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Bruno Masquelier & Ian M. Timæus

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Estimating adult mortality based on maternal orphanhood in populations with HIV/AIDS

Bruno Masquelier [1] **and Ian M. Timæus** [2,3]
[1]Louvain University, [2]London School of Hygiene and Tropical Medicine, [3]University of Cape Town

In countries without adequate death registration systems, adult mortality is often estimated using orphanhood-based methods. The HIV pandemic breaches several assumptions of these methods, for example, by increasing the correlation between maternal and child survival. Using microsimulations we generated 1,152 populations facing HIV epidemics and evaluated different orphanhood-based estimates against the underlying mortality rates. We regressed survivorship probabilities on proportions of respondents with surviving mothers, adjusting for trends in seroprevalence and coverage of antiretroviral therapy, to obtain new coefficients. We tested the different methods on survey and census data from 16 African countries with high HIV prevalence. We found that the original orphanhood method underestimates mortality during an AIDS epidemic, but better estimates can be obtained using new coefficients applied to synthetic measures of maternal survival. The resulting estimates agree well with those of the United Nations Population Division. Orphanhood-based estimates can fill data gaps in adult mortality, including in countries with high HIV prevalence.

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Keywords: adult mortality; indirect estimation; orphanhood method; HIV/AIDS; microsimulation

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Introduction

The highest levels of adult mortality worldwide are found in sub-Saharan Africa (SSA). According to the United Nations (2022), the risk of dying between ages 15 and 50 was greater than 10 per cent in 61 countries in 2022; 48 of these high-mortality countries were located in SSA. However, because of the underdevelopment of systems for civil registration and vital statistics in the region, the magnitude of this mortality burden is hard to quantify. Only a handful of countries can generate reliable mortality estimates from their death registration system, for example, South Africa and Zimbabwe (Feeney 2001; Joubert et al. 2013), while in other countries high-quality data are available for their capital city only (Masquelier et al. 2019).

Available adult mortality estimates, such as those developed by the United Nations Population Division and the Institute for Health Metrics and Evaluation, are therefore based on statistical models that synthesize a fairly limited set of primary estimates from censuses and surveys in SSA (Wang et al. 2020; United Nations 2022). These primary estimates typically stem from three main approaches: evaluating intercensal population change by age and sex; eliciting reports on recent household deaths; and assessing survival among close relatives (Hill et al. 2005). In particular, sibling survival histories have proved useful in reconstructing trends and age patterns of mortality (Timæus and Jasseh 2004). They are, however, relatively time-consuming to collect and inappropriate for use in censuses or rapid-turnaround surveys. In contrast, orphanhood-based

methods generally require only that two questions are asked: 'Is your mother alive?' and 'Is your father alive?' No information is required on the ages of surviving parents, ages at death, or timing of deaths. Mortality is estimated instead from the proportions with surviving parents. Since parents are by definition alive at the time of birth of their children (or the time of conception, for fathers), their duration of exposure to the risk of dying corresponds to the age of the respondents. The average age of parents at the start of the exposure period is simply the mean age at childbearing. Proportions of parents alive as collated from reports by individuals aged a are thus closely related to the probability of surviving from M to $M + a$ ($_ap_M$), where M stands for the mean age at childbearing.

Henry (1960) and Brass and Hill (1973) developed the original orphanhood method based on the theory of stable populations, which enables expression of the frequency and survival of close relatives as a function of mortality and fertility rates. Several revisions have been proposed since (Hill and Trussell 1977; Palloni and Heligman 1985; Timæus 1991a, 1992). About 100 censuses conducted in SSA have included orphanhood questions (Table S1, Appendix A, supplementary material). Nationally representative surveys, such as the Demographic and Health Survey (DHS) and Multiple Indicator Cluster Survey (MICS) also regularly collect data on parental survival among children aged under 18 years. Numerous studies have estimated adult mortality by means of orphanhood-based methods, including in populations with high HIV prevalence (Tollman et al. 1999; Feeney 2001; Dorrington et al. 2004; Hosegood et al. 2004; Nhacolo et al. 2006; Lesotho NSO 2009; Chisumpa and Dorrington 2011; Menashe-Oren and Stecklov 2018; Odimegwu et al. 2018). Yet, orphanhood-based estimates remain less frequently used than sibling survival histories for monitoring trends in mortality. For example, they are not included in the mortality database of the Global Burden of Disease study (Wang et al. 2020).

The patchy use of orphanhood data for mortality estimation is probably due to concerns over data quality. The reporting of fostered orphans as non-orphans, an error referred to as the 'adoption effect', is thought to be common (Blacker and Mukiza-Gapere 1988; Robertson et al. 2008). However, methods have been developed to correct for this: by either estimating mortality from orphanhood among adults only (Timæus 1991b) or constructing synthetic cohorts from two sets of data on orphanhood (Timæus 1986, 1991a).

Another source of scepticism about orphanhood-based methods is related to selection biases. These arise if mothers' and children's probabilities of dying are correlated, if mothers' fertility is associated with their mortality, or when children's mortality varies with their number of siblings. In normal circumstances, these selection biases tend to cancel each other out (Palloni et al. 1984). In recent decades, however, HIV epidemics have amplified these biases. The transmission of HIV from mothers to children ranges from 15 to 45 per cent in the absence of treatment (De Cock et al. 2000). Because of vertical transmission, fewer orphans will survive among those born to HIV-positive parents than those born to seronegative parents; thus, the latter will be oversampled in reports from censuses and surveys. The lower fertility of seropositive mothers will also bias mortality estimates downwards. Additional errors will be introduced when proportions of parents alive are converted into measures of mortality with coefficients calculated based on standard age patterns of mortality. This is because such age patterns do not reflect the 'hump' in adult mortality rates that is typical of populations experiencing a generalized HIV epidemic (Masquelier et al. 2017). Finally, biases will also be introduced because the rapid changes in mortality during the course of the epidemic violate the assumption of a regular trend in mortality that underlies the calculation of reference periods for the estimates (Brass and Bamgboye 1981).

The only attempt to adapt orphanhood-based methods for use in countries facing HIV/AIDS epidemics dates back to the mid-1990s. Timæus and Nunn (1997) developed approximate expressions for the HIV-related selection biases and proposed an adjustment for the proportions of mothers alive. They also suggested a revised set of coefficients for converting the adjusted proportions into survivorship probabilities for females, based on age-specific mortality rates that reflected the burden of AIDS. They warned, however, that the coefficients were provisional because they were based on prospective mortality data collected in a single rural community in Uganda (Asiki et al. 2013). In addition, their method did not account for antiretroviral therapy (ART), which was introduced in the area only in 2004 (Kasamba et al. 2012).

In this paper, we assess the sensitivity of orphanhood-based methods to HIV-related bias using a more diverse set of simulations than in the initial study by Timæus and Nunn (1997). We use micro-simulated populations that model the vertical transmission of HIV, reduced fertility of HIV-positive

mothers, and shifts in age patterns of mortality due to AIDS. The impact of ART, including the prevention of mother-to-child transmission (PMTCT), is also modelled explicitly. A new procedure for making the estimates is developed for use when at least two series of maternal orphanhood reports are available from successive surveys or censuses, in addition to estimates of HIV prevalence and treatment coverage. We develop this new approach in our simulated environment and evaluate it using survey and census data for 16 countries—Botswana, Cameroon, Central African Republic, Cote d'Ivoire, Eswatini, Kenya, Lesotho, Malawi, Mozambique, Namibia, Rwanda, South Africa, Tanzania, Uganda, Zambia, and Zimbabwe—where the peak in HIV prevalence exceeded 5 per cent in females (UNAIDS 2022). Gabon and Equatorial Guinea also experienced severe HIV epidemics with a prevalence among women aged 15–49 exceeding 5 per cent, but these two countries are excluded from the analysis due to the paucity of data on orphanhood.

Data and methods

The conventional orphanhood method

Here we summarize the conventional orphanhood method. We refer readers to Timæus (2013) for a detailed explanation of the method and for Excel templates that facilitate its application. The method is best expounded by starting with a child aged a, taken at random from a population whose fertility rates and survival function are $m(x)$ and $l(x)$ (Keyfitz and Caswell 2005). The probability that the mother is still alive, conditional on her having given birth at age x, is ${}_ap_x$. To eliminate this condition, the survival probabilities should be averaged over all reproductive ages, weighting each age x by the number of births that occurred at that age. In a stable population, the age distribution of the female population is constant and depends on $l(x)$, $m(x)$, and r, the intrinsic growth rate. This leads to the equation introduced by Lotka (1931) for the probability that a child aged a has a surviving mother under the prevailing conditions of mortality and fertility:

$$S(a) = \int_{\alpha}^{\beta} {}_ap_x \, {}_xp_0 e^{-rx} m(x) dx. \quad (1)$$

From this, the proportion of mothers surviving among those who have given birth to a child who is now aged y to $y+5$ years can be expressed as:

$${}_5S_y = \frac{\int_y^{y+5} e^{-r(a)} {}_ap_0 \int_{\alpha}^{\beta} e^{-r(x)} {}_{x+a}p_0 m(x)\, dx\, da}{\int_y^{y+5} e^{-r(a)} {}_ap_0 \int_{\alpha}^{\beta} e^{-r(x)} {}_xp_0 m(x)\, dx\, da}. \quad (2)$$

By specifying a series of fertility and mortality rates through standard age patterns, equation (2) can be used to approximate numerically the proportions ${}_5S_y$ (Brass and Hill 1973). The proportions can be connected to the probabilities ${}_np_M$, calculated in the life tables from which they were generated, for example through linear regression, yielding a set of coefficients for each age group y. For convenience, M is often replaced by 25, a round number close to the mean age at childbearing among women, and an estimate of the mean age at childbearing is included in the regression as a covariate to control for the actual timing of fertility. It can be obtained as the average age of women giving birth in a 12-month period about y years ago. Timæus (1992) used the following equation:

$${}_np_{25} = \beta_0(n) + \beta_1(n)\, M + \beta_2(n) {}_5S_{n-5}, \quad (3)$$

where ${}_np_{25}$ is the chance of a woman surviving between age 25 and $25+n$; M is the mean age at childbearing; and ${}_5S_{n-5}$ is the proportion of respondents in the age group $n-5$ to n whose mother is still alive. The β coefficients are presented in Table S2 (Appendix B, supplementary material). Other regression equations have been tested and provide different sets of coefficients (Hill and Trussell 1977; United Nations 1983; Palloni and Heligman 1985). In the absence of HIV, the estimated probabilities, ${}_np_{25}$, are not very sensitive to the choice of coefficients, especially when based on reports from young respondents (aged $n<35$) (Masquelier 2010). Timæus (1992) also developed coefficients to estimate men's mortality from paternal orphanhood.

