations if the bias adjustment is zero. The scale of the y-axis in the second-row plots is an inverse-logit numerical value for each effect.

Step 2: model for HIV countries

The second modelling step focused on adult mortality in countries with a high HIV prevalence. The non-HIV effects estimated in step 1 were incorporated as inputs with additional effects for HIV prevalence, antiretroviral therapy (ART) coverage, and their interaction included. Specifically,

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

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

The within-country temporal effect $P_{c,t}$ captures fluctuations over time and is modelled as a first-order random walk (RW1):

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

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

The country-specific regression coefficients for the double exponential HIV prevalence exp $(exp(\text{HIV}_{c,t}))$ and double exponential ART coverage exp $(exp(\text{1-ART}_{c,t}))$ follow hierarchical normal distributions:

$$\alpha_c \sim \mathcal{N}(0, 1/\tau_\alpha), \quad \text{for } c \in (1, \cdots, 236) \tag{21}$$

$$\beta_c \sim \mathcal{N}(0, 1/\tau_\beta), \quad \text{for } c \in (1, \cdots, 236) \tag{22}$$

The interaction effect $U_{c,g[t]}$ models the country-specific non-linear interaction between HIV prevalence and the ART coverage for country c year t. Specifically, let $M_{c,t}$ denote the $\text{HIV}_{c,t} \times (\text{1-ART}_{c,t})$ per 1000 for country c in 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. Evaluation locations for $U_{c,g[t]}$ are 3 apart from each other, hence the total number of locations $G = 103$. Each $M_{c,t}$ is matched to the closest λ_g with the smallest absolute difference from $M_{c,t}$, denoting the gth index for year t as $g[t]$. The relationship between $U_{c,g}$ and λ_g was modelled using a second-order random walk (RW2) process. $U_{c,g}$ is assumed to be constant outside the range of λ_1 and λ_G across all c and t. In particular:

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

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

Penalized Complex (PC) priors are assigned to the precision parameters for country-specific temporal and interaction effects, respectively τ_c^U for $c \in (1, \cdots, 236)$, and τ_c^p for $c \in (1, \cdots, 236)$ as follows:

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

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

where z is the standard deviation of all observations.

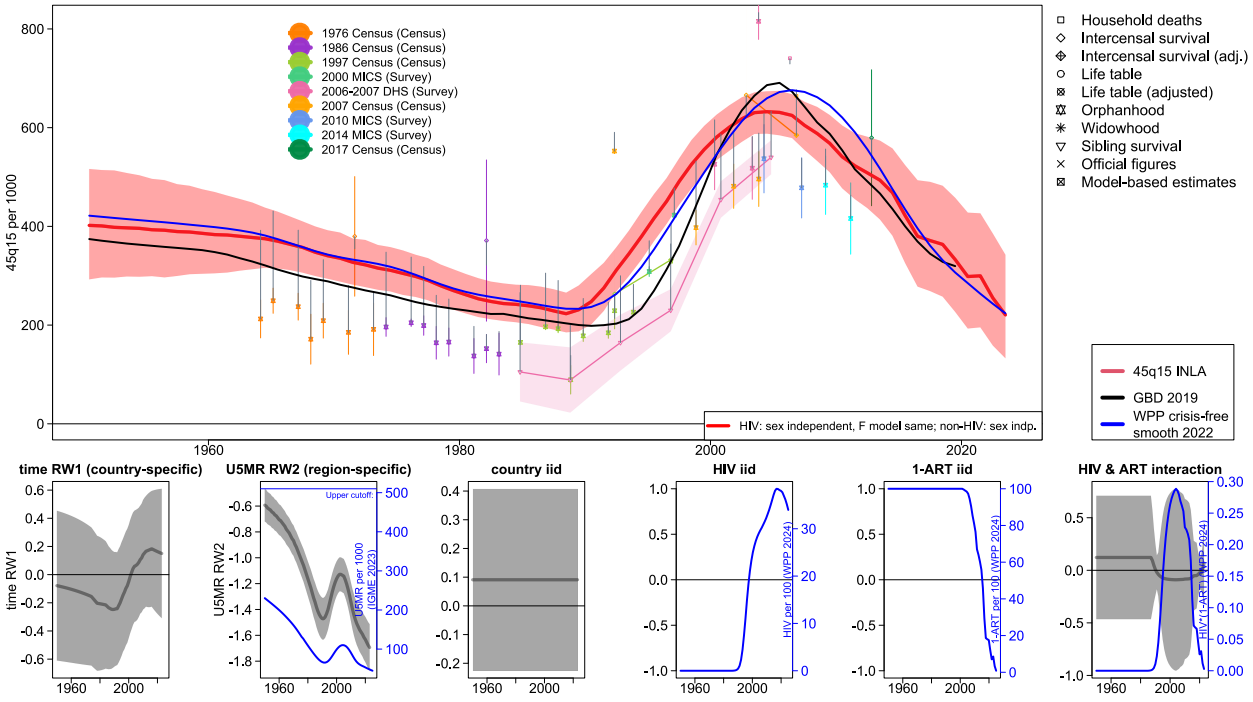
Non-informative priors are used for the global precision parameters $\tau_\alpha = 1/\sigma_\alpha^2$ and $\tau_\beta = 1/\sigma_\beta^2$ as follows:

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

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

Figure 5 illustrates the Bayesian hierarchical model (BHM) applied to adult mortality in Eswatini, a country with high HIV prevalence since the 1990s. The model incorporates estimates of HIV prevalence, the proportion of the population receiving antiretroviral therapy (ART), and their interaction effects, modelled at the country level. Hierarchical structures were used to share these effects across countries to improve their estimations.

Figure 5. Age-sex-specific adult mortality model illustration for female age group 15–59 from Eswatini



Source: United Nations (2024b), IHME (2020) and calculations by authors.

Note: The curves show the posterior medians. The shades show the 95 per cent 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 show the bias adjustment done before the BMH model fitting. Grey bars are absent for observations if the bias adjustment is zero. The scale of the y-axis in the second-row plots is an inverse-logit numerical value for each effect.

B. Data model

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

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

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

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

The sampling/stochastic errors σ_i^2 were pre-calculated for each observation as described in the previous section. They reflect the uncertainty resulting from survey sampling designs or stochastic variability in the vital registration data.

The non-sampling errors ω_s^2 for $s \in (1, \ldots, 5)$ are usually unknown but inevitable during data collection and processing. They represent uncertainty from non-responses, recall bias, and data input errors, among others. For this reason, non-sampling errors are modelled as data-source-specific parameters by assigning vague priors:

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

C. Statistical computing

The model uses the Integrated Nested Laplace Approximation (INLA) for Bayesian inference (Rue and others, 2009), implemented through the R package R-INLA (Martins and others, 2013; R Core Team, 2024).

D. One-country model

While the global BHMs described earlier use observations from all countries, a "one-country model" can be employed for specific countries to get provisional results. This approach utilizes the global and regional average effects as inputs, allowing updated estimates for a single country when new data become available without requiring a full global model re-run.

This enables analysts to update their estimates as needed, which will then be consolidated when the next global run is performed. When such minor data updates occur, the global and regional effects are assumed to be unaffected. Hence, the one-country model uses regional and global effects from the global model as model inputs, and only estimates country-level effects, assuming no change in regional and global effects.

This is especially useful for obtaining results using updated data and can provide immediate feedback on the impact of data inclusion, adjustment, or exclusion on estimates. The advantage of the one-country model is that it runs faster than the global model and can immediately produce updated results.[8] Once the data updates were finalized for all countries, the global model was rerun to produce the final results for the specific revision of the WPP estimates. This ensures that both global and country-specific estimates are comprehensively updated.

[8] For a typical desktop computer, a global run for one sex and an age group takes 70 minutes for 10,000 posterior samples and a one-country run takes about 20 seconds.

IV. Results for selected countries

This section presents the BHM estimates of age-sex-specific adult mortality rates for the selected countries. The aim was to illustrate the results for the four different cases.

1. Countries with high quality and high coverage of data, such as vital registration data from administrative records. Countries in this category are usually high-income or upper-middle-income countries, with complete registration systems for recording vital events.
2. Countries without high-quality vital registration data from administrative records, but with some data from surveys, censuses and estimates, and with proper data coverage over time. Countries in this category usually do not have complete vital registration systems, but sampling surveys and censuses are conducted regularly. These are typically middle- or low-income countries.
3. Countries with very limited data or no information on adult mortality.
4. Countries with high HIV prevalence.

Figure 6 presents the adult mortality rate BHM estimates from Sweden, the United Kingdom and the United States of America, focusing on periods without significant mortality crises. These three countries have had high-quality vital registration data for all broad age groups every year since 1950.

