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Bayesian Population Reconstruction:  
A Method for Estimating Age- and Sex-specific Vital Rates and  
Population Counts with Uncertainty from Fragmentary Data

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**Abstract**

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Current methods for reconstructing human populations of the past by age and sex are deterministic or do not formally account for measurement error. I propose “Bayesian reconstruction”, a method for simultaneously estimating age-specific population counts, fertility rates, mortality rates and net international migration flows from fragmentary data, that incorporates measurement error. Expert opinion is incorporated formally through informative priors. Inference is based on joint posterior probability distributions which yield fully probabilistic interval estimates. Previous methods of reconstruction did not account for measurement error, or imposed fixed age-patterns on some parameters. It is designed for the kind of data commonly collected in modern demographic surveys and censuses. Population dynamics over the period of reconstruction are modeled by embedding formal demographic accounting relationships in a Bayesian hierarchical model. Informative priors are specified for vital rates, migration rates, population counts at baseline, and their respective measurement error variances. Statistical properties of Bayesian reconstruction are investigated through simulation and sensitivity analyzes. The method is applied to real data from Burkina Faso, Laos, New Zealand, Sri Lanka, Thailand and India, demonstrating its applicability to developing and developed countries. It can also be used to compare model life tables. When full populations are reconstructed, probabilistic estimates of sex ratios, such as the sex ratio at birth and sex ratios of mortality, can also be obtained. Bayesian



reconstruction is implemented in the *R* package *popReconstruct*.





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## GLOSSARY

ANOVA analysis of variance.

ARD absolute relative difference.

ASFR age-specific fertility rate.

CCMPP cohort component method of population projection.

CD WEST Coale and Demeny West.

CEB children ever born.

CERPOD Centre d'Etudes et de Recherche sur la Population pour le Développement.

CPS Contraceptive Prevalence Survey.

CRAN Comprehensive R Archive Network.

DCS SRI LANKA Department of Census and Statistics, Sri Lanka.

DHS Demographic and Health Survey.

E0 life expectancy at birth.

GIP generalized inverse projection.

IGME Interagency Group for Child Mortality Estimation.

MAE mean absolute error.

MARE mean absolute relative error.

MCMC Markov chain Monte Carlo.

NFHS National Family Health Survey.

OLS ordinary least squares.

ORSTOM Office de la Recherche Scientifique et Technique Outre Mer.

PES post-enumeration survey.

PLT permanent and long-term.

PSRF potential scale reduction factor.

RCHS Reproductive and Child Health Survey.

SRB sex ratio at birth.

SRM sex ratio of mortality.

SRS Sample Registration System.

SRTP sex ratio in the total population.

TFR total fertility rate.

U5MR under-five mortality rate.

UN United Nations.

UNFPA United Nations Population Fund.

UNPD United Nations Population Division.

UNSA United Nations South Asian.

VITAL RATE fertility and mortality rate.

WFS World Fertility Survey.

WPP *World Population Prospects*.

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## DEDICATION

To my parents.



## Chapter 1

# INTRODUCTION

### 1.1 *Motivation and Background*

The release of *World Population Prospects 2010* (WPP 2010; [United Nations, 2011a](#)) coincided with considerable interest in global demographic statistics in both the popular media (e.g. [nbcnews.com, 2011](#); [foxnews.com, 2011](#); [Gillis and Dugger, 2011](#); [Reuters, 2011](#); [Phillips, 2011](#); [Nagarajan, 2011](#)) and academic literature (e.g. [Chin et al., 2001](#)). This is perhaps unsurprising since these statistics, which include estimates and forecasts of population sizes, fertility and mortality rates and rates of international migration for all countries of the world, are of paramount importance for planning and evaluation in virtually all areas of national and global policy. The current size of the world population received particularly close attention due to the then imminent arrival of the 7 billionth person. For example, the United Nations Population Fund (UNFPA) began its *7 Billion Actions* campaign on *World Population Day* (11th July, 2011) and declared 31st October, 2011 to be “7 billion day”, the day the 7 billionth child was expected to be born. Despite the apparent precision implied by the number 7 billion, attempts to make exact, error-free statements about national populations and fertility, mortality and migration rates are unlikely to succeed due to a lack of data, measurement error and other factors. It is necessary, therefore, to quantify the uncertainty in the estimates one can obtain. The appropriate way to express such uncertainty is through interval estimates which have a probabilistic interpretation. In this dissertation, I introduce and apply a new method called Bayesian reconstruction which is designed to do just this.

WPP is produced by the United Nations Population Division (UNPD) every two years. The statistics it contains can be classified into two broad groups, known as estimates and projections. Projections are predictions about demographic parameters in the future, while estimates concern population structures of the past. I will use the term reconstruction

which is less ambiguous. Nevertheless, use of the term “estimate” agrees with standard usage in statistics; data about demographic parameters in the past are used to estimate the true values. Between the biennial editions of the WPP, new data are collected and old data become available, so revisions must be made to the reconstructions to accommodate it.

Implicit in the previous paragraph is the assertion that there is uncertainty in the measurements. This is hardly controversial; demographers have long acknowledged that some parameters are almost immune to perfect measurement and many so-called indirect methods exist for estimating them (e.g., [United Nations, 1983](#)). Most of these, however, are focused on obtaining a best point estimate of a single quantity. Although it has been standard practice to produce ranges of estimates for many parameters based on different scenarios, high, medium and low fertility for example, the ranges produced cannot be interpreted probabilistically. This approach is still commonly used for projections, but since the mid 1990s new methods began to appear that do yield probabilistic predictions; [Lee \(1998\)](#) and [Booth \(2006\)](#) provided reviews. In contrast, there has been relatively little work on the development of fully probabilistic methods for demographic reconstruction. Bayesian reconstruction accounts for measurement uncertainty and works with the type of demographic data that have commonly been collected for most countries over the last 60 years or so. It has been designed to fit within the UNPD’s existing work-flow, but I hope it is general enough to have broad appeal.

The extra value that probabilistic interval estimates provide over point estimates will vary among countries and parameters. For example, estimates of fertility and mortality rates in most developed countries are derived from vital registration systems. While the resulting estimates are unlikely to be exactly correct, it is reasonable to expect them to be closer to the truth than estimates derived from many sample surveys, these being an important source of vital rate data for many less developed countries. To a lesser extent, the same is true for national censuses. As will be shown, Bayesian Reconstruction can be applied to all countries, no matter the type and quality of data available. However, it has the greatest value for countries without well-resourced statistical systems and which are not able to provide national estimates to the degree of detail required by the UNPD. Roughly half of all the countries and areas included in the WPP fall into this category ([United](#)



Nations, 2011a) and the UNPD is a key partner in the process of compiling, analyzing and publishing the data.

## 1.2 Population Reconstruction

### 1.2.1 The Cohort Component Method of Population Projection

Virtually all methods of population reconstruction in demography employ the cohort component method of population projection (CCMPP) in some form. This is an operationalization of the basic demographic balancing equation which states, quite simply, that the population size in year  $t + \delta$  must equal the population size in year  $t$  plus the intervening births and net migration, minus the intervening deaths (e.g., Whelpton, 1936; Preston et al., 2001). Intricacies arise in practice because the projection is typically done by age and the usual inputs are not simple counts but demographic rates. Furthermore,  $\delta$  is usually five which means that projection is a rather coarse discrete-time approximation to a continuous-time process. Standard adjustments are made to improve accuracy. These lead to a way of concisely expressing projection as a matrix multiplication (Lewis, 1942; Leslie, 1945, 1948).

Population projection is distinct from population forecasting since it merely entails evolving a population forward in time from some given baseline under assumptions about prevailing fertility and mortality rates (vital rates) and migration (Keyfitz and Caswell, 2005). The period of projection may be in the future or the past.

### 1.2.2 Existing Methods of Reconstruction

Many existing methods of population reconstruction in human demography were developed for one of two reasons: reconstructing populations of the distant past from data on births, deaths and marriages recorded in parish registers (e.g., Wrigley and Schofield, 1981; Bertino and Sonnino, 2003; Walters, 2008), or in counter-factual exercises to estimate the excess of mortality due to extreme events such as famine or genocide or country-specific cultural practices (e.g., Boyle and Ó Gráda, 1986; Sen, 1990; Coale, 1991; Daponte et al., 1997; Heuveline, 1998; Merli, 1998; Goodkind and West, 2001; Das Gupta, 2005). Purely deterministic reconstruction methods used in some of these studies include “inverse projection”

(Lee, 1971, 1974), “back projection” (Wrigley and Schofield, 1981) and “generalized back projection” (Oeppen, 1993b).

The CCMPP works by taking age-specific vital rates and population counts at some baseline time, and converting them into population counts at set intervals (usually five-yearly) over the period of reconstruction by successively applying the balancing equation. Inverse projection is so-called since it takes counts of births and deaths (aggregated over age) as inputs and yields estimates of rates as outputs. Population counts at the start of the reconstruction period are also required, as are model age patterns of fertility and mortality. Reconstruction proceeds forward in time. Where at least two independent estimates of population size are available, net migration can also be estimated (Lee, 1985). Back projection, in contrast, takes counts of births and deaths over the reconstruction period and population counts at the terminal year and then recedes, in a series of somewhat complicated steps, backward in time, reconstructing population counts and net migration along the way. Several iterations might be required to produce a satisfactory result. There was considerable debate about the efficacy of back projection, centered partly around identifiability issues that arise from trying to “resurrect” people and simultaneously estimate fertility, mortality and migration rates (Lee, 1985, 1993), prompting the proposal of generalized inverse projection (GIP) by Oeppen (1993a; 1993b).

Bertino and Sonnino (2003) proposed “stochastic inverse projection”. This method is not deterministic but the only form of uncertainty accounted for is that which comes from treating birth and death as stochastic processes at the individual level. Counts of births and deaths are assumed to be known without error and age patterns are fixed. In the cases I treat, accurate data on births and deaths of the parish register kind are often unavailable and uncertainty due to stochastic vital rates is likely to be small relative to uncertainty due to measurement error (Pollard, 1968; Lee, 2003; Cohen, 2006). Moreover, it is designed to work with the kind of data commonly available for developing countries and does not rely on the existence of detailed births and deaths registers, although this information can be used when available.

Daponte et al. (1997) took a fully Bayesian approach to constructing a counterfactual history of the Iraqi Kurdish population from 1977 to 1990. They constructed prior

distributions for fertility and mortality rates using survey data and expert opinion about uncertainty based on historical information and knowledge of demographic processes. Measurement error in the available, fragmentary data was accounted for. However, there were some restrictions such as holding the age pattern of fertility fixed and allowing for mortality variation only through infant mortality. Rural to urban migration was accounted for by treating these populations separately; international migration was assumed negligible. Bayesian reconstruction is similar but no model age patterns are assumed to hold and international migration is explicitly estimated along with fertility, mortality and population counts.

Complex models have also been developed by fisheries researchers to study the population dynamics of marine and land animal populations (e.g., [Quinn and Deriso, 1999](#); [Brooks et al., 2000a, 2002](#)). In most wildlife studies, data collection methods and the type and amount of data available differ somewhat from those in human demography. Nevertheless, there are similar statistical challenges to overcome and these suggest a Bayesian approach is appropriate. For example, multiple sources of data informing the same demographic parameters must be coherently synthesized and over-parameterization in population dynamics models is common. Bayesian approaches have been able to handle both of these challenges (e.g., [Raftery et al., 1995](#); [Givens et al., 1993](#); [McAllister et al., 1994](#); [Brooks et al., 2000b](#); [Catchpole et al., 2001](#)).

### *1.2.3 Bayesian Population Reconstruction*

Bayesian reconstruction also relies on the CCMPP to relate population counts and vital rates through time, but embeds it in a hierarchical statistical model. It reconciles two different estimates of population counts, those based on adjusted census counts (or similar data) and those derived by projecting initial estimates of the baseline population forward using initial estimates of vital rates. Adjusted census counts are raw counts which have been processed to reduce common biases such as undercount and age heaping. Since projection is done using the CCMPP, the parameters for which I require initial point estimates are the CCMPP inputs, namely population counts for the baseline year, vital rates and net

migration, all by age group and sex, over the period of reconstruction. Migration is treated in the same way as fertility, mortality and baseline population counts.

The initial point estimates of the input parameters and estimates of their measurement error are used to define probability distributions for each input. Initial point estimates are derived from data. Baseline population estimates come from adjusted census counts (or similar sources), fertility and mortality estimates from surveys such as the Demographic and Health Surveys (DHSs) and vital registration. The distributions on the input parameters are combined into a joint prior. Typically, the initial point estimates will serve as the marginal medians of this distribution, but this is not a requirement. Estimates of the measurement error for each input parameter are also required. These can be based on expert judgment or preliminary analyzes such as post-enumeration surveys. Data and expert knowledge sufficient to generate these inputs are available for most countries from about 1960.

A probability model is also specified for the two sets of population counts; those obtained by projecting the inputs using the CCMPP, and the adjusted census counts themselves. Viewed as a likelihood, this is a function of the projected counts. Via Bayes theorem, the prior and the likelihood define a posterior distribution on the inputs from which a large sample can be drawn using a Markov chain Monte Carlo (MCMC) algorithm. Inference is based on the marginals of this joint posterior. I use 95 percent credible intervals.

Bayesian population reconstruction is implemented in the *R* package *popReconstruct* and can be downloaded from the Comprehensive R Archive Network (CRAN) (<http://www.r-project.org/>).

### **1.3 Dissertation Outline**

The remainder of the dissertation is structured as follows. In Chapter 2 I review some existing methods of population reconstruction in demography and ecology. Statistical details of Bayesian reconstruction are given and some standard demographic parameters are defined. A simulation study is performed to assess calibration of marginal posterior probability intervals. This is followed by an application to real data involving the reconstruction of the female population of Burkina Faso between 1960 and 2005. Model checking and sensitivity analyzes are given. This chapter is closely based on Wheldon et al. (forthcoming), published

in the *Journal of the American Statistical Association*.

In Chapter 3 the female populations of Laos, Sri Lanka and New Zealand are reconstructed. These examples show that Bayesian reconstruction can be usefully applied to reconstruct the populations of developed, as well as developing, countries (New Zealand); that the method can be used to compare competing model life tables (Laos); and that it can be extended to cases where censuses are not available at regularly spaced intervals (Sri Lanka).

Bayesian reconstruction was initially developed for female populations only. In Chapter 4 a method is proposed to allow reconstruction of two-sex populations. This allows estimation of the sex ratio at birth (SRB) and sex-comparisons of mortality such as the ratio of under-five mortality rates (U5MRs) and the sex-difference in life expectancy at birth ( $e_0$ ). The populations of Laos, Thailand and India are reconstructed to demonstrate. India is an important case because it is widely believed that sex ratios of mortality in this country do not follow the typical worldwide pattern.

Chapter 5 concludes by summarizing the key contributions making suggestions for future work.

Most chapters have their own appendices containing extra information about data sources, additional results and sensitivity analyzes. There are two main appendices to the dissertation. Appendix A discusses the modeling of correlation in age and time. Appendix B, contains a vignette for the *popReconstruct* package which implements Bayesian reconstruction in the *R* environment for statistical computing (R Development Core Team, 2012).

## Chapter 2

## RECONSTRUCTION OF FEMALE-ONLY POPULATIONS

**2.1 Introduction**

Every two years the United Nations Population Division (UNPD) publishes detailed estimates and projections of key demographic quantities for all countries in the world from 1950 to 2100; they appear in *World Population Prospects* (WPP; [United Nations, 2009a,b](#)). The parameters reported include age-specific fertility and mortality rates (vital rates), population counts and international migration rates. These numbers are used for the development and assessment of policy and are of particular importance for countries that lack their own well-resourced official statistical systems. For many of these countries, the UNPD is a key partner in the process of compiling, analyzing and publishing internationally comparable demographic data.

The WPP tables can be classified into two broad groups, known as estimates and projections. Projections are predictions about demographic parameters in the future while estimates concern populations of the past. I will use the term reconstruction which I find less ambiguous. Nevertheless, use of the term “estimate” agrees with standard usage in statistics; data about demographic parameters in the past are used to estimate the true values. Between the biennial editions of the WPP, new data are collected and old data become available, so revisions must be made to the reconstructions to accommodate it.

Demographers have long acknowledged the presence of uncertainty in their measurements and many so-called indirect methods exist for obtaining “best” point estimates (e.g., [United Nations, 1983](#)). It is still common practice to produce ranges of projections of vital rates and population counts based on different scenarios; high, medium and low fertility for example. These ranges cannot be interpreted probabilistically, but methods have been developed that do yield probabilistic projections; [Lee \(1998\)](#) and [Booth \(2006\)](#) provide reviews. In contrast, there has been relatively little work on the development of fully probabilistic

methods for demographic reconstruction. Here I propose a general method for reconstruction that accounts for measurement uncertainty and works with the type of demographic data that have commonly been collected for most countries over the last 60 years or so.

This chapter is closely based on the article [Wheldon et al. \(forthcoming\)](#). It is structured as follows. Existing methods of population reconstruction are reviewed in Section 2.2. In Section 2.3 I define the notation and parameters and describe the method. In Section 2.4, I investigate some statistical properties of the method through simulation before applying it to real data from Burkina Faso in Section 2.5. I close with a summary of the results and a discussion in Section 2.6.

## 2.2 Existing Methods of Population Reconstruction

Outside of official statistical agencies, demographic reconstructions have been undertaken to study historical populations of the past (e.g., [Wrigley and Schofield, 1981](#)) and to estimate excess mortality in crises such as famine or social upheaval (e.g., [Boyle and Ó Gráda, 1986](#); [Heuveline, 1998](#); [Merli, 1998](#); [Goodkind and West, 2001](#)). The most commonly used methods are based on the demographic balancing equations. These are the basic accounting relationships which state that the population size at time  $t + \delta$  is equal to the size at time  $t$  plus births and immigrants, minus deaths and emigrants. These relationships are encoded in the cohort component method of population projection (CCMPP; [Lewis, 1942](#); [Leslie, 1945, 1948](#); [Preston et al., 2001](#)). Given the size and age-structure of a population at some baseline time, its size and structure at any point in the future can be determined from the baseline population and the fertility, mortality and international migration rates that prevail over the period of reconstruction.

The back projection method of reconstruction ([Wrigley and Schofield, 1981](#)) attempts to apply these relationships in reverse by using an estimate of the population structure at the terminal year of the period of reconstruction. This approach is problematic since the CCMPP procedure is not formally invertible. To produce sensible results, some additional constraints have to be imposed or somewhat ad-hoc fixes applied. In response to these concerns, [Lee \(1971, 1974\)](#) proposed the method of inverse projection. Inverse projection enacts the reconstruction forward through time; it is named for the fact that, instead of

estimating counts of births and deaths from rates, count data are used to infer rates. Both of these methods have been further developed since their inception. For example, [McCaa and Barbi \(2004\)](#) and [Rosina \(2004\)](#) described extensions of inverse projection, while [Oeppen \(1993a\)](#) proposed generalized inverse projection (GIP). All of the extended methods remain purely deterministic.

A stochastic reconstruction method was proposed by [Bertino and Sonnino \(2003\)](#) who modeled childbirth and death as inhomogeneous Poisson processes. The method is designed to work with counts of births and deaths aggregated over age and so requires the analyst to specify model age-patterns for fertility and mortality, although different schedules can be chosen for different sub-periods. These schedules are taken as the intensity functions of the process and realizations are simulated through time to produce sequences of empirical estimates of population age structures. Hence, the only source of variation accounted for is natural variation around the demographic rates; the total numbers of deaths by year are assumed to be recorded without error. Moreover, international migration is assumed to be negligible over the period of reconstruction.

Finally, all of the above methods were designed to work with individual data of the kind sometimes found in European parish registers, or aggregated summaries of them. The data available for many countries in the intended application are not as detailed. The aim of this chapter is to introduce a new method of reconstruction that uses measurements of demographic parameters from 50–60 years in the past from multiple noisy data sources, often available only for limited years or periods. Uncertainty due to measurement error is expressed as probability distributions and intervals rather than deterministic, scenario-based ranges. To my knowledge, there are no existing methods of human population reconstruction that have these features.

[Daponte et al. \(1997\)](#) used an approach similar to ours to construct a counterfactual history of the Iraqi Kurdish population between 1977 and 1990. They, too, represented errors in the measurement of demographic parameters as the standard deviations of probability distributions. However, they used a low dimensional parametrization of mortality and fixed the age patterns of fertility. International and sub-national migration was assumed to be negligible.



Where migration is accounted for, it has been handled in different ways. Lee’s inverse projection method estimates it as a residual if censuses are available at intermediate years in the reconstruction interval. [Alho \(1992\)](#) added it as extra error in measuring survival. Here, migration is treated explicitly and age-time specific estimates are available as for the other parameters.

Complex models have also been developed by fisheries researchers to study the population dynamics of marine life (e.g., [Quinn and Deriso, 1999](#)). A large body of work also exists on the dynamics of land animal populations. As with fisheries research, data commonly come from mark-recapture or mark-recovery studies, but radio-telemetry and age-at-harvest data are also common; [Seber \(1982\)](#) is a classic reference and more recent reviews are [Pollock \(1991\)](#) and [Schwarz and Seber \(1999\)](#). Bayesian approaches to the analysis of this type of data were suggested at least as early as [Gaskell and George \(1972\)](#). [Vounatsou and Smith \(1995\)](#) took advantage of modern computers and Markov chain Monte Carlo (MCMC) methods to simultaneously estimate several parameters. Subsequently, a large body of literature developed; [Brooks et al. \(2000a, 2002\)](#) provide reviews while [Barry et al. \(2003\)](#), [Conn et al. \(2008\)](#) and [Corkrey et al. \(2008\)](#) are just a few examples of more recent studies.

In most wildlife studies, data collection methods and the type and amount of data available differ somewhat from those in human demography. Nevertheless, there are similar statistical challenges to overcome and these suggest a Bayesian approach may be appropriate. For instance, in ecology and demography, multiple sources of data informing the same demographic parameters often exist. [Poole and Raftery \(2000\)](#) found that Bayesian melding allowed these to be synthesized in a coherent manner; see also [Raftery et al. \(1995\)](#), [Givens et al. \(1993\)](#) and [McAllister et al. \(1994\)](#). Furthermore, population dynamics models are often over-parameterized (e.g., [Lee, 1985, 1993](#)). The resulting ridges in the likelihood surface posed problems that Bayesian approaches have been able to overcome (e.g., [Brooks et al., 2000b](#); [Catchpole et al., 2001](#)).

Here I propose a Bayesian solution to the reconstruction problem in which the dominant source of uncertainty, measurement error, is adequately accounted for through fully probabilistic estimates. I handle multiple, noisy data sources and I account for uncertainty

about migration as well as fertility and mortality. I do not require individual level data of the European parish register kind.

## 2.3 Method

### 2.3.1 Notation and Parameters of Interest

In this chapter I restrict attention to the dynamics of populations of females only. The parameters of interest are age- and time-specific vital rates, net international migration flows and population counts. I will refer to “international migration” as simply “migration” as this is the only type I consider. I use the symbols  $n$ ,  $s$ ,  $g$  and  $f$  to denote population counts, survival (a measure of mortality), net migration (immigrants minus emigrants) and fertility, respectively. All of these parameters will be indexed by five-year increments of age, denoted by  $a$ , and time, denoted by  $t$ . Reconstruction will be done over the time interval  $[t_0, T]$ . The age scale runs from 0 to  $A > 0$ ; in the application (Section 2.5)  $A$  is 80. To model fertility, I define  $a_L^{[\text{fert}]} \leq a_U^{[\text{fert}]}$  where fertility is assumed to be zero at ages outside the range  $[a_L^{[\text{fert}]}, a_U^{[\text{fert}]} + 5)$ . Throughout, a prime indicates vector transpose.