The proportions of parents alive as derived from reports by adult respondents refer to mortality and fertility rates over a longer period than those based on the reports of young children. A time to which the estimate refers should therefore be calculated. Existing time-location procedures assume a linear trend in mortality levels, captured through the α parameter of the Brass logit system (Brass and Bamgboye 1981) or trends in life expectancy (Palloni and Heligman 1985). These procedures also assume a steady increase in mortality by age. Once time located, the probabilities, ${}_np_{25}$, obtained from the reports of respondents in different five-year age

groups (n–5 to n) need to be converted into a common index of mortality, such as the probability ${}_{35}q_{15}$, to be comparable and depict the general trend in mortality. This can be achieved either through relational models (such as the Brass logit model) or by interpolating within other families of model life tables (Coale et al. 1983; INDEPTH 2004).

Distortions due to HIV/AIDS

As mentioned earlier, the HIV epidemic undermines the validity of the conventional orphanhood method. Three important sources of bias exist. First, selection biases are magnified by the vertical transmission of the virus and the reduced fertility of seropositive women, which both inflate the proportions of mothers reported to be alive. Second, HIV epidemics generate atypical age patterns of mortality: the risk of dying rises rapidly with age across the early adult ages (15–30 years) and then increases more slowly with age than in standard model schedules. This leads the standard coefficients to overestimate survivorship. Third, increases in mortality due to AIDS, and the declines that have followed due to the uptake of ART and behavioural changes, violate the assumption that the trend in all-cause mortality is linear and unidirectional. Thus, the series of estimates made from respondents of different ages can no longer be interpreted as indicative of the period trend in mortality.

To address the first problem, selection biases, Timæus and Nunn (1997) rearranged equation (2) to distinguish between seronegative mothers who remained uninfected, mothers who were seropositive at the time of birth, and mothers who became infected after the birth of their child. They proposed an adjustment to the observed proportions of mothers remaining alive. This adjustment is based on two parameters: F, the ratio of the fertility of seropositive to seronegative women (assumed to be age invariant); and h, the risk of mother-to-child transmission (proportion of children who become infected in the perinatal period out of all those born to seropositive mothers). In addition to F and h, an estimate of the prevalence of HIV infection among women attending prenatal clinics (P) is needed. The corrected proportions of mothers alive (${}_5S'_n$) are obtained from the observed proportions (${}_5S^*_n$), such that:

$$ {}_5S'_n = \frac{1 - hP}{1 + \frac{1-F}{F} \times P} \times {}_5S^*_n. \qquad (4) $$

If an estimate of the HIV prevalence in the population (P^*) is used, the equation becomes:

$$ {}_5S'_n = \left[1 - (1 - (1 - h) \times F) \times P^*\right] \times {}_5S^*_n \,. \qquad (5) $$

We can assume that the risk of mother-to-child transmission is about one-third and that the fertility of seropositive women is about 75 per cent of that of seronegative women (De Cock et al. 2000; Chen and Walker 2010). Thus, a suitable adjustment might be:

$$ {}_5S'_n = \left[1 - 0.5 \times P^*\right] \times {}_5S^*_n \,. \qquad (6) $$

This correction is easy to implement but assumes that all mothers who were already infected when the respondents were born died before the survey. Because this is unrealistic for young respondents, Timæus (2013) later recommended that the adjustment applied to reports from respondents aged 5–9 be halved ($1 - 0.25 \times P^*$) and for 10–14-year-olds be reduced by one-quarter ($1 - 0.375 \times P^*$).

To address the second problem, related to distortions introduced in age patterns of mortality, Timæus and Nunn (1997) developed simulations based on prospective mortality data from the Masaka Health and Demographic Surveillance System (HDSS) in Uganda in 1990–95. Their simulations were based on stable population theory, assuming that the characteristics of the HIV epidemic at that time were kept constant. These simulations allowed them to compute a set of coefficients that can be used to convert the proportions of mothers alive into life-table survivorship estimates when HIV prevalence is 5 per cent or greater. These coefficients are reproduced in Table S3 (Appendix B, supplementary material).

The third problem, relating to the time trend in mortality, has not been explicitly addressed in the literature. Most attempts to estimate mortality from orphanhood in settings with high HIV prevalence have ignored this problem and used time-location procedures that assume a smooth and unidirectional trend in mortality (e.g. Feeney 2001; Hosegood et al. 2004; Nhacolo et al. 2006; Menashe-Oren and Stecklov 2018; Odimegwu et al. 2018). Estimates produced in this way will inevitably smooth out the sudden reversals and accelerations in mortality trends that would be expected in populations experiencing a generalized HIV epidemic.

The microsimulation set

To produce a more robust assessment of the magnitude of the HIV-related biases in orphanhood-based estimates than Timæus and Nunn (1997) obtained with an analytic approach, we resorted to demographic microsimulations. These are models in which individuals experience vital events as a result of stochastic experiments with predefined probabilistic rules (Zagheni 2015). We used SOCSIM, a discrete-time microsimulation model that keeps track of kinship links between individuals (Wachter et al. 1997; Verdery et al. 2020).

In the simulations, the first period corresponds to the conditions of a stable population and lasts from year 0 to year 200. Populations reach about 100,000 individuals at that point. Ten periods of five years follow, during which the populations face an HIV epidemic. The growth rate during these 50 years evolves according to the severity of the epidemic; some populations reach 150,000 individuals in year 250, while others decline to 85,000 survivors.

For the long period preceding the onset of the HIV epidemic, the mortality and fertility rates are similar to those used by Timæus (1992) although fewer parameters are retained, to allow for the introduction of additional parameters related to HIV while limiting the number of simulations and the computational burden of producing them. Populations are exposed to various levels of non-AIDS mortality, modelled using the Brass relational model, specifying three values for the α_m parameter (capturing variations in the level of mortality) and two values for the β_m parameter (capturing differences in age patterns), using Brass's general standard (Brass 1971). Fertility is also modelled with a relational model, with two values of α_f (capturing the age location of the fertility schedule) and two values of β_f (capturing the spread of the fertility schedule) (Brass 1974). The standard used for the fertility schedule was created by Booth (1984) for populations with high fertility. The waiting time to each event is generated randomly from a piecewise exponential distribution. The stable equivalent population obtained analytically from the survival curve, the shape of the fertility schedule, and the growth rate is used to specify the age structure of the starting population. The initial growth rate is set at 2 per cent and kept constant until the onset of the epidemic, for consistency with the method's original calculations (Hill and Trussell 1977; Timæus 1992). Using a single value for the growth rate is adequate, as variations in age structure have little effect on mortality estimates derived from orphanhood (Timæus 1992). The corresponding non-AIDS life expectancies at birth range from 43.1 to 68.3 years, while the mean ages at childbearing range from 25.1 to 29.8 years.

The parameters used to model the HIV epidemic were inspired by those underpinning the UNAIDS Spectrum package (Stover et al. 2012, 2017). Following Zagheni (2011), we modelled HIV/AIDS in SOCSIM by splitting the population into subgroups: (1) seronegative individuals; (2) those who had been infected with HIV through sexual transmission but were in the asymptomatic phase; (3) those who had developed acquired immunodeficiency syndrome (AIDS); (4) children infected with HIV through vertical transmission; and (5) individuals who had initiated antiretroviral treatment (Figure S1, Appendix C, supplementary material). In the simulations, HIV infection is governed by age-specific rates, depending on trends in incidence. A gamma distribution is used to impose a plausible shape on the HIV incidence curve (Heuveline 2003). It depends on two parameters, α_{hiv} and β_{hiv} (Clark et al. 2012), as follows:

$$\Gamma_{t_2-t_1} = \int_{t_1}^{t_2} \frac{x^{\alpha_{hiv}-1} e^{-x/\beta_{hiv}}}{(\alpha_{hiv}-1)!\beta_{hiv}^{\alpha_{hiv}}} dx. \qquad (7)$$

This curve defines the trend in HIV incidence between times t_1 and t_2; the scale of the epidemic is determined by an additional parameter H, such that the proportion of individuals that are uninfected at time t_1 and both alive and HIV-positive at time t_2 is:

$$i_{t_1} = 1 - \exp(-\Gamma_{t_2-t_1} H). \qquad (8)$$

The age distribution of HIV infections was obtained as an average of patterns derived from cross-sectional measurements of HIV prevalence in the DHS (Stover et al. 2010). Once infected, individuals remain exposed to background mortality and progress to AIDS according to a Weibull distribution (with a median time from infection to AIDS of 8.55 years for females) (Figure S2, Appendix C, supplementary material). These progression rates were used in the Spectrum program before the approach was revised to accommodate changes in the criteria for eligibility for ART (Stover 2009). In our simulations, the transition to AIDS is governed solely by the time since infection. The transition from the AIDS stage to death is also modelled with a Weibull distribution, with a median time from AIDS to death of 1.95 years. The fertility of infected women relative to uninfected women is fixed at 1.26 for women aged 15–19, 0.76 for women aged 20–24,

and 0.67 for those aged 25+, based on ratios between age-specific fertility in HIV-positive women and HIV-negative women observed in 19 community-based studies (Lewis et al. 2004).