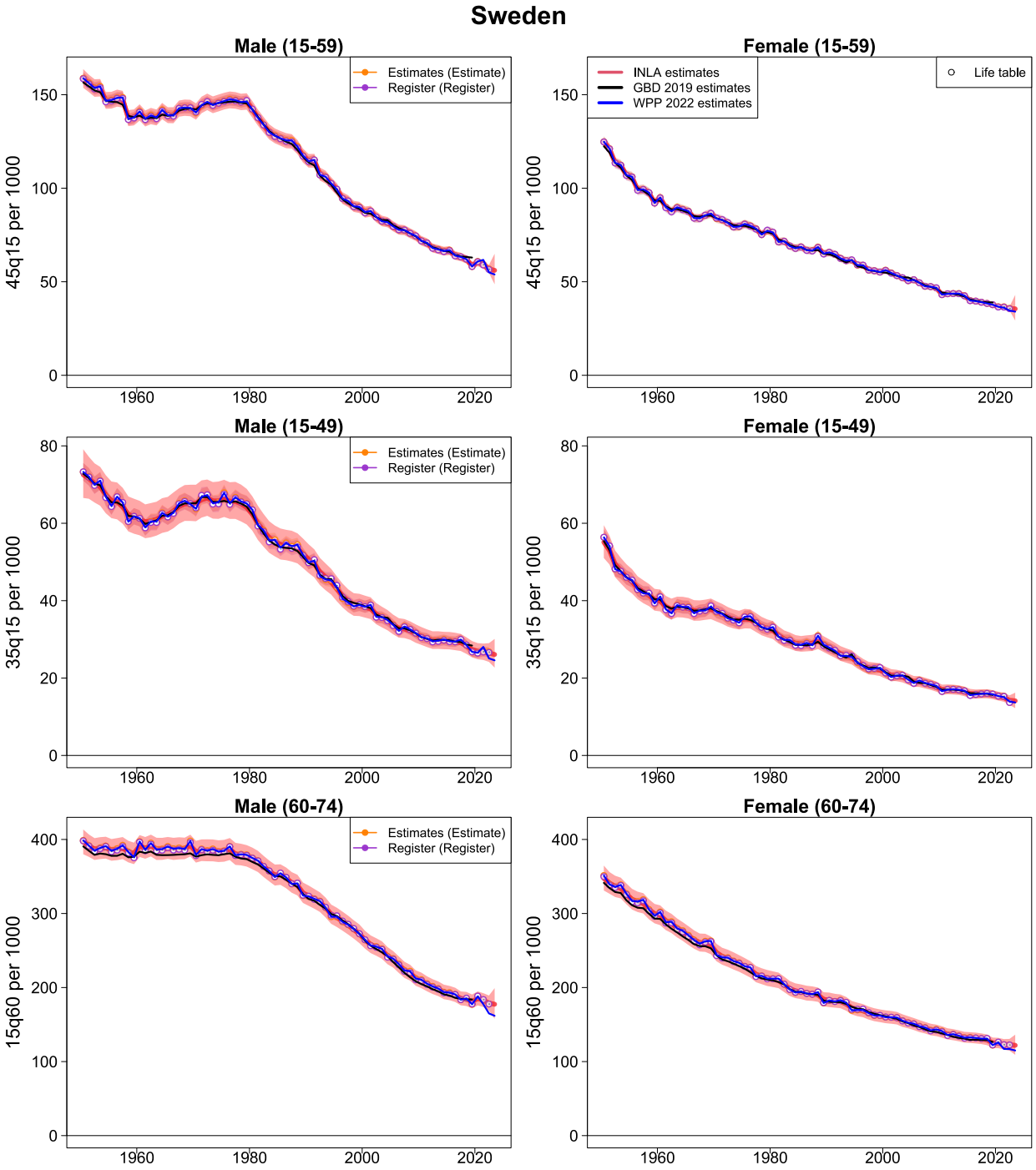
The BHM median estimates closely follow the observed levels and trends within each country over time, with narrow uncertainty bounds reflecting the high quality of the data and the model's consideration of stochastic errors only. However, the uncertainty bounds for recent years are wider owing to the absence of recent data for some age groups or their exclusion because of the excess mortality associated with the COVID-19 pandemic, which introduces larger stochastic errors into the vital registration data.

Figure 7 shows the adult mortality rate BHM estimates for Egypt, Malaysia and Mexico. These countries have mortality statistics based on deficient vital registration data but with additional direct and indirect mortality estimates from surveys and censuses, providing some overall good time coverage since 1950. The data coverage was generally good in recent decades, but variable in earlier ones. Additional direct and indirect estimates for age groups 15-49 and 60-74 years were also more limited.

The BHM model estimates follow the data trends for the country-periods in which the data are available. If there are multiple observations for a certain country-year, the BHM model can use all of them. In such cases, the model estimates are closer to higher-quality observations (corresponding to smaller sampling errors) and less towards data points with lower quality (equivalent to larger sampling errors). For country-periods with limited or no data, the BHM estimates are mainly driven by the following model assumptions: the regional effect of U5MR, country-level temporal effect, and offset.

Figure 6. Age-sex-specific adult mortality model estimates for several broad age groups from selected countries with high-quality and high completeness of vital registration data

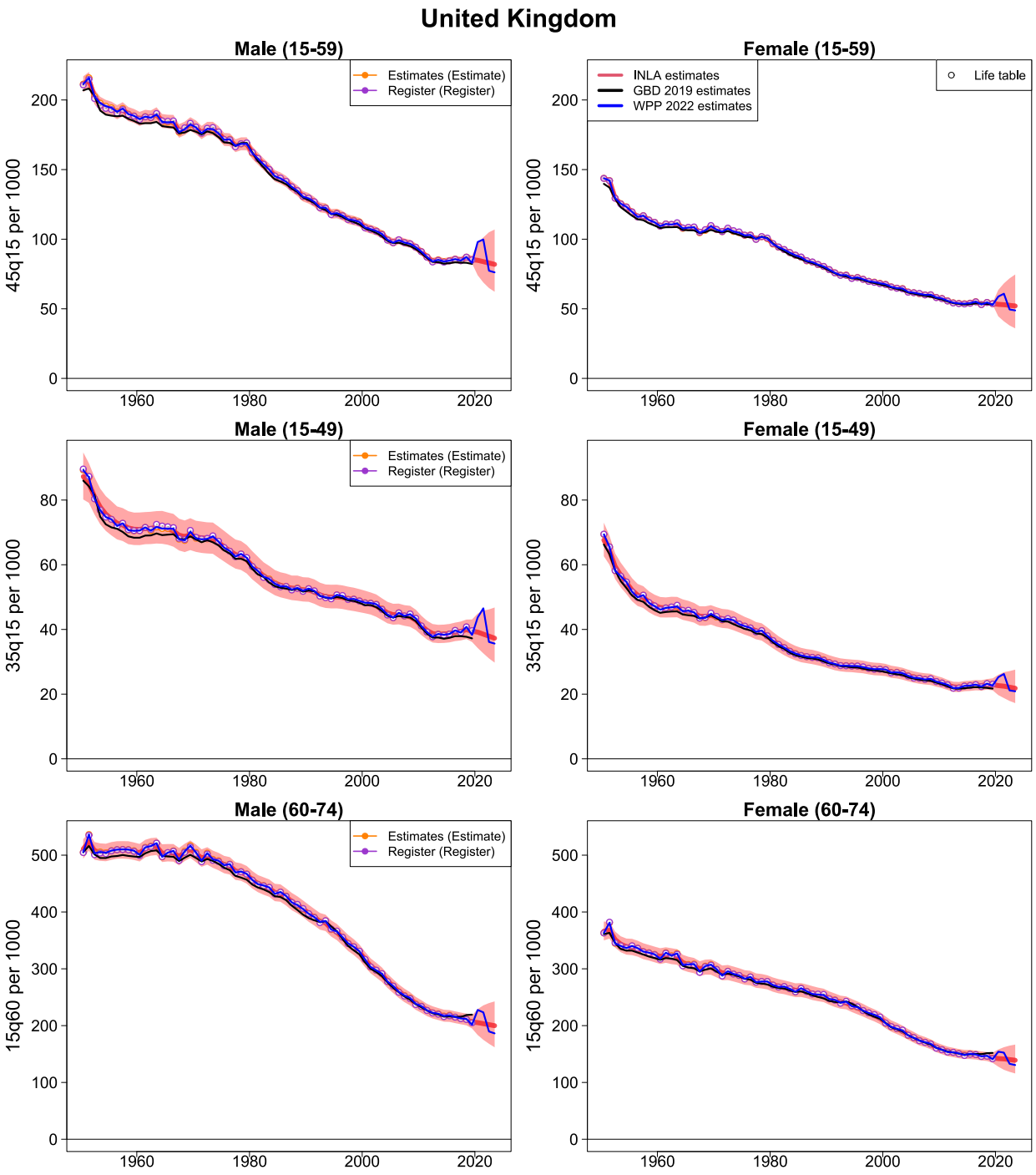
Examples of Sweden, United Kingdom and United State of America



Source: United Nations (2024b), IHME (2020) and calculations by authors.

Note: The red curves show the posterior medians. The shades show 95 per cent uncertainty bounds. Dots are the observations used for modelling. The shading and vertical lines around the dots represent 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.

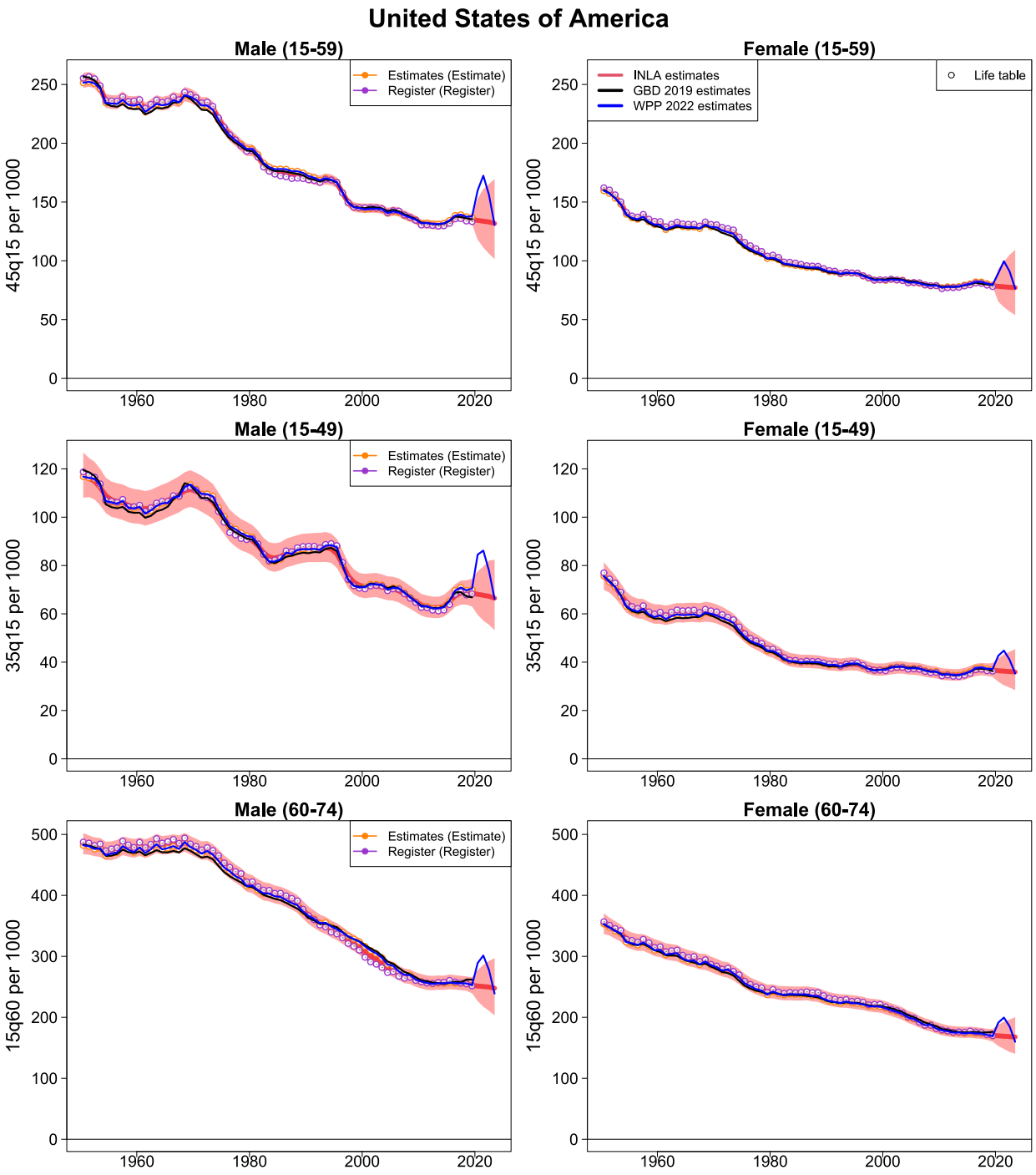
Figure 6. Continued



Source: United Nations (2024b), IHME (2020) and calculations by authors.