Given  $\mathbf{n}_{t_0} = (n_{0,t_0}, n_{5,t_0}, \dots, n_{A,t_0})'$ , the vector of age-specific female population counts at baseline  $t_0$ , and using “ $\circ$ ” to denote entry-wise product, the CCMPP gives  $\mathbf{n}_{t+5} = \mathbf{Q}_t(\mathbf{n}_t + \mathbf{n}_t \circ \mathbf{g}_t / 2) + \mathbf{n}_t \circ \mathbf{g}_t / 2$ ,  $t = t_0, t_0 + 5, \dots, T - 5$ . Here,  $\mathbf{Q}_t$  is a  $K$  by  $K$  matrix encoding fertility and mortality and  $K$  is the number of age groups. The quantity  $\mathbf{g}_t$  is the net number of migrants expressed as a proportion of the population size so that  $\mathbf{n}_t \circ \mathbf{g}_t$ , is the net number of migrants, a count. Projection proceeds in discrete steps; those alive at the beginning of each step are subjected to the fertility, mortality and migration prevailing during the projection interval. This is a discrete time approximation to a continuous time process and there are standard adjustments to improve accuracy. Adding half of the migrants at the beginning of the projection step and the remainder at the end is one such adjustment. The

specific form I use is:

$$\begin{bmatrix} n_{0,t+5} \\ n_{5,t+5} \\ \vdots \\ n_{A-5,t+5} \\ n_{A,t+5} \end{bmatrix} = \begin{bmatrix} \tilde{f}_{0,t} & \tilde{f}_{5,t} & \cdots & \tilde{f}_{A-5,t} & \tilde{f}_{A,t} \\ s_{5,t} & 0 & & 0 & 0 \\ \vdots & \vdots & \ddots & \vdots & \vdots \\ 0 & 0 & \cdots & 0 & 0 \\ 0 & 0 & \cdots & s_{A,t} & s_{A+5,t} \end{bmatrix} \begin{bmatrix} n_{0,t} + g_{0,t}n_{0,t}/2 \\ n_{5,t} + g_{5,t}n_{5,t}/2 \\ \vdots \\ n_{A-5,t} + g_{A-5,t}n_{A-5,t}/2 \\ n_{A,t} + g_{A,t}n_{A,t}/2 \end{bmatrix} + \begin{bmatrix} g_{0,t}n_{0,t}/2 \\ g_{5,t}n_{5,t}/2 \\ \vdots \\ g_{A-5,t}n_{A-5,t}/2 \\ g_{A,t}n_{A,t} \end{bmatrix} \quad (2.1)$$

where

$$\tilde{f}_{a,t} \equiv s_{0,t}(1 + SRB)^{-1}(f_{a,t} + f_{(a+5),t} \cdot s_{a+5,t})(5/2) \quad (2.2)$$

(Preston et al., 2001). Annualized, age specific fertility rates enter (2.1) through the transformation defined in (2.2). This transformation maps the rates into proportions so that projection can be compactly expressed as a matrix multiplication. I use a tilde to represent this transformation and discuss it further below.  $SRB$  is the sex ratio at birth (the ratio of males to females among all births). Multiplication by  $SRB$  in (2.2) ensures only the female births are kept. Throughout, I take  $SRB$  to be fixed at 1.05, a demographic convention. I will use  $M(\cdot)$  to represent CCMPP and abbreviate (2.1) as

$$\mathbf{n}_{t+5} = M(\mathbf{n}_t, \mathbf{f}_t, \mathbf{s}_t, \mathbf{g}_t). \quad (2.3)$$

The survival parameters,  $s_{a,t}$ , give the proportion of those aged  $a - 5$  to  $a$  at time  $t$  who survive to be aged  $a$  to  $a + 5$  at time  $t + 5$ , for  $a = 0, 5, \dots, A + 5$ . That is,  $s_{a,t}$  is the proportion of people surviving into the age range  $[a, a + 5)$  over the 5 years between  $t$  and  $t + 5$ . Also,  $s_{A,t}$  is the proportion aged  $[A - 5, A)$  at exact time  $t$  who survive to time  $t + 5$ , by which time they are in the age group  $[A, \infty)$ . I allow for subsequent survival in this age group by letting  $s_{A+5,t}$  be the proportion aged  $[A, \infty)$  at time  $t$  who survive five more years.

Age-specific mortality during a given time period will be summarized by life expectancy at birth ( $e_0$ ), where

$$e_{0,t} \equiv 5 \sum_{a=0}^A \prod_{i=0}^a s_{i,t} + 5 \left( \prod_{i=0}^A s_{i,t} \right) (s_{A+5,t} / (1 - s_{A+5,t})). \quad (2.4)$$

The derivation is straightforward but requires additional concepts from demography; see Appendix 2.A. The quantity  $e_{0,t}$  is the average age at death in a hypothetical cohort sub-

jected for its entire life to the mortality conditions represented by the set of age-specific survival proportions,  $s_{a,t}$ .

The net number of migrants aged  $[a, a + 5)$  to the population during the time period  $[t, t + 5)$  is  $g_{a,t}n_{a,t}$ . The age summarized measure of migration I use will be the average annual total net number of migrants which, for the period  $[t, t + 5)$ , is  $(1/5) \sum_a g_{a,t}n_{a,t}$ . I model  $g_{a,t}$  instead of  $g_{a,t}n_{a,t}$ , however, because I expect variation over time and age in the former to be less dependent on magnitude.

The  $\tilde{f}_{a,t}$  represent a combination of age-specific fertility and under-five mortality. When multiplied by  $n_{a,t}$ , they give the number of female births surviving to time  $t + 5$ . That is, the  $\tilde{f}_{a,t}$  give the number of surviving female babies at  $t + 5$  as a proportion of the number of females aged  $[a, a + 5)$  alive at time  $t$ . I do not model  $\tilde{f}_{a,t}$ , however, because data are typically gathered to estimate fertility rates,  $f_{a,t}$ , not the proportions,  $\tilde{f}_{a,t}$ . Fertility rates are annualized occurrence/exposure rates. They give the ratio of births of both sexes to women aged  $a$  to  $a + 5$  (occurrence) to person-years lived (exposure) during  $[t, t + 5)$ . Thus the number of births in the projection step  $t$  to  $t + 5$  is not quite  $5f_{a,t}n_{a,t}$  because the denominator of  $f_{a,t}$  is not  $n_{a,t}$  (I need the factor of five because  $f_{a,t}$  are single-year rates but the projection intervals are five years wide). The expression in (2.2) is more accurate. To illustrate, calculating  $n_{0,t+5}$  (and taking  $g_{a,t} = 0$  for clarity) gives

$$n_{0,t+5} = s_{0,t}(1 + SRB)^{-1} \sum_{a=a_L^{[fert]} }^{a_U^{[fert]}} 5f_{a,t} \left\{ \frac{n_{a,t} + n_{a-5,t}s_{a,t}}{2} \right\} \quad (2.5)$$

(where I use the  $SRB$  to keep only the female births). The quantity in the right-most parentheses in (2.5) is a better approximation for the denominator of  $f_{a,t}$  than  $n_{a,t}$ . I multiply by  $s_{0,t}$  to account for mortality of births during the projection step.

Age-specific fertility rates (ASFRs) for a given time period will be summarized by the total fertility rate (TFR) which, for the period  $[t, t + 5)$ , is defined as

$$TFR_t \equiv 5 \cdot \sum_{a=a_L^{[fert]} }^{a_U^{[fert]}} f_{a,t}. \quad (2.6)$$

It is the average number of children born to members of a hypothetical cohort of women

who survive from age  $a_L^{[\text{fert}]}$  to age  $a_U^{[\text{fert}]} + 5$  and experience the ASFRs that were in effect during the period  $[t, t + 5)$ .

### 2.3.2 Data and Initial Estimates

Data on the parameters of interest come from numerous sources of varying quality and coverage. For example, estimates of fertility rates come from registers of births or from surveys such as the Demographic and Health Surveys (DHSs), depending on the country. Moreover, several data points for the same age-time specific parameter are often available due to multiple overlapping surveys. The UNPD often adjusts these outputs to reduce systematic biases. They apply existing demographic techniques and draw on their expert knowledge about the specific data sources. Further details about the UNPD's methodology can be found in [United Nations \(2010b\)](#). In many cases, this bias-reduction stage is highly specific to country and parameter, and so I do not propose a general approach to replace this part of the analysis.

Instead, I take the outputs of this stage, which are single bias-reduced age-time series for all four parameters, as inputs to the model. I call the elements of these biased-reduced single series *initial estimates* and use an asterisk (\*) to distinguish them from the true values. For example, I let  $f_{a,t}$  be the true (unknown) fertility rate and  $f_{a,t}^*$  be an initial estimate of it; similarly for the other parameters. I also use an asterisk to indicate estimates of population counts based on bias-reduced census counts (e.g., adjusted census counts based on post-enumeration surveys) or similarly adjusted counts from a comprehensive demographic survey. Hence I let  $n_{a,t}$  be the true population count and  $n_{a,t}^*$  a census-based estimate of it.

### 2.3.3 Model Description

I will take  $t_0$  and  $T$  to be, respectively, the earliest and most recent years for which census-based population counts are available. These will usually be bias-adjusted census counts, and I will just call them census counts. I will denote the years after  $t_0$  for which census-based

estimates of population counts are available by  $t_0 < t_L^{[\text{cen}]}, \dots, t_U^{[\text{cen}]} \leq T$ . Let

$$\boldsymbol{\theta} = (\mathbf{n}_{t_0}, \mathbf{f}_{t_0}, \mathbf{f}_{t_0+5}, \dots, \mathbf{f}_T, \mathbf{s}_{t_0}, \dots, \mathbf{s}_T, \mathbf{g}_{t_0}, \dots, \mathbf{g}_T)$$

be the vector of all age-time-specific vital rate and migration parameters, as well as population counts at  $t_0$ . These are precisely the inputs required by the CCMPP,  $M(\cdot)$  in (2.3). Census counts for years  $t_L^{[\text{cen}]}, \dots, t_U^{[\text{cen}]}$  are not included in  $\boldsymbol{\theta}$  because they are not inputs to  $M(\cdot)$ .

Reconstruction is equivalent to estimation of  $\boldsymbol{\theta}$ . To achieve this, I propose the following hierarchical model which depends on the original data only through the initial estimates. I model the census counts after the earliest census at Level 1, conditional on the outputs of the CCMPP, which appear in Level 2. The initial estimates of fertility, mortality and migration, as well as census counts at  $t_0$ , are modeled at Level 3. Level 4 specifies informative prior distributions. I assume, *a priori*, that the elements of  $\boldsymbol{\theta}$  are mutually independent given  $\boldsymbol{\theta}^*$ .

$$\begin{aligned} \text{Level 1 :} \quad \log n_{a,t}^* | n_{a,t}, \sigma_n^2 &\sim \text{Normal}(\log n_{a,t}, \sigma_n^2), \quad a = 0, 5, \dots, A \\ &t = t_L^{[\text{cen}]}, \dots, t_U^{[\text{cen}]} \end{aligned} \quad (2.7)$$

$$\begin{aligned} \text{Level 2 :} \quad n_{a,t} | \mathbf{n}_{t-5}, \mathbf{f}_{t-5}, \mathbf{s}_{t-5}, \mathbf{g}_{t-5} &= M(\mathbf{n}_{t-5}, \mathbf{f}_{t-5}, \mathbf{s}_{t-5}, \mathbf{g}_{t-5}), \\ &a = 0, 5, \dots, A; t = t_0 + 5, t_0 + 10, \dots, T \end{aligned} \quad (2.8)$$

$$\begin{aligned} \text{Level 3 :} \quad \log n_{a,t_0} | n_{a,t_0}^*, \sigma_n^2 &\sim \text{Normal}(\log n_{a,t_0}^*, \sigma_n^2), \quad a = 0, 5, \dots, A \\ \log f_{a,t} | f_{a,t}^*, \sigma_f^2 &\sim \begin{cases} \text{Normal}(\log f_{a,t}^*, \sigma_f^2), & a = a_L^{[\text{fert}]}, \dots, a_U^{[\text{fert}]} \\ \text{undefined}, & \text{otherwise} \end{cases} \end{aligned} \quad (2.9)$$

$$\text{logit } s_{a,t} | s_{a,t}^*, \sigma_s^2 \sim \text{Normal}(\text{logit } s_{a,t}^*, \sigma_s^2), \quad a = 0, 5, \dots, A + 5 \quad (2.11)$$

$$g_{a,t} | g_{a,t}^*, \sigma_g^2 \sim \text{Normal}(g_{a,t}^*, \sigma_g^2), \quad a = 0, 5, \dots, A, \quad (2.12)$$

(where  $t = t_0, t_0 + 5, \dots, T$  in (2.9)–(2.12))

$$\text{Level 4 :} \quad \sigma_v^2 \sim \text{InvGamma}(\alpha_v, \beta_v), \quad v \in \{n, f, s, g\}. \quad (2.13)$$

For  $0 < x < 1$ ,  $\text{logit } x \equiv \log(x/(1-x))$ .

To ensure that all population counts are non-negative I multiply the joint prior on  $\boldsymbol{\theta}$  at time  $t$  by

$$I(M(\mathbf{n}_t, \mathbf{f}_t, \mathbf{s}_t, \mathbf{g}_t) > 0) \equiv \begin{cases} 1 & \text{if, for all } a = 0, \dots, A, n_{a,t+5} \geq 0 \\ 0 & \text{otherwise.} \end{cases} \quad (2.14)$$

In practice, this tends to exclude values of  $g_{a,t}$  in the range  $(-\infty, -1]$ . The truncation (2.14) is equivalent to re-defining the prior as

$$p(\boldsymbol{\theta}_t | C_t) = \frac{p(\boldsymbol{\theta}_t, C_t)}{\Pr(C_t)} \quad (2.15)$$

where  $C_t$  is the event

$$CCMPP(\mathbf{n}_{t-5}, \mathbf{f}_{t-5}, \mathbf{s}_{t-5}, \mathbf{g}_{t-5}) > 0. \quad (2.16)$$

Since (2.16) always has positive probability, (2.15) is well defined. For example, the Borel paradox (e.g, Wolpert, 1995) should not occur.

In standard Bayesian terms, (2.7) is the likelihood of  $\mathbf{n}_{t_L^{[\text{cen}]}}^{\text{cen}}, \dots, \mathbf{n}_{t_U^{[\text{cen}]}}^{\text{cen}}$ , while (2.13) is the prior distribution of  $\sigma_v^2$ , specified by the user-defined hyperparameters  $\alpha_v$  and  $\beta_v$ . Population counts at baseline are treated differently because (2.8) is essentially a standard difference equation with initial condition  $\boldsymbol{\theta}$ , which contains  $\mathbf{n}_{t_0}$ . These are the only population counts that  $M(\cdot)$  takes as inputs. The remaining census counts, at times  $t_L^{[\text{cen}]}, \dots, t_U^{[\text{cen}]}$ , are compared with the outputs of  $M(\cdot)$  via (2.7). Inference will be based on the joint posterior distribution of  $\boldsymbol{\theta}$ .

The quantities involved, and their dependence relations, are summarized in Figure 2.1.

#### 2.3.4 Determining the Hyperparameters

To determine plausible values of  $\alpha_v$  and  $\beta_v$ ,  $v \in \{n, f, s, g\}$ , I view the  $\sigma_v^2$  as representing the variance of the errors in the initial estimates of the respective demographic parameters.

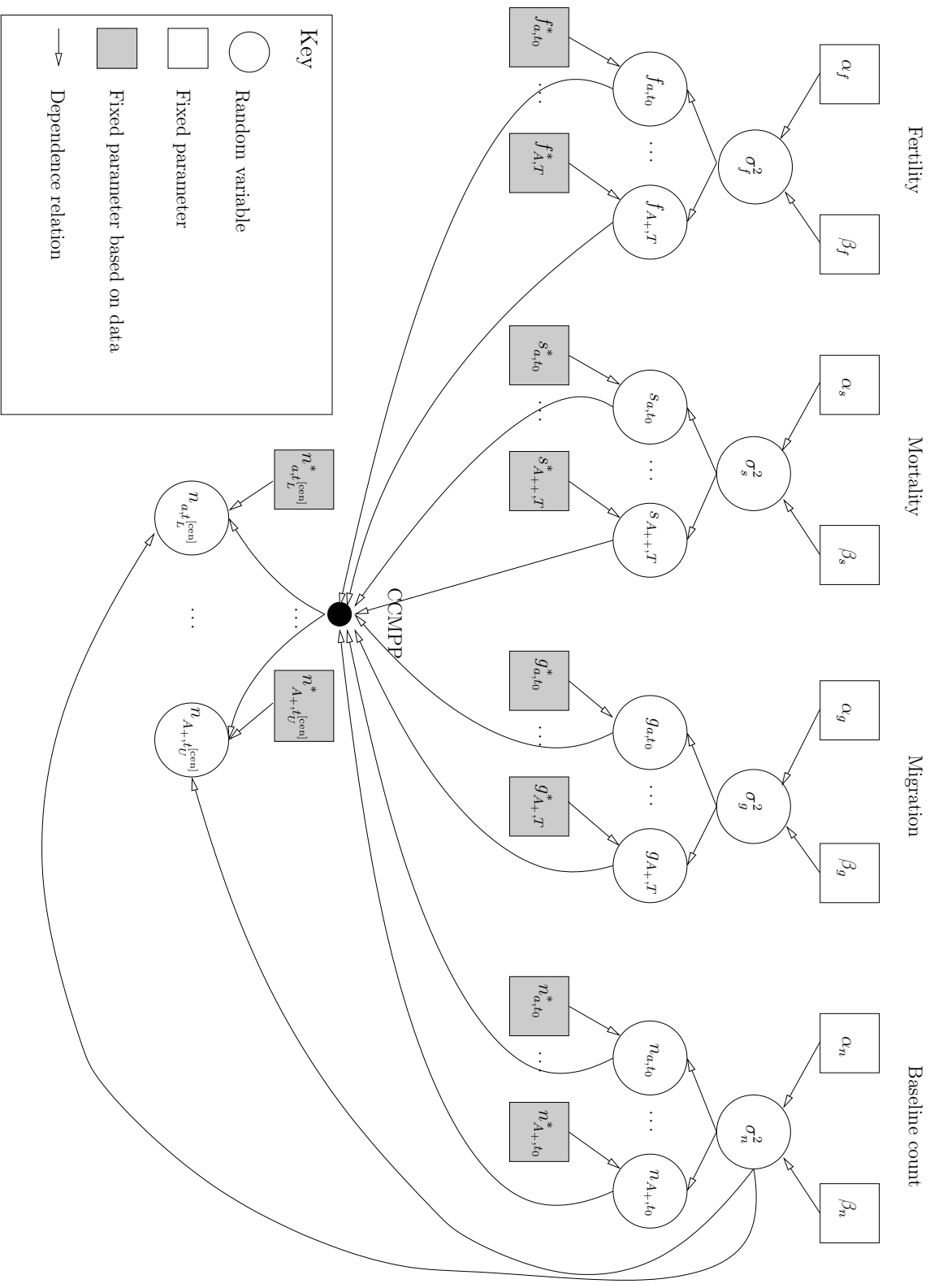


Figure 2.1. Plot showing the relationships between parameters, initial estimates and the cohort component method of population projection in the estimation model.



Although prior knowledge about these variances is unlikely to be exact, I expect that informative estimates can be derived from experts' knowledge of the data sources. Methods for eliciting prior information from experts are numerous (e.g., O'Hagan et al., 2006). Here, I use a straightforward method based on the mean absolute error (MAE) of the transformed initial estimates.

Taking fertility rate as an example, note that (2.10) implies that  $\text{MAE}(\log f_{a,t} | \sigma_f^2) \equiv E(|\log f_{a,t} - \log f_{a,t}^*| | \sigma_f^2) = \sigma_f \sqrt{2/\pi}$ . The prior distribution for  $\sigma_f^2$  can be specified by choosing quantiles for  $\text{MAE}(\log f_{a,t} | \sigma_f^2)$ . Suppose expert opinion is that  $\text{MAE}(\log f_{a,t} | \sigma_f^2)$  is likely to be close to 0.1, but could be as high as 0.5. This suggests setting  $\text{median}(\sigma_f^2) = (0.1)^2 \pi / 2 = 0.016$  and the 0.975 quantile to  $(0.5)^2 \pi / 2 = 0.393$ . To find an inverse gamma distribution with these quantiles, I would fix  $\alpha_f$  at a range of values between 0.3 and 6 and chose  $\beta_f$  such that  $\text{median}(\text{MAE}(\log f_{a,t} | \sigma_f^2)) = 0.1$ . The parameter  $\alpha_f$  would then be chosen such that the 0.975 quantile of  $\text{MAE}(\log f_{a,t} | \sigma_f^2)$  was about 0.5. This would give  $\alpha_f = 1$  and  $\beta_f = 0.0109$ .

Since demographers are more used to thinking about untransformed fertility rates, it is useful to consider what specifying  $\text{MAE}(\log f_{a,t} | \sigma_f^2)$  means on the original scale. MAE on the log scale approximates mean absolute relative error (MARE) on the original scale, where  $\text{MARE}(f_{a,t} | \sigma_f^2) \equiv E(|f_{a,t} - f_{a,t}^*| | \sigma_f^2) / f_{a,t}^*$ . This approximation is good for the MAE values used here. The MARE has been used previously by demographers as a way of quantifying measurement accuracy (Keilman, 1998). For the migration parameter, which is already proportion, I specify the MAE directly.

The population count variance,  $\sigma_n^2$ , is also modeled on the log scale and  $\alpha_n, \beta_n$  are found in the same way as  $\alpha_f$  and  $\beta_f$ . Survival is measured on the logit scale, but this should not be too difficult to interpret. Note that  $E(|\text{logit } \bar{s}_{a,t} - \text{logit } \bar{s}_{a,t}^*| | \sigma_s^2) = E(|\text{logit } s_{a,t} - \text{logit } s_{a,t}^*| | \sigma_s^2)$  where  $\bar{s}_{a,t} = 1 - s_{a,t}$ . In practice, the  $\bar{s}_{a,t}$  are close to zero, so that  $\bar{s}_{a,t} \approx \bar{s}_{a,t} / (1 - \bar{s}_{a,t})$ . Thus specifying the MAE of the log-odds of survival is not that different from specifying it for the log probability of death.

### 2.3.5 Estimation

I draw samples from the joint posterior using an MCMC sampler (Metropolis et al., 1953; Hastings, 1970; Geman and Geman, 1984). Without the restriction in (2.14), the full conditional posterior distributions for the variance hyperparameters would be the usual conjugate inverse gamma distributions. For example, the full conditional for  $\sigma_f^2$  would be

$$\sigma_f^2 | \boldsymbol{\theta} \sim \text{InvGamma} \left( \alpha_f + \frac{(\sum_{a=a_L}^{a_U} 1)(\sum_{t=t_0}^T 1)}{2}, \beta_f + \frac{1}{2} \sum_{a=a_L}^{a_U} \sum_{t=t_0}^T (\log f_{a,t} - \log f_{a,t}^*)^2 \right). \quad (2.17)$$

With the restriction, the conjugate forms are not exactly correct but will probably be close to the true full conditionals. Therefore, to update these parameters I use the conjugate full conditional distributions as proposal densities in Metropolis-Hastings steps. Using a Metropolis-Hastings proposal instead produced very similar results. The posterior densities of the remaining parameters are not easy to express analytically since each vital rate enters the likelihood through the map  $M(\cdot)$ . Therefore, these parameters are updated using Metropolis-Hastings steps with univariate normal proposal densities, with variances tuned by the method of Raftery and Lewis (1996) ( $q = 0.025, 0.975$ ,  $r = 0.0125$ ,  $s = 0.95$ ). Metropolis acceptance rates were kept within the range  $[0.2, 0.5]$ . The diagnostic was applied to the chains for each Level 4 (variance) parameter, each age- time-specific Level 3 (vital rate) parameter and the age- time-specific Level 2 parameters (the projected population counts,  $n_{a,t}$ ). I will use the term “iteration” to refer to one complete sweep through all age-time specific parameters and variance parameters. Further details are in Appendix 2.E.

The *R* environment for statistical computing (R Development Core Team, 2010), together with the *CODA* package (Plummer et al., 2006, 2010) were used for all data manipulation, model estimation and output analysis. The method is implemented in the *R* package “popReconstruct” described in Appendix B at the end of the dissertation.

## 2.4 Simulation Study

I now describe the results of a simulation study carried out to investigate the calibration of posterior probability intervals for  $f_{a,t}$ ,  $s_{a,t}$ ,  $g_{a,t}$  and  $n_{a,t_0}$  under repeated sampling of the initial estimates.