The probability of vertical transmission in utero or during delivery for a child born to an HIV-positive mother is assumed to be 20 per cent in the absence of treatment (Stover et al. 2012). The probability of infection through breastfeeding varies by child's age and depends on an average proportion of children who received exclusive or mixed breastfeeding. The survival of HIV-infected children is defined by a double Weibull curve and varies with age at infection, based on Stover et al. (2012). Using data from 16 countries where the peak prevalence of HIV reached at least 5 per cent according to UNAIDS (2022), we developed three scenarios for the expansion of coverage of treatment with ART and PMTCT: rapid treatment scale-up, slow treatment scale-up, and no treatment (Figure S3, Appendix C, supplementary material). In the two scenarios with treatment, the proportion of children infected vertically is revised downwards based on PMTCT trends. We assume that there is no dropout from ART treatment, that patients on ART also benefit from PMTCT, and that the fertility of women receiving ART is similar to that of those who have not yet initiated treatment. The probability of survival on ART is fixed at 85 per cent in the first year and 95 per cent for each additional year on treatment (Stover et al. 2008). Adults on ART are also exposed to mortality from other causes. All the simulations were run twice, once with and once without vertical transmission and reduced fertility due to HIV.

The values of the main parameters used to set up these simulations are shown in Table 1. Their combination results in 1,152 different simulations. Figure 1 presents the following model inputs: (a) the survival curves from the non-AIDS life tables; (b) the fertility schedules for seronegative women; and (c) the HIV incidence curves. It also displays the resulting trends in HIV prevalence among women aged 15–49 in Panel (d).

Results

Effect of the HIV epidemic on orphanhood prevalence and adult mortality

As a calibration exercise, Figure 2(a) presents trends in orphanhood prevalence among children aged 5–9 and 10–14 years in one simulation set, selected to broadly reflect the HIV epidemic in Zimbabwe. For this illustration, the years of the simulation are recoded such that the onset of the epidemic is around 1977. Proportions of orphaned children aged 5–9 and 10–14 observed in surveys and censuses in Zimbabwe are represented by circles. In Zimbabwe, the prevalence of maternal orphanhood among 5–9-year-olds increased from 2 per cent in the 1982 Census to 9 per cent in the 2009 MICS then declined to 3 per cent in the 2019 MICS. The orphan prevalence recalculated from the simulation follows a similar trend, hovering around the expected prevalence in the stable equivalent population until the mid-1980s (2 per cent) then increasing rapidly to peak at 10 per cent in 2006 before declining to reach 3 per cent in 2019.

In this simulation representing Zimbabwe, AIDS-free life expectancy at birth is 68 years for women and the risk of dying between ages 15 and 50 is 89 per 1,000 before the HIV epidemic unfolds (Figure 2(b)). This probability then increases to reach 513 per 1,000 in 2004. Sibling histories collected in the DHS in Zimbabwe depict a similar mortality increase, from 142 per 1,000 for the six-year period preceding the 1994 DHS to 443 per 1,000 for the same period preceding the 2005 DHS (Central Statistical Office Zimbabwe and Macro International 1995, 2007). In this simulation the prevalence of HIV infection among women of reproductive age peaks at 23 per cent in 2001, which is close to the

Table 1 Parameters used to set up the microsimulations

Background mortality		Incidence curve	
α_m	0, −0.4, −0.8	α_{hiv}	5, 7
β_m	0.8, 1.1	β_{hiv}	3, 5
		H	0.08, 0.13
Fertility (seronegative women)		HIV settings	
α_f	−0.35, 0.25	Treatments	No, Slow, Rapid scale-up
β_f	0.85, 1.15	Vertical transmission and reduced fertility due to HIV	Yes, No

Source: Parameters adapted from Timæus (1992) and Heuveline (2003).

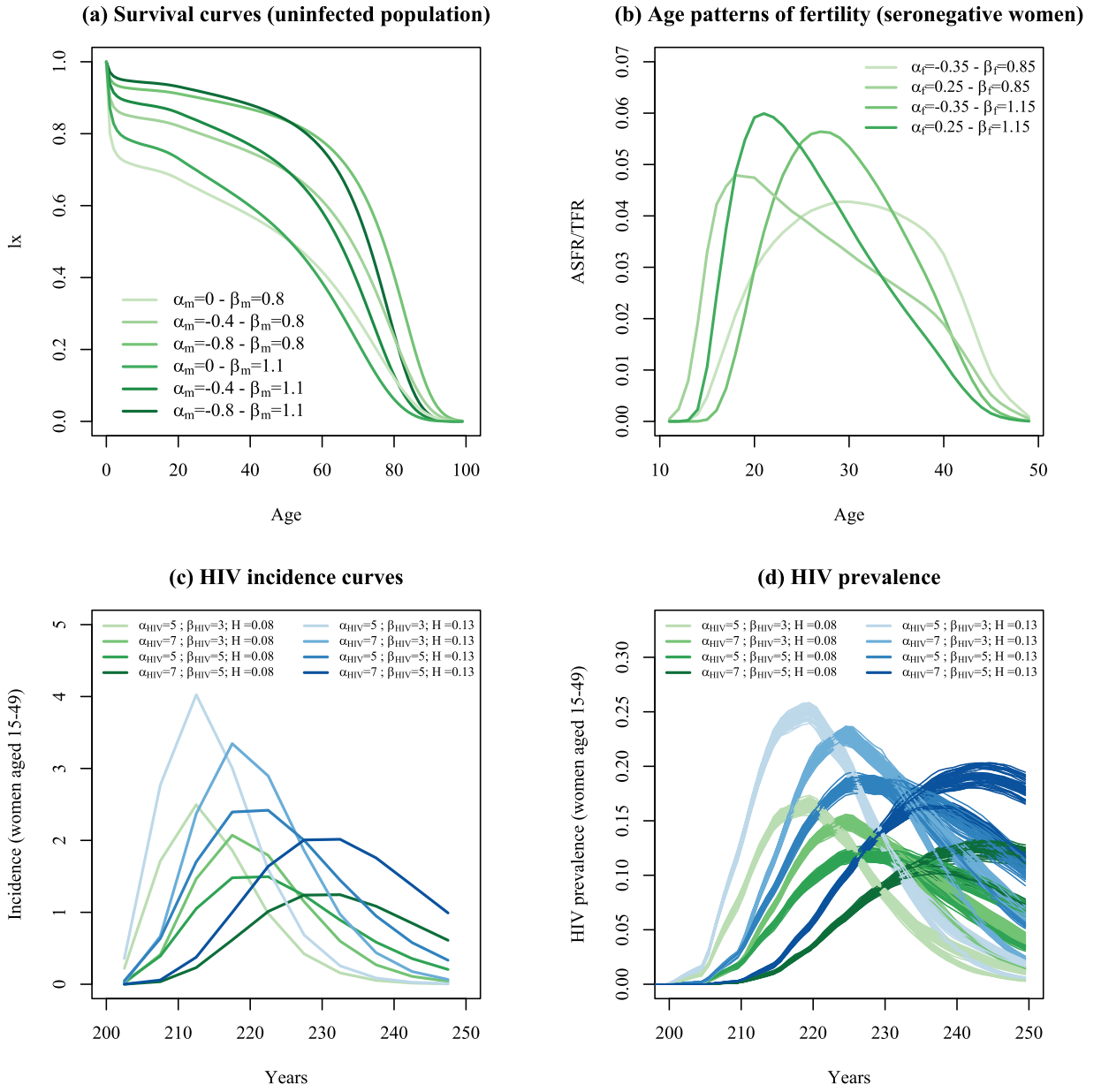

Figure 1 Inputs to simulation models: (a) Age patterns of non-AIDS mortality; (b) Fertility schedules in the absence of HIV; (c) HIV incidence curves; and Results: (d) Simulated trends in HIV prevalence

Note: This figure is best viewed online in colour.

Source: Authors' analysis based on the 576 different simulations with reduced fertility of HIV-positive mothers and vertical transmission.

prevalence measured in the 2005–06 DHS (21.1 per cent). According to UNAIDS, the peak in prevalence in women aged 15–49 was higher and earlier, at 28.3 per cent in 1996. The simulation, therefore, does not reproduce the evolution of the HIV epidemic in Zimbabwe exactly but follows a similar enough pathway to be used here for illustrative purposes. Figure S4 (Appendix C, supplementary material) compares the proportions of maternal orphans in all DHS conducted in high-HIV countries with those observed in the microsimulation set and also compares adult and child mortality rates in these two series. These comparisons suggest that our simulations are well calibrated.

Estimates obtained from the conventional method: One survey/census and standard coefficients

We first examine HIV-related biases in the orphanhood estimates obtained from the conventional

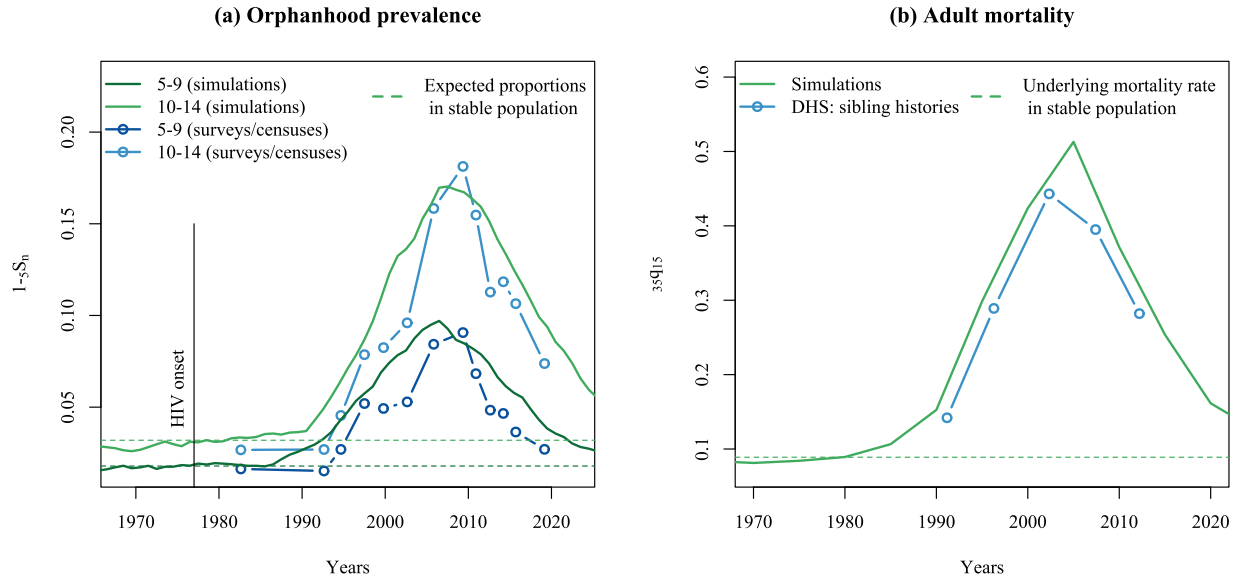

Figure 2 Calibration: (a) Orphanhood prevalence in children aged 5–14 in one simulation resembling Zimbabwe and in surveys and censuses from this country; (b) Adult women's mortality ($_{35}q_{15}$) in the same simulation set and in sibling histories from DHS from Zimbabwe

Note: This figure is best viewed online in colour.