Note: The red curves show the posterior medians. The shades show 95 per cent uncertainty bounds. Dots are the observations used for modelling. The shading and vertical lines around the dots represent 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.

Figure 6. Continued

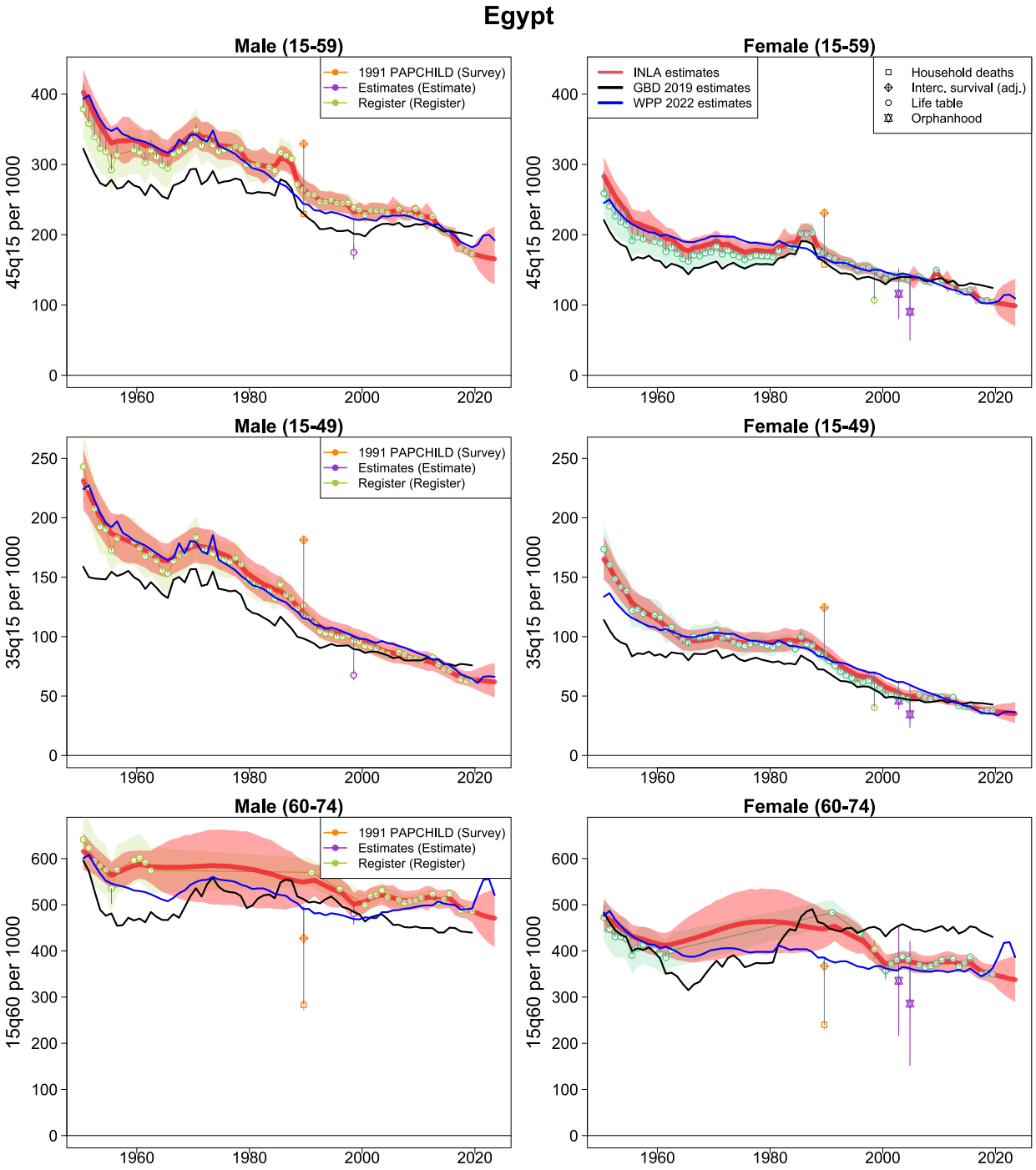


Source: United Nations (2024b), IHME (2020) and calculations by authors.

Note: The red curves show the posterior medians. The shades show 95 per cent uncertainty bounds. Dots are the observations used for modelling. The shading and vertical lines around the dots represent 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.

Figure 7. Age-sex-specific adult mortality model estimates for several broad age groups from selected countries with deficient vital registration data, but with estimates from surveys and censuses, and good time coverage since 1950

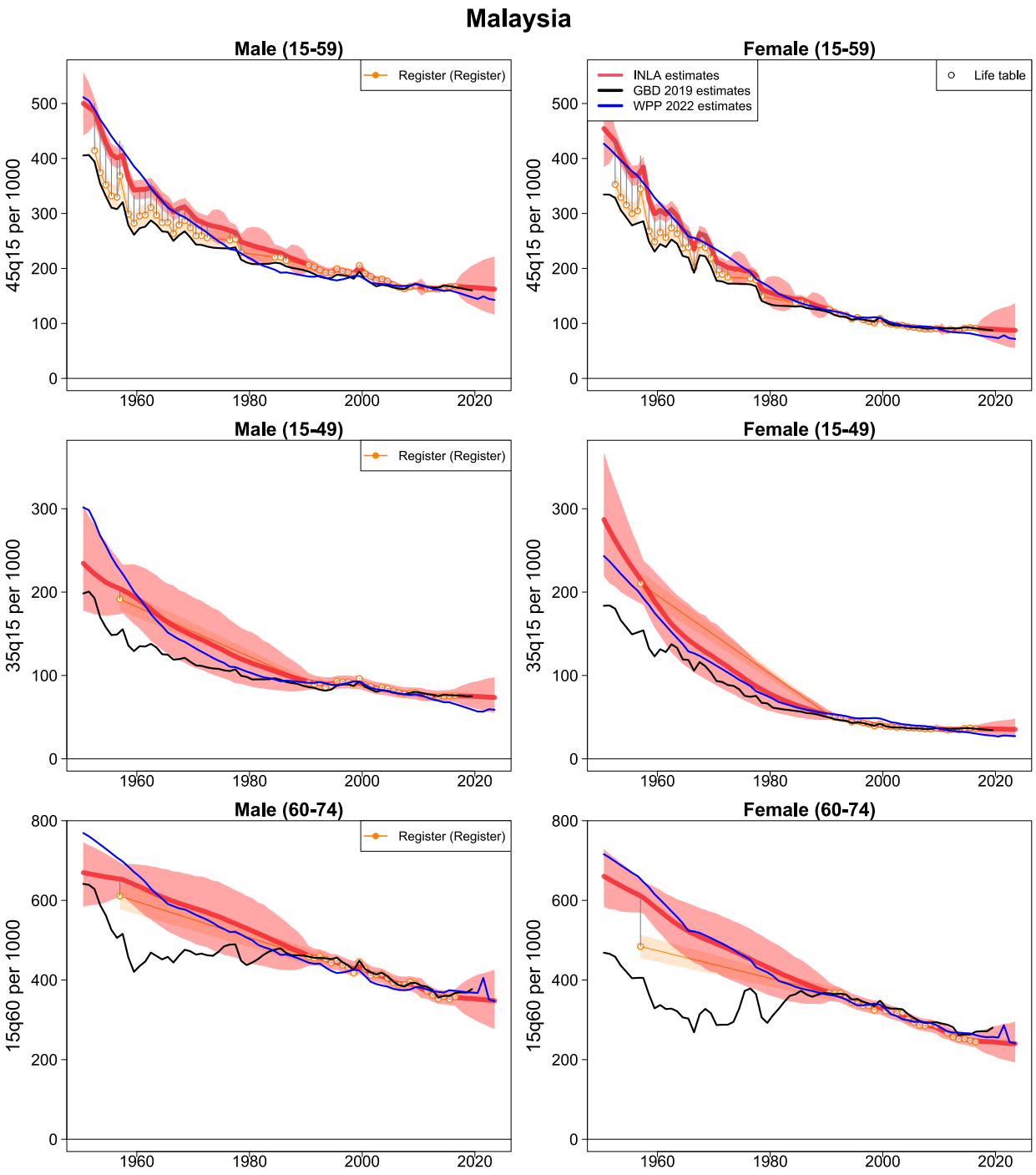
Examples of Egypt, Malaysia and Mexico



Source: United Nations (2024b), IHME (2020) and calculations by authors.

Note: The red curves show the posterior medians. The shades show 95 per cent uncertainty bounds. Dots are the observations used for modelling. The shading and vertical lines around the dots represent 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.