### 2.4.1 Inputs

The true vital and migration rates assumed to have prevailed in this population are shown in Tables 2.1 and 2.2. I denote these by  $f_{a,t}^{[\text{true}]}$ ,  $s_{a,t}^{[\text{true}]}$ ,  $g_{a,t}^{[\text{true}]}$  and  $n_{a,t_0}^{[\text{true}]}$ . In practice, these would be the unknown, true values of the parameters  $f_{a,t}, s_{a,t}, g_{a,t}, n_{a,t_0}$  which appear in (2.9)–(2.12). This is not intended to be a realistic model of a human population; datasets typically encountered in human demography have up to 18 age categories and any number of time periods. However, I believe that this reduced population model is of sufficient size and complexity to explore the characteristics of the statistical model while not being too computationally expensive. The TFR and life expectancy at birth were kept constant at 0.7 births per woman per year and 15.61 years, respectively, for the duration of the reconstruction. A varying pattern of migration was chosen which consisted of net out-migration in the first half of the reconstruction period followed by net in-migration in the second half. The magnitude of the flows was quite volatile, varying from 13 percent to 26 percent of the receiving population. Migration in both directions was concentrated in the two middle age groups.

The true population counts, denoted  $n_{a,t}^{[\text{true}]}$ , are shown in Table 2.2. Those for 1960 were chosen to represent a young population. Those for the subsequent time periods were derived by applying the CCMPP to the 1960 population using the vital rate and migration parameters in Table 2.1. Therefore, the underlying true population dynamics over the reconstruction period were completely and deterministically defined by (2.1). The entries in Table 2.2 correspond to  $n_{a,t}^{[\text{true}]}$ ,  $t = t_0, t_L^{[\text{cen}]}, \dots, t_U^{[\text{cen}]}$  in (2.8).

The hyperparameters of the inverse gamma distributions were determined as described in Section 2.3.4. The median MAEs for log fertility rate, logit survival and log population counts were set to 0.1 with 0.975 quantiles of approximately 0.5. The same quantities for

*Table 2.1.* True vital rates used in the simulation study.

age	Time period			
	[1960, 1965)	[1965, 1970)	[1970, 1975)	[1975, 1980)
Fertility Rate				
0	0.00	0.00	0.00	0.00
5	0.40	0.40	0.40	0.40
10	0.30	0.30	0.30	0.30
15	0.00	0.00	0.00	0.00
Survival Proportion				
0	0.90	0.90	0.90	0.90
5	0.95	0.95	0.95	0.95
10	0.85	0.85	0.85	0.85
15	0.80	0.80	0.80	0.80
20+	0.10	0.10	0.10	0.10
Migration Proportion				
0	-0.03	-0.05	0.03	0.05
5	-0.05	-0.10	0.05	0.10
10	-0.06	-0.11	0.06	0.11
15	-0.01	-0.01	0.01	0.01

Table 2.2. True population counts used in simulation study.

age	Year				
	1960	1965	1970	1975	1980
0	7500	8482	9453	11436	14504
5	6000	6886	7512	9280	11600
10	4000	4862	5293	6690	8651
15	3000	3404	3998	4762	6149

Table 2.3. Level 4 hyperparameters and selected implied quantiles of the mean absolute error (MAE) of the demographic parameters used in the simulation study and the application to Burkina Faso.  $f$  and  $n$  are modeled on the log scale,  $s$  is modeled on the logit scale and  $g$  is untransformed.

		Quantiles of MAE( $v$ )					
$v$	$\alpha$	$\beta$	0.025	0.25	0.5	0.75	0.975
$f, s, n$	1	0.0109	0.0433	0.0707	0.1	0.1552	0.5232
$g$	1	0.0436	0.0867	0.1414	0.2	0.3104	1.0465

migration were set to 0.2 and approximately 1, respectively. The resulting values of  $\alpha_v$ ,  $\beta_v$  and MAE quantiles are shown in Table 2.3. For fertility,  $\text{MAE}(\log f_{a,t} | \sigma_f^2) = \sigma_f \sqrt{2/\pi}$ ; similarly for population count. For survival,  $\text{MAE}(\text{logit } s_{a,t} | \sigma_s^2) = \sigma_s \sqrt{2/\pi}$  and for migration  $\text{MAE}(g_{a,t} | \sigma_g^2) = \sigma_g \sqrt{2/\pi}$ .

#### 2.4.2 Study Design

The values in Tables 2.1–2.3 remained fixed throughout the simulation study and the initial estimates  $f_{a,t}^*$ ,  $s_{a,t}^*$ ,  $g_{a,t}^*$  and  $n_{a,t}^*$  were treated as random. I drew  $n_{a,t}^* | \sigma_n^2$  from a  $\text{logNormal}(\log n_{a,t}^{[\text{true}]}, \sigma_n^2)$  distribution in accordance with (2.7). The remaining initial estimates were drawn from distributions derived from (2.9)–(2.12) in an analogous manner. For example, the  $f_{a,t}^* | \sigma_f^2$  were drawn from a  $\text{logNormal}(\log f_{a,t}^{[\text{true}]}, \sigma_f^2)$  distribution.

The coverage of central marginal credible intervals (or Bayesian confidence intervals) under the model was estimated by the following experiment. For  $j = 1, \dots, J$ :

1. Randomly sample  $\sigma_v^{2[j]}$ ,  $v = n, f, s, g$ , from (2.13).
2. Generate initial estimates  $f_{a,t}^{*[j]}, g_{a,t}^{*[j]}, n_{a,t}^{*[j]}$  for  $a = 0, \dots, 15+$ ,  $t = 1960, \dots, 1980$ ,  $s_{a,t}^{*[j]}$ , for  $a = 0, \dots, 20+$   $t = 1960, \dots, 1980$ , as described above.
3. Check that (2.14) is satisfied by the initial estimates; if not return to step 1.
4. Draw a large MCMC sample from the joint posterior and find the 0.025, 0.5 and 0.975 quantiles of the marginal distribution of each parameter.

The estimated coverage is then the proportion of the  $J$  credible intervals containing the known, true value for each parameter.

I set  $J = 200$  and applied the estimation method described in Section 2.3.5. Start values for the population counts, vital rates and migration proportions were set to the initial estimates. Start values for the variances were arbitrarily set to 5 as they appeared to have a negligible effect on the final results.

### 2.4.3 Results and Discussion

Point estimates of the coverage of the marginal 0.95 posterior probability intervals are shown in Table 2.4. These are all close to 0.95. In practical applications with real data sets, where the true parameter values are unknown, interest will be in interval estimates of the demographic parameters. These should be based on the joint posterior distribution. For illustration, I have plotted central marginal credible intervals of a selection of age-specific and age-summarized parameters that might be of interest based on the MCMC sample from a single replicate of the simulation study (Figure 2.2). For comparison, I have also plotted the true parameter values used throughout the simulation and the noisy initial estimates generated under the model.

credible intervals can be plotted for age-specific parameters as has been done for ASFRs in Figure 2.2a. Confidence intervals for any function of the age-specific parameters can be

Table 2.4. Estimated coverage probabilities of 95 percent credible intervals for Level 3 parameters from the simulation study.

Years	Ages	Demographic Parameter			
		Population	Fertility	Survival	Migration
1960	[0, 5)	0.930			
	[5, 10)	0.940			
	[10, 15)	0.945			
	[15, 20)	0.920			
	20+				
[1960, 1965)	[0, 5)			0.940	0.940
	[5, 10)			0.945	0.935
	[10, 15)		0.965	0.950	0.950
	[15, 20)		0.935	0.955	0.960
	20+			0.960	
[1965, 1970)	[0, 5)			0.950	0.940
	[5, 10)		0.920	0.945	0.940
	[10, 15)		0.960	0.935	0.965
	[15, 20)			0.925	0.955
	20+			0.935	
[1970, 1975)	[0, 5)			0.915	0.960
	[5, 10)		0.920	0.955	0.950
	[10, 15)		0.930	0.950	0.935
	[15, 20)			0.965	0.940
	20+			0.890	
[1975, 1980)	[0, 5)			0.950	0.930
	[5, 10)		0.920	0.950	0.970
	[10, 15)		0.955	0.945	0.950
	[15, 20)			0.950	0.955
	20+			0.975	

obtained immediately by transforming each vector of age-specific values in the MCMC sample and computing the sample quantiles. Quantities of particular interest are the summary measures defined in Section 2.3.1. I show TFR,  $e_0$  and the average annual total net number of migrants in Figures 2.2b–d.

## 2.5 *Reconstruction of the Population of Burkina Faso, 1960–2005*

I now illustrate the method by reconstructing the female population of Burkina Faso from 1960 to 2005. Uncertainty in this case is non-negligible due to the fragmentary nature of the available data. This application shows how the method is able to quantify this appropriately by producing probabilistic interval estimates.

### 2.5.1 *Initial Estimates*

Brief descriptions of the initial estimates are given below; see Appendix 2.B for further details. The parameters  $\alpha_v$  and  $\beta_v$ ,  $v \in \{n, f, s, g\}$ , were set to the same values as in the simulation study (Table 2.3); the MAEs given there were based on expert opinions provided by UNPD analysts for the case of Burkina Faso.

#### *Population Counts*

Population counts,  $n_{a,t}^*$ , in exact years 1960, 1975, 1985, 1995 and 2005 by sex were taken from United Nations (2009a) which are based on a 1960–1961 demographic survey and censuses in 1975, 1985, 1996 and 2006. The United Nations (UN) figures are preferred over the raw census counts because important adjustments were made for underenumeration. This form of bias is more common in certain age groups and efforts to reduce it are based on post-censal surveys.

Burkina Faso experienced a high level of population growth between 1960 and 2005; the total female population increased from 2.3 million to 6.9 million, an average of 2.4 percent per year. The population has a young age structure, as illustrated by the age-specific population counts in Figure 2.3.



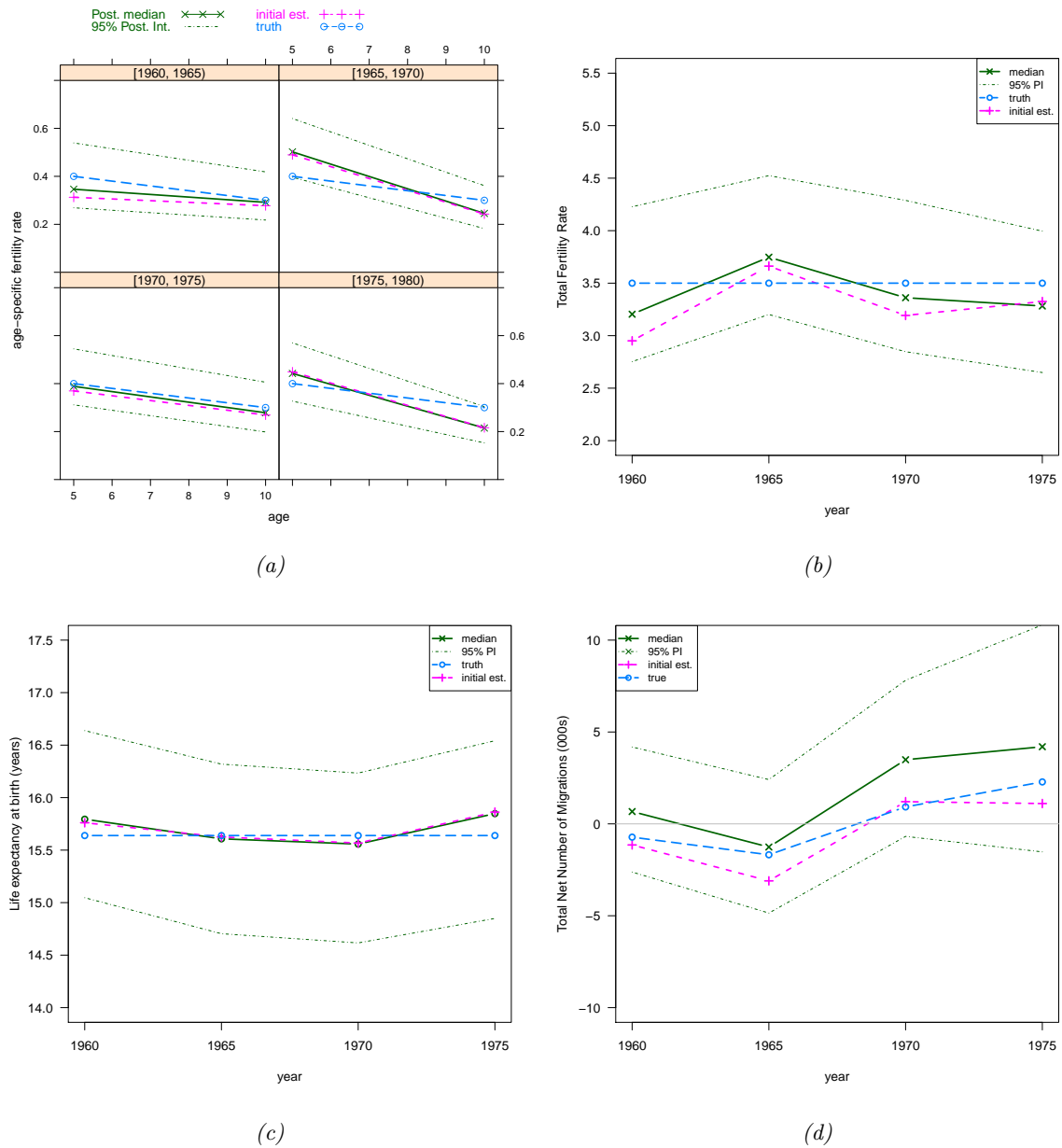


Figure 2.2. Ninety-five percent credible intervals for selected parameters from a single replication of the simulation study. (a) age-specific fertility rate (ASFR). (b) total fertility rate (TFR). (c) life expectancy at birth ( $e_0$ ). (d) Average annual total net number of migrants.

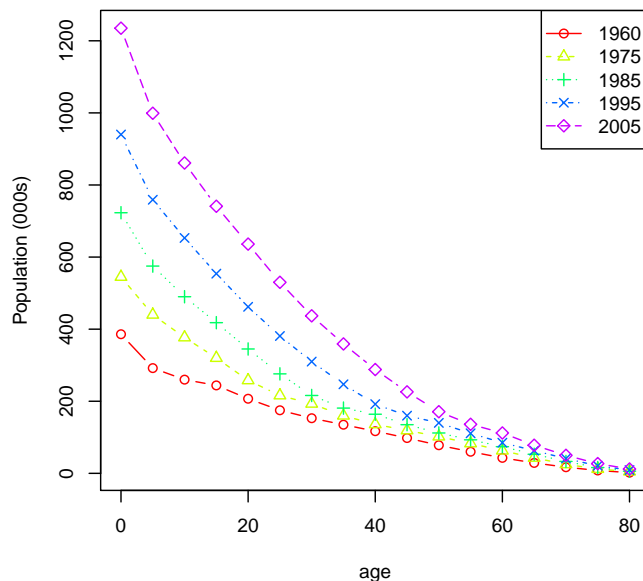


Figure 2.3. Population counts by five-year age group for the reconstructed female population of Burkina Faso, 1960–2005.

### Fertility Rates

Initial estimates of ASFRs,  $f_{a,t}^*$ , were derived from multiple, overlapping series of point estimates taken from the 1960 and 1991 demographic surveys, the 1976 census post-enumeration survey, the 1985, 1996 and 2006 censuses and the 1992–93, 1998–99 and 2003 DHSs. [Alkema et al. \(2012\)](#) studied estimates of TFR using these data and found evidence of bias. Therefore, I took [Alkema et al.’s \(2012\)](#) median bias-adjusted estimates as the initial estimates of TFR and multiplied them by age-specific fertility patterns.

Age patterns sum to one and indicate the share of fertility attributable to each age group. I obtained a separate pattern for each projection interval in the reconstruction period by smoothing the available point estimates over age, within interval, using *loess* ([Cleveland, 1979](#); [Cleveland et al., 1992](#)) and normalizing. The *loess* method performs a series of locally weighted regressions. Smoothing within five-year sub-interval (Figure 2.4) yielded trends

that were also sensible, *a priori*, when viewed by five-year age group (Figure 2.5). No point estimates were available for the period 1965–1970. To generate initial estimates for this period, I multiplied the 1960–1965 age-pattern by [Alkema et al.’s \(2012\)](#) adjusted TFR estimate for 1965–1970.

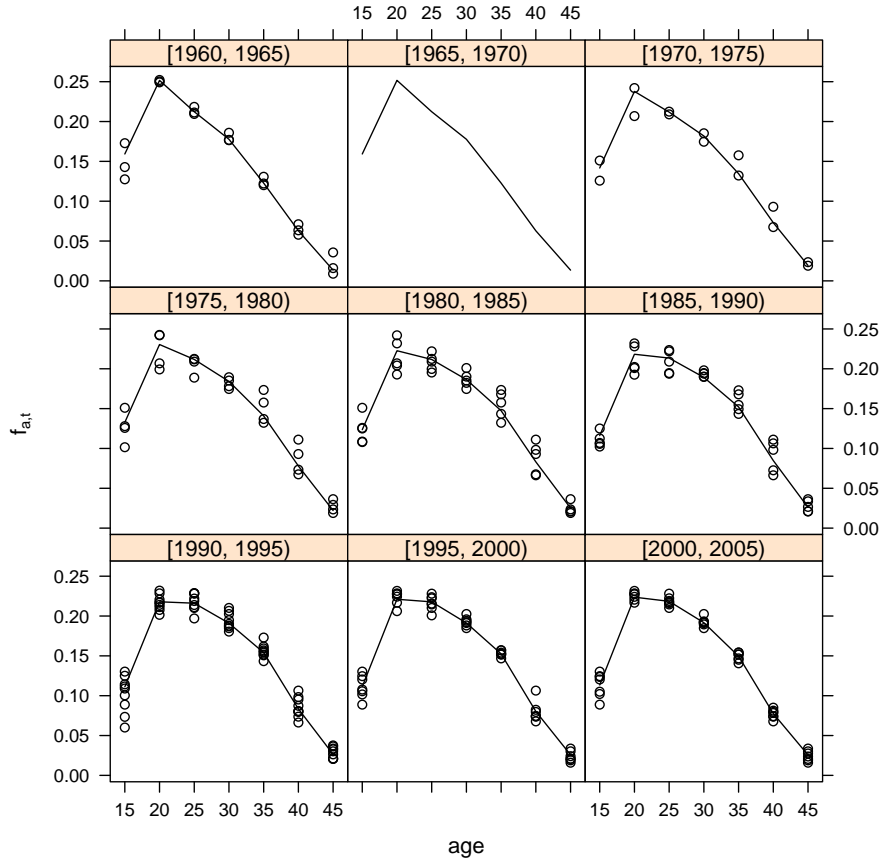


Figure 2.4. Data points for the initial estimates of age-specific fertility patterns of Burkina Faso females, 1960–2005, grouped by five-year time period. The lines are the within-time loess smooths.

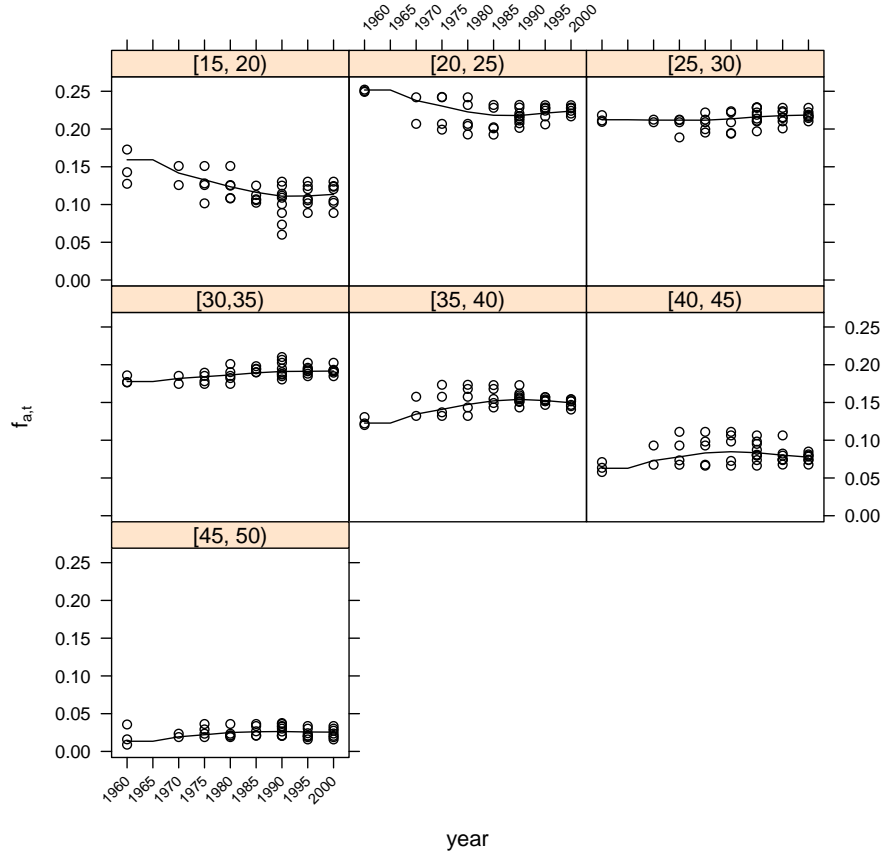


Figure 2.5. Data points for the initial estimates of age-specific fertility patterns of Burkina Faso females, 1960–2005, grouped by five-year age group. The lines are the within-time loess smooths, the same as those plotted in Figure 2.4.

### Survival Proportions

Initial estimates of survival proportions,  $s_{a,t}^*$ , were derived from abridged demographic life tables constructed using data on under five and adult mortality from the 1960–1961 and 1991 national demographic surveys, the 1992–1993, 1998–1999 and 2003 DHSs, UNICEF’s Multiple Indicator Cluster Survey—Round 3 conducted in 2006. The tables were created by applying the Brass two-parameter relational logit model (Brass, 1971b) with the Timæus Sahelian standard (Timæus, 1999). Standard methods were used to derive survival propor-

tions from the life tables.

### *Migration Proportions*

Estimates of migration of comparable detail to those for vital rates are seldom available for many countries. Some estimates for Burkina Faso by broad age group and sex are given by [Condé \(1980\)](#) for the period 1960–1975 who concluded that migration during this period was primarily labor migration. In addition, whole-population estimates for 1960–2005 are available from [United Nations \(2009a\)](#) and [United States Census Bureau \(2008\)](#) which indicate sustained net out-migration over the period 1960–2000. The latter source suggests a reversal to net in-migration over 2000–2005.

I designed the initial estimates to reflect the direction and approximate magnitude suggested by these sources. The  $g_{a,t}^*$  were set to -0.055 for  $15 \leq a \leq 50$ ,  $1960 \leq t \leq 1995$ , 0.055 for  $15 \leq a \leq 50$ ,  $t = 2000$  and zero otherwise. Thus, for example, the initial estimate for the net number of migrants over the five-year period  $[1960, 1965)$  is centered at -5.5 percent of the 1960 population, an average of -1.1 percent of the 1960 population per year for the five years in the projection interval. The direction is reversed over  $[2000, 2005)$  since Burkina Faso likely received refugees from the civil war which broke out in neighboring Côte D’Ivoire during this period. The greater uncertainty about these initial estimates than about those for the other parameters is accounted for by setting  $\alpha_g, \beta_g$  such that the median and the 0.975 quantile of the MAE were twice as large as the values used for the other parameters (Table 2.3).

### *2.5.2 Results*

I summarize the full joint posterior distribution with posterior medians and 95% central credible intervals based on the marginal distributions of age-specific input parameters and age-summarized versions such as TFR and  $e_0$ . I use half the width of the confidence intervals (“half-widths”) to indicate the magnitude of posterior uncertainty. Summarizing the joint posterior distribution of  $\theta$  by quantiles of marginal distributions provides coherent and probabilistic interval estimates. They are coherent because uncertainty about all other

parameters is accounted for. The simulation study suggests that the intervals are also well calibrated in that they achieve their nominal coverage over repeated random sampling of the initial estimates and census data, under the model.

### *Population Counts*

The posterior medians for population counts at baseline (Figure 2.6) are very close to their initial estimates; across age groups, the maximum absolute difference is 2.3 percent of the initial estimate. All of the intervals have half-widths less than 7.4 percent of the median, indicating that posterior uncertainty about this quantity is low.

