A Bayesian parametric model to estimate and reconstruct male age-specific fertility rates

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Abstract

Research on human fertility has primarily focused on women, with male fertility remaining underexplored. The biggest differences in timing and magnitude between male and female fertility is observed in the Global South, where data on male fertility is not widely available. In this project we propose a Bayesian parametric model to estimate and reconstruct male fertility rates for countries with no civil registration and vital statistics systems for past, present, and future periods. We draw on the own-children method applied to Demographic and Health Surveys (DHS) from various countries. The statistical model we propose, which centers on a skew-normal distribution, accounts for missing data, small samples, and data quality issues. The model is flexible enough to capture variations in male age-specific fertility rates across different populations and periods, and its parameters can be interpreted in terms of fertility trends. The approach allows reconstructing estimates for years without data, combine surveys covering the same year, and incorporating sampling errors from surveys. The methodology also ensures that yearly estimated male age-specific fertility rates are coherent with yearly births estimates from the United Nations World Population Prospects. Our results suggest that there is a general convergence between male and female TFRs over time but the mean age at parenthood remains substantially higher for males compared to females in the countries studied. This research will contribute to a more comprehensive understanding of male fertility trends and provide essential inputs for modeling kinship structures, orphanhood, and conducting indirect mortality estimates.

1 Introduction

Research on human fertility has historically focused on women, leaving male fertility largely understudied. This is particularly evident in the lack of global databases on male fertility. While data on past, current, and projected fertility are widely available for women (for example, the UN-World Population Prospects (UN-WPP) estimates and projections (United Nations 2024)), such information is limited for men (Schoumaker 2019). Given the central role of reproduction in human life and society, understanding fundamental aspects of male fertility is important for population studies. Theories of fertility transitions have long recognized the role of men in fertility behavior, but these ideas often lack empirical support and remain 'in search of evidence' (Coleman 2000). Improved measures of male fertility are also critical for mortality research, such as measuring paternal and double orphans (Hillis et al. 2021) or conducting indirect mortality estimates (Paget and Timaeus 1994, Timaeus 1991). Male fertility also has implications for evolutionary demography (Tuljapurkar et al. 2007) and for modeling kinship structures through patrilineal descent (Alburez-Gutierrez et al. 2023, Caswell 2022), among other areas.

Some recent studies have attempted to fill this gap by documenting male fertility from a comparative perspective. Dudel and Klüsener (2021) reconstructed a time series of male age-specific fertility rates in 17 Western countries between the 1960s-1970's and 2010s. Recent attempts have tried to project future male fertility but have again focused on countries in the Global North where good quality data are available (Ellison et al. 2024). For countries without civil registration and vital statistics (CRVS) systems, Schoumaker (2017) compared three methods applied on Demographic and Health Surveys (DHS) to calculate age-specific male fertility rates. Estimates from the own-children method were found to be the most reliable. This method requires the household roster data from the DHS (or similar surveys), which are widely available in many countries. Following this work, Schoumaker (2019) produced estimates of age-specific fertility rates and total fertility rates for 163 countries in 2013, using the own-children method with survey data and census data. However, estimates of male fertility are still lacking for many countries and time periods, in part due to a lack of data and data quality issues.

This lack of male fertility estimates has led to the frequent use of the 'androgynous approximation' in kinship modeling, where female fertility patterns are used to approximate male fertility patterns (Caswell 2022). While the androgynous assumption may hold in some regions of the world, it may be unrealistic in some others, particularly, sub-Saharan Africa. From a global perspective where data are available, variations in male fertility are much more pronounced than in female fertility (Schoumaker 2019). For example, while in European countries, male and female total fertility rates (TFRs) are similar, in half of sub-Saharan countries, male TFRs are above 8.5 children, significantly higher than female TFRs. In half of the countries included in Schoumaker's study, male fertility is at least 15 percent higher than female fertility. In addition to the difference in fertility levels, men also tend to have their children at older ages. This can be partly explained by the differences in age at marriage between men and women (Mignot 2010). These results suggest that age heterogeneity in male age-specific fertility rates (ASFRs) is higher than in female ASFRs.