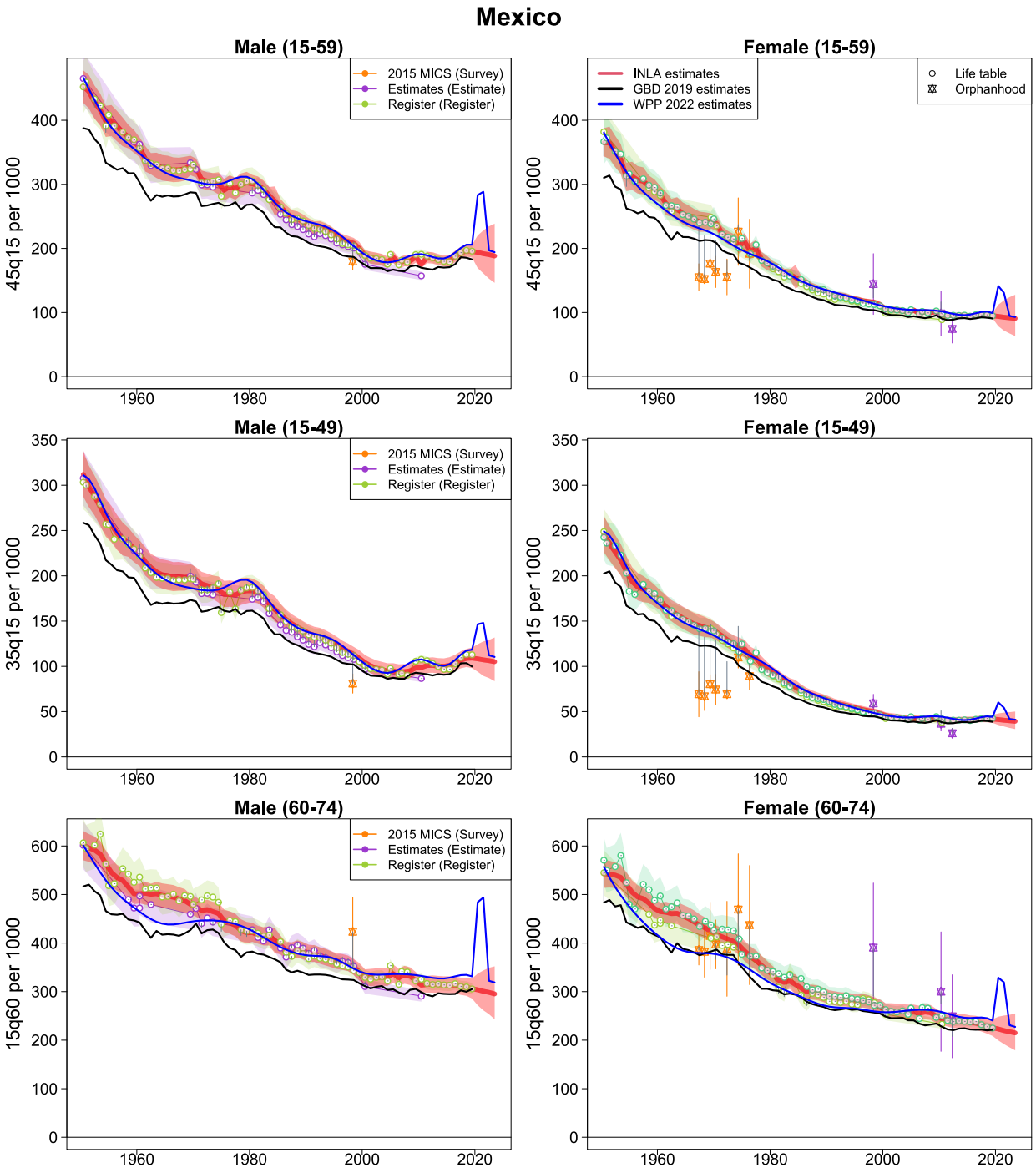
Figure 7. Continued



Source: United Nations (2024b), IHME (2020) and calculations by authors.

Note: The red curves show the posterior medians. The shades show 95 per cent uncertainty bounds. Dots are the observations used for modelling. The shading and vertical lines around the dots represent 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.

Figure 7. Continued



Source: United Nations (2024b), IHME (2020) and calculations by authors.

Note: The red curves show the posterior medians. The shades show 95 per cent uncertainty bounds. Dots are the observations used for modelling. The shading and vertical lines around the dots represent 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.

Figure 8 presents the adult mortality rate BHM estimates from Bangladesh, Solomon Islands and Sudan. The three selected countries did not have vital registration observations. However, they do have some observations from other data sources such as international surveys, DHSs, MICSs, Bangladesh-specific surveys for sample vital registration, and censuses. In general, data coverage has been good in recent decades, and the data coverage was low or zero before the 1970s.

The BHM model estimates follow the data trends for country periods in which data are available. If there are multiple observations for a certain country-year, the BHM model makes use of all observations, and estimates are pooled more towards the levels of observations with higher quality (corresponding to smaller sampling errors) and less towards the data points with lower quality (equivalent to larger sampling errors).

For country-periods with limited or no data, for example, before the 1970s in all the selected countries, the BHM estimates are mainly driven by the following model assumptions: the country-level effect of HIV prevalence, country-level effect of proportion of population receiving ART, regional effect of U5MR, country-level temporal effect, and offset. Since prior the 1970s, there has been no HIV prevalence, and consequently, no one receiving ART; the levels and trend of adult mortality prior to 1970 are from the regional U5MR effect.

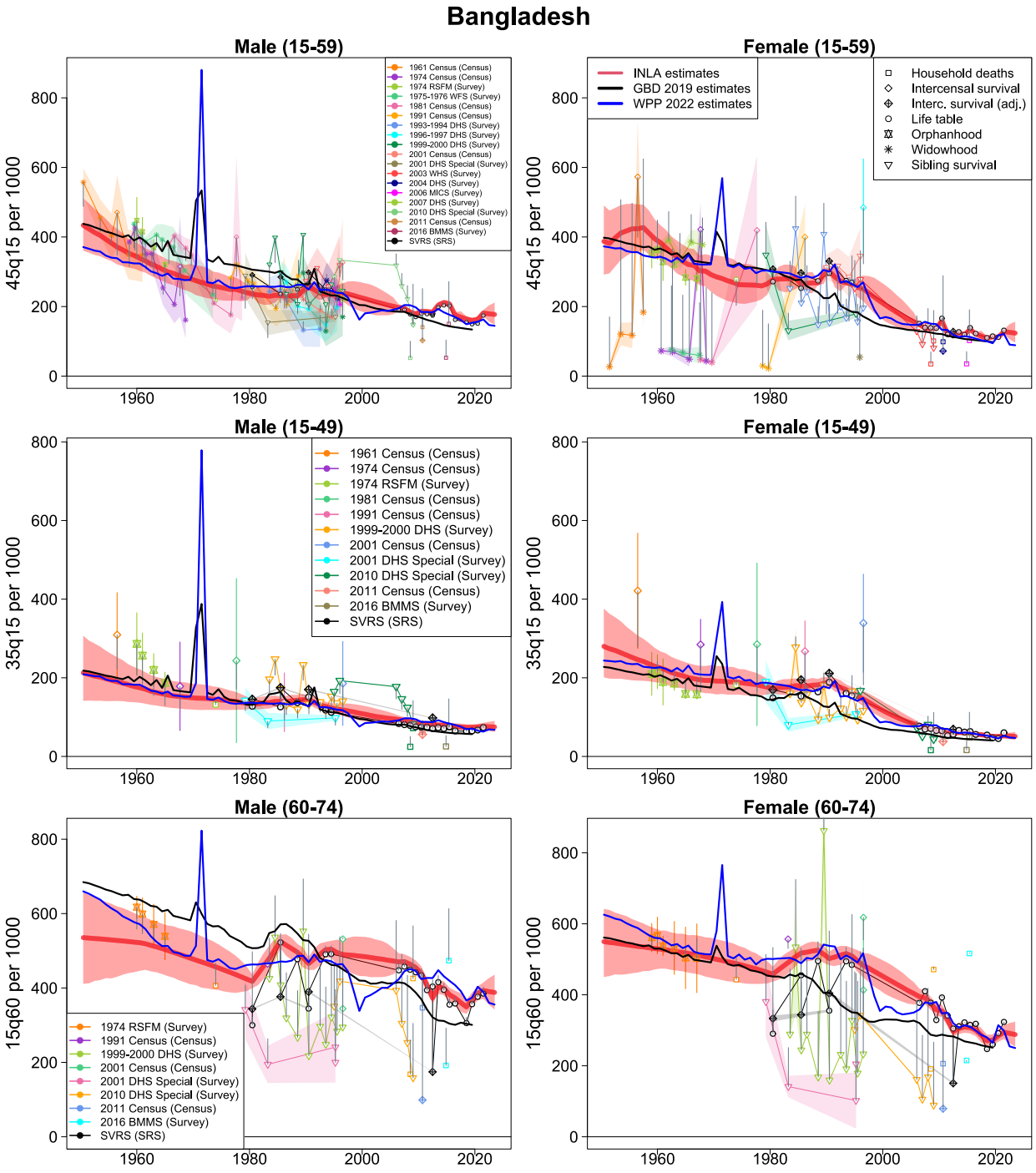
Figure 9 shows the adult mortality rate BHM estimates for Senegal, Saudi Arabia and Somalia. The selected countries had a very limited number of available observations and did not have any data points before the 1980s. The BHM estimates are driven entirely by the model assumptions for the entire estimation period 1950-2023. Hence, as a result of the hierarchical model structure, the effect of U5MR is the average effect from all countries in the same region and the temporal effect, which is the average of all countries.

Figure 10 depicts the adult mortality rate BHM estimates from Burundi, Eswatini and Malawi, three countries significantly affected by a high HIV prevalence. These countries have had reasonably good data coverage in recent decades, primarily derived from surveys and census data.

The increase in HIV adult prevalence since the 1990s is reflected in the mortality data collected during this period. Through the inclusion of HIV adult prevalence and ART coverage effects in the second step of the estimation, the BHM effectively captured the upward trend in mortality rates during the 1990s. As HIV prevalence decreased and ART coverage increased, BHM also estimated a corresponding downward trend in mortality rates, demonstrating the impact of these interaction effects on the estimates.