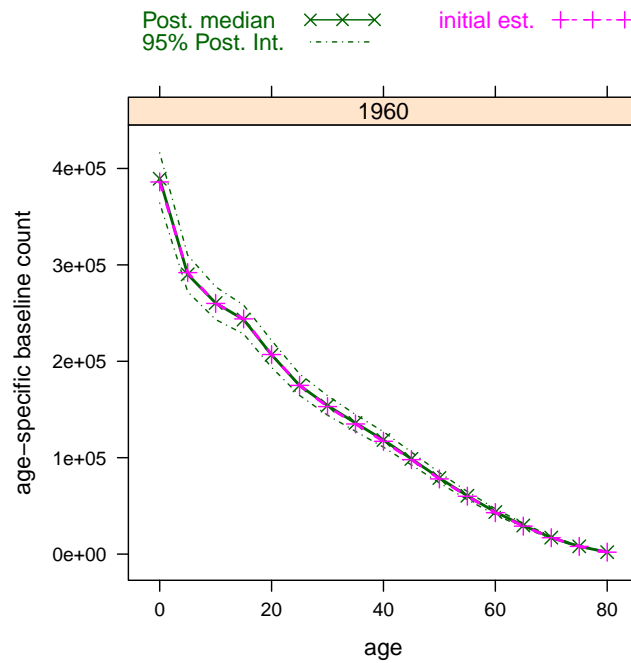


Figure 2.6. Ninety five percent credible intervals and initial estimates for population count for the reconstructed female population of Burkina Faso by age, 1960.

### *Fertility*

A similar plot for ASFRs is shown in Figure 2.7. Again, the posterior medians are close to their respective initial estimates, but the half widths of the posterior intervals are wider, ranging from 18–21 percent of the median. This is because most of the information about fertility in the non-fertility parameters comes from the population counts in the age range  $[0, 5)$ , and this depends mainly on the level of fertility, not how it is distributed across age group of mother. Information about the age pattern of fertility in the posterior distribution comes mostly from the data-derived initial estimates. The interval widths narrow as age-specific fertility approaches zero, which occurs at the extremes of the age-range of non-zero fertility. Due mainly to biology, human fertility is known to be low at the extremes of this range with a high degree of certainty. The shape of the posterior intervals reflects this.

Posterior median estimates of TFR (Figure 2.8a) increased from 7.1 children per woman in 1960–1965 to about 7.4 over the period 1965–1980, and then decreased to 6.4 children per woman in 2000–2005. Over the entire reconstruction period, the limits of the 95 percent intervals are equivalent to about plus or minus half a child. The posterior medians are slightly lower than the initial estimates, which were based only on information about fertility collected mainly in surveys. The posterior distribution for TFR also takes population counts, mortality and migration into account. There is more information about TFR in these parameters than there is about the fertility age pattern, explaining why the interval half-widths for TFR are narrower, relatively, than those for the age-specific rates; all are less than 7.5 percent of the posterior median.

### *Mortality*

Posterior estimates of mortality are presented in terms of life expectancy at birth,  $e_0$ , and under-five mortality,  $1 - s_{0,t}$  (Figures 2.8c and d). Under-five mortality is often viewed as an indicator of a country's level of development. The posterior marginal distributions for these two parameters reflect a sustained improvement in mortality conditions in Burkina Faso over the period. Posterior median estimates of  $e_0$  for 1960–1965 and 2000–2005 are 35 and 52 years, respectively. The interval half-widths decrease from 2.2 years in 1960–1965 to

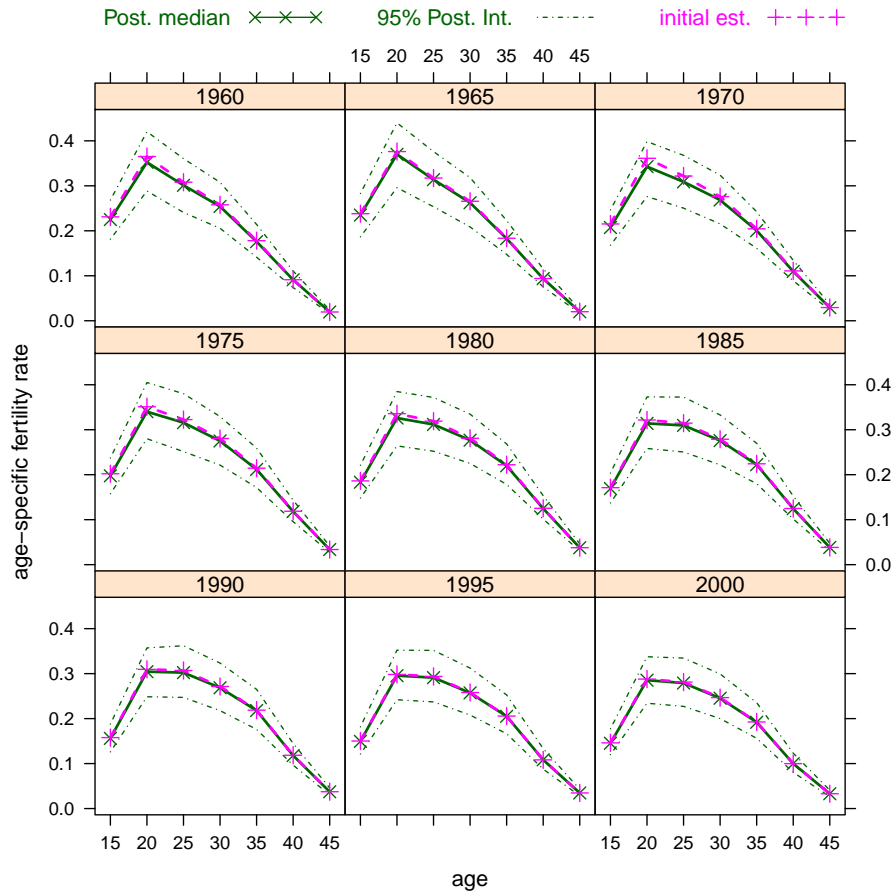


Figure 2.7. Ninety-five percent credible intervals and initial estimates for age-specific fertility rates (ASFRs) for the reconstructed female population of Burkina Faso, 1960–2005

1.8 years in 2000–2005, indicating a decrease in uncertainty about this parameter over the interval of reconstruction. Posterior median estimates of under five mortality declined from 0.25 to 0.12 over the period (95 percent intervals: [0.21, 0.29] and [0.1, 0.15], respectively).

### Migration

I summarize age-specific migration by the average annual net number of migrants added to the population, in units of 1000 (Figure 2.8b). The average of the posterior median estimates between 1960 and 2000 is  $-18$  (thousand women) per year. Importantly, the 95



percent intervals contain zero at all time periods and, moreover, they are very wide. The interval for 1960–1965 is  $[-28, 13]$ , while it is  $[-73, 11]$ , for 1995–2000.

Burkina Faso has been characterized as a country of emigration between 1960 and 2000, with migration dominated by people moving to find work in neighboring countries. This view is consistent with knowledge about the labor market during that period, as well as with data collected in neighboring countries (United States Census Bureau, 2008; Condé, 1980). These data are fragmentary, however, and there are no reliable estimates of the magnitude of the migratory flow. The results reflect this situation. The marginal posterior distribution is centered below zero which suggests that, on balance, the available data are more consistent with a net outflow up to 2000. Nevertheless, there is insufficient information to rule out a zero, or even a small positive, net flow.

For 2000–2005 the 95 percent interval is  $[-29, 70]$  with posterior median 22. While a positive net flow is suggested, the interval is very wide and contains zero. Clearly, there is a great deal of uncertainty about migration during this period, even after taking information about all the other parameters into account.

### 2.5.3 Model Checking and Sensitivity Analysis

The census counts,  $n_{a,t}^*$ , play a central role in the model; all vital rate and migration parameters are related to one another *a posteriori* through these counts. I report two checks here; one to assess sensitivity to the form of the likelihood and another to assess out-of-sample predictive performance. Further checks related to MCMC sampling can be found in Appendix 2.E.

I assessed sensitivity to the use of the relatively light tailed normal likelihood with constant variance using the approach of Carlin and Polson (1991). Replacing  $\sigma_n^2$  with  $\lambda_{a,t}\sigma_n^2$ ,  $\lambda_{a,t} \sim \text{InvGamma}(1, 1)$ ,  $t = 1960, 1965, \dots, 2005$ ,  $a = 0, 5, \dots, 80+$ , in (2.7) and (2.9) relaxes the assumption of constant variance. Moreover, in comparison with (2.7), the (marginal) likelihood under this formulation is the heavier tailed Student’s  $t$  (mean =  $\log n_{a,t}$ , scale =  $\sigma_n$ ,  $\text{df} = 2$ ) distribution. I refer to this modification as the “ $t_2$  likelihood model”.

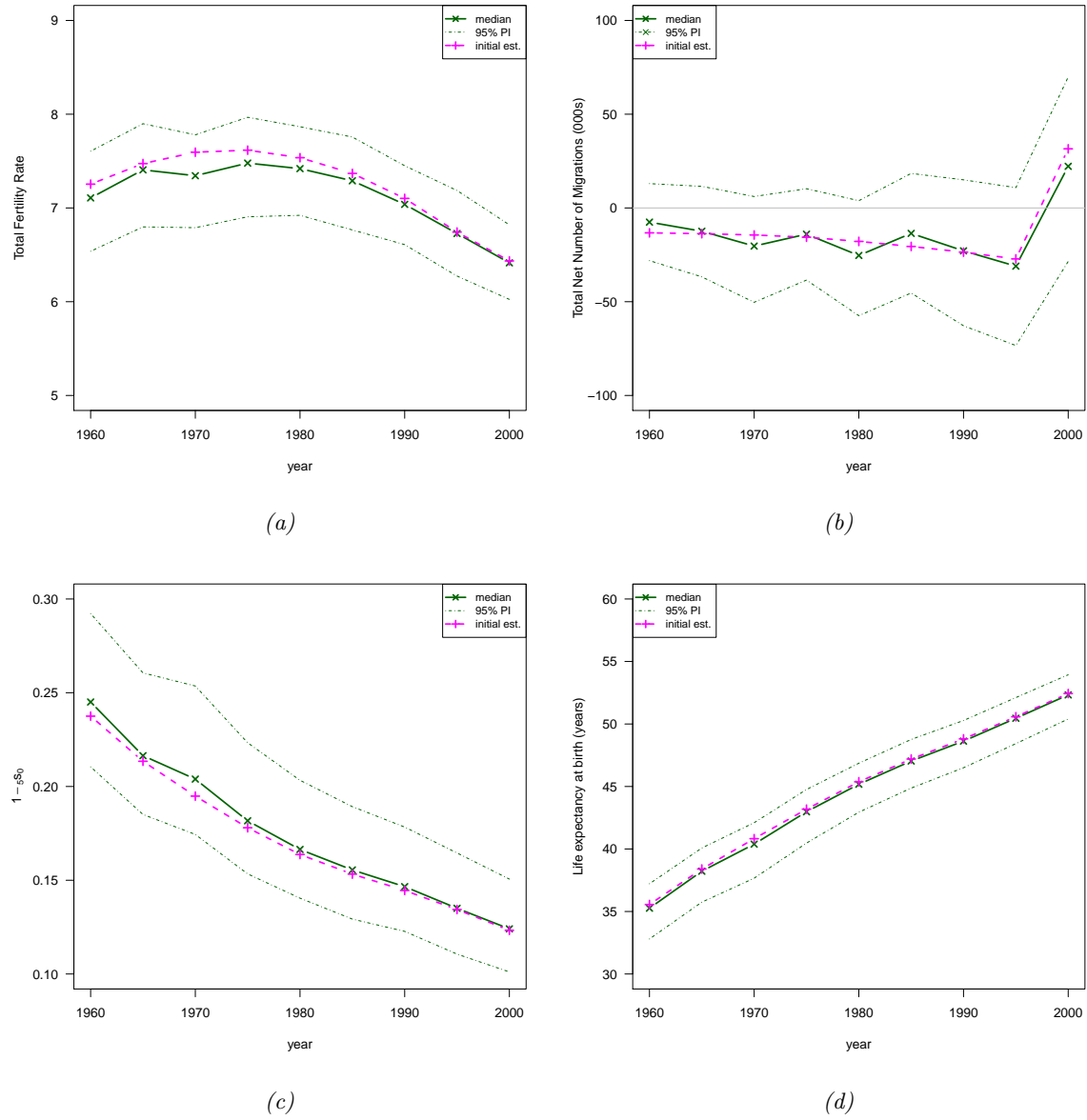


Figure 2.8. Ninety-five percent credible intervals for selected age-summarized parameters for the reconstructed female population of Burkina Faso, 1960–2005. (a) total fertility rate (TFR). (b) Average annual total net number of migrants. (c) Under-5 mortality. (d) life expectancy at birth ( $e_0$ ).

Posterior marginal quantiles of the demographic parameters were examined to assess the need for this additional flexibility. I compared the empirical 0.025, 0.5 and 0.975 quantiles of the posterior marginal distributions of each age-time-specific parameter using the MCMC samples from the runs under the modified and original models. This involved comparing two sets of multivariate distributions. Within each parameter, except migration, I calculated the absolute relative differences (ARDs) for each age and time, expressed as a percentage, and summarized them by their averages and maxima, taken over all ages and times. For example, the mean of the ARDs of the 0.025 quantiles for fertility rate was calculated as

$$\frac{100}{(17)(9)} \sum_a \sum_t \frac{|f_{a,t}^{[0.025, \text{orig}]} - f_{a,t}^{[0.025, t_2]}|}{f_{a,t}^{[0.025, \text{orig}]}}$$

where  $f_{a,t}^{[0.025, \text{orig}]}$  and  $f_{a,t}^{[0.025, t_2]}$  are the 0.025 quantiles of the posterior distribution for  $f_{a,t}$  under the original and  $t_2$  likelihood models. The 17 and 9 correspond to the number of age groups and time periods, respectively. The maximum ARDs were computed similarly. Migration is expressed as a proportion so I calculated absolute (non-relative) differences for this parameter.

Posterior distributions of the  $\lambda_{a,t}$  were also examined to assess the need for the additional flexibility of the  $t_2$  likelihood model. Posterior distributions of the  $\lambda_{a,t}$  concentrated away from 1 would indicate that the original normal-based model fits poorly (Carlin and Louis, 2009, Ch. 4).

The predictive ability of the original model was tested by re-running the analysis four times, each time omitting one of the census data sets. For  $t = 1975, 1985, 1995, 2005$ , I compared the posterior predictive distributions  $n_{a,t} | n_{a,-t}^*$  with the point values  $n_{a,t}^*$ , where  $n_{a,-t}^*$  is the set of census counts for age  $a$  for all years except  $t$ . I call this the “out-of-sample validation”. For each of the four runs, I summarized the difference between the posterior predictive median and the census counts using MARE, expressed as a percentage, where

$$MARE \equiv \frac{100}{(17)(4)} \sum_a \sum_{t=t_L^{[\text{cen}]} }^{t_U^{[\text{cen}]}} \frac{|n_{a,t}^* - \tilde{n}_{a,t}|}{n_{a,t}^*},$$

$\tilde{n}_{a,t}$  is the sample median of the  $n_{a,t}$  based on the MCMC sample and the 17 and 4 refer to

the number of age groups and censuses, respectively. Small values of MARE suggest that the model predicts the observed counts well.

### *Results*

Quantiles of the posterior marginal distributions from the  $t_2$  likelihood model were close to those from the original model (Table 2.5). All mean ARDs were below five percent and most maximum ARDs were below nine percent. Large ARDs were found between the extreme quantiles of some population counts, the largest for the 0.975 quantile in 1960, age group 65–69 (ARD = 36 percent). However, on the raw scale, this represented a difference of less than 10,000 people, which is small relative to the total population size, the median estimate of which was slightly over 2 million in 1960 under both models.

The posterior distributions of the  $\lambda_{a,t}$  were virtually all centered around 1. That of  $\lambda_{80,1975}$  had the median furthest from 1, but was still very spread out; its 0.025, 0.25, 0.5, 0.75 and 0.975 quantiles were, respectively, 0.30, 0.93, 2.4, 9.4, and 167. This suggests that the extra flexibility of the  $t_2$  likelihood model is not needed.

The MARE from the out-of-sample validation was 3.9 percent, indicating that the posterior predictive estimates of the census counts were close to the observed census counts.

Overall, these results indicate that the normal-based model as originally formulated in Section 2.3.3 fits the data reasonably well.

## **2.6 Discussion**

I have described a method for reconstructing past populations by age and sex which is designed to work with the type of data commonly collected in modern demographic surveys and censuses, especially in developing countries. Population dynamics are modeled by the well-known cohort-component method of population projection and measurement error is accounted for in a coherent, fully probabilistic manner through a Bayesian hierarchical model. Inference is based on the joint posterior distribution of all parameters, which depends on data through bias-reduced initial estimates. I applied the method to a real data set and found that the widths of the posterior intervals indicated a non-negligible amount of

*Table 2.5.* Mean and maximum absolute relative differences (ARDs) between posterior marginal quantiles of the posterior distributions from the  $t_2$  likelihood and original models for the reconstructed female population of Burkina Faso, 1960–2005. Absolute differences (ADs) are given for migration (see Section 2.5.3).

parameter	quantile	mean ARD (%)	max ARD (%)
fertility rate	0.025	0.79	4.09
	0.500	0.22	0.65
	0.975	0.52	1.87
survival proportion	0.025	0.38	2.67
	0.500	0.06	1.67
	0.975	0.30	2.39
migration proportion	0.025	0.68	0.29
	0.500	0.72	2.36
	0.975	1.81	2.20
pop. count, 1960	0.025	0.92	1.73
	0.500	0.20	0.48
	0.975	5.38	36.48
pop. count, 1965–2005	0.025	0.92	19.08
	0.500	0.24	1.87
	0.975	1.07	24.36

uncertainty about all parameters, but were of magnitudes within the range of variation demographers are used to when working with estimates and projections.

Inferences are likely to be sensitive to changes in the initial estimates. However, these are primarily data-derived and the goal here is to synthesize all of the available information; changes in these parameters should have an influence on the posteriors. In the application to the female population of Burkina Faso, the posterior medians were similar to the initial estimates in many cases. This suggests that the initial estimates of each parameter agreed closely with the census counts and the initial estimates of the other parameters. I would expect to see a greater difference between the posterior medians and initial estimates of parameters for which this agreement is weaker. This is investigated further in [Appendix 2.D](#) and [Section 3.4](#).

[Lee \(1971, 1974\)](#) and [Oeppen \(1993a\)](#) proposed deterministic methods of population reconstruction. I have assumed a deterministic model only for the population dynamics. That is, given the true vital and migration rates, the evolution of the population is modeled deterministically. In contrast, [Bertino and Sonnino \(2003\)](#) give a method in which the population dynamics are stochastic and the vital rates function as mean parameters. I agree with [Pollard \(1968; see also Cohen, 2006\)](#) and expect that, in typical applications, variation due to measurement error will overwhelm any additional variation arising from a stochastic population dynamics model. Moreover, [Bertino and Sonnino's \(2003\)](#) method cannot be easily applied in this context because it was designed to take counts of baptisms and deaths by year as inputs. Information of this kind is seldom available in most of the cases where I wish to apply the method. Key features of the approach, therefore, are that the major source of uncertainty in population reconstruction, namely measurement error, is appropriately accounted for through fully probabilistic estimates and the method can be used with the kind of data available for most countries over past sixty years.

I made the simplifying assumption of constant variance across age and time for each demographic parameter on the log or logit scale. This might seem restrictive; more complex variance structures for the other parameters could be proposed to allow for the fact that more is typically known about infant and child mortality than old-age mortality, for example. Correlations between measurement errors in adjacent time periods and age groups for the

vital rate parameters are studied in Appendix A. However, the benefits of this extension would have to be weighed against the additional complexity of having to estimate more parameters. As my checks indicated, using separate age-time specific variance parameters for population counts made little difference to the final results, probably because there was not enough information in the initial estimates to estimate them. The story might be different if estimation is done simultaneously for groups of countries. For instance, with demographically similar countries, it might be realistic to set some of the variance parameters constant across countries but allow for variation over time or age.

Alternatively, a small number of variance parameters could be chosen representing different degrees of uncertainty, for example,  $\sigma_{SML}^2 < \sigma_{MED}^2 < \sigma_{LGE}^2 < \sigma_{XL}^2$ . These could then be assigned to the age-specific parameters by following expert opinion. An advantage is that the number of parameters can be determined by the analyst as opposed being dependent on the number of age groups or sub-intervals.

Census counts, or data of comparable reliability, are assumed available for the baseline year. This requirement could be removed by modifying (2.9) so as to accommodate values of  $n_{a,t_0}^*$  derived from non-census sources. Since these would probably be less reliable than census-derived estimates, this would mean replacing  $\sigma_n^2$  in (2.9) with a new variance parameter to account for the extra uncertainty. This could be modeled in the same way as the existing variance parameters per (2.13). The period of reconstruction in my example was delimited by the years of the earliest and most recent data on population counts. This modification would permit the period of reconstruction to begin earlier if some initial estimate of population counts at an earlier baseline year were to be obtained.

No modifications are required to continue reconstruction beyond the year of the most recent census where initial estimates of vital rates and migration are available. However, the posterior distribution of the vital rates and migration for years beyond the most recent census will be based entirely on the initial estimates.

The structure of the model could be extended to produce more detailed reconstructions in several ways. An extension to two-sex populations is implemented in Chapter 4.

I used the method to reconstruct national populations. There are at least two ways in which sub-national reconstructions could be obtained. The most straightforward would

be to obtain sets of initial estimates for each sub-national region of interest, and apply the model separately to each. Sub-national estimates of population counts by age can be obtained from many censuses. In developed countries, vital registration systems would likely provide initial estimates of regional fertility and mortality. Less developed countries often lack these systems and such data might be difficult to obtain. Obtaining sub-national estimates of net migration is likely to be difficult for most countries.

A more feasible approach is to use sub-national initial estimates of population counts and set initial estimates of sub-national vital rates to their national-level estimates. A minimal set of modifications to allow this could involve replacing the national-level population count vectors,  $\mathbf{n}_t$ , in (2.1) with vectors of stacked sub-national counts. For  $R$  regions, the population count vector at time  $t$ ,  $\mathbf{n}_{\cdot,t} \equiv (n_{0,t}, \dots, n_{A,t})'$ , would be  $(\mathbf{n}'_{\cdot,1}, \dots, \mathbf{n}'_{\cdot,R})'$ . The projection matrix would take a block diagonal form with  $R$  blocks, one for each region. Similarly, the  $g_{a,t}$  would be national-level initial estimates of migration proportions. Level 1, (2.7), and Level 3, (2.9)–(2.12), of the hierarchical model would be extended to include additional, similar terms for each region. For example, (2.11) could be replaced by  $\text{logit } s_{a,t,r} \mid s_{a,t}^*, \sigma_s^2 \sim \text{Normal}(\text{logit } s_{a,t}^*, \sigma_s^2)$  for regions  $r, \dots, R$ . Level 4, (2.13), would be unchanged for  $v = f, s, g$  since I only have national-level initial estimates, but models with separate variance parameters for each region (i.e.,  $\sigma_{n,r}^2$ ,  $r = 1, \dots, R$ ) would be worth investigating.

An advantage of this modification is that “hybrid” cases where sub-national data are available for some time periods and/or parameters could be accommodated by using them to derive specific initial estimates and substituting these for the national-level estimates in the modified Level 3. Corresponding, additional variance parameters could also be added at Level 4. A possible shortcoming of this approach is lack of flexibility in cases where a few regional vital rates differ greatly from the national-level rates since the national level initial-estimates are used as fixed medians at Level 3. This might be detected by applying the approach of Carlin and Polson (1991) to the vital rate variance parameters, as was done in Section 2.5.3 for  $\sigma_n^2$ . Alternatively, dependence among sub-national vital rates could be explicitly modeled, perhaps using a spatial model in Level 3.

Migration is not split into its constituent inflows and outflows since the projection model



(2.1) requires net migration as an input. Reliable data on migration over long periods are not usually available, especially for developing countries. Even where data on flows are collected, such as in the European Union, there can be significant disagreement in estimates of bi-national flows between the records of the sending and receiving countries (e.g., [Raymer et al., 2011](#)). The UNPD has considered this issue and net migration is currently their preferred measure.