Even where survey data allow for measurement of male fertility, data are often erratic, subject to high standard errors, and not collected regularly, making the underlying trend in male fertility unclear. In these cases, a statistical model is needed. To our knowledge, only one model has been proposed to estimate male ASFR (Paget and Timaeus 1994). The authors' contribution was to develop a standard male fertility schedule that can be used in the Brass relational Gompertz model (Booth 1984). This followed their observation that male and female fertility schedules have a similar shape, being unimodal and right-skewed, but male fertility is distributed over a wider age range. This is explained by the fact that men in good health are sexually competent into their seventies and eighties (Hogan 1980). To account for the greater heterogeneity across ages, they used a 'stretch factor' to convert the Booth's female standard into a male standard (Paget and Timaeus 1994).

In contrast to the sparse literature on modeling male fertility, numerous models have been proposed for female fertility. For example, Hoem et al. (1981) compared classical functions such as the Hadwiger (Hadwiger 1940), the Coale-Trussell (Coale and Trussell 1974), and other functions and densities in their ability to fit the Danish ASFR over the period 1962-1971. More recently, several statistical approaches have been developed for modeling female fertility, ranging from classical parametric functions to more flexible probabilistic models (Peristera and Kostaki 2007, Schmertmann 2003, Mazzuco and Scarpa 2015). Mazzuco and Scarpa (2015) proposed a model based on flexible skew symmetric probability density functions, which allows for the fitting of fertility schedules with two modes. Importantly for the current paper, the authors observed that the skew-normal density, developed by Azzalini (1985), performs better than classical fertility models for modeling unimodal fertility curves.

The skew-normal model is a parametric model summarizing main patterns across populations and over time using a reduced set of parameters that can be interpreted in terms of prevailing fertility trends. Indeed, Azzalini and Capitanio (2003) proposed a reparametrization of the skew-normal model to overcome the difficulty of maximizing the likelihood when the skewness parameter is close to zero. In this form, the function estimates the entire ASFR age schedule with four parameters that can be interpreted in terms of fertility trends: the total fertility rate, the mean age at birth, the concentration of fertility rates around their mean or heterogeneity, and the skewness of the fertility schedule (Mazzuco and Zanotto 2025). Furthermore, the model has all the desired characteristics to model demographic processes: smoothness, parsimony, interpolation, comparison, trends and forecasting, and analytic manipulation (Congdon 1993).

Our work is part of an effort to produce age-specific male fertility rates around the world for current, past and future periods. Using a Bayesian framework, we will estimate male ASFRs in countries and periods with deficient, or limited data on male fertility. Unlike previous models that rely on simplifying assumptions about male fertility patterns, our approach incorporates more flexibility through the skew-normal density function while remaining parsimonious. The Bayesian framework allows for the sampling error of the survey estimates to be taken into account, combine different surveys for the same period, and also allows male fertility patterns to be reconstructed for periods when the DHS data are not available. In addition, our methodology uses the United Nations World Population Prospects births estimates (United Nations 2024) to compute male TFRs. In this way, we ensure that yearly estimated male ASFRs are coherent with yearly births estimates from the UN-WPP.

In what follows, we first present the data used to measure male fertility in countries that do not have a functioning CRVS systems. We then describe the Bayesian skew-normal model we propose to estimate male age-specific fertility rates. The results section is divided into three subsections. First, we compare the performance of the skew-normal model with Brass's relational Gompertz model for four selected countries with different fertility levels. Second, we look at the reconstructed time series of male fertility schedules for an example country. Third, we show the temporal evolution of the estimated parameters for a selection of eight countries, and compare the trends in TFR and mean age at parenthood between males and females. We conclude with a discussion.

2 Data and Methods

2.1 Own-children method applied to the DHS

As shown in previous work, the own children method can be used to calculate male age-specific fertility rates with household roster data from demographic surveys (Schoumaker 2017; 2019). The method, which is adapted from the own children method for women, uses data collected on living children and their biological fathers. Children are linked to their father if they live in the same household. Children whose father is deceased are dropped from the file, as this greatly simplifies the method (Schoumaker 2017). For the other children who do not live with their father (unmatched children), the father's age is imputed using random hot-deck imputation based on the child's and mother's ages. Next, each unmatched child is matched with a father of the same age as the imputed age. In this way, we obtain a data file of men and children (whose father is alive). Finally, each surviving child is weighted by the inverse of the survival probability corresponding to their age to compute the number of births. The survival probabilities of the children are obtained from the birth histories of women collected in the DHS surveys. Age-specific fertility rates are calculated by dividing the number of births in each age group by the corresponding exposure.