Source: As for Figure 1. In addition, for Figure 2(a) orphanhood estimates for Zimbabwe were extracted from the 1982, 1992, 2002, and 2012 Censuses, the 1997 Intercensal Survey, the 1994, 1999, 2005–06, 2010–11, and 2015 DHS, and the 2009, 2014, and 2019 MICS. For Figure 2(b), sibling-based estimates of the probability $_{35}q_{15}$ were extracted from the 1994, 1999, 2005–06, 2010–11, and 2015 DHS.

method. Proportions of maternal orphans classified by five-year age groups were computed from simulations as if a survey or census had been conducted every five years. Indirect estimates were obtained using the coefficients developed by Timæus (1992) and time-located following Brass and Bamgboye (1981). The 'true' mortality rates were obtained by dividing the number of deaths by age, sex, and year by the corresponding exposure, using the exact dates of birth and death of all females who ever lived in the simulation. Figure 3(a) is based on the simulation that approximates the trends observed in Zimbabwe. It contrasts the indirect mortality estimates obtained from maternal orphanhood in respondents aged 5–9 and 15–19 (dashed lines) with the 'true' mortality rates (solid lines). The circles correspond to estimates derived from surveys and censuses in Zimbabwe. In the simulations, the indirect estimates agree well with the direct measures in the pre-HIV period. After the onset of the epidemic, the probability of dying between exact ages 25 and 35 ($_{10}q_{25}$) inferred from orphanhood (based on respondents aged 5–9) starts to deviate from the underlying mortality rates and is underestimated by as much as 58 per cent in 2004. The probability $_{20}q_{25}$, based on respondents aged 15–19, is also substantially biased, with a 44 per cent underestimate in 2004. To quantify the magnitude of the errors across all simulations with different mortality rates and compare age groups, we computed the ratio of the odds of surviving according to the indirect estimates to the 'true' odds of surviving, as follows:

$$\frac{{}_{n}p_{25}^{\text{indirect}}}{1-{}_{n}p_{25}^{\text{indirect}}} = \frac{1-{}_{n}p_{25}^{\text{true}}}{{}_{n}p_{25}^{\text{true}}}. \qquad (9)$$

Figure 3(b) displays the median ratios for the 576 simulations with vertical transmission and reduced fertility (see also Table S4, Appendix D, supplementary material). As in the Zimbabwe example, the indirect estimates are close to the underlying mortality rates before HIV is introduced: the median ratios range between 1.00 and 1.05. (Small deviations are to be expected as we did not use exactly the same parameters as Timæus (1992) to build the simulations.) Once HIV is introduced, the median ratios first decline below 1.00, indicating that mortality is overestimated in the 10–15 years following the onset of the epidemic. This is because trends are overly smoothed by the conventional time-location procedure: estimates for the beginning of the epidemic are capturing some of the subsequent mortality increase. This effect is most pronounced when estimating $_{20}p_{25}$ (median ratios = 0.93, seven

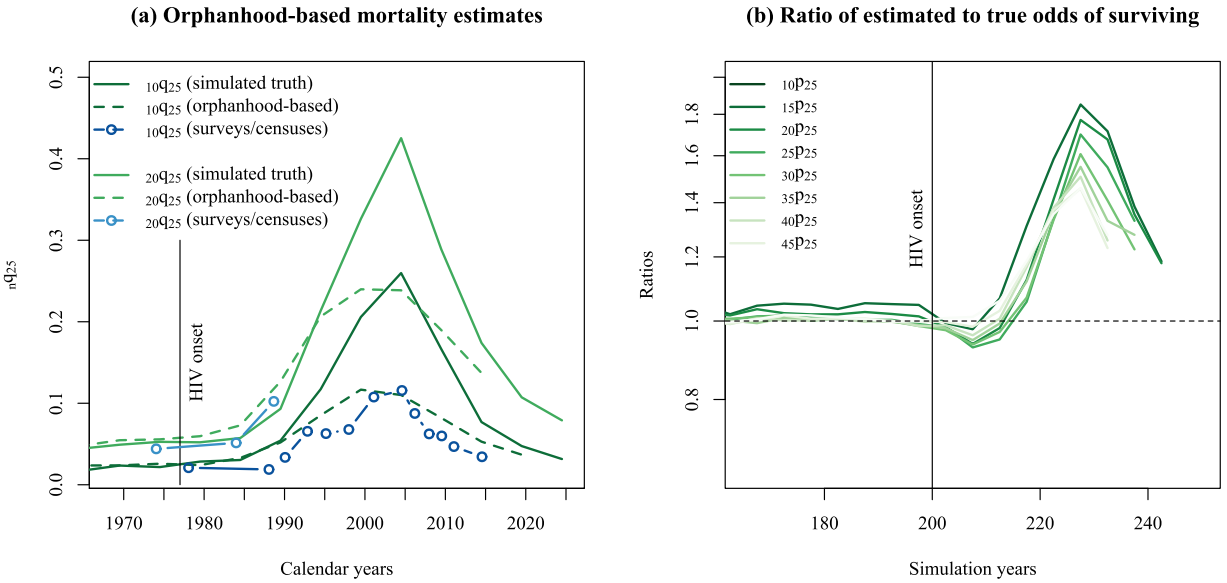

Figure 3 Conventional method: (a) Probabilities ${}_{10}q_{25}$ and ${}_{20}q_{25}$ estimated from orphanhood in surveys and censuses from Zimbabwe and in the simulation resembling Zimbabwe, compared with the simulated truth; (b) Median ratios of estimated to 'true' odds of surviving across the 576 simulations with reduced fertility and vertical transmission

Note: This figure is best viewed online in colour.

Source: As for Figure 2.

years after the onset of HIV). As the epidemic unfolds, the median ratios rise substantially for all survivorship probabilities before shrinking as the epidemic recedes. The bias is larger when estimates are inferred from reports from younger respondents, but the errors are still substantial for the older age groups. The odds of surviving between ages 25 and 35 are overestimated by as much as 85 per cent about 30 years after the onset of the epidemic, against 46 per cent for the probability ${}_{45}p_{25}$.

Existing adjustments for HIV-related bias

We detailed earlier the different adjustments developed by Timæus and Nunn (1997). Figure 4(a) shows the risks of dying obtained from the simulation resembling Zimbabwe and from surveys or censuses conducted there, after applying these adjustments when HIV prevalence at the time of birth is higher than 5 per cent. The indirect estimates of mortality are now much closer to the underlying mortality for the youngest respondents (5–9 years) but seem too high in the most recent periods. In addition, the indirect estimates for ${}_{20}q_{25}$ remain considerably lower than the underlying mortality rates. To generalize across all simulations with vertical transmission and reduced fertility, Figure 4(b) displays the median ratios of the estimated to 'true' life-table odds of surviving. For the youngest age group (n = 10), the errors are substantially reduced compared with estimates obtained without any adjustment for HIV. However, the odds of survival are overestimated about 20 years after the onset of the epidemic, before becoming underestimated, with median ratios approaching 0.60. Biases are much reduced for the probabilities ${}_{15}p_{25}$ to ${}_{20}p_{25}$, but the latest ratios are also lower than 1.00. For the older age groups, biases are similar to those observed with the original method. This is because at the time Timæus and Nunn (1997) conducted their study, Uganda was only about 15 years into its HIV epidemic and no evidence existed as to how large an impact it would have in future on the mortality of older women.

The remaining errors might have three sources, again related to biases in the proportions of mothers surviving, the conversion of proportions into life-table survivorship, and the procedure for estimating mortality trends. First, the adjustment for proportions of surviving mothers does not incorporate the effects of PMTCT on the risk of vertical transmission. Nor is the effect of ART on fertility and survival in HIV-positive women accounted for. The adjusted proportions of surviving mothers will therefore be too low once treatment has been scaled up. Figure 5 illustrates this. Figure 5(a) shows proportions of respondents with a surviving

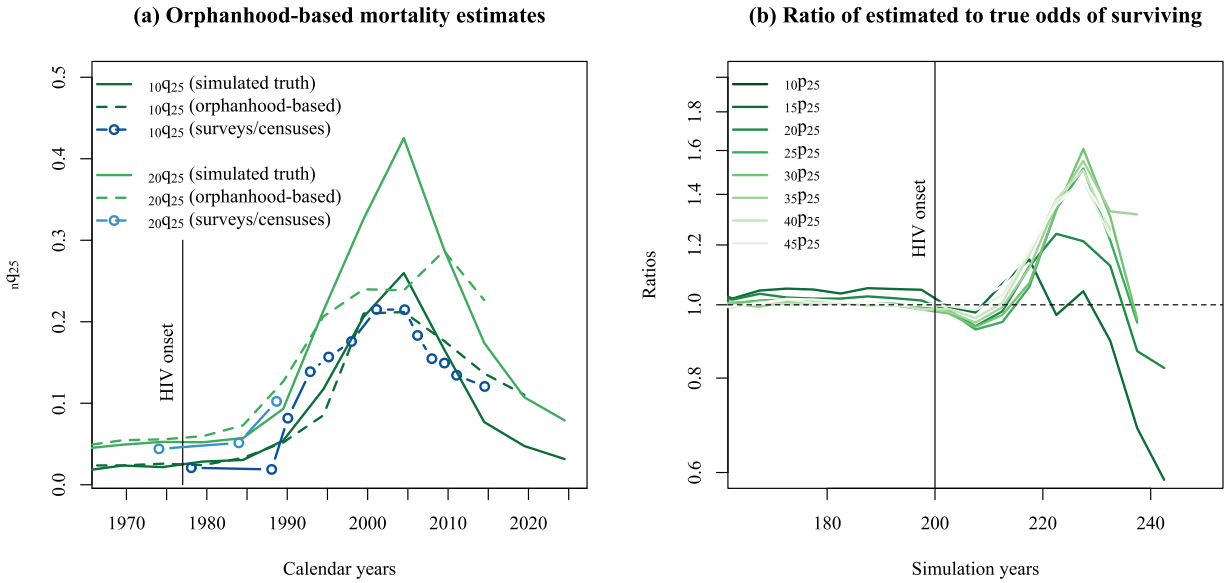

Figure 4 Timæus and Nunn (1997) method: (a) Probabilities ${}_{10}q_{25}$ and ${}_{20}q_{25}$ estimated from orphanhood in surveys and censuses from Zimbabwe and in the simulation resembling Zimbabwe, compared with the simulated truth; (b) Median ratios of estimated to 'true' odds of surviving across the 576 simulations with reduced fertility and vertical transmission

Note: This figure is best viewed online in colour.