However, in cases where good information about both in- and out-migration is collected by means of population registers or border control agencies it might be reasonable to model the two flows separately on a country-by-country basis. To allow this, the  $g_{a,t}$  would be replaced with  $g_{a,t}^I$  and  $g_{a,t}^E$ , say, for immigration and emigration, respectively. A minimal modification would then be to replace  $g_{a,t}$  with  $g_{a,t}^I - g_{a,t}^E$  in (2.1) and replace (2.12) with two similar terms for  $g_{a,t}^I$  and  $g_{a,t}^E$ . If good information about the accuracy of the immigration and emigration data were available, then  $\sigma_g^2$  could be replaced with two separate parameters; otherwise it would be unchanged.

## **Appendix 2.A Derivation of $e_0$**

Here, I derived the expression given in (2.4). Data on the  $s_{a,t}$  are seldom available; most surveys and registration systems are designed to estimate mortality rates (these are annualized occurrence/exposure rates where the “occurrence” is death and exposure is measured in total person-years lived). Standard practice is to use the estimated mortality rates to construct an abridged life table for each five-year time period. An abridged life table has one row for each of the five-year age groups and columns for various mortality parameters. For consistency of notation, label these age groups  $[0, 5)$ ,  $[5, 10)$ ,  $\dots$ ,  $[A, A + 5)$ ,  $[A + 5, \infty)$ .  $A$  is usually between 80 and 100. The life table describes the mortality experience of a birth cohort of arbitrary size (e.g., [Preston et al., 2001](#), Ch. 3). I take this to be one and relate the life table to familiar concepts from survival analysis. In what follows I suppress dependence on  $t$  for clarity.

Once column of the life table gives the probability of surviving to exact age  $a$ ; this is simply the survival function evaluated at the integers  $0, 5, \dots, A + 5$ . In statistics, the survival function is often denoted  $S(a)$ ; standard demographic notation is  $l(a)$ . I denote

the entries in this column by  $l_a$  and set  $l_0 = 1$ . Information about survival between the tabulated ages is captured in a column called  $L_a$ , where  $L_a \equiv \int_a^{a+5} l(a)da$ ,  $a = 0, 5, \dots, A$  and  $L_{A+5} = \int_{A+5}^{\infty} l(a)da$ . The standard way to derive survival proportions  $s_a$  from these columns is via the relationships

$$s_0 = L_0/(5l_0); \quad s_a = L_a/L_{a-5}, a = 5, \dots, A; \quad s_{A+5} = L_{A+5}/(L_A + L_{A+5}) \quad (2.18)$$

These are ratios of the areas under the survival curve in adjacent age intervals.  $e_0$  is simply the expected length of life:

$$e_0 = \int_0^{\infty} l(a)da = \sum_a L_a \quad (2.19)$$

where the summation is over  $0, 5, \dots, A + 5$ . Using (2.18) to express  $L_a$  in terms of  $s_a$  and substituting into (2.19) gives

$$e_0 = 5 \sum_{a=0}^A \prod_{i=0}^a s_i + 5 \left( \prod_{i=0}^A s_i \right) (s_{A+5}/(1 - s_{A+5}))$$

as required.

## **Appendix 2.B Data Sources**

### *2.B.1 Fertility Rates*

Estimates of ASFRs for Burkina Faso based on data from recent births (in the preceding 12 months) were obtained from the 1960 and 1991 demographic surveys, the 1976 census post-enumeration survey and the 1985, 1996 and 2006 censuses. Retrospective birth histories for the preceding 20 years, taken from the 1992–93, 1998–99 and 2003 DHSs, were also used. In addition, for each of these data sources, adjusted fertility rates for the most recent period were estimated using women’s lifetime parity information and the Brass-Feeney P/F ratio method (Brass, 1964; Feeney, 1996, United Nations, 1983, Ch. II, Sect. B).

Alkema et al. (2012) studied estimates of TFR for seven West African countries, including Burkina Faso, and found evidence of bias in the estimates from the various available data sources. Therefore, the initial estimates were based on Alkema et al.’s (2012) median bias-adjusted estimates of TFRs for Burkina Faso at five-year increments between 1962 and 1997, inclusive. These are the mid-points of the five-year sub-intervals [1960, 1965), [1965,

1970), ..., [1995, 2000). The TFRs were then disaggregated into age-specific rates by applying an age-specific fertility pattern. These patterns, which sum to one, indicate the share of fertility attributable to each age group. Therefore, the final ASFRs are the product of TFRs and the age patterns. The patterns were obtained through a process I now describe.

Since I require average fertility rates for the sub-intervals [1960, 1965), ..., [1995, 2000), I grouped the available estimates by the sub-interval into which they fell. Data of this kind are often summarized by a single series of age-specific values per sub-interval using a relational model or a smoothing technique. Relational models take a fixed age-pattern, often derived from a combination of data collected in similar populations and theory about the underlying social and biological processes, and adjust it to fit the observed data, usually by way of a parsimonious parameterization on a transformed scale. The method of [Coale and Trussell \(1974\)](#), updated by [Xie \(1990\)](#) and [Xie and Pimentel \(1992\)](#), is an example. However, the validity of these methods rests, in part, on an appropriate choice of model age pattern. Data-driven smoothing techniques avoid this problem, albeit at the cost of not modeling the underlying mechanisms. Since I am not primarily concerned with such mechanisms, I used *loess* ([Cleveland, 1979](#); [Cleveland et al., 1992](#)) to smooth the age-specific fertility patterns within five-year sub-interval. The *loess* method performs a series of locally weighted regressions. Smoothing within five-year sub-interval (Figure 2.4) yielded trends that were also sensible, *a priori*, when viewed by five-year age group (Figure 2.5). No age-pattern data were available for the period [1965,1970). To generate initial estimates for this period, I assumed that the [1960,1965) pattern held over this period but used [Alkema et al.'s \(2012\)](#) median TFR estimate for 1967. The resulting initial estimates are shown in Figure 2.7. The Level 4 hyperparameters were set so that the median MARE was 0.1 and the 0.975 quantile was approximately 0.5.

### 2.B.2 Survival Proportions

Abridged life tables for Burkina Faso can be computed from data on recent household deaths in years for which data is available. However, potential biases arise due to the omission of deaths, recall period errors, age heaping and age exaggeration by survey respondents. The

approach favored by the UN in this context has been to use a Brass two-parameter relational logit model (Brass, 1971a), with the Timæus Sahelian standard mortality pattern (Timæus, 1999), to estimate a complete set of abridged life tables for each five-year sub-interval of the reconstruction period. Relational models use data to adjust a standard mortality pattern such that it reflects the pattern in the population of interest. Brass’s method treats the logit of the life table for the population of interest as a linear function of the logit of an appropriately selected standard life table. The intercept and slope are estimated using ordinary least squares (OLS).

Brass’s model was fitted to robust estimates of under-five mortality and adjusted estimates of adult mortality. Under-five mortality estimates were based on three types of data: (i) recent household deaths from the 1960–1961 and 1991 national demographic surveys and the 1976, 1985, 1996 and 2006 censuses; (ii) births and deaths to under-fives calculated from maternity-history data from the 1992–1993, 1998–1999 and 2003 DHSs; and (iii) data on children ever-born and surviving classified by age of mother (and the South model of the Coale-Demeny Model Life Tables) from the data sources in (ii) as well as from UNICEF’s Multiple Indicator Cluster Survey—Round 3 conducted in 2006. Estimates of adult mortality were based on three sources: (i) recent household deaths data (unadjusted and adjusted for underregistration using the growth-balance and synthetic-extinct generation methods) from the 1960–1961 and 1991 national demographic surveys and the 1976, 1985, 1996 and 2006 censuses; (ii) parental orphanhood from the 1993 and 2003 DHSs and the 2006 census; (iii) sibling deaths from the 1998–1999 and 2003 DHSs.

Age-specific survival proportions are obtained from the resulting life-tables using (2.18). As with population counts and fertility rates, the Level 4 hyperparameters were set so that the median MARE was 0.1 and the 0.975 quantile was approximately 0.5.

### 2.B.3 Migration Proportions

Estimates of migration for many countries, even those with well-resourced official statistics systems, are often unavailable, unreliable or available only at the whole population level. Common practice in such situations has been to estimate net migration as a “residual”, that

is, apply the CCMPP in (1) with migration set to zero for all ages and years, compare the projected counts with observed counts (from censuses, for example) and use the difference as an estimate for net migration. This approach is not satisfactory for producing initial estimates in my framework because it explicitly uses the census data “twice”; first to derive the initial estimates of migration and then again in the likelihood in (7).

Whole-population estimates of net migration in Burkina Faso for the reconstruction period are available from [United Nations \(2009a\)](#) and [United States Census Bureau \(2008\)](#). Both draw on information from UNHCR statistics on refugee movements and the former also used information from Centre d’Etudes et de Recherche sur la Population pour le Développement (CERPOD) and surveys of migrants in Côte d’Ivoire. It is possible that residual methods were also used in the process of producing these figures (e.g., [United States Census Bureau, 2010](#)).

[Condé \(1980\)](#) gives a detailed analysis of migration in Burkina Faso between 1960 and 1975 by broad age group and sex. The report uses data from the 1960–61 National Demographic Sample Survey, a survey of migration conducted by Office de la Recherche Scientifique et Technique Outre Mer (ORSTOM), Paris, in 1973 and migration-related questions from the 1975 census and post-enumeration survey. The economic, historical and geographical context and data from other West African countries is also considered. No reference is made to residual methods. Key conclusions were that international migration between 1960 and 1975 was driven primarily by people leaving to work in neighboring countries. An estimate of  $-33,000$  people is given for the total (all-sex) net flow around 1975 (p. U.V. 31).

The sources above give only an incomplete picture of age specific net migration over the whole period 1960–2005. Therefore, I designed the initial estimates to reflect sustained, net out-migration up to 2000. This is followed by a reversal in the period [2000, 2005) motivated, in part, by refugee movements due to conflict in Côte d’Ivoire during this period. I assumed that migration was concentrated in the age range 15–55. The,  $g_{a,t}^*$  were set to  $-0.055$  for  $15 \leq a \leq 55$ ,  $1960 \leq t \leq 1995$ ,  $0.055$  for  $15 \leq a \leq 50$ ,  $t = 2000$  and zero otherwise. Thus, for example, the initial estimate for the net number of migrants over the five-year period [1975, 1980) is centered at  $-5.5$  percent of the 1975 population between ages 15 and 55, an average of  $-1.1$  percent per year. This amounts to approximately half of the all-sex flow

estimated by Condé (1980) for this period. There is considerably greater uncertainty about these initial estimates than about those for the other parameters. To account for this, the Level 4 hyperparameters were set so that the median MAE was 0.2 and the 0.975 quantile was approximately 1, both twice as large as the values used for the other parameters.

## **Appendix 2.C Extra Results**

Posterior medians and 95 percent central credible intervals for the survival and migration proportions are in Figures 2.9 and 2.10, respectively. Prior and posterior kernel density estimates for the variance parameters  $\sigma_v$ ,  $v = \{n, f, s, g\}$  are shown in Figure 2.11.

## **Appendix 2.D Sensitivity to Initial Estimates**

I expect the posterior to be sensitive to changes in the initial estimates. This is not of concern because these are based heavily on data; it is desirable that the posterior respond to changes in such inputs. The purpose of this appendix is to investigate how the posteriors change with large, simple changes in the initial estimates.

### *2.D.1 Method*

The reconstruction of the female population of Burkina Faso (Section 2.5) was re-run three more times. Each re-run used a different set of initial estimates for fertility, survival or migration. I call these *i*) “fert plus”, *ii*) “surv plus”, and *iii*) “mig plus”. Initial estimates for all age- time-specific values of these parameters were modified as follows. For “fert plus”, the initial estimates for age- time-specific fertility rates,  $f_{a,t}^*$ , were derived by adding ten percent to the original initial estimates described in Section 2.5.1. All other initial estimates were the same as those used in the main example. Initial estimates for the “surv plus” and “mig plus” runs were derived similarly; for “surv plus” the original initial estimates of survival were inflated by ten percent on the logit scale, for “mig plus” the original estimates of migration proportions were inflated by multiplying the originals by two. These modified sets of initial estimates were developed for investigatory purposes only and are not intended to represent any specific demographic scenario.

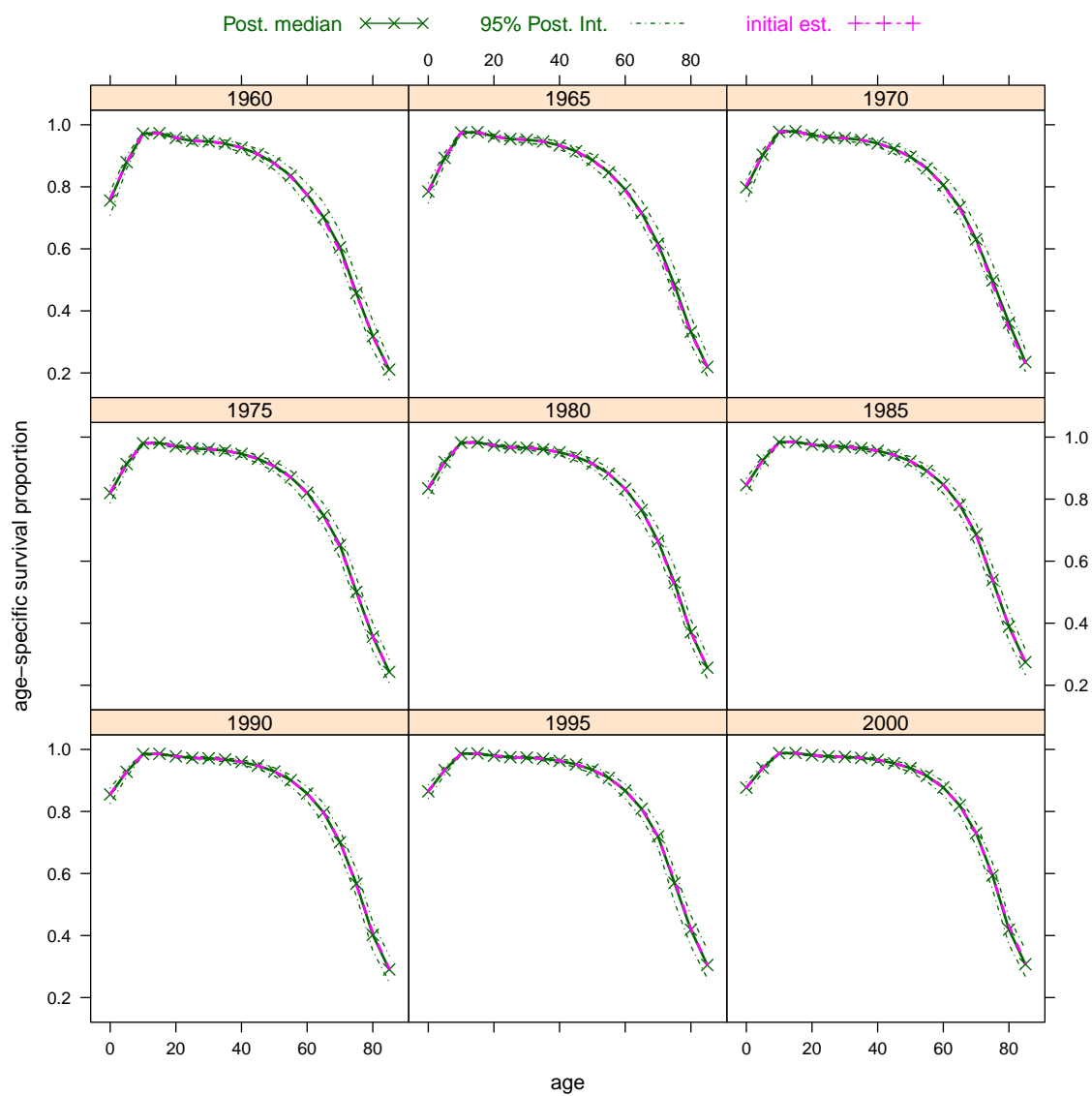


Figure 2.9. Ninety-five percent credible intervals and initial estimates for age-specific survival proportion for the reconstructed female population of Burkina Faso, 1960–2005.

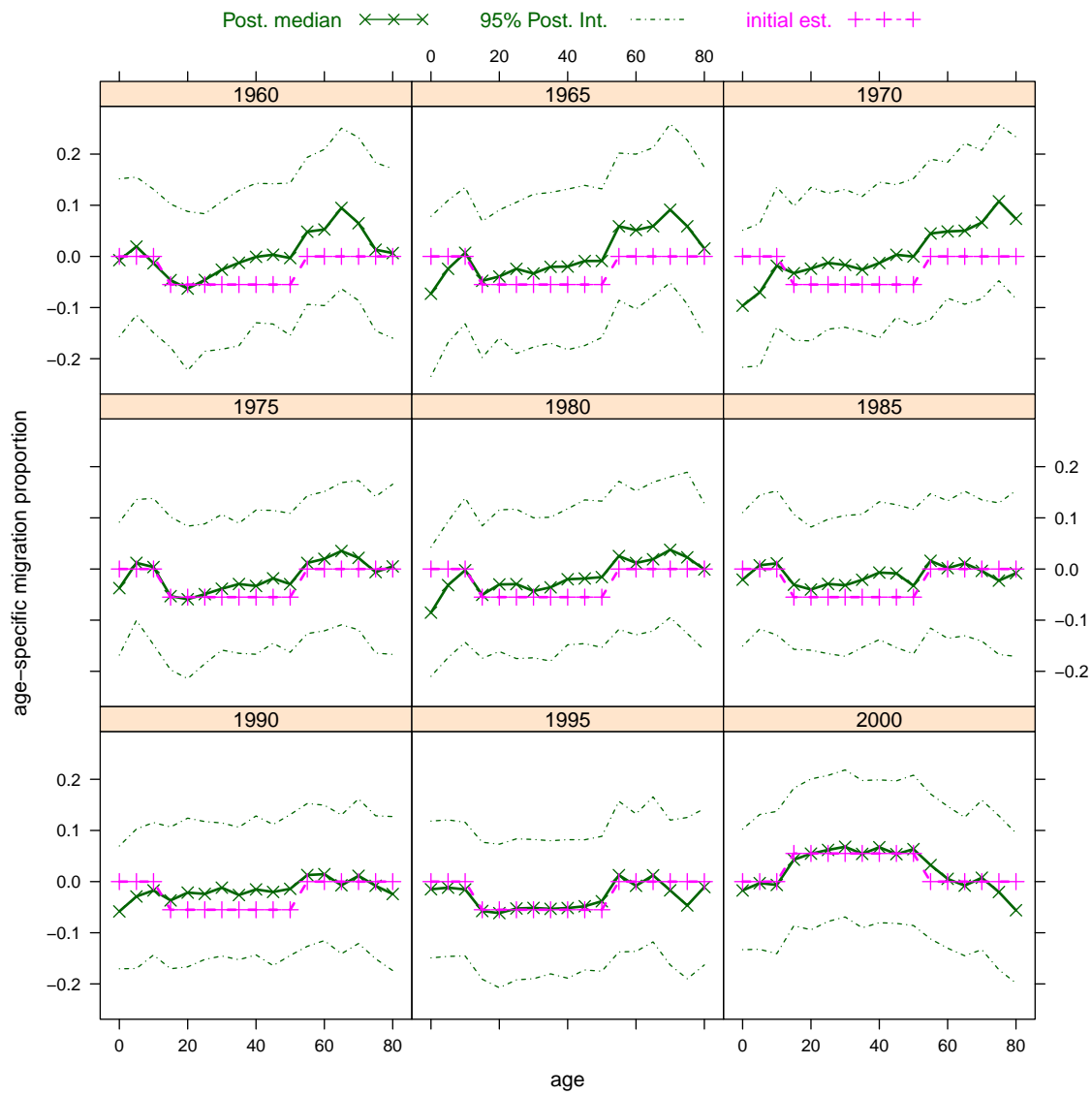


Figure 2.10. Ninety-five percent credible intervals and initial estimates for age-specific migration proportion for the reconstructed female population of Burkina Faso, 1960–2005.



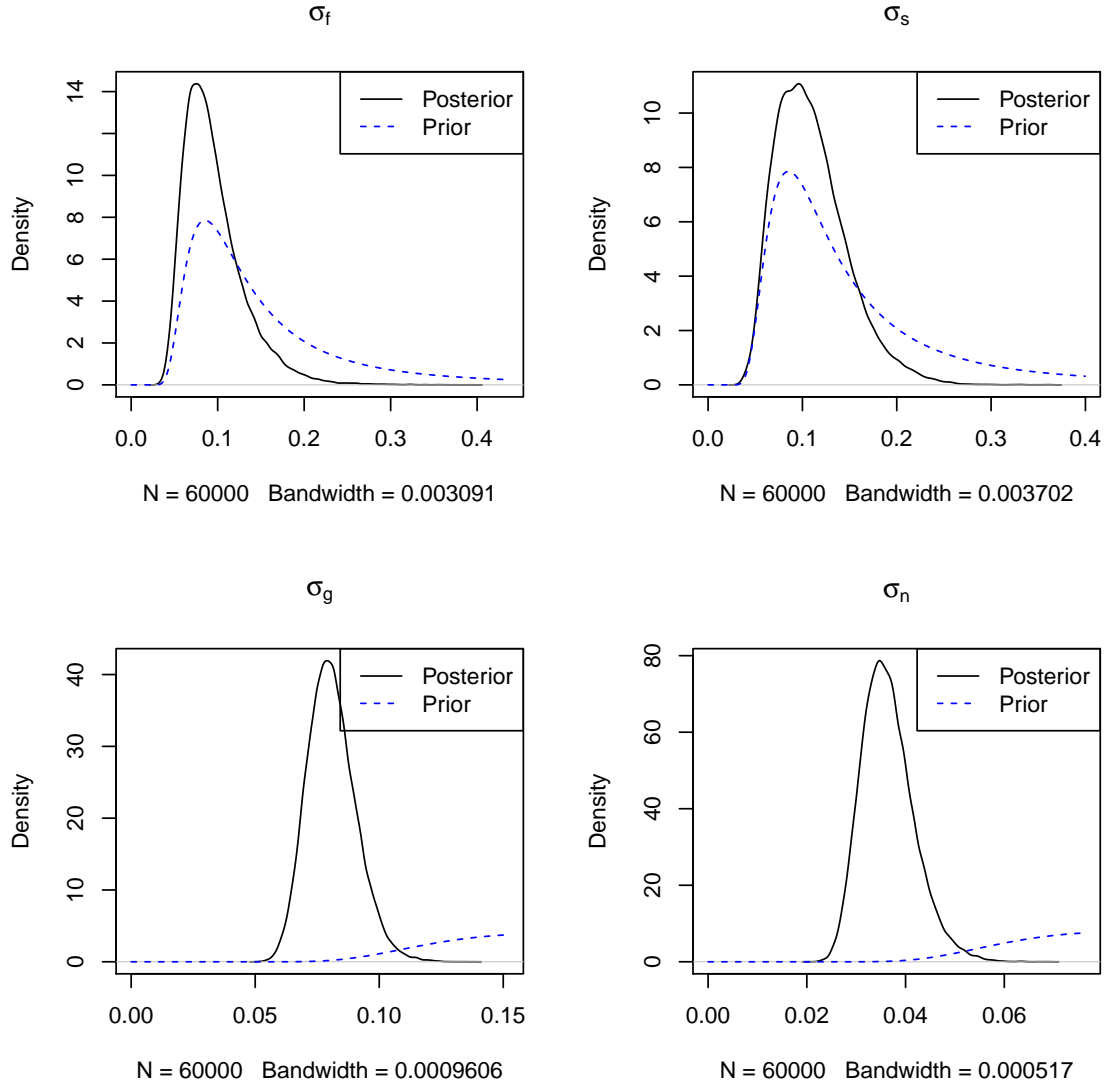


Figure 2.11. Prior densities and posterior densities of Level 4 parameters (standard deviations,  $\sigma_v$ ,  $v = \{n, f, s, g\}$ ) for the reconstructed female population of Burkina Faso, 1960–2005. Posterior densities are kernel density estimates.