In this paper, this method is used to compute age-specific fertility rates by 5-year age groups, annually for 15 years preceding each survey. When multiple surveys are available, as is often the case, age-specific fertility rates from successive surveys usually overlap for several years. Combining information from successive surveys also allows the calculation of rates over long periods, close to 50 years in some cases. Taylor linearized variance estimation is used to account for clustering within primary sampling units. In addition, we adjust for the sampling variability introduced by random imputation of paternal age, using the standard multiple imputation formulas (Allison 2009).

2.2 Modeling framework

Following Hoem et al. (1981), the age schedule of fertility rates can be written as

$$g(x;\delta,\theta_1,...,\theta_{r-1}) = \delta h(x;\theta_1,...,\theta_{r-1}) \tag{1}$$

where x are ages 15, 16,..., 79, 80 years old, $h(x;\theta_1,...,\theta_{r-1})$ is a probability density function (PDF) on the real line with $r-1$ parameters, and δ is the rth parameter representing the total fertility rate (TFR). Several functions and densities can be used for $h(x;\theta_1,...,\theta_{r-1})$. Here we use the skew-normal distribution (Azzalini 1985, Mazzuco and Zanotto 2025),

$$h(x;\xi,\omega,\lambda) = \frac{2}{\omega}\phi(\frac{x-\xi}{\omega})\Phi(\lambda\frac{x-\xi}{\omega}) \tag{2}$$

where $\phi(\cdot)$ is the standard normal probability distribution function and $\Phi(\cdot)$ the standard normal cumulative distribution function. The location parameter is $\xi \in \mathbb{R}$, the scale parameter is $\omega \in \mathbb{R}^+$ and the skewness parameter is $\lambda \in \mathbb{R}$. Estimating the model in its direct parametrization can be problematic when $\lambda \approx 0$ (Azzalini and Capitanio 1999). Instead, we will estimate a centered parametrization. The estimated centered parameters are the mean, μ, the variance, σ^2, and the skewness index γ. Conveniently, when estimating age-specific fertility rates, the mean μ is then the mean age at fatherhood. The parameter σ is the standard deviation which measures the age heterogeneity in ASFR. Finally, if γ is positive, we obtain a skewness on the right; otherwise, the skewness is on the left.

For a given country, we estimate male proportionate age-specific fertility rates (PASFR) – dividing each ASFR by their sum – in year t, $f^0_{x,t}$, as follows

$$\log(f^0_{x,t}) \sim \text{Normal}(\log\left(h(x;\mu_t,\sigma_t,\gamma_t)\right), \text{se}^2_{x,t}) \tag{3}$$

where $\mathrm{se}_{x,t}$ is the estimated standard error on the log scale that accounts for sampling error around the male PASFR, $f^0_{x,t}$. In order to smooth PASFR estimates over time and allow for reconstruction and projection of estimates, we place a second order random walk prior on each of the three parameters. For example, a second order random walk on μ_t is defined as

$$\mu_t \sim \text{Normal}(2\mu_{t-1} - \mu_{t-2}, \sigma^2_\mu). \tag{4}$$

We set weakly informative priors on the random walk variance parameters

$$\sigma_\mu, \sigma_\sigma, \sigma_\gamma \sim \text{logNormal}(-1.5, 0.5). \tag{5}$$

We estimate ASFR (and hence the male TFR) indirectly using UN-WPP estimates. We rely on the following equation (Schoumaker 2019),

$$TFR_t = \frac{B_t}{\sum_{x=15}^{80} h(x; \hat{\mu}_t, \hat{\sigma}_t, \hat{\gamma}_t) N_{x,t}} \tag{6}$$

where B_t is the annual number of births during year t, $h(x; \hat{\mu}_t, \hat{\sigma}_t, \hat{\gamma}_t)$ are PASFR for age x and year t estimated with the Bayesian skew-normal model, and $N_{x,t}$ is the number of men aged x at mid year t. The number of births and the number of men are estimated by UN-WPP. This step ensures that estimated male TFR and UN-WPP female TFR lead to the same number of births in year t.

We obtain samples of posterior distributions of parameters using Hamiltonian Monte Carlo (HMC), a type of Markov Chain Monte Carlo sampling, implemented in Stan. We monitor for convergence using standard diagnostic measures. R-hat values for all parameters are under 1.02, and visual inspection of traceplots do not indicate sampling pathologies.