Figure 8. Age-sex-specific adult mortality model estimates for several broad age groups from selected countries with reasonable data coverage from surveys and censuses

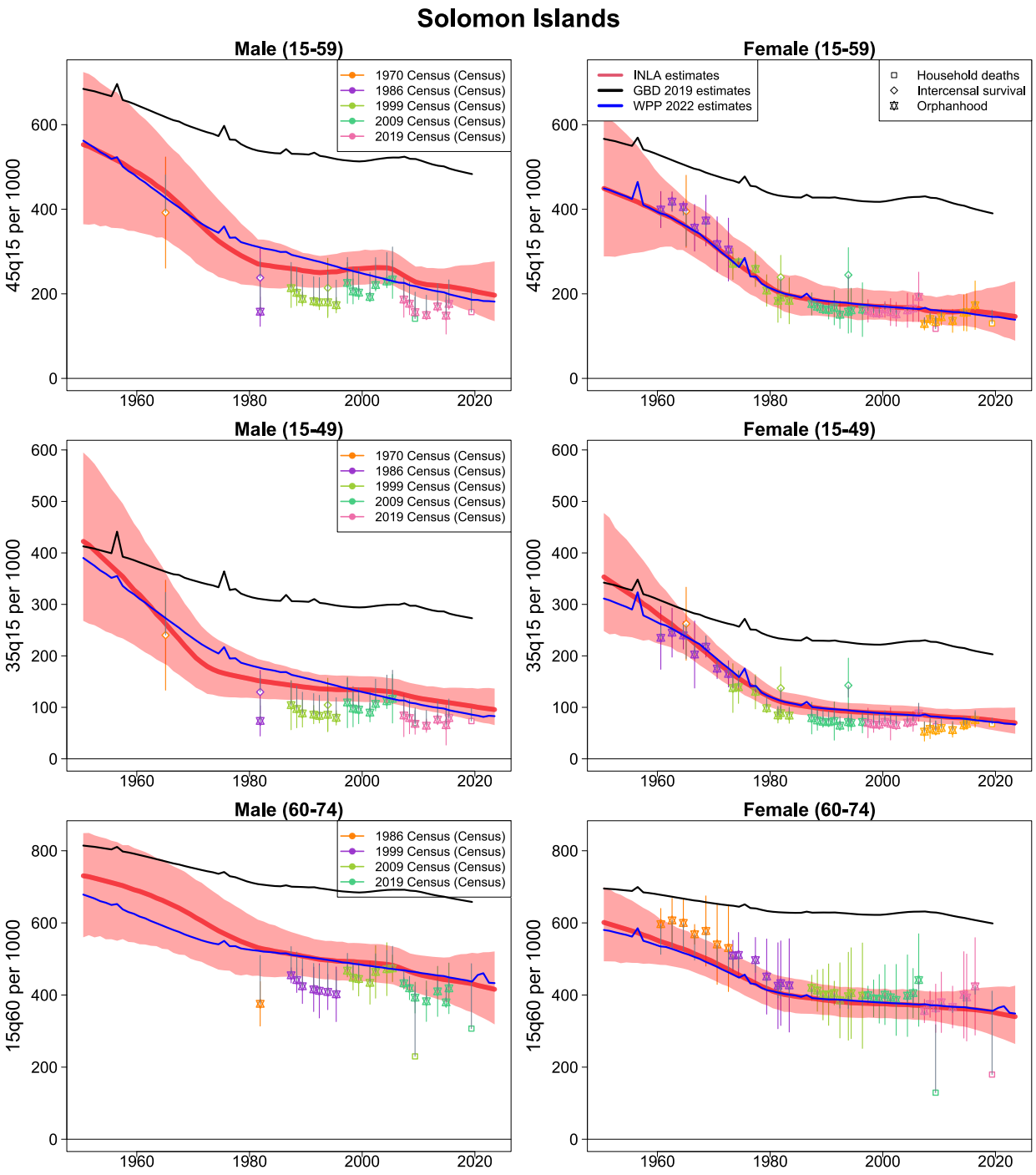
Examples of Bangladesh, Solomon Islands and Sudan



Source: United Nations (2024b), IHME (2020) and calculations by authors.

Note: The red curves show the posterior medians. The shades show 95 per cent uncertainty bounds. Dots are the observations used for modelling. The shading and vertical lines around the dots represent sampling errors (if available). The vertical grey bars at dots show the bias adjustment done before BMH model fitting. Grey bars are absent for observations if bias adjustment is zero.

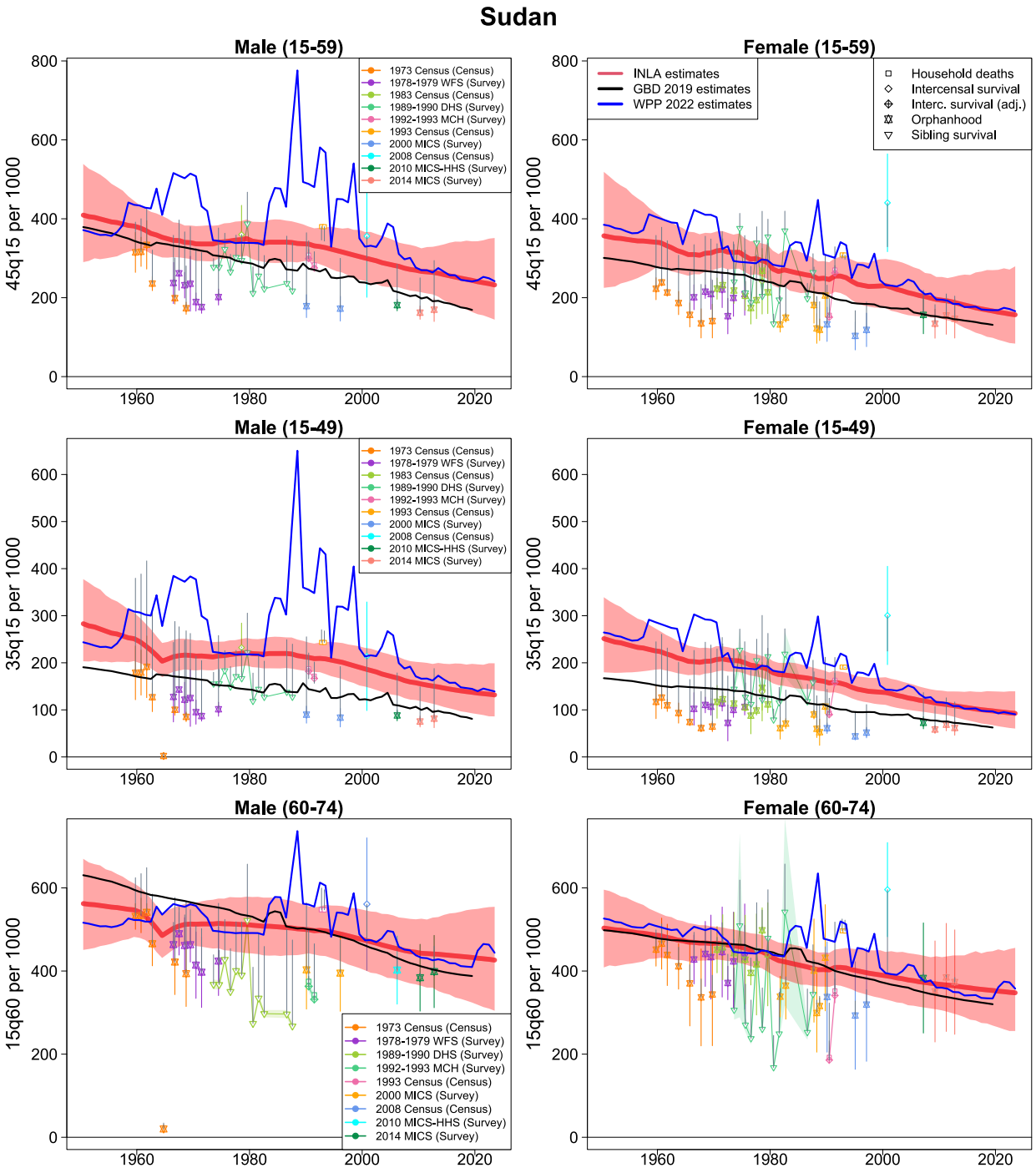
Figure 8. Continued



Source: United Nations (2024b), IHME (2020) and calculations by authors.

Note: The red curves show the posterior medians. The shades show 95 per cent uncertainty bounds. Dots are the observations used for modelling. The shading and vertical lines around the dots represent sampling errors (if available). The vertical grey bars at dots show the bias adjustment done before BMH model fitting. Grey bars are absent for observations if bias adjustment is zero.

Figure 8. Continued

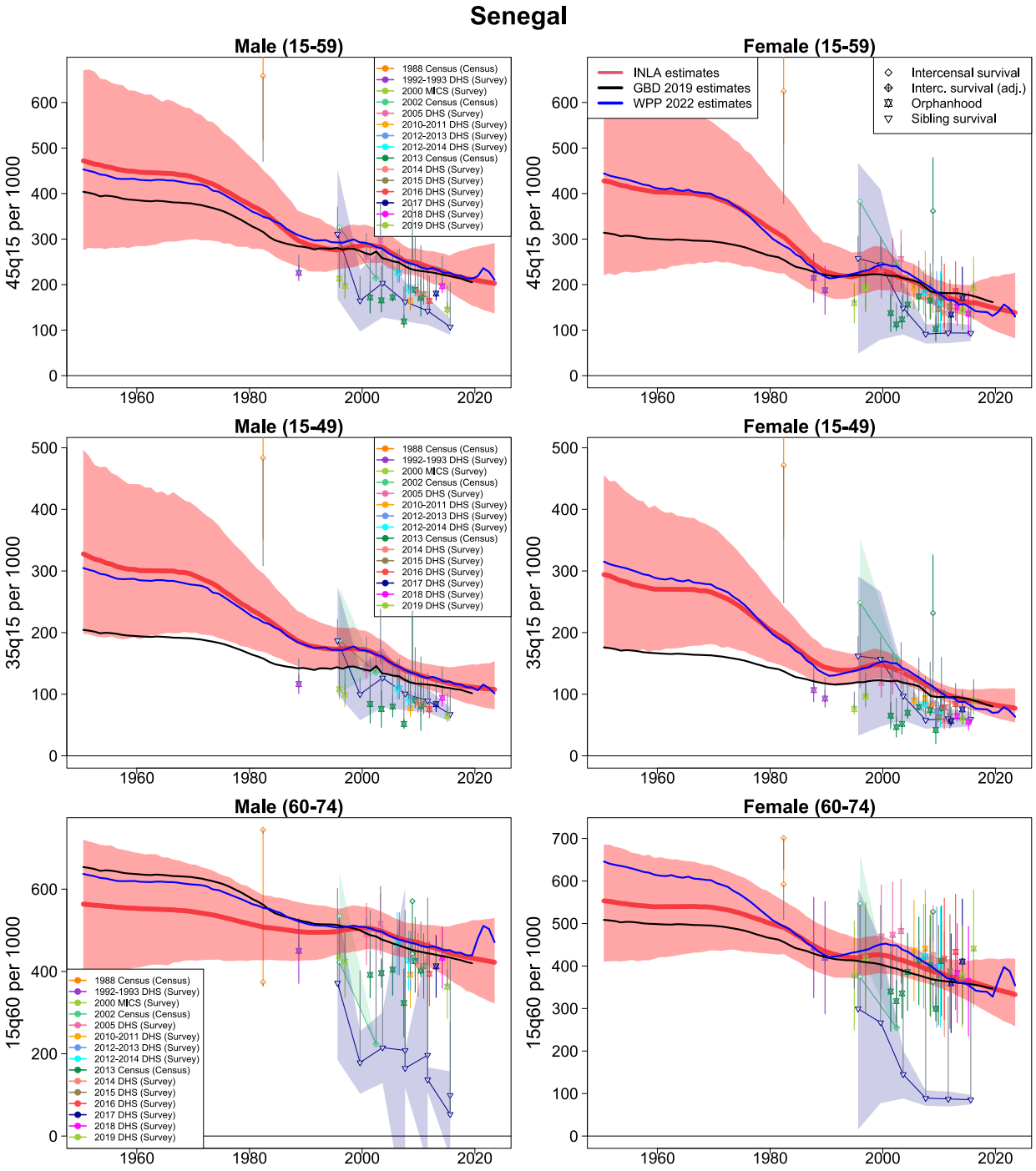


Source: United Nations (2024b), IHME (2020) and calculations by authors.