### 2.D.2 Results

#### *“fert plus”*

Increasing the initial estimates for ASFRs had a noticeable impact on the posterior for these quantities, as well as for TFR (Figures 2.12 and 2.13). The spread of the marginal posteriors under the “fert plus” initial estimates is much larger than under the original ones. Moreover, there appears to have been an over-correction. In the age groups where fertility is highest, most of the posterior medians are lower than the posterior medians under the original run.

The marginal posteriors for the non-fertility parameters do not differ greatly from the originals except for age-specific migration proportions in some time periods (Figure 2.19). In the periods beginning 1965 through 1980, posterior median migration proportions in the age group 0–4 is higher under the “fert plus” initial estimates, and lower for the period beginning 2000. The extra births implied by the higher initial fertility rate estimates have been partly compensated for by a change in posterior medians for migration.

#### *“surv plus”*

Increasing the initial estimates for age-specific survival proportions had a noticeable effect on the posterior distributions of fertility, survival and migration parameters (Figures 2.15–2.19). The marginal posteriors for age-specific survival are centered at the initial estimates in both the original and “surv plus” runs (Figure 2.17) and the results for  $e_0$  are similarly sensitive to the initial estimates (Figure 2.18). Posteriors for TFR (Figure 2.16) and migration proportions (Figure 2.19) have also changed under the re-run to compensate for the larger cohorts implied by higher initial estimates of age-specific survival. For example, the posterior median for TFR is lower under the re-run. This implies fewer births and so compensates for the reduction in number of deaths in the 0–4 age group the “surv plus” initial estimates imply.

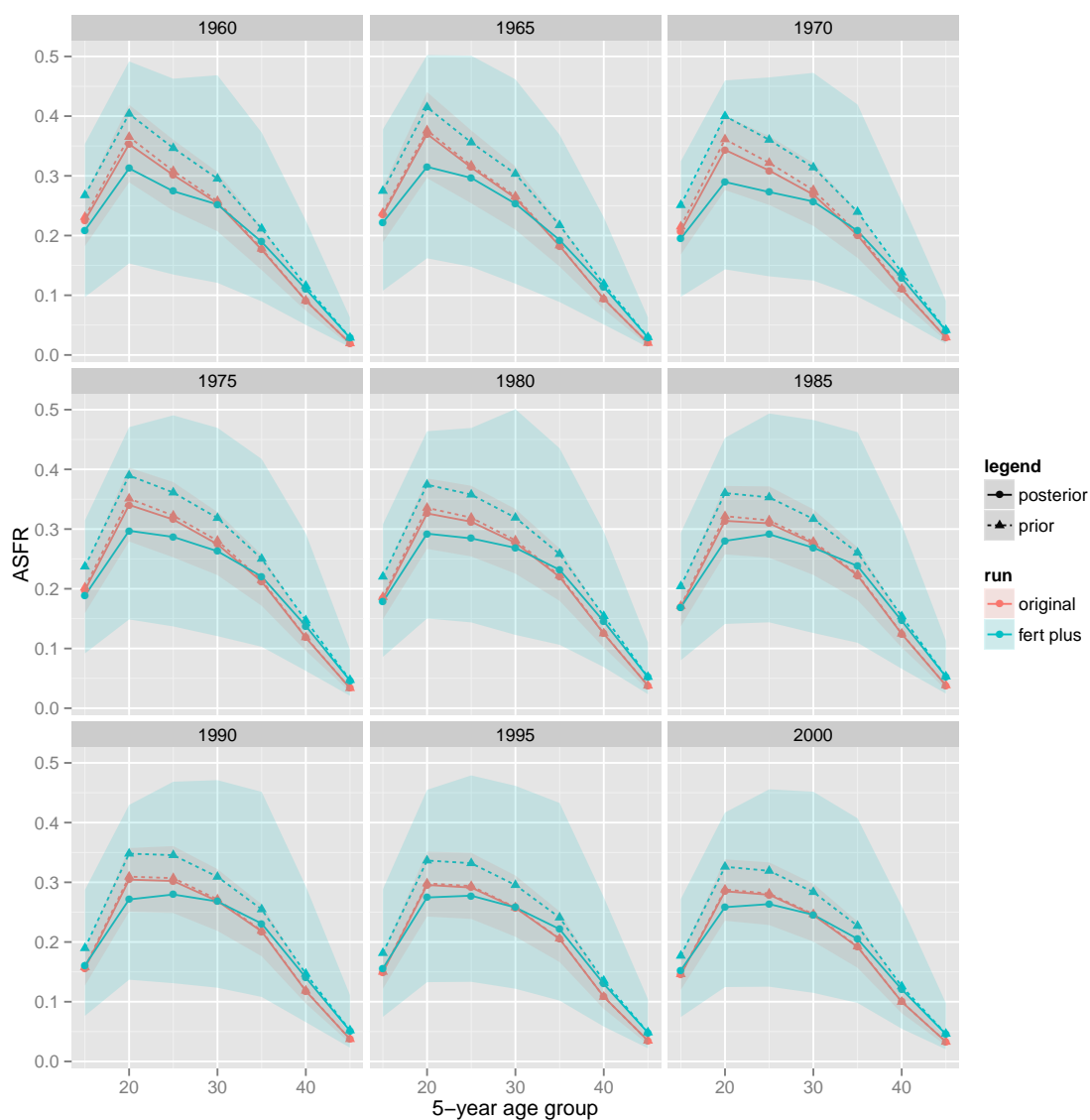


Figure 2.12. Initial estimates, posterior medians and 95 percent credible intervals for age-specific fertility rate (ASFR) under the “fert plus” and original initial estimates, for the reconstructed female population of Burkina Faso, 1960–2005.

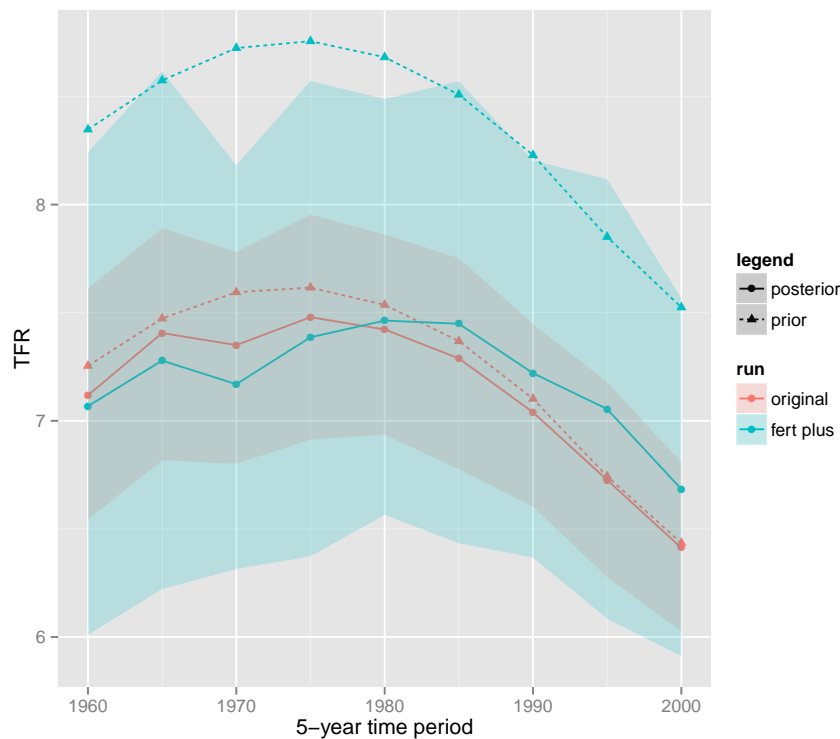


Figure 2.13. Initial estimates, posterior medians and 95 percent credible intervals for total fertility rate (TFR) under the “fert plus” and original initial estimates, for the reconstructed female population of Burkina Faso, 1960–2005.

### “mig plus”

The “mig plus” re-run resulted in only small changes in the posterior median for age-specific migration proportions (Figure 2.21) for all but the last time period. In this period, the posterior medians follow the initial estimates very closely. Migration proportions in earlier periods affect population counts for several subsequent reconstructed periods for which there are census counts to compare against. This is not the case for the final time period which could explain why the initial estimates have a greater influence on the posterior. The width of the marginal credible intervals under the “mig plus” re-run is greater than under the original run. This could be seen as an indication that original initial estimates agree more closely with the census counts and initial estimates for the other input parameters.

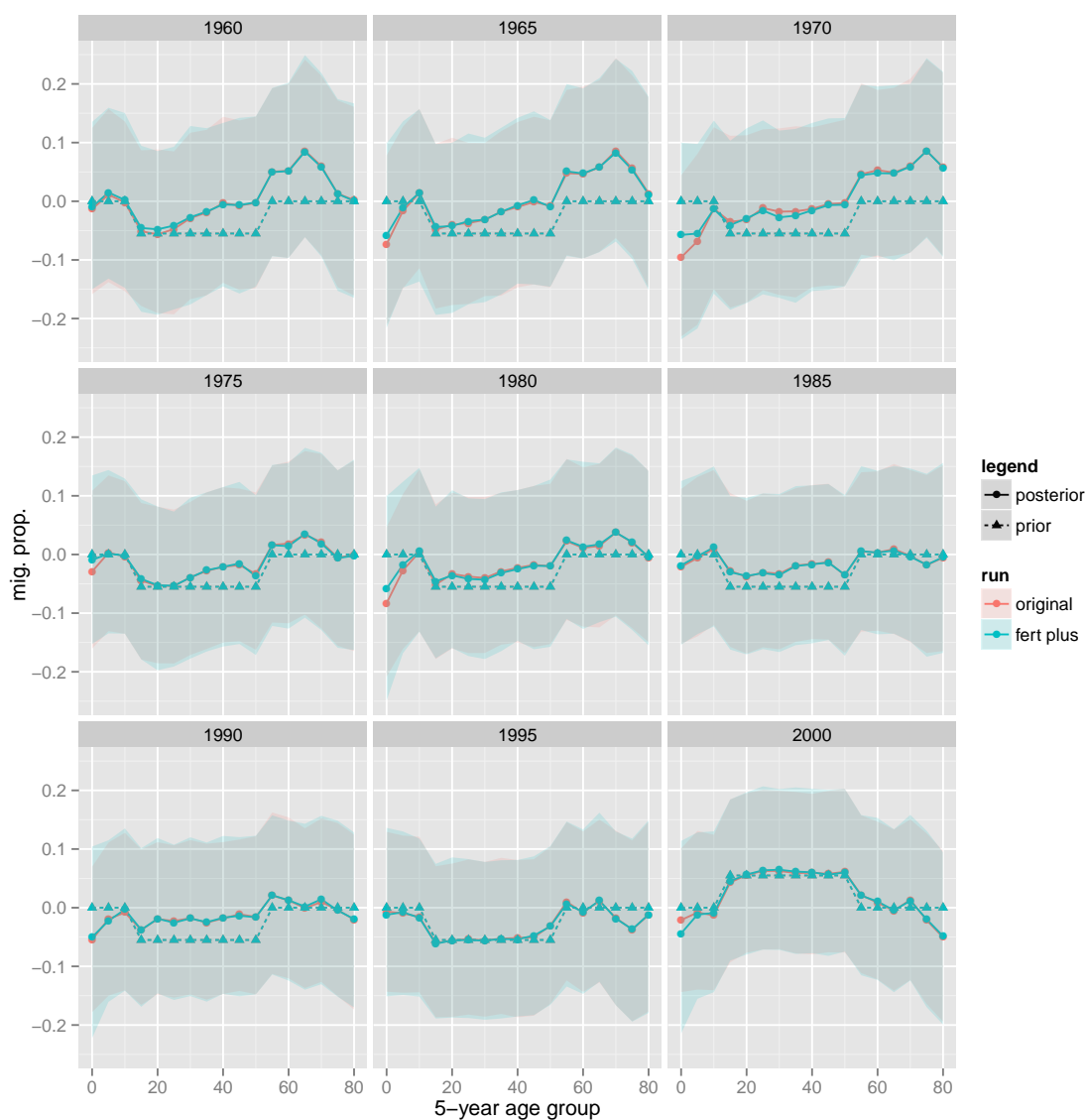
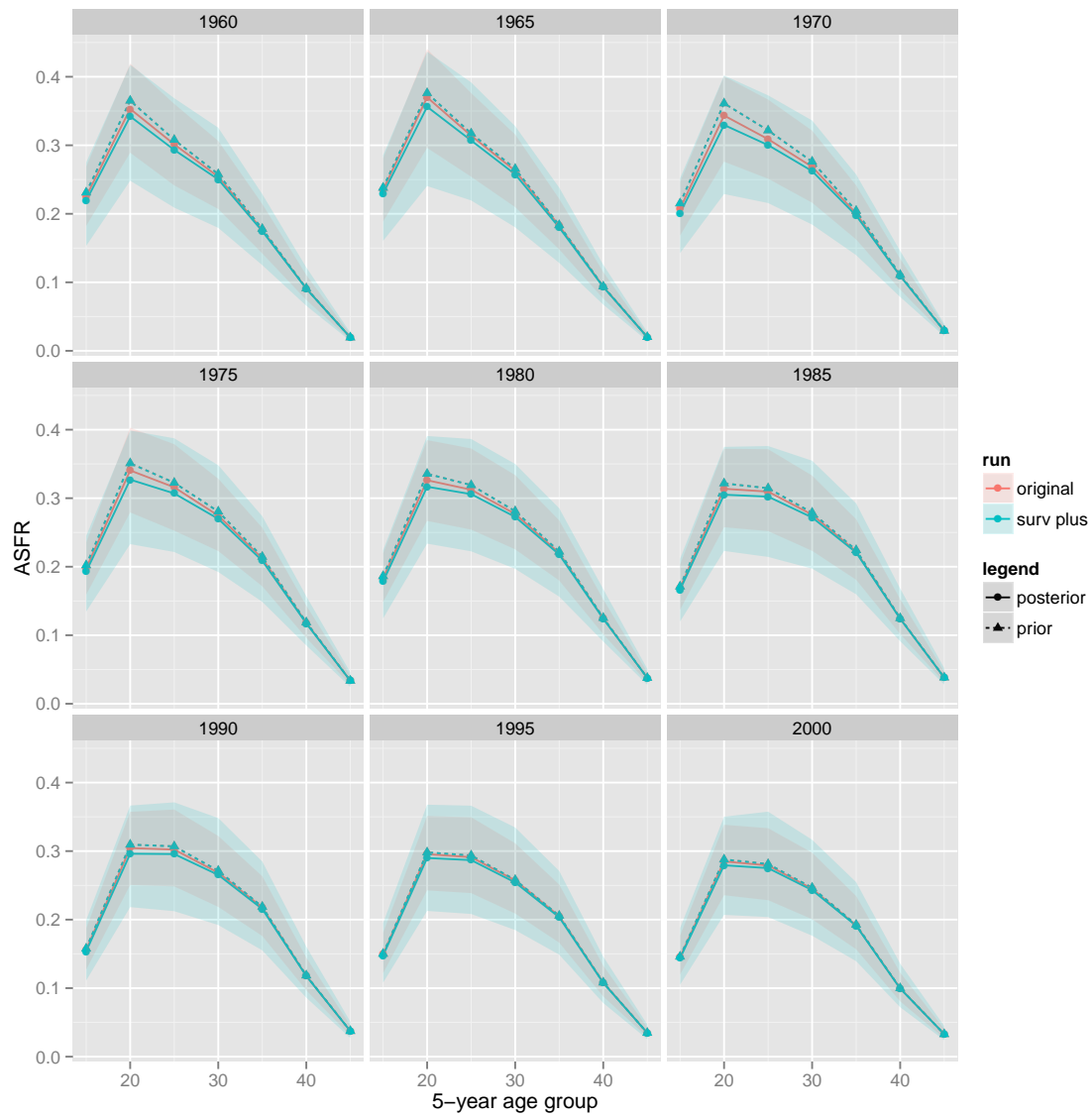
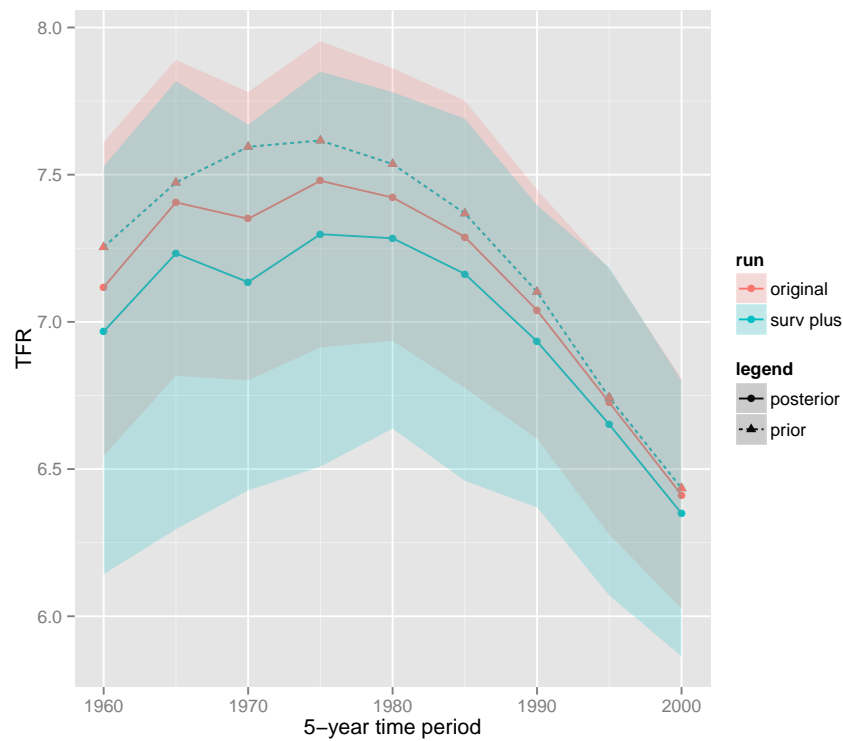


Figure 2.14. Initial estimates, posterior medians and 95 percent credible intervals for age-specific migration proportion under the “fert plus” and original initial estimates, for the reconstructed female population of Burkina Faso, 1960–2005.



*Figure 2.15.* Initial estimates, posterior medians and 95 percent credible intervals for age-specific fertility rate (ASFR) under the “surv plus” and original initial estimates, for the reconstructed female population of Burkina Faso, 1960–2005.



*Figure 2.16.* Initial estimates, posterior medians and 95 percent credible intervals for total fertility rate (TFR) under the “surv plus” and original initial estimates, for the reconstructed female population of Burkina Faso, 1960–2005. The vertical axis has been transformed to the logit scale.

Marginal posteriors for the non-migration parameters appear to have been affected only slightly except that the posterior for TFR (Figure 2.20) is centered higher than under the original run (other outputs not shown). This increase would compensate for the higher level of emigration implied by the “mig plus” initial estimates.

### 2.D.3 Conclusions

The sensitivity analyzes show that the marginal posterior distributions are sensitive to changes in the initial estimates. This is desirable since the initial estimates are based on data.

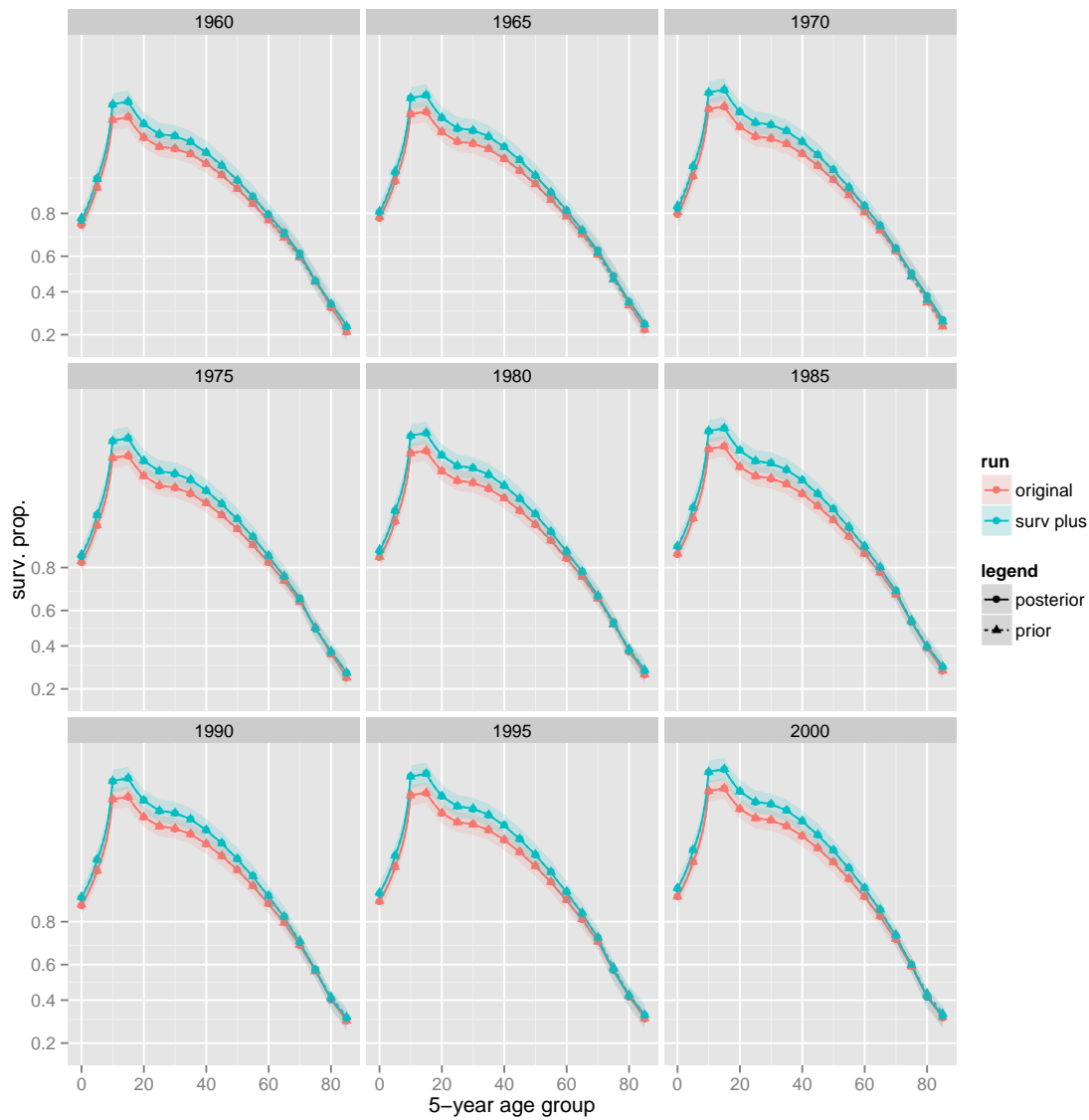


Figure 2.17. Initial estimates, posterior medians and 95 percent credible intervals for age-specific survival proportion under the “surv plus” and original initial estimates, for the reconstructed female population of Burkina Faso, 1960–2005.