2.3 Evaluation of model performance

To assess the skew normal model's performance, we compare it to the Brass relational Gompertz model (Paget and Timaeus 1994). In this model, a standard fertility schedule is related to the observed fertility of a population by the equation

$$Y_x = \alpha + \beta Y^s_x \tag{7}$$

where $Y_x^s = -\log(-\log(F_x^s))$, F_x^s is the cumulated fertility in the standard schedule, and $Y_x = -\log(-\log(F_x/F_\omega))$ with ω the highest age group considered (here 75-79 years old). We use two standards. First, the one proposed by Paget and Timaeus (1994). Second, the first principal component of a Singular Value Decomposition (SVD) performed on all male proportional age-specific fertility rates (PASFR), except the ones belonging to the countries selected for comparing the models. We selected four countries to compare the models: Albania, Colombia, Ghana, and Burkina Faso. These countries reflect low, middle, and high fertility levels.

For model comparison purposes, we estimate the skew-normal model independently for each country-survey-year and hence, do not assume random walks on the parameters. Models were compared by computing the root mean squared error (RMSE) associated with a given country-survey-year,

$$RMSE = \sqrt{\frac{1}{G}\sum_{x=1}^{\omega}(\hat{f_x^0} - f_x^0)} \tag{8}$$

where G refers to the number of 5-year age groups considered. The lower the RMSE, the better the model's fit to the data.

3 Results

3.1 Comparing models' performance

Figure 1 compares the RMSE between the skew-normal model and Brass's relational Gompertz model for four selected countries: Albania, Burkina Faso, Colombia, and Ghana. The Brass relational model was estimated using two different standards, that of Paget and Timaeus (1994), P&T, and the first principal component of an SVD performed on male fertility schedules, PC1 (see Figure 5 in the Appendix). Figure 1 shows that the skew-normal model generally has the lowest RMSE in all four selected countries. This is explained by a higher flexibility compared to the the relational model, allowing the function to fit a diversity of fertility schedules (see Figure 6 in the Appendix). Focusing on Brass's relational model, the standard based on the first principal component (PC1) provides a better fit to the data.

3.2 Reconstructing male PASFR

Figure 2 focuses on Ghana and shows PASFR estimates from the Bayesian skew-normal model over the period 1978-2022. The model provides a good fit to the survey estimates. The model fit seems

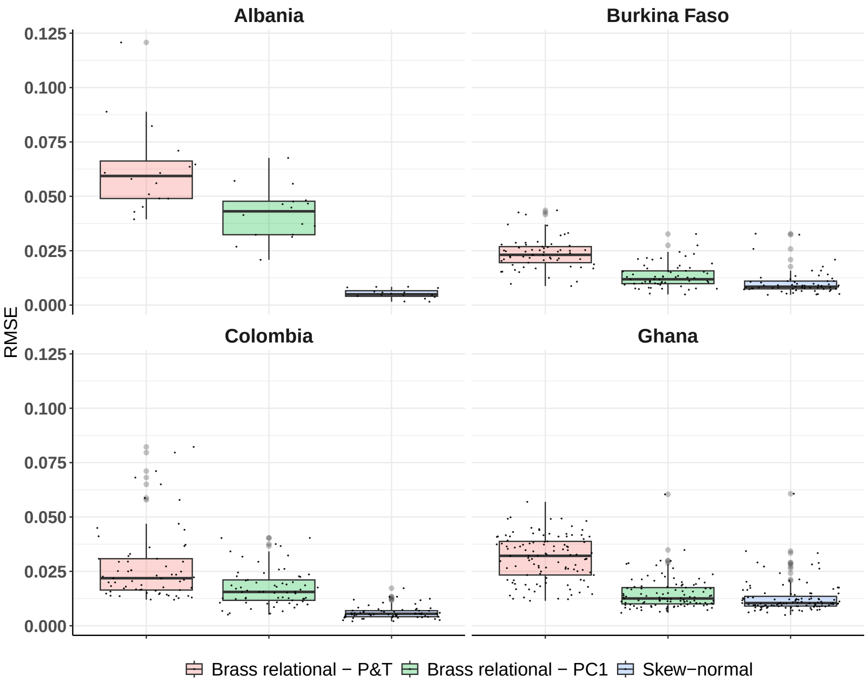

Figure 1: Comparison of the root mean squared errors (RMSE) between the skew-normal model and the Brass's relational Gompertz models for Albania, Burkina Faso, Colombia, and Ghana.

unaffected by the high stochasticity in fertility rates, especially visible at old ages. In addition, in years with data from multiple surveys, the model estimates are a trade-off between the different survey point estimates according to their sampling errors.