Note: The red curves show the posterior medians. The shades show 95 per cent uncertainty bounds. Dots are the observations used for modelling. The shading and vertical lines around the dots represent sampling errors (if available). The vertical grey bars at dots show the bias adjustment done before BMH model fitting. Grey bars are absent for observations if bias adjustment is zero.

Figure 9. Age-sex-specific adult mortality model estimates for several broad age groups from selected countries with limited data

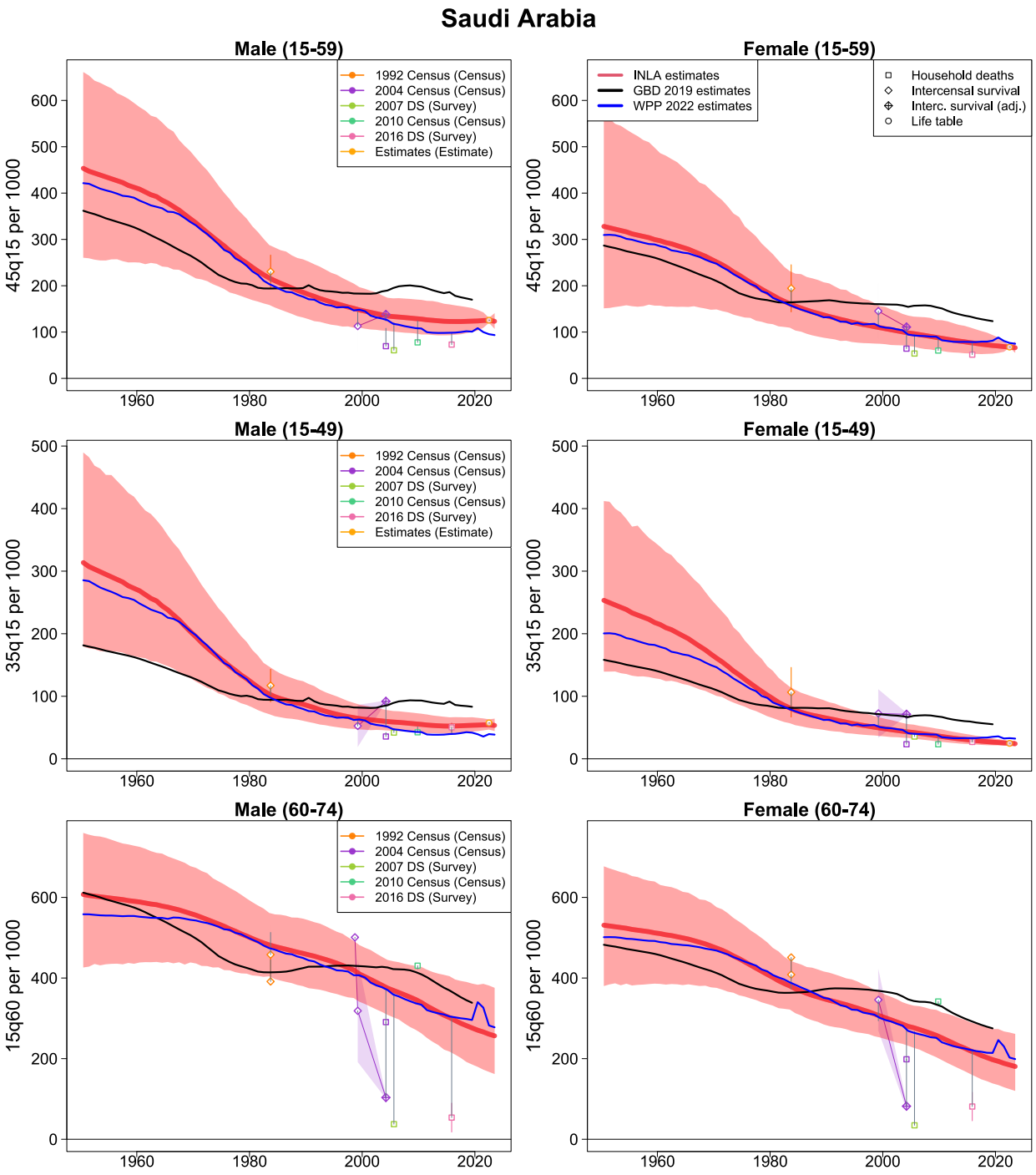
Examples of Senegal, Saudi Arabia and Somalia



Source: United Nations (2024b), IHME (2020) and calculations by authors.

Note: The red curves show the posterior medians. The shades show 95 per cent uncertainty bounds. Dots are the observations used for modelling. The shading and vertical lines around the dots represent sampling errors (if available). The vertical grey bars at dots show the bias adjustment done before BMH model fitting. Grey bars are absent for observations if bias adjustment is zero.

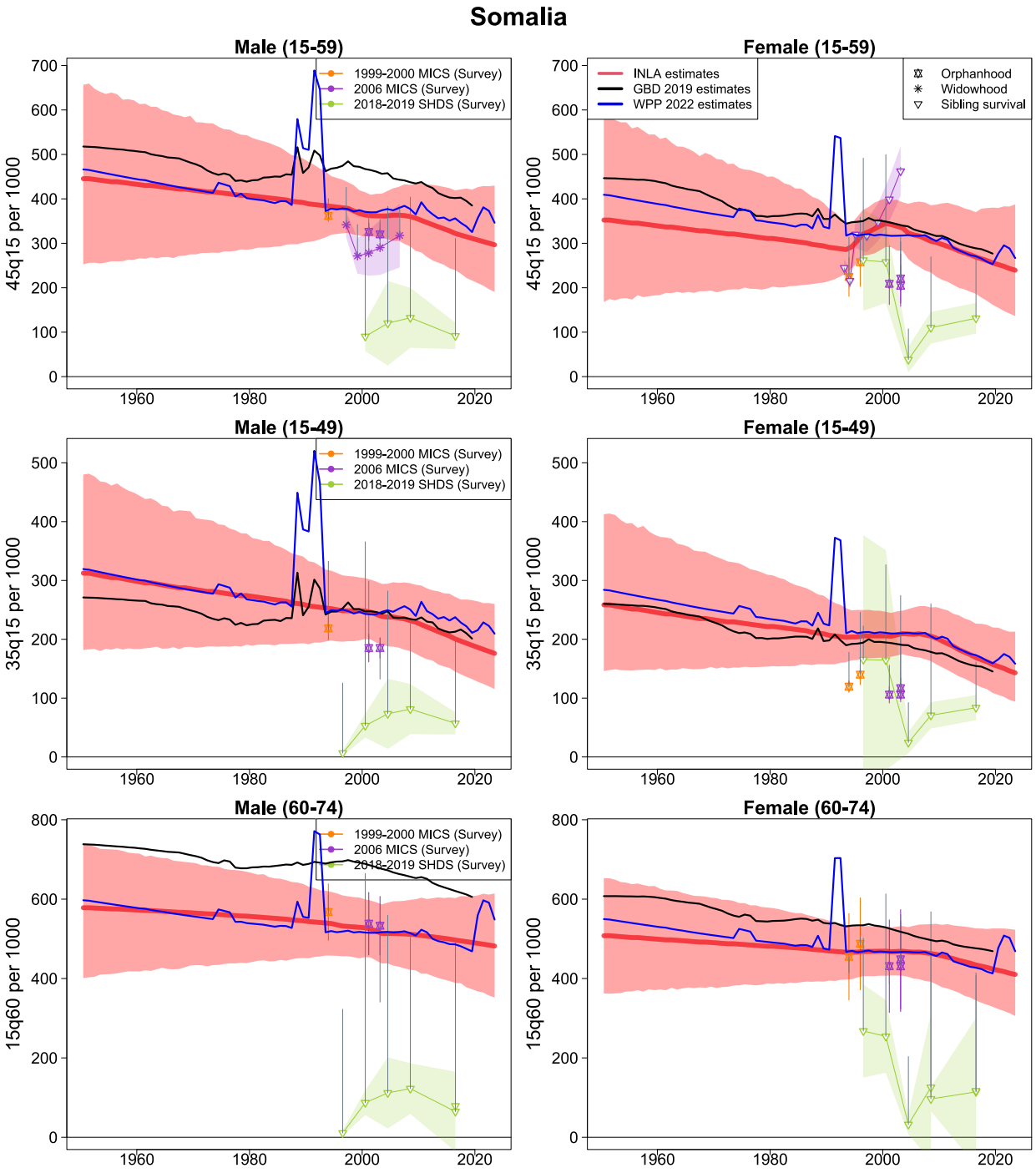
Figure 9. Continued



Source: United Nations (2024b), IHME (2020) and calculations by authors.

Note: The red curves show the posterior medians. The shades show 95 per cent uncertainty bounds. Dots are the observations used for modelling. The shading and vertical lines around the dots represent sampling errors (if available). The vertical grey bars at dots show the bias adjustment done before BMH model fitting. Grey bars are absent for observations if bias adjustment is zero.