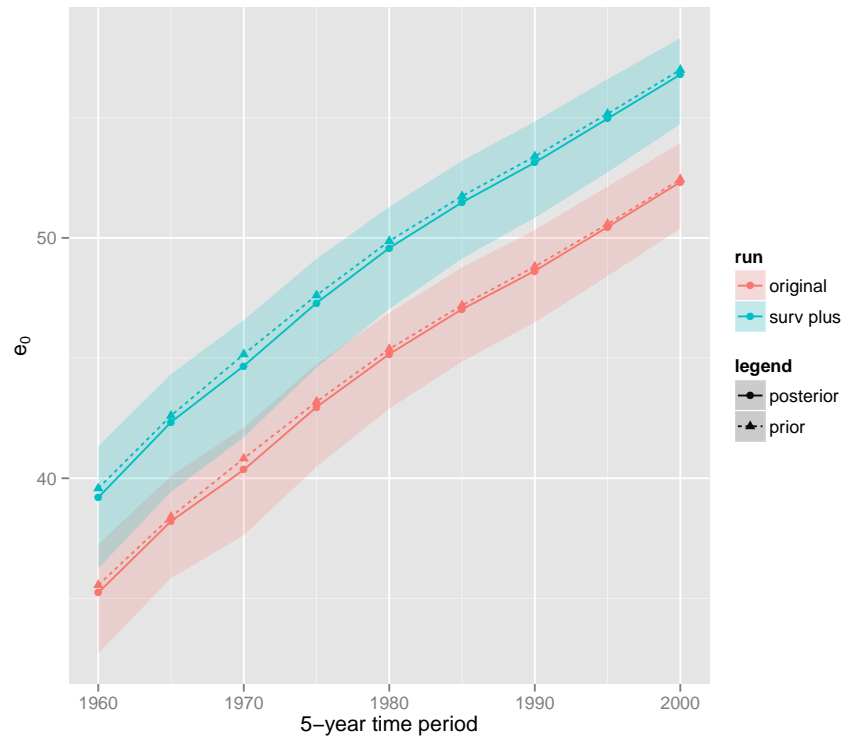
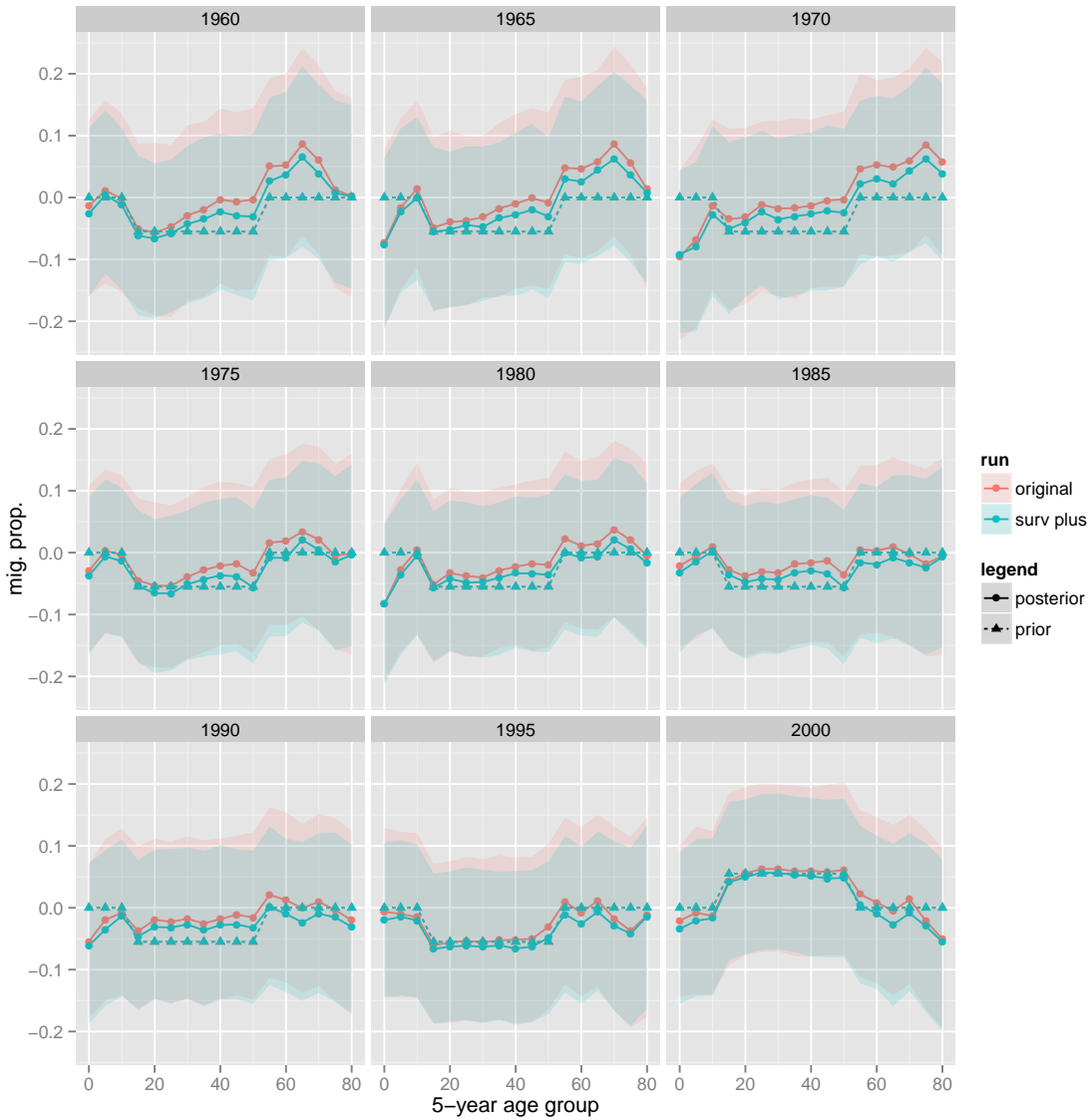
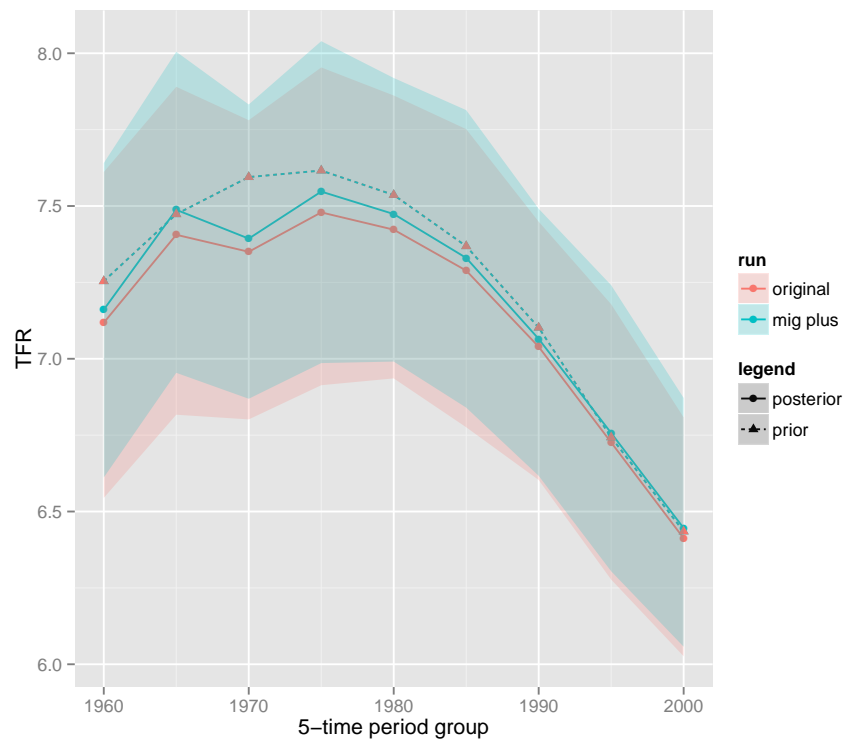


Figure 2.18. Initial estimates, posterior medians and 95 percent credible intervals for life expectancy at birth ( $e_0$ ) under the “surv plus” and original initial estimates, for the reconstructed female population of Burkina Faso, 1960–2005.

Changes in initial estimates for survival or migration affected the posteriors for all parameters, while changes in the initial estimates of age-specific fertility affected only the posteriors for the fertility parameters. This could be because survival and migration have a more profound effect on the population size and structure. The values of these parameters affect cohort sizes in all age groups while fertility rates only affect cohort sizes in the 0–4 age group. The changes in the marginal posteriors for the parameters with modified initial estimates were in the same direction as the changes made to the initial estimates themselves. For example, increasing initial estimates for age-specific survival proportions resulted in higher posterior medians for these parameters. Conversely, the changes in the posteriors for the parameters with unmodified initial estimates appeared to be compensatory. Poster



*Figure 2.19.* Initial estimates, posterior medians and 95 percent credible intervals for age-specific migration proportion under the “surv plus” and original initial estimates, for the reconstructed female population of Burkina Faso, 1960–2005.



*Figure 2.20.* Initial estimates, posterior medians and 95 percent credible intervals for total fertility rate (TFR) under the “mig plus” and original initial estimates, for the reconstructed female population of Burkina Faso, 1960–2005.

median fertility rates were lower under the “surv plus” re-run, for example.

The modified initial estimates in the “surv plus” re-run led to changes in the marginal posteriors for fertility and migration parameters, as well as survival proportion parameters. Moreover, if only the original and “surv plus” results were available, it would be difficult to conclude which set of initial estimates are the more accurate. The posterior uncertainty about age-specific survival under the “surv plus” initial estimates appears to be very similar to the uncertainty under the original run. This differs from the “fert plus” results, for example, where posterior uncertainty about age-specific fertility is much greater under the re-run. The “surv plus” modification was somewhat artificial, however. In Section 3.4 a more subtle modification is made to initial estimates of survival proportions and the

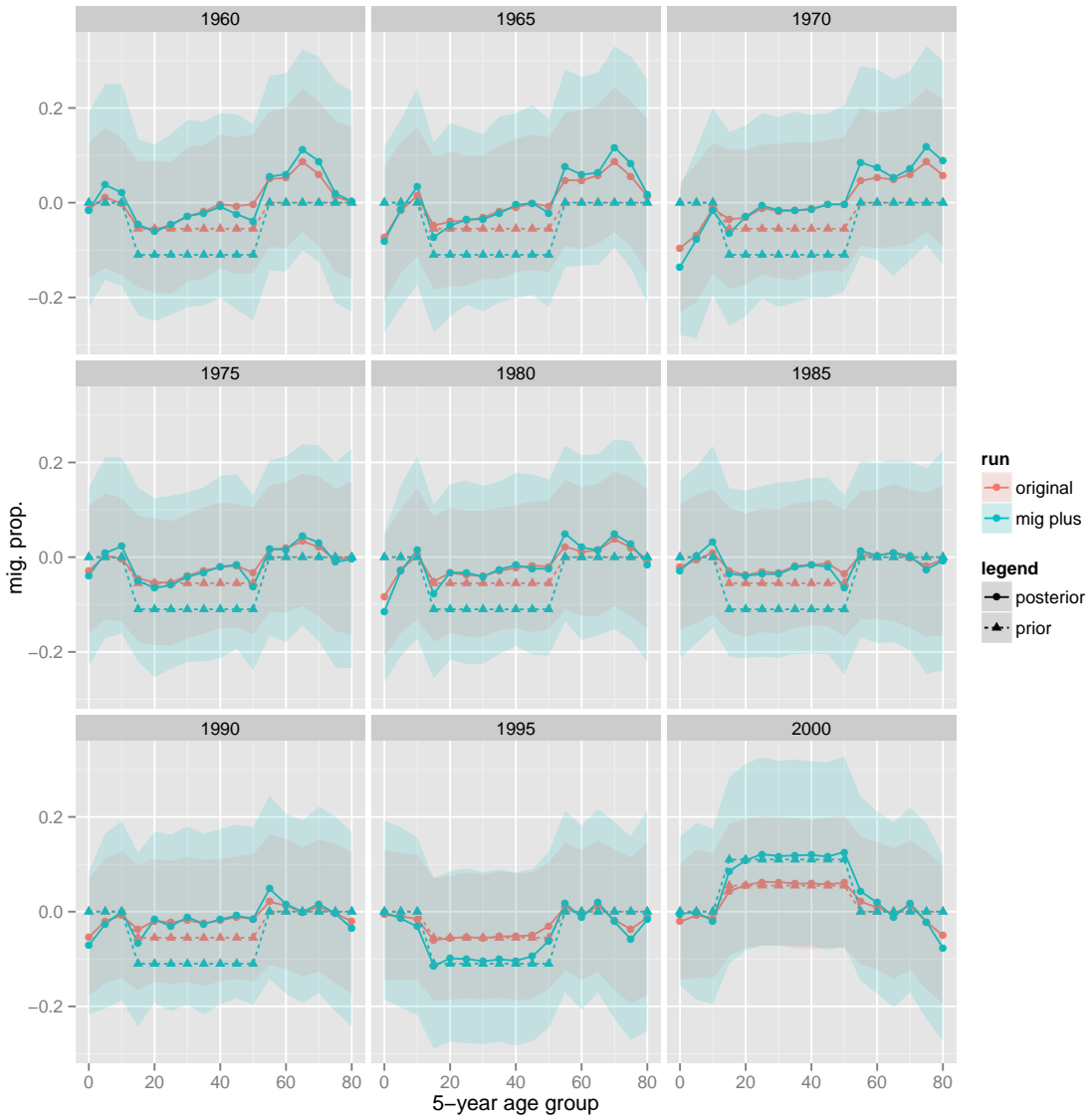


Figure 2.21. Initial estimates, posterior medians and 95 percent credible intervals for age-specific migration proportion under the “mig plus” and original initial estimates, for the reconstructed female population of Burkina Faso, 1960–2005.

posterior uncertainty does increase, suggesting that the modified initial estimates are less accurate. The modification there was done by choosing a different model life table and a different fitting method, and is more indicative of what a demographer might do in practice to generate competing sets of initial estimates.

## ***Appendix 2.E MCMC Diagnostics***

MCMC algorithms are designed to generate dependent, finite samples from a “target” distribution. In Bayesian inference, this is the joint posterior. More precisely, the algorithm generates a sequence, or chain, which is a realization of a stochastic process having the posterior as its stationary distribution. One may have to run the algorithm for many iterations before the sequence of sampled values converges. From this point on, all subsequent values generated by the algorithm are random draws from the stationary distribution. A general method of proving that convergence has been reached for any chain of finite length is unavailable (Cowles and Carlin, 1996; Gilks et al., 1996). However, several diagnostic checks can be performed which are useful for assessing algorithm performance such as chain mixing (Carlin and Louis, 2009). Good mixing means that the chain has explored the posterior parameter space well. I used the Raftery-Lewis (Raftery and Lewis, 1996) and Gelman-Rubin (Gelman and Rubin, 1992; Brooks and Gelman, 1998) diagnostics. All results reported in this appendix refer to the original application to the female population of Burkina Faso discussed in Section 2.5.

### *2.E.1 The Raftery-Lewis Diagnostic*

The Raftery-Lewis diagnostic aims to find the chain length required to estimate the specific quantile,  $q$ , of a chosen parameter to within  $\pm r$  units, with probability  $s$ . I applied the diagnostic to all age-specific input parameters in Level 3 ( $n_{a,t_0}, \dots, g_{a,t}$  in eqns (2.9)–(2.12)), as well as the variance parameters in Level 4 ( $\sigma_n, \dots, \sigma_g$  in eqn (2.13)) with  $q = 0.025, 0.975$ ,  $r = 0.0125$ ,  $s = 0.95$ . The 0.025 and 0.975 quantiles are of interest since I report 95 percent credible intervals for the Level 3 parameters. In the application to Burkina Faso, the maximum of the suggested chain lengths across vital rate (Level 3) parameters

was  $3.5 \times 10^4$ , the maximum across variance (Level 4) parameters was  $2.2 \times 10^4$ . I used un-thinned chains of length  $6 \times 10^4$  for inference, with a burn-in of 500.

### *2.E.2 The Gelman-Rubin Diagnostic*

To generate the chains used for inference, MCMC start values for the population counts, vital rates and migration proportions were set to the initial estimates. Start values for the variances were arbitrarily set to 5 as they appeared to have a negligible effect on the final results. The Gelman-Rubin diagnostic was applied to assess convergence of the chains for the variance (Level 4) parameters, and check that the start values did not have an impact on the MCMC sample used for inference.

The diagnostic of [Gelman and Rubin \(1992\)](#) requires that  $m > 1$  chains, each with different start values. The set of start values should be over-dispersed relative to the posterior. For each scalar parameter of interest, a potential scale reduction factor (PSRF) is calculated that is the ratio of two variance estimates. The numerator is a weighted average of the mean within chain variance and the variance of the chain means (these are the “within” and “between” mean-squares from analysis of variance (ANOVA)). The denominator is the mean within chain variance. Values of the PSRF larger than 1 indicate that, either the estimate of the variance of the parameter of interest can be reduced by running the chain for more iterations, or the chain has not yet fully explored the posterior distribution. Conversely, values close to 1 suggest that the sample is close to the posterior distribution. “Close to 1” has been taken to mean values in the interval  $[1, 1.2]$  ([Brooks and Gelman, 1998](#)). A multivariate extension was proposed by [Brooks and Gelman \(1998\)](#). These authors also recommend plotting the PSRF for successively larger chunks of the chains to monitor its evolution as the number of iterations increase. This helps to guard against incorrectly concluding that too few iterations are sufficient.

The main reason I used this diagnostic is to ensure that the start values did not have an unduly large effect on the posterior sample used for inference. The method of [Raftery and Lewis \(1996\)](#), which involves monitoring Metropolis acceptance proportions as well as the required chain length for a given degree of accuracy, has already been used to guard

against using too few iterations and poor mixing.

To apply the diagnostic, six sets of start values were chosen based on combinations of very low and very high start values of 0.001 and 5, respectively (Table 2.6). These correspond to MAREs of 0.025 and 1.78 and are very extreme relative to what one would expect to observe (most elicited MAREs were between 0.1 and 1). The *gelman.diag* function in the *R* package *coda* was used to compute PSRFs. The chains were of length  $6 \times 10^4$  with burn-in of 500. The function’s transform argument was used to improve the normal approximation used to calculate the confidence intervals.

Table 2.6. Scheme of Level 4 parameter start values used to generate multiple chains for the Gelman-Rubin diagnostic for the reconstructed female population of Burkina Faso, 1960–2005.

Series	Level 4 Parameter			
	$\sigma_f^2$	$\sigma_s^2$	$\sigma_g^2$	$\sigma_n^2$
A	5	5	5	5
B	5	5	5	0.001
C	5	0.001	5	0.001
D	0.001	5	0.001	5
E	0.001	0.001	0.001	5
F	0.001	0.001	0.001	0.001

The PSRFs for the variance parameters were all very close to 1. The maximum of the upper limits of the 95 percent confidence intervals was 1.01. PSRF evolution plots for each parameters are in Figures 2.22 and 2.23. These suggest that a burn-in of 2000 is more appropriate than the 500 used in Section 2.5. I re-ran the analyzes with a burn-in of 5000 but the results were unchanged, hence I report the originals.

Traceplots of the chains used are in Figure 2.24. From these plots, it appears that, regardless of start value, the chains have explored the same range of values in the posterior parameter space. This suggests that the start values for the variance parameters used in the application (which correspond to series “A”) did not have an effect on the inferences.

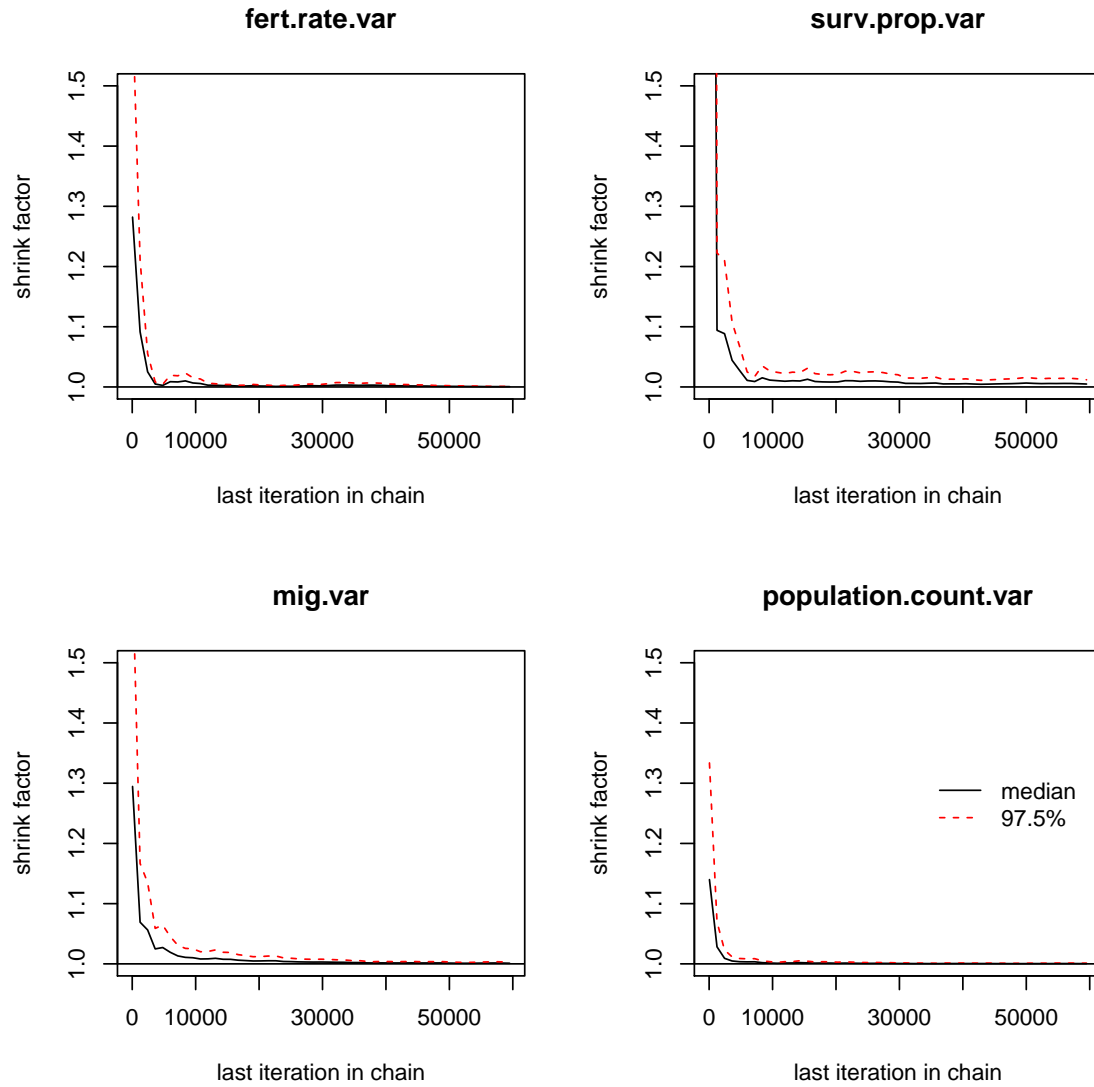


Figure 2.22. Potential scale reduction factor (PSRF) evolution plots for the Level 4 parameters calculated from six chains with dispersed start values, for the reconstructed female population of Burkina Faso, 1960–2005 (“fert.rate.var”= $\sigma_f^2$ , “surv.prop.var”= $\sigma_s^2$ , “mig.prop.var”= $\sigma_g^2$ , “population.count.var”= $\sigma_n^2$ ).