Source: As for Figure 2.

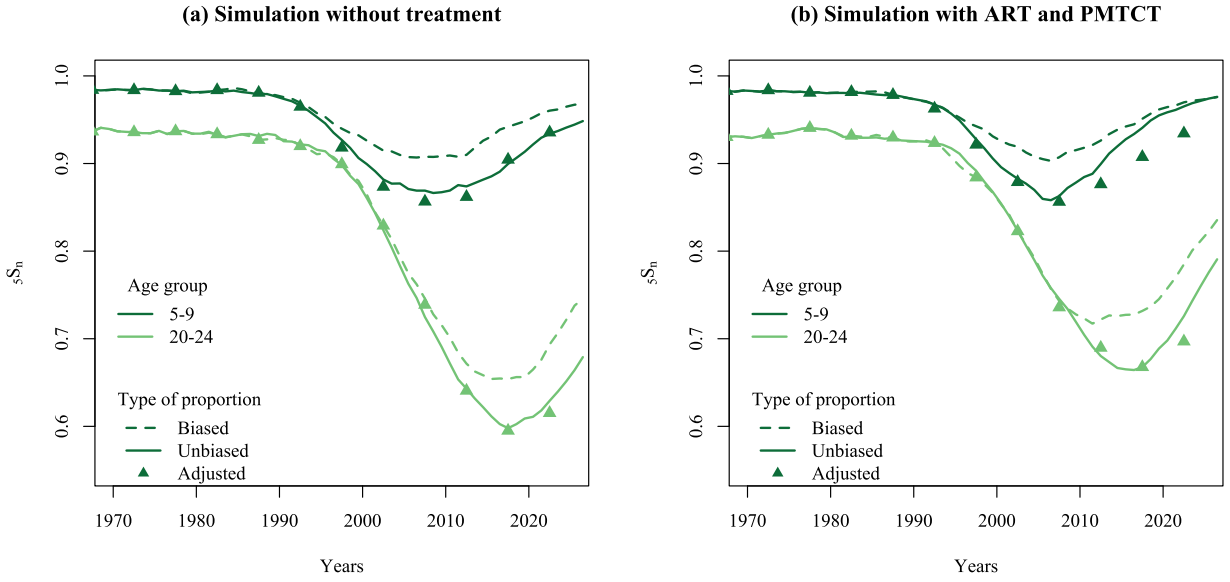

Figure 5 Effect of vertical transmission and reduced fertility in trends in proportions of respondents aged 5–9 and 20–24 with a surviving mother: (a) Simulation without treatment; (b) Simulation with treatment

Note: This figure is best viewed online in colour.

Source: Authors' analysis based on the simulation presented in Figure 2 and three variants, reflecting different scenarios for treatment and vertical transmission / reduced fertility. Adjustments applied to proportions with a surviving mother are based on Timæus and Nunn (1997).

mother in a simulation using the same parameters as the one resembling Zimbabwe, except that nobody receives ART. Figure 5(b) shows the same proportions but with treatment coverage reaching 90 per cent. The dashed lines refer to the proportions that according to the simulations would be observed

in surveys, while the solid lines represent the unbiased proportions. These unbiased proportions were obtained without any HIV-related bias and were computed in simulations with exactly the same parameters, except that we disabled vertical transmission and the reduced fertility of HIV-infected mothers. The proportions adjusted as suggested by Timæus and Nunn (1997) are displayed with triangles. In the absence of treatment (Figure 5 (a)), the adjusted proportions are consistent with the unbiased proportions, suggesting that vertical transmission and reduced fertility can indeed be accounted for in this way before ART and PMTCT are introduced. By contrast, in the simulation that includes ART and PMTCT (Figure 5(b)), the adjusted proportions are found to be too low once the treatments are introduced. To develop their adjustment, Timæus and Nunn (1997) had to assume that all HIV-positive mothers died when their child reached age five, so they then reduced the adjustment by a fixed age factor to account for the fact that many of the mothers of young children would still have been alive at the time of data collection. However, this procedure is no longer adequate, as the bias cannot be approximated based solely on h and F once a substantial proportion of infected women are receiving ART. This is because the numerators in equations (1) and (2) of Timæus and Nunn (1997) are no longer identical. Using their formulation, $N^{+}(a)$ (corresponding to the number of living HIV-positive women who would have given birth a years ago if their fertility were the same as other women's) is no longer zero in the presence of the treatment.

A second source of bias is that the coefficients developed in the 1990s were based on the limited evidence available at that time and also do not account for the introduction of treatment, which became available later. Timæus and Nunn (1997) used prospective mortality data from an HDSS where HIV prevalence among the adult population was about 8 per cent, a level well below the peak observed since in several countries. The age pattern of HIV prevalence was also assumed to be fixed, with seroprevalence peaking among women in their mid-20s. In our simulations, the age pattern of HIV varies over time. In the first 10 years after HIV is introduced, prevalence peaks among women aged 20–24, but it gradually shifts to older ages and by 20 years into the epidemic prevalence peaks among women aged 25–29 in about half the simulations. In addition, the scale-up of ART changes the age patterns of mortality. Since the mid-2000s, ART coverage has dramatically increased in SSA. By 2021, it had reached 82 per cent in West and Central Africa and 79 per cent in East and Southern Africa (UNAIDS 2022). As noted earlier, a third source of bias is that deriving a series of dated estimates from a single set of proportions is inappropriate when mortality trends have been highly disrupted.

A new method based on two sets of proportions of mothers alive

To address these three sources of error, we first re-examined the relationship between the unbiased proportions of mothers surviving and the proportions affected by fertility reduction and vertical transmission. In Figure 6, the graphs in the upper panel present the ratios of the unbiased to the observed proportions, according to HIV prevalence at birth, without any adjustment to the proportions, based only on simulations without treatment ($_5S_n/_5S_n^*$). Bias is linearly associated with prevalence, as established previously by Timæus and Nunn (1997). The coefficient of the slope of the linear regression is −0.248 for the 5–9 age group, −0.378 for the 10–14 age group, and −0.477 for the 15–19 age group. These coefficients are remarkably consistent with the adjustments that Timæus and Nunn (1997) developed analytically (i.e. $1 - 0.25 \times P$, $1 - 0.375 \times P$, and $1 - 0.5 \times P$; see Distortions due to HIV/AIDS subsection). In the middle panels of Figure 6, we present the ratios based on proportions after using such adjustments ($_5S_n/_5S_n'$) but considering now all simulations, including those with treatment. On average, these ratios are too high. Moreover, for the first age group, the error is directly related to PMTCT coverage at the time of birth. For the 15–19 age group, the magnitude of the bias is associated with ART coverage at the time of the survey.

We tested seven regression models to predict the bias in the proportions based on covariates made available for all countries by UNAIDS. We included as covariates various combinations of HIV prevalence, PMTCT, and ART coverage measured at time of survey or at birth (Table S5, Appendix E, supplementary material). The dependent variable was the ratio of the unbiased to the observed proportions. All the models were run separately for each age group. To evaluate model performance, we randomly selected 80 per cent of the simulations to fit the models and calculated the out-of-sample root mean square error (RMSE) based on predictions in the remaining simulations. The prediction