Figure 9. Continued

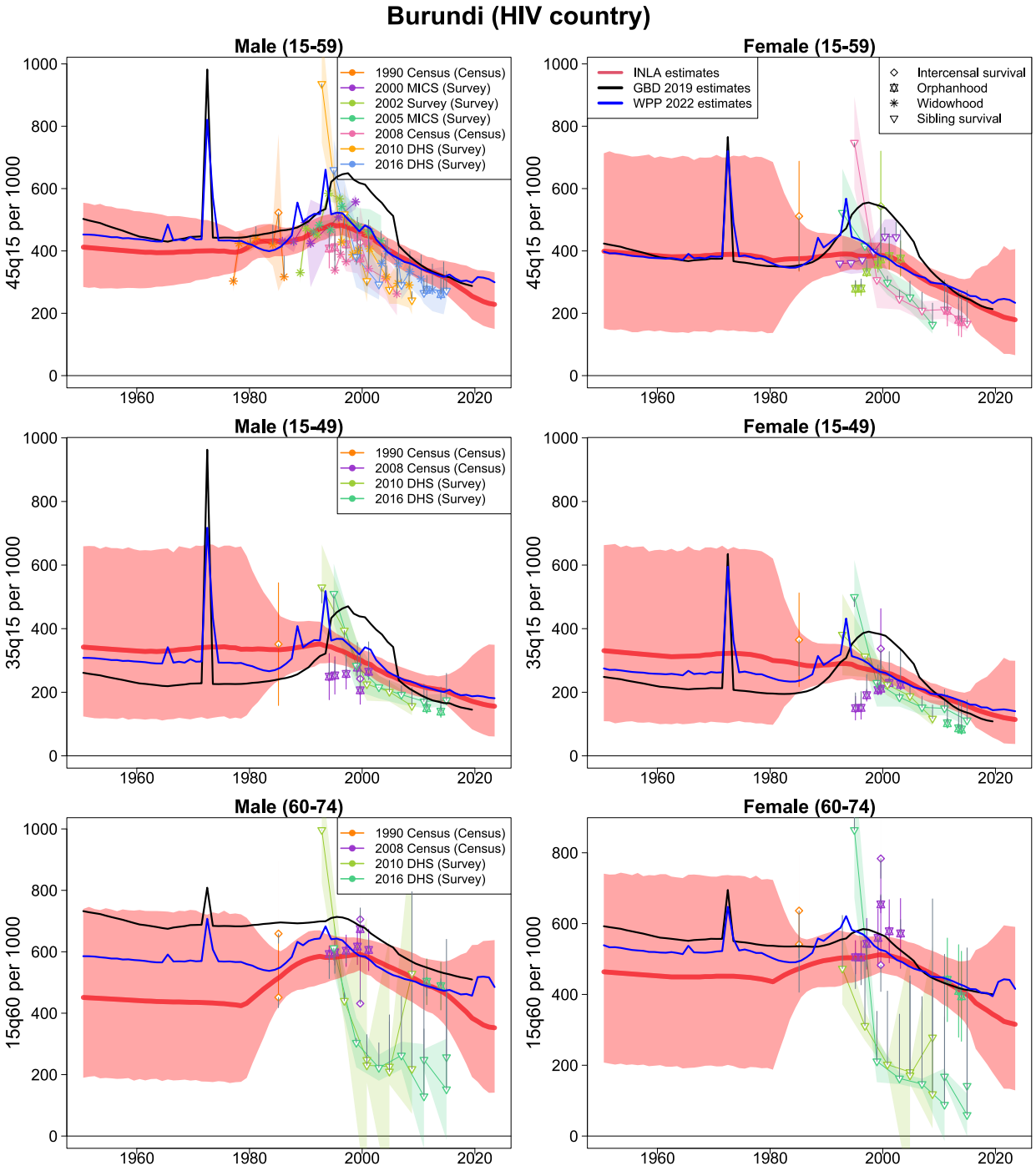


Source: United Nations (2024b), IHME (2020) and calculations by authors.

Note: The red curves show the posterior medians. The shades show 95 per cent uncertainty bounds. Dots are the observations used for modelling. The shading and vertical lines around the dots represent sampling errors (if available). The vertical grey bars at dots show the bias adjustment done before BMH model fitting. Grey bars are absent for observations if bias adjustment is zero.

Figure 10. Age-sex-specific adult mortality model estimates for several broad age groups from selected countries with high HIV prevalence

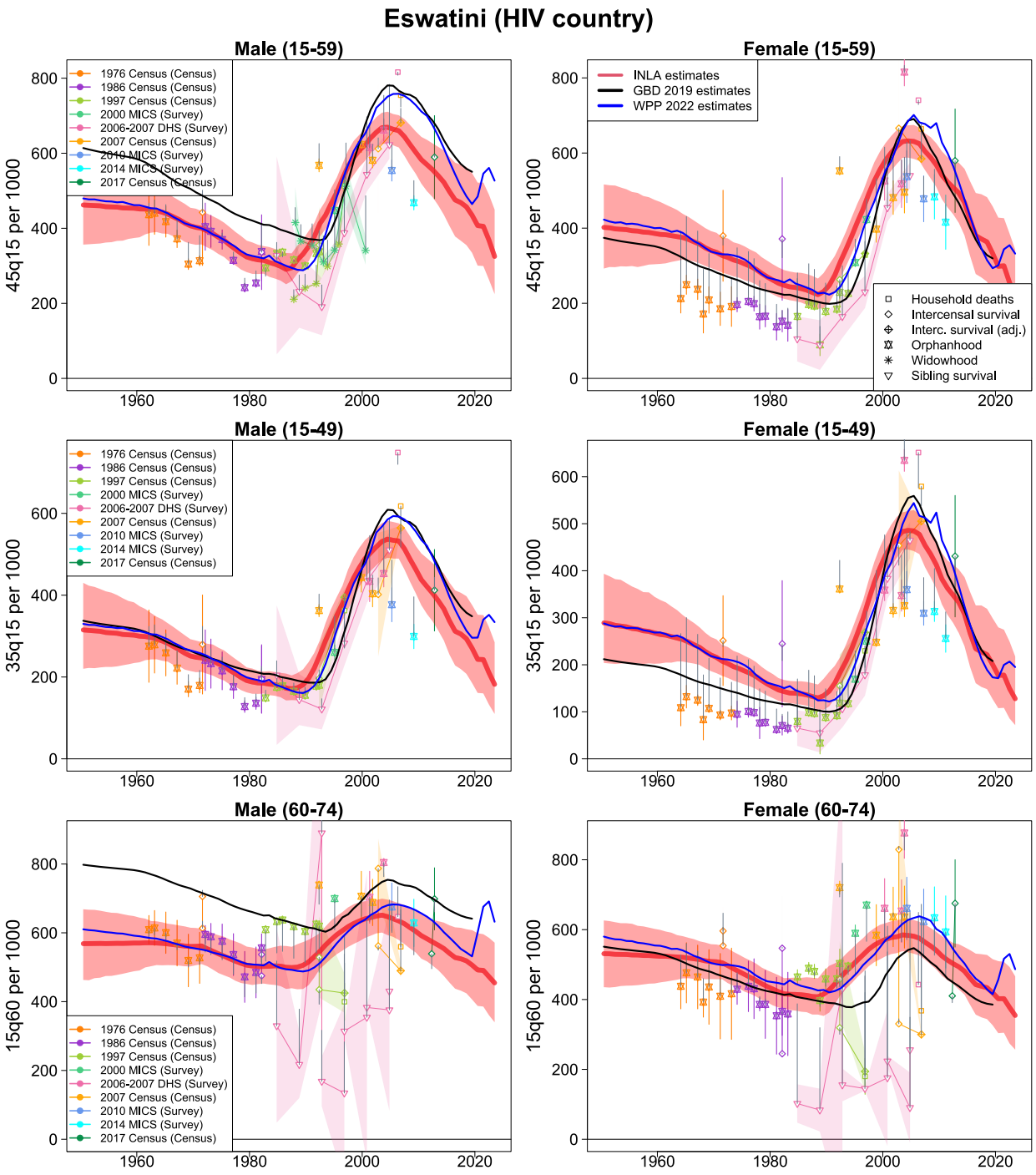
Examples of Burundi, Eswatini and Malawi



Source: United Nations (2024b), IHME (2020) and calculations by authors.

Note: The red curves show the posterior medians. The shades show 95 per cent uncertainty bounds. Dots are the observations used for modelling. The shading and vertical lines around the dots represent sampling errors (if available). The vertical grey bars at dots show the bias adjustment done before BMH model fitting. Grey bars are absent for observations if bias adjustment is zero.