3.3 Temporal evolution in the estimated parameters

Figure 3 shows the estimated parameters for Albania, Burkina Faso, Colombia, Democratic Republic of the Congo (D.R. Congo), Egypt, Ghana, Guatemala, and Kenya. Focusing on the mean age at fatherhood, all countries except Albania experienced a decrease over the period studied. For example in Ghana, the mean age at fatherhood decreased from 44.9 (95% CI: 44.5–45.2) years old in 1978 to 37.6 (95% CI: 36.9–38.3) years old in 2022. Similar decline are observed in Burkina Faso, D.R. Congo, and Kenya. The TFRs have also decreased significantly for all countries studied. The drop was especially visible for Burkina Faso, Kenya, and Ghana from 11.7 (95% CI: 11.5–11.9) children per man to 6.7 (95% CI: 6.6–6.9) children per man, from 13.4 (95% CI: 13.0–13.8) children per man to 4.5 (95% CI: 4.4–4.6) children per man, and from 11.1 (95% CI: 10.9–11.2) children per man to 4.1 (95% CI: 4.0–4.2) children per man, respectively. The heterogeneity has decreased in all countries except in Albania, reflecting a general narrowing of the fertility age schedule over time. Finally, the skewness parameters do not show any specific temporal trend. This parameter converges to zero for Albania indicating that the male fertility age schedule is more and more

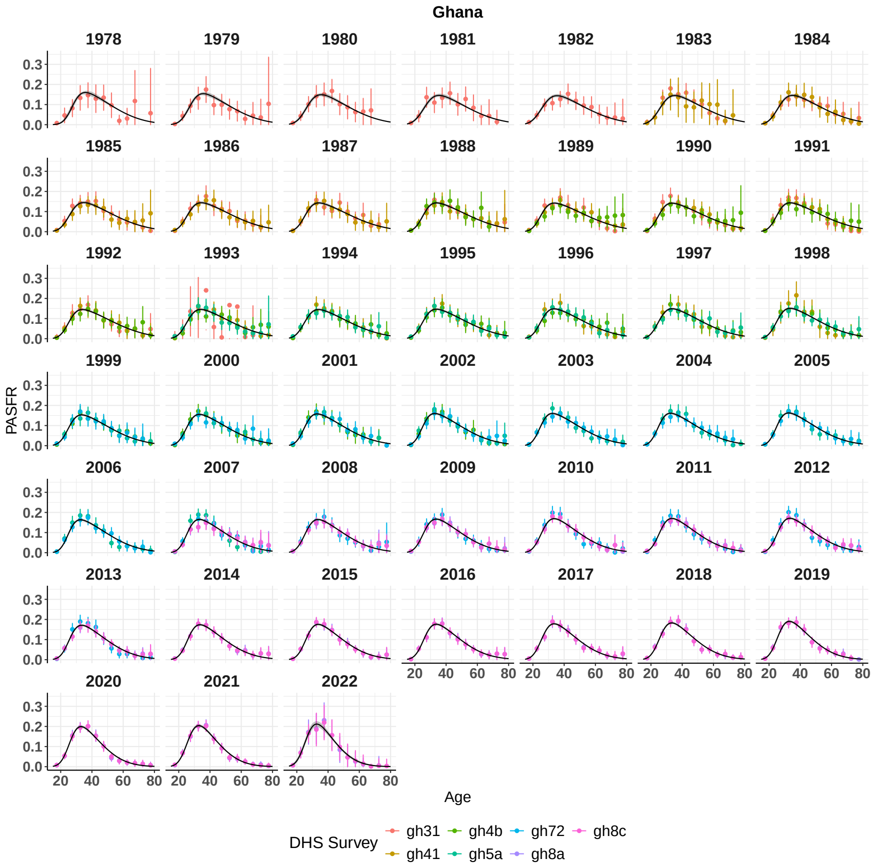

Figure 2: Median PASFR estimates (line) and 95% CI (shaded area) of the Bayesian skew-normal model for Ghana over the period 1978-2022. Points are survey estimates from the own-children method applied to DHS data.

symmetric around its mean.