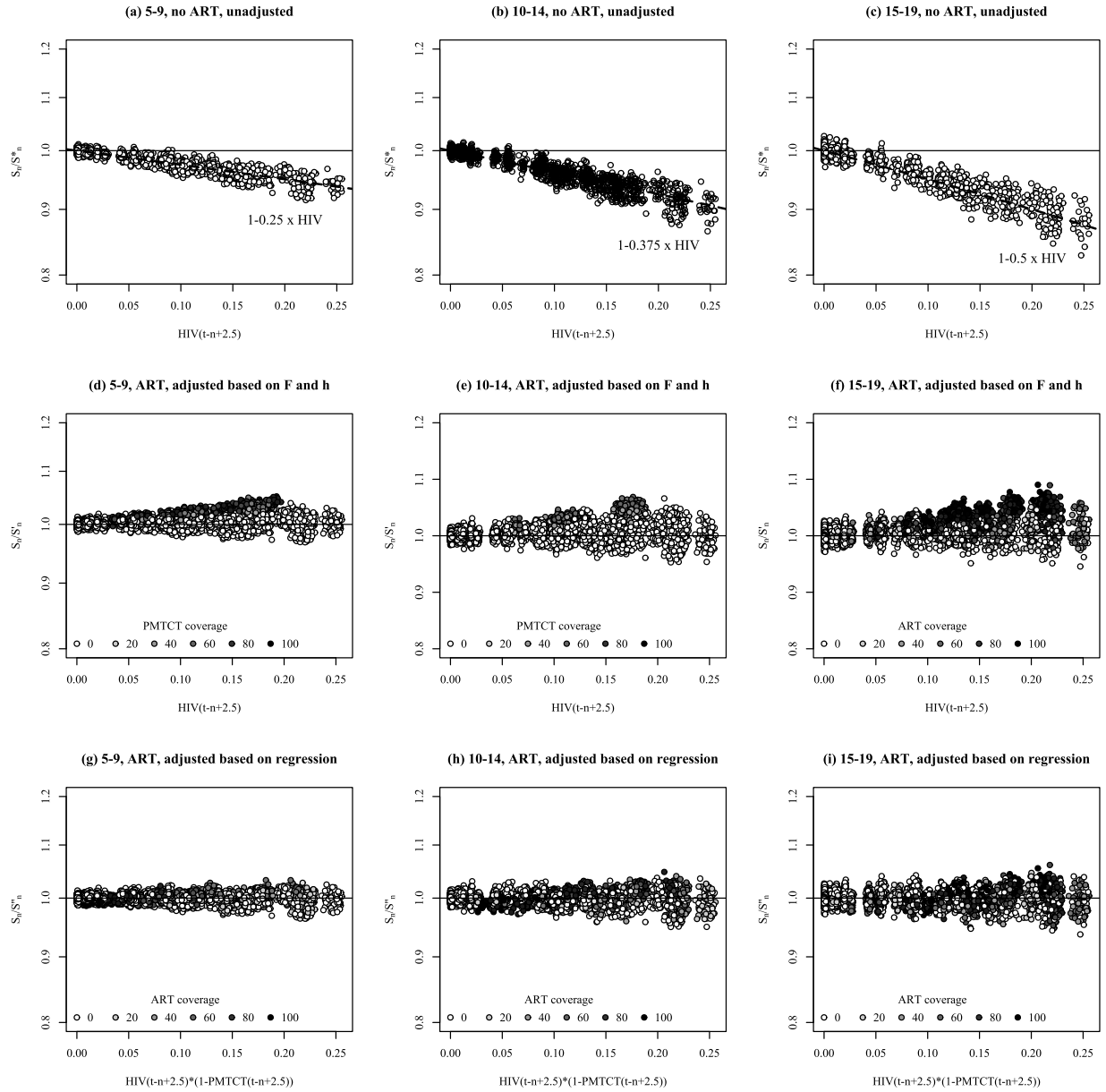

Figure 6 Ratios of unbiased to observed proportions of mothers surviving for three age groups (5–9, 10–14, and 15–19): (a–c) In simulations without treatments (${}_5S(h)_n$/ ${}_5S(h)^*_n$); (d–f) In all simulations with adjustments developed by Timæus and Nunn (1997) (${}_5S(h)_n$ / ${}_5S(h)'_n$); and (g–i) With adjustments obtained through regression (${}_5S(h)_n$ / ${}_5S(h)''_n$)

Source: Authors' analysis based on all 1,152 simulations outlined in the Data and methods section.

errors are displayed in Table S5. Across age groups, the best-performing model is as follows:

$$\begin{aligned}\frac{{}_5S_n}{{}_5S^*_n} = {} & \beta_0(n) \\ & + \beta_1(n)\,[HIV_{t-n+2.5} \times (1 - \mathrm{PMTCT}_{t-n+2.5})] \\ & + \beta_2(n) ART_t \end{aligned} \tag{10}$$

where $HIV_{t-n+2.5}$ and $\mathrm{PMTCT}_{t-n+2.5}$ are HIV prevalence and PMTCT coverage, respectively, at the time of respondents' birth, while ART_t refers to ART coverage at the time of survey. The β coefficients are presented in Table 2. The ratios obtained from proportions corrected by means of these coefficients $\left(\frac{{}_5S_n}{{}_5S''_n}\right)$ are displayed in the bottom panels of Figure 6 and show the reduction in the errors.

Once the proportions of mothers surviving had been corrected for HIV-related bias in the reports, they could be related to the underlying mortality levels, but this raised the question of the reference

Table 2 New coefficients for adjusting proportions of mothers surviving to account for HIV-related bias, by age

n	β_0	β_1	β_2	RMSE	R^2
0	1.0000	−0.0813	−0.0013	0.0015	0.8401
5	1.0000	−0.2296	0.0032	0.0031	0.8975
10	1.0000	−0.3594	0.0164	0.0042	0.9121
15	1.0000	−0.4672	0.0264	0.0048	0.9144
20	0.9999	−0.5200	0.0154	0.0053	0.9026
25	0.9999	−0.5500	0.0054	0.0056	0.8538
30	1.0000	−0.5550	0.0007	0.0065	0.6352

Source: Authors'analysis based on simulations outlined in the Data and methods section.

period to consider. It did not seem possible to develop a new procedure for dating the estimates that captured the diversity of temporal changes in mortality in HIV/AIDS-affected settings or that adequately addressed the built-in tendency of the lifetime proportions to smooth out abrupt discontinuities in mortality trends. To circumvent this problem, we used two sets of proportions from successive surveys or censuses to construct synthetic cohorts ($_5S(h)_5$) for periods of time centred on h. The construction of synthetic cohorts was first proposed by Zlotnik and Hill (1981), who suggested chaining together changes experienced by a given birth cohort (in terms of the survival of their parents) during the intercensal or intersurvey period. As an alternative, Preston (1987) proposed working with the changes experienced by a given age group between two censuses or surveys, by computing a correction factor based on the growth rate in the proportion of parents alive. This provides the proportion of parents alive that pertains to the intercensal period and would be observed in a stationary population. This approach was originally developed to generate estimates that refer to more recent periods than the measures derived from a single inquiry and that are less biased by the underreporting of parental deaths (Timæus 1986). In contexts affected by HIV, synthetic cohorts offer the additional advantage that they do not require any assumption made about the mortality trend prior to collection of the first set of data.

Proportions for a hypothetical cohort were obtained by adjusting each set of proportions for HIV-related bias based on equation (10) and chaining successive sets as suggested by Preston (1987). The remaining task was then to convert these proportions into life-table survivorship estimates. From microsimulations, Figure 7(a) presents the

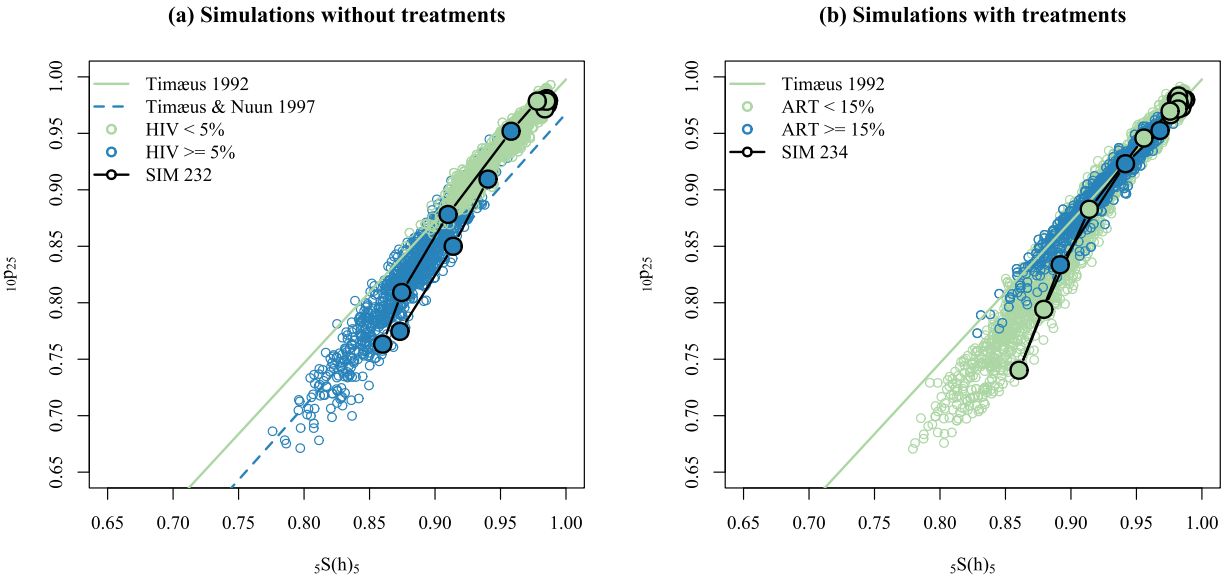

Figure 7 Relationship between growth-corrected proportions of respondents with a mother surviving, $_5S(h)_5$, and life-table survivorship, $_{10}p_{25}$
Note: This figure is best viewed online in colour.
Source: As for Figure 1.

relationship between the probabilities ${}_{10}p_{25}$ and proportions ${}_5S(h)_5$, in simulations without treatment. The simulation highlighted with large, bold circles has the same parameters as the one that resembles Zimbabwe but without any treatment. When HIV prevalence is less than 5 per cent, the relationship between the two series is well represented by the coefficients from Timæus (1992) (straight solid line, for a value of M of 25). However, as HIV prevalence increases, the slope of the regression line steepens, as already demonstrated by Timæus and Nunn (1997). They thus recalculated the intercept and slope of the regression line but without introducing HIV as a covariate. Such a recalculation will lead to discontinuities in the trends when shifting from one set of coefficients to the other, due to the large difference in their intercepts (dashed line in Figure 7(a)). It has also become important to incorporate ART as a covariate, as the slope of the regression line declines again when ART coverage increases, as illustrated in Figure 7(b).

To calculate new coefficients, we evaluated different regression models predicting survivorship probabilities from the simulated proportions, by testing combinations of predictors including HIV prevalence and ART coverage, measured at the midpoint between two surveys or at respondents' time of birth (Table S6, Appendix F, supplementary material). We also evaluated the predictive performance of models including $HIV \times (1 - ART)$, which captures the percentage of women who are seropositive and have not initiated treatment. Because the synthetic proportions are based on changes over time in the proportions of mothers surviving, in some models we included the absolute difference in HIV prevalence or in $HIV \times (1 - ART)$ between the two surveys. Some models were fitted over the full data set; others used two regressions, one for data points without any treatment and one for data points with a least some women on ART. This helps to capture potential changes in age patterns of mortality in growing and receding epidemics, as in most countries the early phases of ART roll-out correspond to the start of the decline in adult mortality (Reniers et al. 2014). Across age groups, the best-performing approach uses separate models for the pre-ART period and the period after treatment programmes are introduced:

$$
{}_np_{25} = \begin{cases} \left\{ \begin{array}{l} \beta_0(n) + \beta_1(n)\, M + \beta_2(n){}_5S(h)_{n-5} \\ + \beta_3(n) HIV_t + \beta_4(n)\, \Delta HIV \end{array} \right\} (ART_t = 0) \\ \left\{ \begin{array}{l} \beta_5(n) + \beta_6(n)\, M + \beta_7(n){}_5S(h)_{n-5} \\ + \beta_8(n)[HIV_t \times (1 - ART_t)] \\ \quad + \beta_9(n)\, \Delta[HIV \times (1 - ART)] \end{array} \right\} (ART_t > 0) \end{cases} \tag{11}
$$

Here HIV_t and ART_t refer to HIV prevalence and ART coverage at the time of data collection and are obtained as the average of estimates from each survey (since two series are required to calculate synthetic proportions). The indicators of trends, ΔHIV and $\Delta[HIV \times (1 - ART)]$, refer to the absolute difference in the measures between the two surveys. The corresponding β coefficients are displayed in Table 3. An Excel workbook is available in the supplementary material to facilitate the calculations.