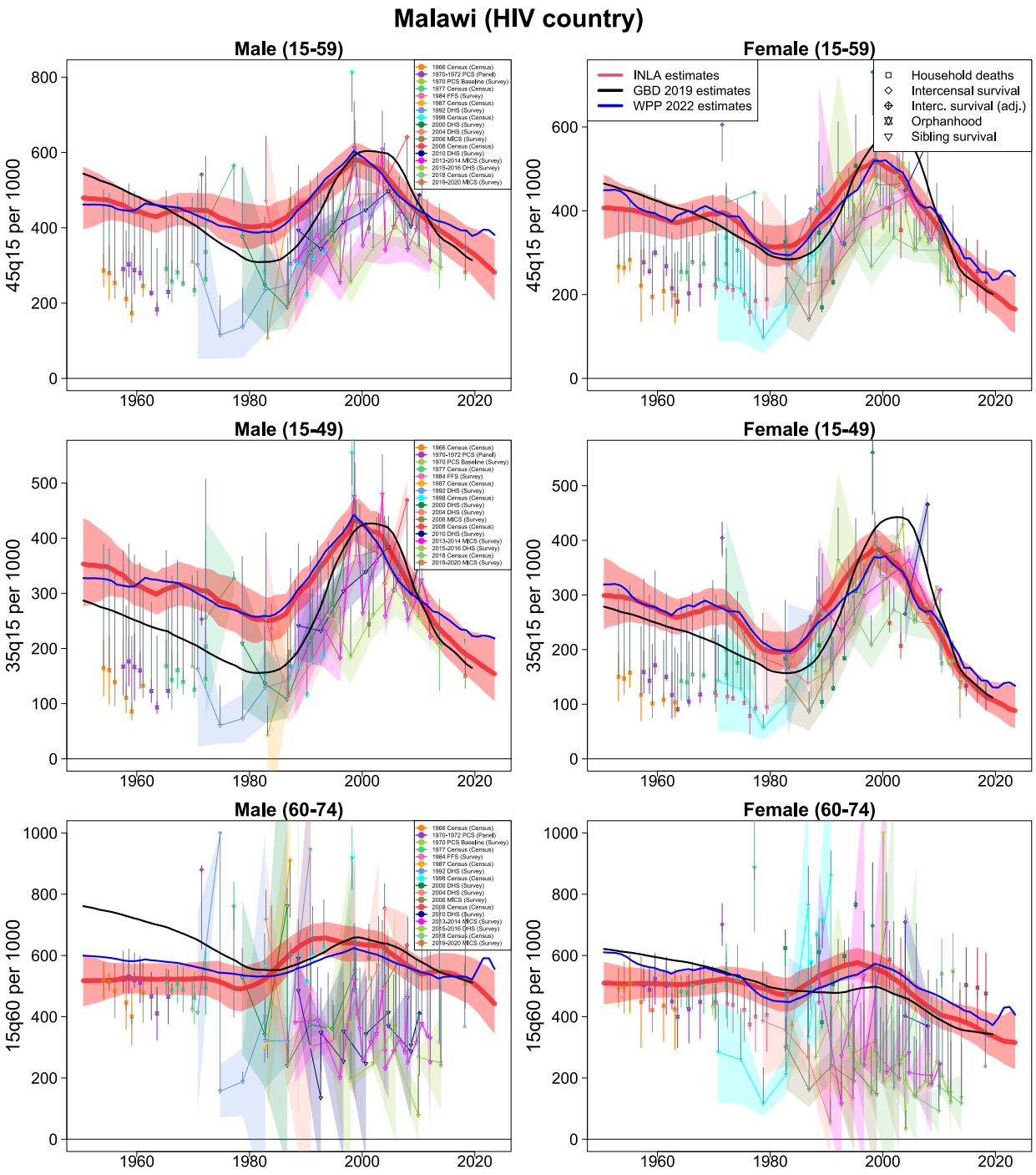
Figure 9. Continued



Source: United Nations (2024b), IHME (2020) and calculations by authors.

Note: The red curves show the posterior medians. The shades show 95 per cent uncertainty bounds. Dots are the observations used for modelling. The shading and vertical lines around the dots represent sampling errors (if available). The vertical grey bars at dots show the bias adjustment done before BMH model fitting. Grey bars are absent for observations if bias adjustment is zero.

Figure 9. Continued



Source: United Nations (2024b), IHME (2020) and calculations by authors.

Note: The red curves show the posterior medians. The shades show 95 per cent uncertainty bounds. Dots are the observations used for modelling. The shading and vertical lines around the dots represent sampling errors (if available). The vertical grey bars at dots show the bias adjustment done before BMH model fitting. Grey bars are absent for observations if bias adjustment is zero.

VI. Conclusions

This technical paper presents a comprehensive Bayesian Hierarchical Model (BHM) for estimating age-sex-specific adult mortality across all countries and territories from 1950 onwards. The model's design addresses the inherent challenges of limited, incomplete, or biased data, offering a reproducible, consistent, and comparable approach to estimating mortality rates globally. The approach utilizes an extensive database of age-sex-specific adult mortality data by broad age groups to produce annual estimates globally. All estimates are based on comprehensive databases of available data sources. The underlying data and estimates are publicly accessible through the United Nations Population Data Portal[9] as part of the most recent revision of the *World Population Prospects*.

The BHM effectively integrates diverse data sources, including vital registration systems, censuses, and surveys, to produce robust mortality estimates. It adapts to varying data quality by borrowing information from regional patterns and employing systematic adjustments for biases. For countries with high-quality data, such as Sweden, the United Kingdom and the United States of America, the model produces estimates that closely follow observed trends with narrow uncertainty bounds. In contrast, for countries with limited, low-quality, or biased data, such as Somalia or Bangladesh, the model relies on hierarchical structures to borrow information from neighbouring countries in the region and covariates like under-five mortality rates to provide reasonable estimates. The inclusion of HIV prevalence and ART coverage in the modelling process is particularly notable for capturing the unique mortality trends in countries significantly affected by the HIV epidemic, such as Eswatini and Malawi. The model successfully reflects the upward trends in mortality during periods of high HIV prevalence and the subsequent declines as ART coverage increases.

The BHM sets a new standard for demographic modeling by integrating diverse data sources and addressing systematically, uncertainties. Its flexibility to adapt to varying data availability makes it an essential tool for global and regional demographic analyses. However, no model can replace real empirical data, and the lack of timely and reliable adult mortality data for many countries remains a significant limitation. Key challenges include:

- Data Coverage: Many countries, especially in low-income regions or conflict-affected areas, lack comprehensive civil registration and vital statistics (CRVS) systems. While surveys and censuses help fill these gaps, they are conducted infrequently, resulting in delays in data availability.

- Data Completeness: Even when data are available, issues such as under-registration of deaths, non-sampling errors and reporting biases reduce their reliability.

- Emerging Challenges: The COVID-19 pandemic underscored the critical need for real-time mortality data to understand its full impact on public health and mortality trends.

Timely and high-quality adult mortality data are essential for effective policymaking, resource allocation and progress monitoring toward global health goals, including the Sustainable Development Goals (SDGs). Strengthening existing data collection systems, particularly civil registration systems, is a high priority. Further investments and support are needed to ensure more regular updates to mortality data.

[9] Please see https://population.un.org/dataportal/home

These improvements are crucial for evaluating interventions, detecting emerging public health challenges, and making informed adjustments to health policies and programs.

The Bayesian Hierarchical Model described in this report represents a significant advancement in the field of demographic estimation. By addressing challenges related to sparse, biased, or unavailable data, the model ensures that mortality estimates are robust, reliable and useful for a wide range of applications. Future enhancements, particularly in data availability and computational efficiency, will further strengthen its utility for global population monitoring and policy development. The continued development and application of such models will be instrumental in advancing our understanding of global mortality trends and supporting sustainable development efforts.

VII. References

Bijak, J., and J. Bryant (2016). Bayesian demography 250 years after Bayes. *Population studies*, vol. 70, No. 1, pp. 1-19. doi: 10.1080/00324728.2015.1122826.

Hill, K. (2017). *Analytical methods to evaluate the completeness and quality of death registration: current state of knowledge*. Technical Paper, No. UN DESA/POP/2017/TP/No.2, New York, United Nations.

Institute for Health Metrics and Evaluation (IHME) (2020). *Global Burden of Disease Study 2019 (GBD 2019)*. University of Washington. Available at http://www.healthdata.org/gbd. Accessed 10 October 2020.

Li, N., and P. Gerland (2013). Using census data to estimate old-age mortality for developing countries. Paper presented at the XXVII IUSSP International Population Conference, Busan, South Korea.

Liu, P., and A. E. Raftery (2020). Accounting for uncertainty about past values in probabilistic projections of the total fertility rate for most countries. *The Annals of Applied Statistics*, vol. 14, No. 2, pp. 685-705. doi: 10.1214/19-aoas1294.

Liu, P., and others (2023). Probabilistic estimation and projection of the annual total fertility rate accounting for past uncertainty: A major update of the bayesTFR R Package. *Journal of Statistical Software*, vol. 106, No. 8, pp. 1 - 36. doi: 10.18637/jss.v106.i08.

Martins, T. G., and others (2013). Bayesian computing with INLA: New features. *Computational Statistics and Data Analysis*, vol. 67, pp. 68-83. doi: 10.1016/j.csda.2013.04.014.

Mathers, C. D., and others (2005). Counting the dead and what they died from: An assessment of the global status of cause of death data. *Bulletin of the World Health Organization*, vol. 83, pp. 171-177c.

Max Planck Institute for Demographic Research (Germany), and others (2023a). *Human Life Table Database*. Date accessed 7 July 2023.

_____ (2023b). *Human Mortality Database (HMD)*. Date accessed 21 Dec. 2023.

Moultrie, T. A., and others (2013). *Tools for Demographic Estimation. In: International Union for the Scientific Study of Population*. Available at http://demographicestimation.iussp.org/.

Palloni, A., and others (2021). *Latin American Mortality Database* (LAMBdA). Madison: University of Wisconsin. Date accessed 21 Sept. 2021.

Preston, S. (1984). The use of direct and indirect techniques for estimating the completeness of death registration systems. In *Data Bases for Mortality Measurements*, United Nations, ed, pp. 66-76. New York.

Preston, S. H., and others (2001). *Demography : Measuring and Modeling Population Processes*. Malden, MA: Blackwell Publishers.

R Core Team (2024). *R: A language and environment for statistical computing. R Foundation for Statistical Computing*. Available at www.R-project.org/.

Rao, C., and others (2020). *Estimating Completeness of Birth and Death Registration: Methods and Options for Estimating Completeness of Civil Registration*. New York: Vital Strategies.

Rue, H., and others (2009). Approximate Bayesian inference for latent Gaussian models by using integrated nested Laplace approximations. *Journal of the Royal Statistical Society Series B: Statistical Methodology*, vol. 71, No. 2, pp. 319-392.

Simpson, D., and others (2017). Penalising model component complexity: A principled, practical approach to constructing priors. *Statistical Science*, vol. 32, No. 1, pp. 1-28.

United Nations (2002). *Methods for estimating adult mortality*. Technical Paper, No. ESA/P/WP.175, New York, United Nations.

United Nations (2004). *Handbook on the Collection of Fertility and Mortality Data*. Statistical Papers. Series F, Studies in methods. No. 92, ST/ESA/STAT/SER.F/92. New York: United Nations.

United Nations (2014). *Principles and Recommendations for a Vital Statistics System, Revision 3*. Statistics Division, Department of Economic and Social Affairs, ed., New York: United Nations.

_____ (2022). *World Population Prospects 2022: Online Edition*. Population Division, Department of Economic and Social Affairs.

_____ (2024a). *World Population Prospects 2024: Methodology of the United Nations population estimates and projections*. UN DESA/POP/2024/DC/NO.10. Population Division, Department of Economic and Social Affairs.

_____ (2024b). *World Population Prospects 2024: Online Edition*. Population Division, Department of Economic and Social Affairs.