Figures 4 compares the time trend in mean age at parenthood, and TFR from the Bayesian skew-normal model for males and United Nations World Population Prospects (UN-WPP) estimates for females. On the one hand, female and male TFRs are converging quickly to similar levels for all countries studied. On the other hand, despite a rapid decline in the mean age at parenthood for male over time, the gap between male and female generally remains substantial (e.g a difference of 5.8 and 7.6 years for Colombia and Egypt, respectively).

4 Discussion & Next Steps

In this paper, we develop a Bayesian parametric model allowing to estimate and reconstruct male age-specific fertility rates, focusing on countries without CRVS systems. In such countries, the

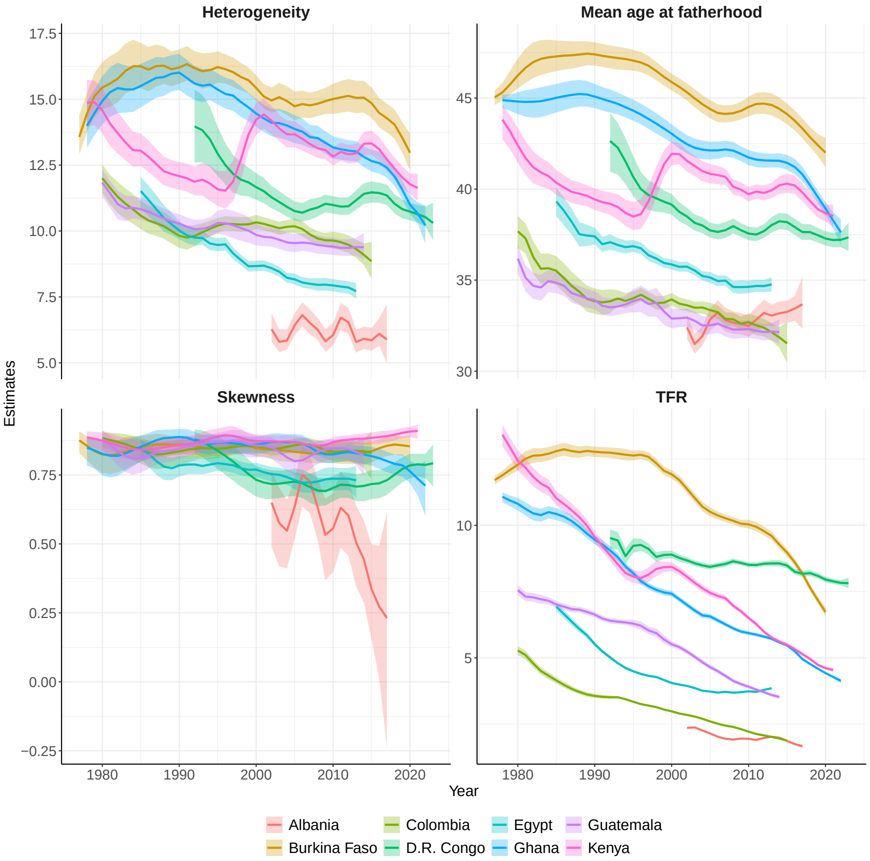

Figure 3: Comparison of the estimated parameters of the Bayesian skew-normal model for a selection of countries.

model uses data obtained by applying the own-children method to DHS surveys and accounts for the sampling error associated with the surveys. At the core of the model is the skew-normal distribution. The proposed model has at least five advantages. First, the model is flexible while remaining parsimonious. Second, all four parameters have straightforward interpretations in terms of fertility patterns. Third, the modeling framework accounts for sampling error and allows for reporting uncertainty around estimates. Fourth, the model allows the estimation of long time series of fertility age schedules even when surveys have not been conducted regularly. Fifth, we ensure coherence in terms of the yearly number of births that is estimated by the UN-WPP. Providing male fertility age schedules in the Global South is critical, as this is the region where male and female fertility differ the most (Schoumaker 2019). In these cases, it is unrealistic to use female ASFR estimates as a proxy for male ASFRs.