As with other orphanhood-based methods, this new variant is based on approximating the proportion of surviving mothers from the proportion of children whose mothers are survivors. This entails assuming that maternal survival remains unaffected by both child survival and fertility and also that child survival is independent of sibship size. After correcting for biases associated

Table 3 New coefficients for converting proportions of mothers surviving into life-table survivorship in the presence of HIV and ART, by age

	Pre-ART period					Post-ART period				
n	β_0	β_1	β_2	β_3	β_4	β_5	β_6	β_7	β_8	β_9
10	−0.2742	0.0010	1.2455	−0.2039	0.2609	−0.3532	0.0021	1.3030	−0.1336	−0.0017
15	−0.1488	0.0016	1.1053	−0.2611	0.3539	−0.2393	0.0026	1.1732	−0.1056	0.0183
20	−0.1123	0.0027	1.0387	−0.2747	0.3711	−0.1693	0.0031	1.0854	−0.1071	−0.0330
25	−0.1336	0.0047	1.0082	−0.2841	0.3386	−0.1559	0.0045	1.0442	−0.1866	−0.1147
30	−0.2051	0.0075	1.0078	−0.2701	0.2995	−0.1915	0.0069	1.0223	−0.2466	−0.0751
35	−0.3074	0.0113	1.0182	−0.2213	0.2649	−0.2708	0.0100	1.0241	−0.2220	−0.0228
40	−0.4580	0.0162	1.0530	−0.1323	0.1770	−0.3801	0.0136	1.0536	−0.1708	−0.0691
45	−0.6244	0.0215	1.1031	−0.0343	0.0671	−0.5119	0.0176	1.1132	−0.1318	−0.2382

Source: As for Table 2.

specifically with HIV/AIDS, any resultant selection biases arising from violations of these assumptions are expected to be minimal (Palloni et al. 1984). When combining age-specific estimates of ${}_np_{25}$ into a summary index, an additional assumption is required: that the chosen model life table reflects the underlying age pattern of mortality. We suggest converting all age-specific estimates into ${}_{35}q_{15}$ using a model life table that incorporates mortality attributable to AIDS (INDEPTH 2004) and then averaging the resulting probabilities.

Orphanhood-based estimates of adult mortality for selected countries in sub-Saharan Africa

This subsection describes our testing of the different estimation approaches on real data for 16 countries where peak HIV prevalence has exceeded 5 per cent (UNAIDS 2022). We extracted proportions of surviving mothers by age group from censuses, DHS, MICS, and other nationally representative surveys (see Appendix G, supplementary material) and constructed two sets of estimates:

- The first set considers each census or survey separately. We used standard coefficients when HIV prevalence was less than 5 per cent and those developed by Timæus and Nunn (1997) when it was greater than or equal to 5 per cent. The proportions of surviving mothers were adjusted for HIV/AIDS bias based only on HIV prevalence. The reference periods were calculated using the method developed by Brass and Bamgboye (1981). This series corresponds to the procedure generally followed in previous research.
- The second set adjusts the proportions for HIV-related bias using the coefficients in Table 2 and chains successive sets of proportions together to construct synthetic cohorts. We combined inquiries separated by at least three years but less than 11 years to avoid irregularities associated with very short intervals and to allow the combination of successive censuses, typically conducted every 10 years. Synthetic proportions were converted into life-table estimates using the coefficients derived from microsimulations (Table 3), combined with estimates of HIV prevalence and ART coverage from UNAIDS (2022). The resulting mortality estimates are available in Appendix H (supplementary material).

In the absence of a gold standard, Figure 8 contrasts the orphanhood-based estimates with mortality rates from *World Population Prospects* (WPP) (United Nations 2022), after interpolating these rates to obtain a value referring to the same

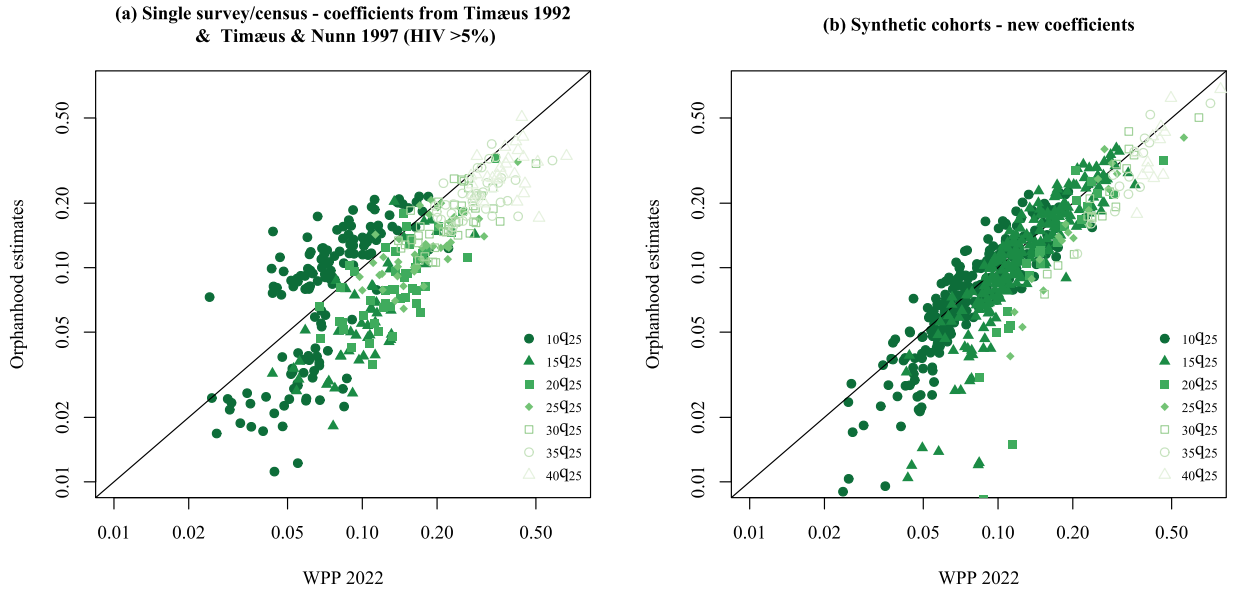

Figure 8 Comparison of women's probabilities of dying (${}_nq_{25}$) obtained from maternal orphanhood and WPP data using two estimation approaches

Notes: A logarithmic scale is used for both axes. This figure is best viewed online in colour.

Source: Surveys and censuses detailed in Appendix G (supplementary material) and *World Population Prospects* (United Nations 2022).

time period. The country-specific estimates of the probabilities ${}_{10}q_{25}$ and ${}_{15}q_{25}$ calculated with the new approach are displayed in Figure 9 (for comparison, see Figure S5, Appendix H, supplementary material, for the first set of estimates, based on a single survey or census). Orphanhood data are one input into the existing WPP estimates of mortality. Thus, the WPP estimates and ours are not entirely independent. In most of the 16 countries though, the documentation available suggests that direct estimates calculated from sibling histories and questions about recent deaths in the household and the comparison of successive census counts have more influence on the WPP estimates than the orphanhood data. In Figure 9, mortality estimates are also compared with those extracted from sibling survival histories collected in the DHS for the six years prior to each survey (Masquelier et al. 2014). There we focus on the probabilities ${}_{10}q_{25}$ and ${}_{15}q_{25}$ because these are obtained from respondents aged 5–9 and