In future work, we plan to project male ASFRs by making assumptions about the trend in the parameters of the skew-normal model. For example, we could assume that by a certain time horizon, the mean age at fatherhood and childbearing will be equal. An extension of this work could also be to modify the model to estimate subnational male ASFRs, taking advantage of the fact

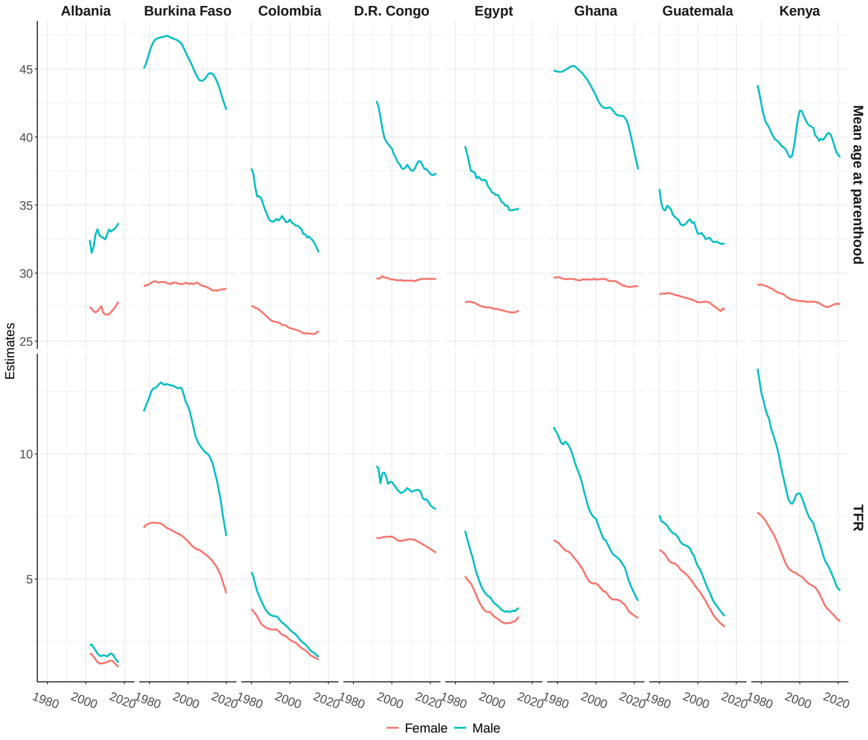

Figure 4: Comparison of the Bayesian skew-normal male estimates against UN-WPP female estimates for TFR and mean age at parenthood.

that the DHS survey is representative at the subnational level and moving towards a hierarchical Bayesian model (Li et al. 2019). In a similar vein, we could estimate ASFRs by education level as this information is collected in DHS surveys. Comparing the estimated parameters across education groups would summarize key differences in fertility behaviors.

Finally, in future it would be interesting to examine how the use of male fertility estimates in countries such as Ghana changes estimates of kinship bereavement. For example, focusing on paternal orphanhood, our results suggest that using male fertility estimates instead of the ”androgynous assumption” (Caswell 2022) could lead to a higher number of children losing their father (higher male TFR relative to female) but also losing them earlier in life (older mean age at fatherhood relative to mean age at motherhood).

Our modeling approach has several limitations currently, which we aim to improve on in future. First, model performance is only compared with the Brass relational model. In the future, we plan to evaluate the performance of classical female fertility models on male fertility. Other surveys such as the Multiple Indicator Cluster Surveys (MICS) and the Pan Arab Project for Family Health (PAPFAM), as well as census data, are also available. These data sources have different degrees of uncertainty. We plan to combine different data sources for a given year and country, taking into account their respective uncertainty, using the Bayesian framework (Alkema and New

2014). Third, when estimating TFRs, we use births and male population estimates from UN-WPP. Currently, we do not account for uncertainty in these estimates. We will do so in future work by using the posterior distribution of these estimates. Fourth, we estimate the model independently for each country. To improve the estimation for countries with few data, we can move to a hierarchical model allowing to pool information on temporal trend across countries belonging to the same region (see Alexander and Alkema (2018) for an example).

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5 Appendix

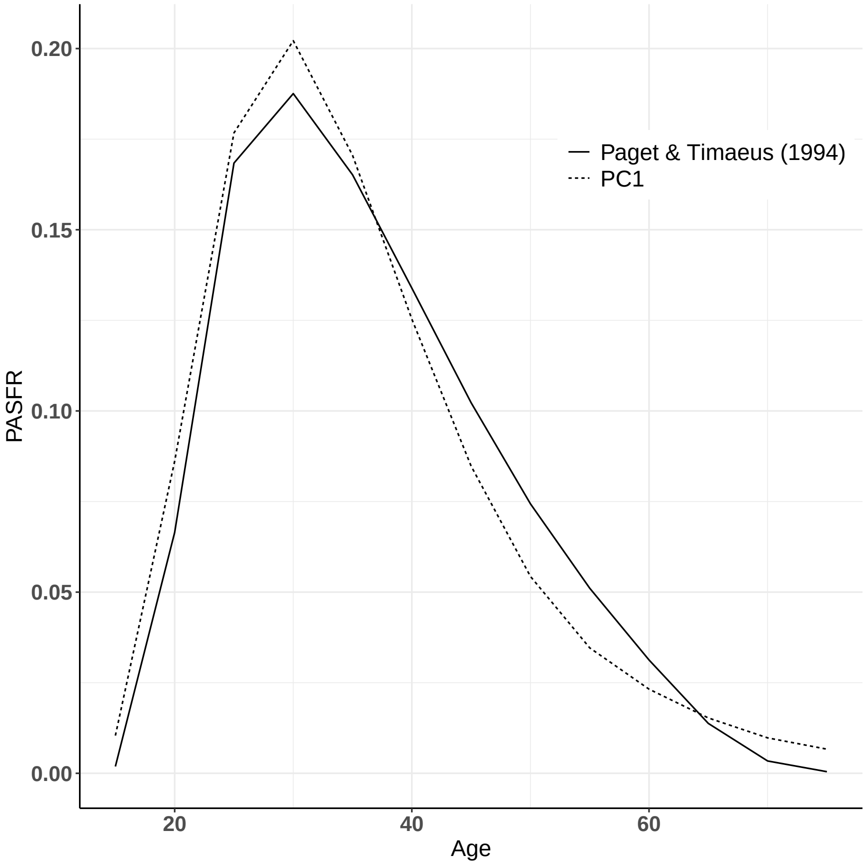

Figure 5: Two male standard PASFR schedules for the Brass's relational Gompertz model of male fertility

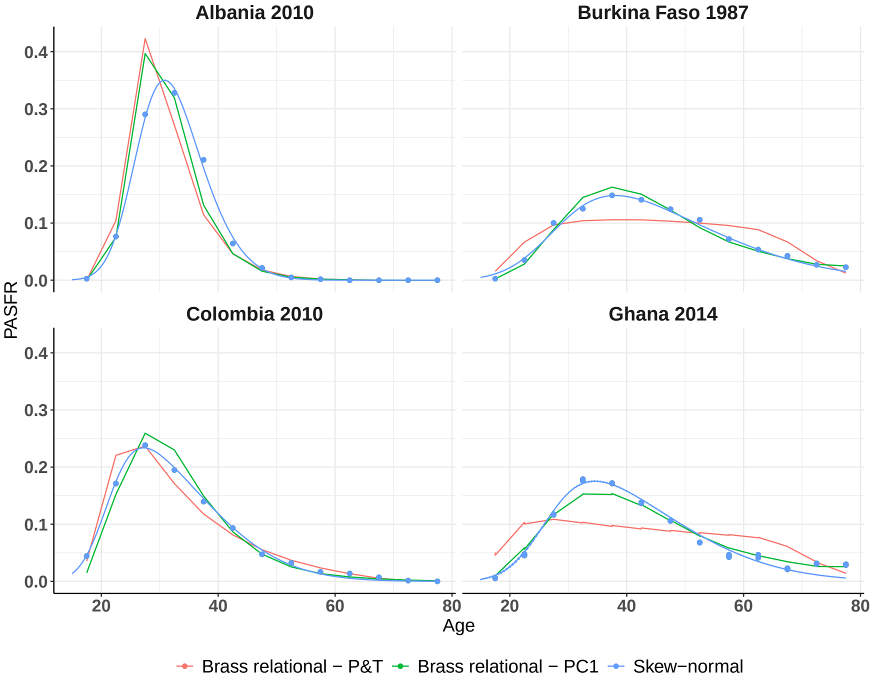

Figure 6: PASFR estimates comparison between the Brass's relational Gompertz models and the skew-normal model for selected countries and years. Points are survey estimates from the own-children method applied to DHS data.