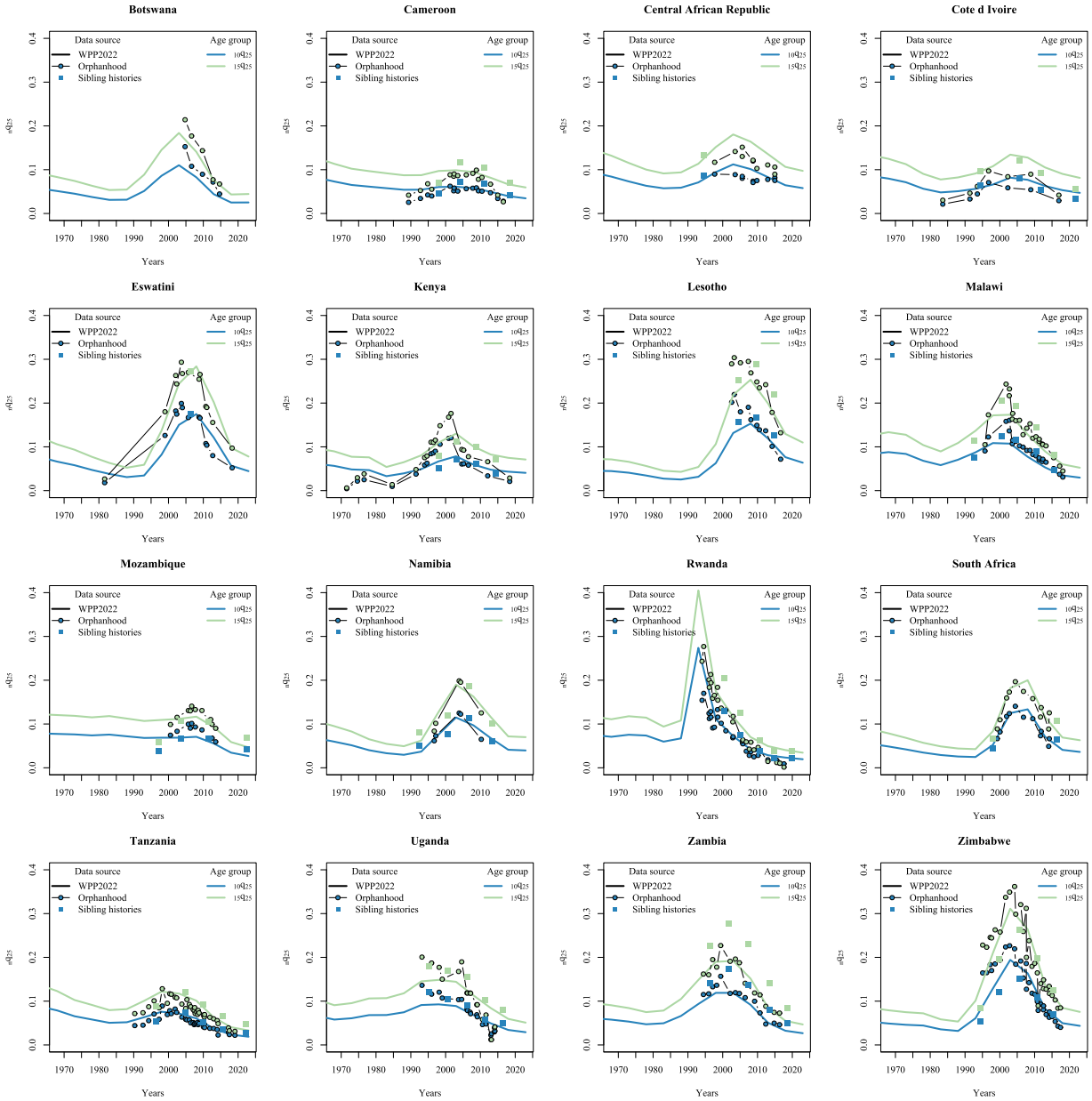

Figure 9 Trends in women's probabilities of dying (${}_{10}q_{25}$ and ${}_{15}q_{25}$) using the new coefficients on data from three sources: orphanhood data from surveys/censuses, estimates from *World Population Prospects* 2022, and sibling histories

Note: This figure is best viewed online in colour.

Source: Surveys and censuses detailed in Appendix G (supplementary material) and *World Population Prospects* (United Nations 2022).

10–14. More observations are available for these age groups than for older ones since the DHS and MICS do not ask adults about parental survival.

According to the patterns observed in simulations, when mortality is high we expect the first set of mortality rates to be overestimated based on reports from children aged 5–9 and underestimated when based on older respondents. This is indeed what is observed in Figure 8(a): the probability ${}_{10}q_{25}$ inferred from maternal survival tends to be below the levels predicted by WPP when the risk of dying is below 0.07, whereas it tends to be higher when mortality increases above this threshold. The overestimation is likely reduced because of adoption bias, which was not introduced in the simulations, and will predominantly affect estimates from a single survey or census, with the proportions in synthetic cohorts being less affected. Overall, the median ratio between probabilities ${}_{10}q_{25}$ derived from orphanhood and WPP estimates is 1.26. This ratio drops below one (0.83) when mortality is lower than 0.07 in WPP, and it reaches 1.28 when mortality is higher. This pattern is also visible in the country-specific plots in Figure S5. There are fewer data points for evaluating the bias on the ${}_{15}q_{25}$ probability, but it appears to be consistently lower than the WPP estimates. The median ratio between orphanhood-based probabilities and WPP estimates is as low as 0.54 for this age group. This is likely due to a combination of recall and modelling biases.

Estimates obtained with the new estimation approach do not refer to the same periods: there are fewer estimates available from respondents aged 5–9 years (since it is necessary to combine surveys or censuses) but slightly more from those aged 10–14 (since the Brass dating method, which requires values up to age 19, is no longer used). Overall, there is a better congruence with WPP than in the previous set of orphanhood estimates: the median ratio between orphanhood-based rates and WPP is 0.99 for ${}_{10}q_{25}$ and 0.91 for ${}_{15}q_{25}$ (compared with 1.26 and 0.54 with the previous set of orphanhood estimates). Moreover, these median ratios remain stable over time: for the ${}_{10}q_{25}$ probability, the ratio is 1.05 for the pre-ART period and 0.98 for the post-ART period, while the corresponding indices for the ${}_{15}q_{25}$ probability are 0.91 at both periods. The country-specific trends suggest that the new estimates track the WPP probabilities of death remarkably well (Figure 9). This is especially the case in Malawi, Namibia, Rwanda, South Africa, Tanzania, Uganda, Zambia, and Zimbabwe. The rises and falls in probabilities are well reproduced, and the difference between the ${}_{10}q_{25}$ and ${}_{15}q_{25}$ probabilities is comparable to that predicted by the WPP. In most countries (except Zimbabwe in the 1990s and 2000s), the orphanhood estimates are also in line with the probabilities of death from sibling histories.

Discussion

Our results demonstrate the large impact of HIV-associated biases on mortality levels inferred from maternal survival data. We built on previous work by Timæus and Nunn (1997) by generalizing the series of simulations and relaxing the assumption of a stable population. We showed that without any adjustment, the conventional orphanhood method will overestimate mortality in the first few years following the onset of an HIV epidemic and then substantially underestimate mortality as the epidemic matures. Biases are considerably reduced when using the adjustments developed by Timæus and Nunn (1997), but they can be further reduced by incorporating information on HIV prevalence, PMTCT coverage, and ART coverage. The construction of synthetic cohorts also avoids the heavy smoothing of abrupt changes in the trend in mortality imposed by the basic orphanhood method. This new variant makes use of prevalence and treatment trends, so unlike estimates from sibling survival histories or recent household deaths, it does not provide a direct measure of mortality. The resulting estimates can, however, complement other series of primary estimates to help reconstruct mortality trends during the epidemic better. When applied to survey and census data from 16 countries in SSA, this new approach provides estimates that better reflect the timing of the epidemic and are more consistent with expectations based on WPP and on sibling histories. Once treatment programmes are scaled up to the point that HIV-positive adults benefit from the same survival chances as HIV-negative adults, and vertical transmission is suppressed in the general population, no correction will be needed. However, reports on parental survival being collected currently are still affected by selection biases. Moreover, estimates based on existing data need to be made with methods that adequately reflect mortality patterns before, during, and after the scale-up of ART.

The new method proposed in this study has some limitations. First, the adjustments proposed here are designed for estimating women's mortality only. Mortality estimates for men made from paternal

orphanhood data will also be biased because fathers can infect or be infected by mothers, who themselves can transmit the virus to their children. Unfortunately, due to the complexity of modelling the concordance between the HIV status of mothers and fathers and the impact of HIV on men's fertility, no adjustment has yet been developed for men's mortality. One avenue for future development in this regard might be to leverage the sophisticated modelling of paternal orphanhood in the Spectrum package (Grassly and Timæus 2005), but this would require revising the software to produce outputs on orphanhood in youth and adults as well. Second, this study was limited by the assumptions made to model the demographic impact of HIV. For example, treatment allocation was carried out randomly at five-year intervals, and the mortality of orphans was assumed to be the same as that of children with living parents (apart from vertical transmission). Most of the model inputs for the HIV epidemic, such as HIV survival and the age pattern of incidence, were considered fixed. Third, and perhaps most importantly, we focused here only on selection biases, leaving aside other possible reporting biases. The most pervasive problem is the adoption effect. The potential magnitude of this adoption bias can be gauged from a cohort study conducted in Manicaland (Zimbabwe). Robertson et al. (2008) analysed the consistency of reporting of parent survival status across successive rounds and found that out of 198 children reported as maternal orphans in the first round (and followed up to the third round), as many as one-third were reported as non-orphans at least once in the next two rounds. Another problem is non-response. Although the proportions of missing data on questions about orphanhood are usually rather low, they can be of the same order of magnitude as the proportions of young children that are orphans. Researchers thus need to make assumptions about the orphanhood status of children with missing data. Finally, ages reported in censuses and surveys can be affected by inaccuracies, such as age exaggeration and heaping on round digits. Because of these different sources of error, estimates from orphan data should always be viewed with caution and compared with other sources. Nevertheless, in this study, when they were compared with sibling survival data, they provided comparable estimates of mortality after making the adjustments proposed here for HIV-related bias.

Despite these limitations, this study has demonstrated that parental survival data remain useful for estimating mortality in countries lacking a complete death registration system. Provided disaggregated prevalence and treatment data are available, the new variant of the orphanhood method we developed could also be used to study mortality differentials in settings affected by HIV. More research is needed to investigate recall errors and develop ways of adjusting for bias in paternal orphanhood data. Statistical models could also be developed to combine orphanhood estimates with data from recent household deaths in censuses and from sibling histories, similarly to well-established models used for child mortality (Alkema and New 2014). Data on parental survival should be more systematically collected as they can help fill important data gaps in SSA and track progress against the HIV epidemic. In the DHS and MICS, questions on parental survival should be extended to adult respondents as well as children under 18. Additional questions could also be asked in surveys about the ages of living parents, ages at death for parents who have died or, most promisingly, their dates of death, to allow more direct calculation (Chackiel and Orellana 1985). Although HIV/AIDS-related mortality has declined significantly in recent decades, the epidemic is far from over, and the true extent of excess mortality associated with this epidemic remains difficult to assess to this day.

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1 Bruno Masquelier is based at the Centre for Demographic Research (DEMO), UCLouvain, Belgium. Ian M. Timæus is affiliated with the Population Studies Group, London School of Hygiene and Tropical Medicine, UK, and the Centre for Actuarial Research, University of Cape Town, South Africa.

2 Please direct all correspondence to Bruno Masquelier, Centre for Demographic Research (DEMO), UCLouvain, Louvain-la-Neuve 1348, Belgium; or by E-mail: bruno.masquelier@uclouvain.be.

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ORCID

Bruno Masquelier http://orcid.org/0000-0002-9585-891X

Ian M. Timæus http://orcid.org/0000-0001-8011-4806

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