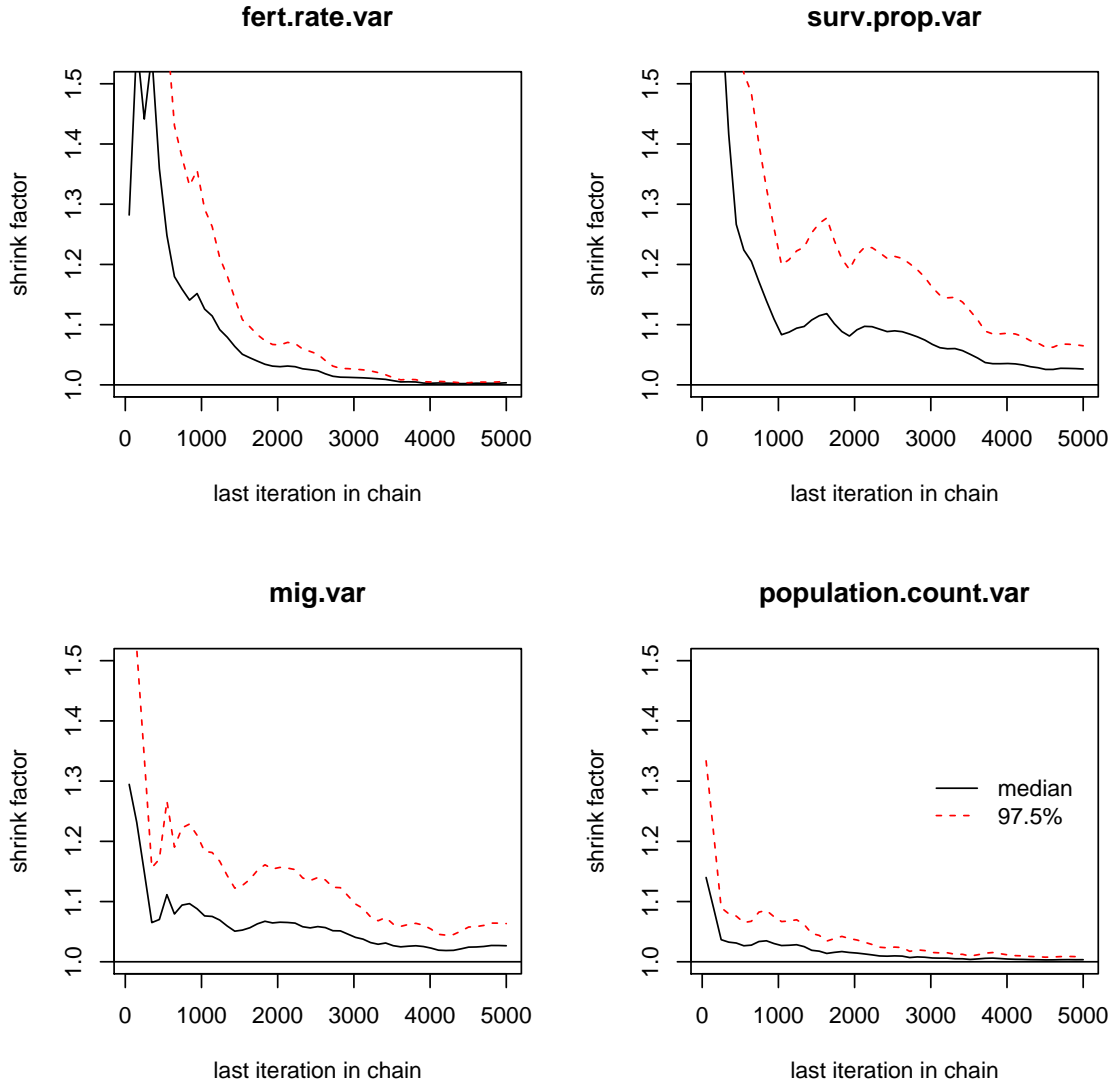


Figure 2.23. The Potential scale reduction factor (PSRF) evolution plots from Figure 2.22 for iterations 1–5000 only (“fert.rate.var”= $\sigma_f^2$ , “surv.prop.var”= $\sigma_s^2$ , “mig.prop.var”= $\sigma_g^2$ , “population.count.var”= $\sigma_n^2$ ).

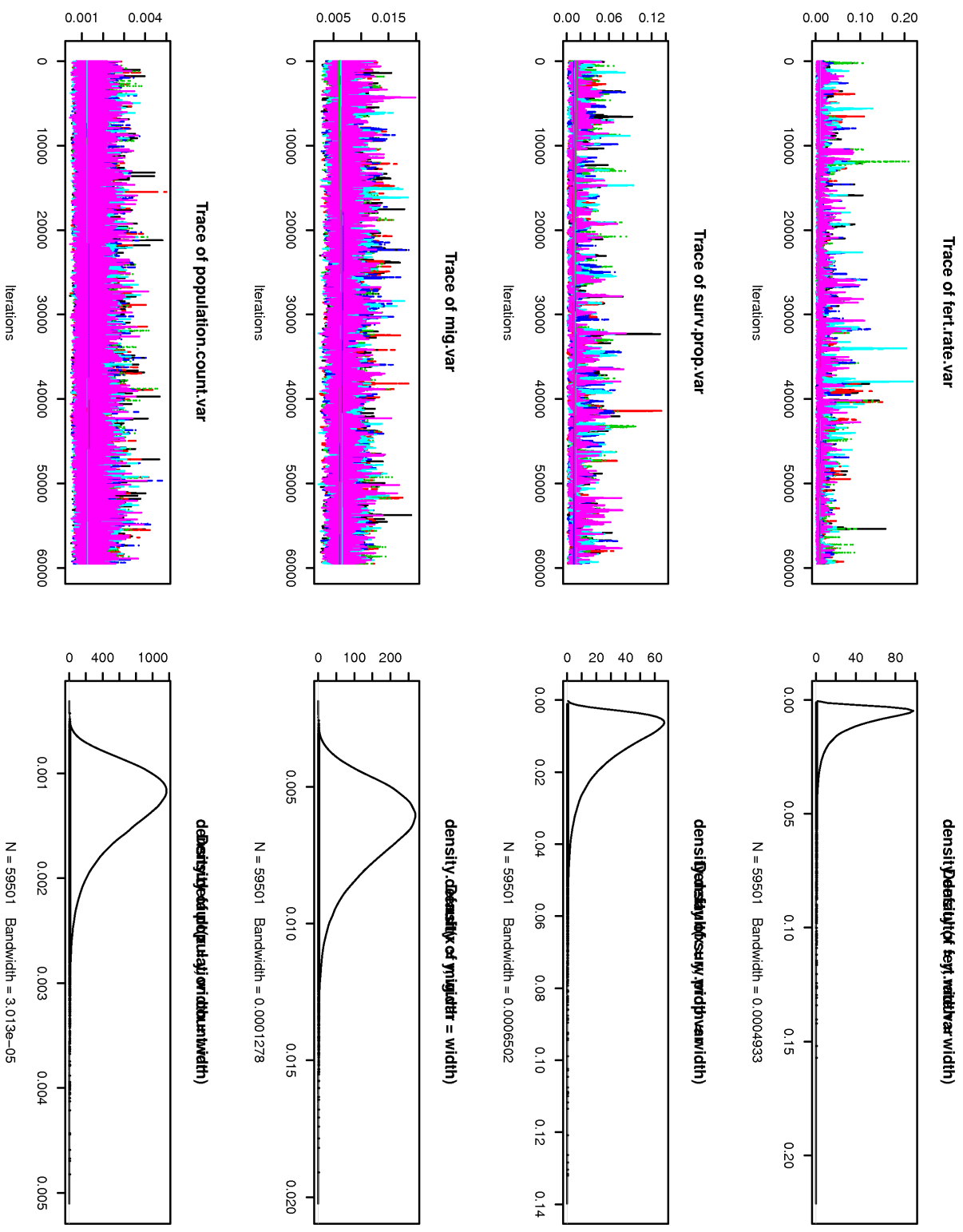


Figure 2.24. Traceplots and kernel density estimates for the six Level 4 chains (superimposed) used for the Gelman-Rubin diagnostic for the reconstructed female population of Burkina Faso, 1960–2005 (“fert.rate.var”= $\sigma_f^2$ , “surv.prop.var”= $\sigma_s^2$ , “mig.prop.var”= $\sigma_g^2$ , “population.count.var”= $\sigma_n^2$ ).

PSRF values, evolution plots and superimposed traceplots were also examined for all Level 3 parameters. The results were similar to those for the variance parameters.

Formal diagnostics were not performed for different start values for the Level 3 parameters. However, experimentation suggested that the chains for the vital rate (Level 3) parameters settle down very quickly regardless of start values, perhaps due to the fact that the marginal priors for these parameters are centered at the initial estimates, which are fixed throughout. I do apply the Gelman-Rubin diagnostic to chains with different start values for the Level 3 parameters in Appendix [3.E.2](#) (appendix to Chapter 3).

## Chapter 3

# POPULATION RECONSTRUCTION FOR DEVELOPED AND DEVELOPING COUNTRIES AND THE COMPARISON OF MODEL LIFE TABLES

Information about uncertainty in demographic statistics can be conveyed by providing interval estimates, rather than simply point estimates as is currently done for many official releases. Such intervals should have a probabilistic interpretation; they should contain the true value with some specified probability, conditional on the assumed statistical model. Bayesian reconstruction, the method introduced in Chapter 2, produces such intervals. It reconstructs population structures of the past by embedding formal demographic relationships in a Bayesian hierarchical model. The outputs are joint probability distributions of demographic rates and population counts from which fully probabilistic interval estimates can be derived in the form of credible intervals (or Bayesian confidence intervals). The method has been designed to fit within the United Nations Population Division (UNPD)’s current work-flow and to deal with the lack of reliable data commonly experienced in many developing countries. Nevertheless, I hope it is general enough to be useful for other demographers interested in estimating population structures of the past.

The aims for this chapter are as follows. I show that Bayesian reconstruction is useful in a wide range of data quality contexts by reconstructing the populations of countries for which data quality varies from poor to extremely good. In all cases, Bayesian reconstruction indicates when estimates of vital rates are inconsistent with census results. This means that the method can be used to compare competing model life tables. I also extend the method to unevenly spaced censuses.

In the next section I review existing methods of population reconstruction. Following that, I describe the method. Then I apply Bayesian reconstruction to the female populations of three countries: Laos, Sri Lanka and New Zealand. The New Zealand case shows that the model performs sensibly for countries with very good data and the Laos case for fragmentary

data. I use the case of Sri Lanka to demonstrate the extension to unevenly spaced censuses. Bayesian reconstruction detected inconsistencies between survey-based estimates of fertility and intercensal population changes, and provided a correction. There is relatively little mortality data for Laos and I use this case to illustrate how Bayesian reconstruction can be used to choose between competing model life tables. I conclude with a discussion. This chapter forms the basis of the working paper by [Wheldon et al. \(2012\)](#).

### **3.1 *Population Reconstruction Methods***

This Section is a summary of the literature reviews in Sections 1.2.2 and 2.2. Many human population reconstructions in the demography literature fall into one of two categories: reconstruction of populations of the distant past using data of the kind commonly found in European parish registers (e.g. [Lee, 1971, 1974](#); [Wrigley and Schofield, 1981](#); [Oeppen, 1993a,b](#); [Bertino and Sonnino, 2003](#)) and reconstruction of population dynamics after extreme crises such as famine or genocide (e.g. [Boyle and Ó Gráda, 1986](#); [Daponte et al., 1997](#); [Heuveline, 1998](#); [Merli, 1998](#); [Goodkind and West, 2001](#)). General methodology has been primarily developed in the former context, the latter being necessarily focused on special cases. In some form or another, the cohort component method of population projection (CCMPP) ([Lewis, 1942](#); [Leslie, 1945, 1948](#)) is central to almost all methods of population reconstruction.

Significant developments include Lee’s ([1971](#); [1974](#)) “inverse projection” and [Wrigley and Schofield’s \(1981\)](#) “back projection”. Further developments are described by [Barbi et al. \(2004\)](#). [Oeppen \(1993a\)](#), [Oeppen \(1993b\)](#) and [Bonneuil and Fursa \(2011\)](#) frame reconstruction as a high dimensional optimization problem. All of the above methods are deterministic and produce point estimates only. Stochastic inverse projection (SIP) was proposed by [Bertino and Sonnino \(2003\)](#), but did not account for measurement error or different age-patterns of vital events. The aim of [Daponte et al. \(1997\)](#) was to construct a counterfactual history of the Iraqi Kurdish population from 1977 to 1990, a period during which it was the target of considerable state-sponsored violence. This Bayesian approach took account of uncertainty due to measurement error and made use of contextual knowledge to make up for fragmentary, unreliable data. However, there were some restrictions, such

as allowing mortality to vary only through the infant mortality rate and specifying fixed age patterns of fertility. My approach is similar in spirit but more flexible as no model age patterns are assumed to hold throughout the period of reconstruction.

## 3.2 Method

Mathematical details can be found in Chapter 2. Here I give a more conceptual overview. All computation was done using the freely available statistical software package *R* (R Development Core Team, 2012); Bayesian population reconstruction is implemented in the package *popReconstruct* described in Appendix B at the end of the dissertation.

### 3.2.1 Description of the Model

The method reconciles two different estimates of population counts, those based on adjusted census counts (or similar data) and those derived by projecting initial estimates of the baseline population forward using initial estimates of vital rates. Adjusted census counts are raw counts which have been processed to reduce common biases such as undercount and age heaping. Since projection is done using the CCMPP, the parameters for which I require initial point estimates are the CCMPP inputs, namely population counts for the baseline year, fertility rates, survival proportions and the net number of migrants, all by age group, over the period of reconstruction. Migration is treated in the same way as fertility, mortality and baseline population counts.

Estimates of the measurement error for each parameter are also required. These can be based on expert judgment or preliminary analyzes such as post-enumeration surveys. Data and expert knowledge sufficient to generate these inputs are available for most countries from about 1960. The comparison is through a Bayesian hierarchical (or multilevel), statistical model which provides probabilistic posterior distributions of the inputs, as well as population counts at each projection step in the period of reconstruction.

Initial point estimates of the input parameters are derived from data. Baseline population estimates come from adjusted census counts (or similar sources), fertility and mortality estimates from surveys such as the Demographic and Health Surveys (DHSs) and vital registration. The model defines a joint prior distribution over these parameters which is

parametrized by the initial point estimates and standard deviations. Typically, the initial point estimates will serve as the marginal medians of this distribution, but this is not a requirement. The standard deviations represent measurement uncertainty about the point estimates. These distributions induce a probability distribution on the population counts at the end of each projection step within the period of reconstruction. Uncertainty about the true population numbers at the time of a census is also modeled by probability distributions. Adjusted census counts are taken as the median of these distributions and measurement uncertainty is represented analogously by standard deviations.

It is important that counts (adjusted or otherwise) from censuses in years after the baseline year not be used to derive initial estimates of fertility, mortality and migration. This means, for example, that intercensal survival rates should not be used to estimate mortality, and that “residual” counts, the difference between census counts and counts based on a projection using fertility and mortality alone, should not be used to estimate migration. Doing so would amount to using the census data twice, once to derive initial estimates of vital rates and once to derive adjusted census counts, which would lead to an underestimate of uncertainty.

In standard Bayesian terms, treating the induced distribution of projected counts as a prior and the distribution of census counts as a likelihood, Bayesian reconstruction yields a posterior distribution of the inputs via Bayesian updating. This distribution can be usefully summarized by marginal credible intervals for each input parameter which express uncertainty probabilistically. Furthermore, credible intervals for age-summarized parameters such as total fertility rate (TFR) and life expectancy at birth ( $e_0$ ) can be obtained. Using simulation, it was shown in Chapter 2 that Bayesian reconstruction produced well-calibrated marginal credible intervals.

Often, projected counts based on a sample from the joint prior on the input parameters will not equal the same-year adjusted census counts. This discrepancy is sometimes called an “error of closure” (Preston et al., 2001). The discrepancy can be reduced by making appropriate adjustments to any, or all, of the CCMPP input parameters and census counts. Many different combinations of adjustments will have the same effect on the discrepancy; for example, adding a migrant of age  $x$  has the same effect on the age- $x$  population count as

removing a death to a person of age  $x$ . The posterior distribution is a distribution over all possible combinations of CCMPP input parameters which assigns higher probability to those combinations leading to larger reductions in the discrepancy. This means that each age-time specific component of the input parameters is not affected equally, but proportionately according to the effect it has on the joint posterior.

In the case studies, the periods of reconstruction are delimited by the earliest and most recent censuses. Reconstruction can be done beyond the year of the most recent census if initial estimates of vital rates and international migration are available, but these latter initial estimates cannot be updated without a census.

### *3.2.2 Bias*

Estimates of vital rates and population counts from surveys and censuses are susceptible to bias. For example, fertility rate estimates based on birth histories suffer from omission and misplacement of births due to recall error and census counts may be biased due to undercount in certain age groups (Zitter and McArthur, 1980; Preston et al., 2001). Bayesian reconstruction does not treat bias explicitly because demographic data differ markedly across parameters, time and countries. Many methods for estimating and reducing these biases have been proposed such as post-censal enumeration surveys (e.g., United Nations, 2008, 2010a), “indirect” methods (e.g., United Nations, 1983), and Alkema et al.’s (2012) method for TFR. Methods appropriate for adjusting census data will not, in general, be applicable to vital registration or survey data. Even within these broad categories, there is great variation among countries and time which makes development of a general approach infeasible. Therefore, the analyst applying Bayesian reconstruction will need to select bias reduction methods appropriate to the data being used. I illustrate some possibilities in the case studies.

### *3.2.3 Measurement Error Uncertainty*

Bias reduced initial estimates of the CCMPP input parameters are still subject to measurement error; that is, variation that is non-systematic and cannot realistically be eliminated



or otherwise modeled. In Bayesian reconstruction, measurement error is represented by the prior standard deviations of the initial estimates. In many cases there is not much data with which to estimate these parameters, but there is often a great deal of relevant expert knowledge. This can be included by giving the variances themselves prior distributions and using the expert knowledge to set the fixed hyperparameters of these distributions. This can be done by eliciting a value for  $p$  in statements of the form “there is a 90 percent probability that the true fertility rates are within plus-or-minus  $p$  percent of the initial point estimates”, and similarly for survival proportions, migration proportions and population counts. I asked UNPD analysts to provide  $p$ , which I refer to as the “elicited relative error”. This quantity is used to set the hyperparameters,  $\alpha_v$  and  $\beta_v$ ,  $v \in \{f, s, g, n\}$  in equation (4.14).

#### *Determining the Hyperparameters $\alpha$ and $\beta$*

The distributions of the vital rate and population count parameters in equations (4.11)–(4.13) are conditional on the unknown variance parameters, hence draws from them are not observable. However, standard calculations show that the marginal (unconditional) distributions of these parameters are Student’s  $t$  centered at the initial point estimates and with variance and degrees of freedom dependent on  $\alpha$  and  $\beta$ . Draws from these distributions are observable. It is about these observable quantities that I elicit expert opinion. This differs from the method used in Chapter 2 which is based on the unobservable quantities modeled by the conditional distributions.

I set  $\alpha_v = 0.5$  for all  $v$  in  $\{f, s, g, n\}$ . This gives the initial estimates a weight equivalent to a single data point. The  $\beta_v$  were then determined by specifying the limits of the central ninety percent probability interval of the marginal distributions. Population counts and fertility rates are modeled on the log scale so this amounts to making a statement of the form “the probability that the true parameter values are the within  $p$  percent of the initial point estimates is ninety percent”. Migration is explicitly modeled as a proportion so this interpretation is direct for this parameter. The survival parameters are also proportions but they are modeled on the logit scale. I set  $\beta_s$  such that the untransformed  $s_{a,t,l}$  lie within the elicited intervals.

### *Estimating Measurement Error Uncertainty*

In statistical models, this type of error is typically accounted for by standard deviation parameters and is estimated from the sample standard deviation of independent, repeated observations. This approach is not suitable for demographic data of the kind I treat since repeated observations may not be available or, when they are, they are not typically independent. For example, in countries with vital registration systems I might have only a single data point for each age-time specific vital rate parameter, in which case there is no replication. For countries without these systems several surveys may each yield estimates of the same parameters and, moreover, more than one bias-reduction technique may have been applied to the same source. There is replication in these cases, but it is incorrect to estimate the measurement error variance from the empirical variance of these observations because they are not independent. For example, the results of applying several different indirect methods to the results of the same survey are clearly not independent. Given detailed information about the sampling methodology for specific surveys, one might be able to extract some quantitative estimate of error due to sampling variability. However, the required information is not always available. Even if it were, developing such estimates for each parameter in each country would be a substantial undertaking and would have to be done case-by-case. Therefore, I take a different approach and model measurement error through the prior standard deviations of the initial estimates. These, in turn, are given their own probability distributions at a higher level of the model.

### **3.3 Case Studies**

To show that Bayesian reconstruction works in a variety of situations, I used the subjective but useful evaluations of UNPD analysts to select three countries based on the quality of their mortality rate data: 1) New Zealand, with complete vital rate data based on vital registration; 2) Sri Lanka with good vital rate data requiring only small adjustments; 3) Laos with only limited under-five mortality estimates available and fertility data from a few demographic surveys. Thus I analyze New Zealand with excellent data, Sri Lanka with intermediate data, and Laos with poor data. Burkina Faso was analyzed in Chapter 2. In

terms of data availability, it sits between Laos and Sri Lanka, having data on both adult and under-five mortality.

In each case, a large sample from the joint posterior was drawn using a Markov chain Monte Carlo algorithm (Metropolis et al., 1953; Hastings, 1970; Geman and Geman, 1984), as described in Section 2.3.5. The method of Raftery and Lewis (1996) was used to choose chain lengths ( $q = 0.025$ ,  $0.975$ ,  $r = 0.0125$ ,  $s = 0.95$ ). Start values for the population counts, fertility and mortality rates (vital rates) and migration proportions were set to the initial estimates. Start values for the variances were arbitrarily set to 5 as they appeared to have a negligible effect on the final results. See Appendix 3.E for further details.

Results for each country are discussed separately below. I briefly describe the original data sources and the processes used to derive the initial estimates, and present results for TFR, net number of migrants,  $e_0$  and under-five mortality rate (U5MR). U5MR is defined as the number of deaths between ages 0 and 5 per 1,000 live births; it is a period measure. Life tables are used in the derivation of initial estimates for all case studies. The separation factors implicit in these tables were used to convert posterior estimates of age-specific survival proportions, a cohort measure, into period mortality (Shryock et al., 1980, Ch. 14,15; Thomas Buettner (pers. comm.)).

I give the limits of 95 percent credible intervals of the prior and posterior distributions of selected parameters using the notation: “(lower, upper)”. I compare my results for fertility and mortality to those published in *World Population Prospects* (WPP) 2010 for years with comparable estimates. WPP 2010 was based on a different procedure but the same data, therefore the comparison is useful.

Only the highlights are given here; more detailed descriptions of the data sources and initial estimates, further results, sensitivity to elicited relative errors and MCMC chains are in Appendices 3.A–3.E at the end of the chapter.

### 3.3.1 Laos, 1985–2005

#### *Data and Initial Estimates*

National censuses were conducted in 1985, 1995 and 2005. These data allow me to reconstruct the female population between 1985 and 2005. I used the census year counts in WPP 2010; there were no post-enumeration surveys, but these counts were adjusted to compensate for undercount in certain age groups.

Initial estimates of age-specific fertility rates (ASFRs) were based on direct and indirect estimates from the available surveys. Age-specific initial estimates were obtained by multiplying smoothed estimates of TFR by smoothed estimates of the age-pattern of fertility. Due to the small number of data points, smoothing was done by taking medians across data sources within age groups and time periods.

The only available mortality data are for infant and under-five mortality. Therefore the initial estimates came from the Coale and Demeny (1983) West (CD West) model life tables with values of  ${}_1q_0$  and  ${}_5q_0$  close to those estimated from available data.

Elicited relative errors for population counts, fertility and mortality were set to 10 percent.

There is not much information about migration. To model this, I set initial point estimates to zero for all ages and time periods, but used a large elicited relative error of 20 percent.

Sensitivity to increased elicited relative errors was studied by re-running the reconstruction. The results are reported in Appendix 3.C.

#### *Results*

Figure 3.1 shows the prior and posterior distributions for the demographic parameters together with WPP 2012 estimates for fertility and mortality. Detailed descriptions are in Appendix 3.B.1 at the end of this chapter. The Bayesian reconstruction estimate of TFR differs from the initial estimates in the five-year periods beginning 1985, 1990 and 2000. While both imply consistent decreases in fertility, the initial estimates appear to be too high in all but the third five-year period. The posterior intervals suggest a level of fertility

more similar to WPP 2010, except my estimates suggest that the acceleration in the decline begins one five-year period later.

Migration is estimated simultaneously with fertility and mortality. Posterior uncertainty for the average annual total net number of migrants has been significantly reduced relative to prior uncertainty (Figure 3.1b). The mean half-width of the posterior intervals is 47,331 (compared with 3,953,406) for the prior intervals.

Figure 3.1a shows that the posterior intervals are not constrained to lie inside the prior intervals. Moreover, the posterior intervals can be wider than the prior intervals. This is the case for ASFRs for Laos. See Appendix 3.B.1 at the end of this chapter for further details.

### 3.3.2 Sri Lanka, 1951–2001

#### *Data and Initial Estimates*

Censuses were conducted in Sri Lanka in 1953, 1963, 1971, 1981 and 2001 so I reconstruct the female population between 1953 and 2001. I took population counts from WPP 2010 which were adjusted to account for under-enumeration. Initial estimates of ASFRs were derived in a manner similar to that used for Laos, although at the level of TFR I used *loess* (Cleveland et al., 1992; Cleveland, 1979) to smooth multiple data points across time period. Initial estimates of age-specific survival proportions were based on abridged national life tables calculated from death registration and available surveys. Elicited relative errors for all of these parameters were set at 10 percent.

I used the same default initial estimate of international migration as for Laos. Luther et al. (1987) provide age-specific estimates for the periods 1971–1975 and 1976–1980 using census data as well as information about vital rates. Their results are not suitable as a basis for initial estimates because they were derived, in part, from census counts, so I use them for comparison instead.

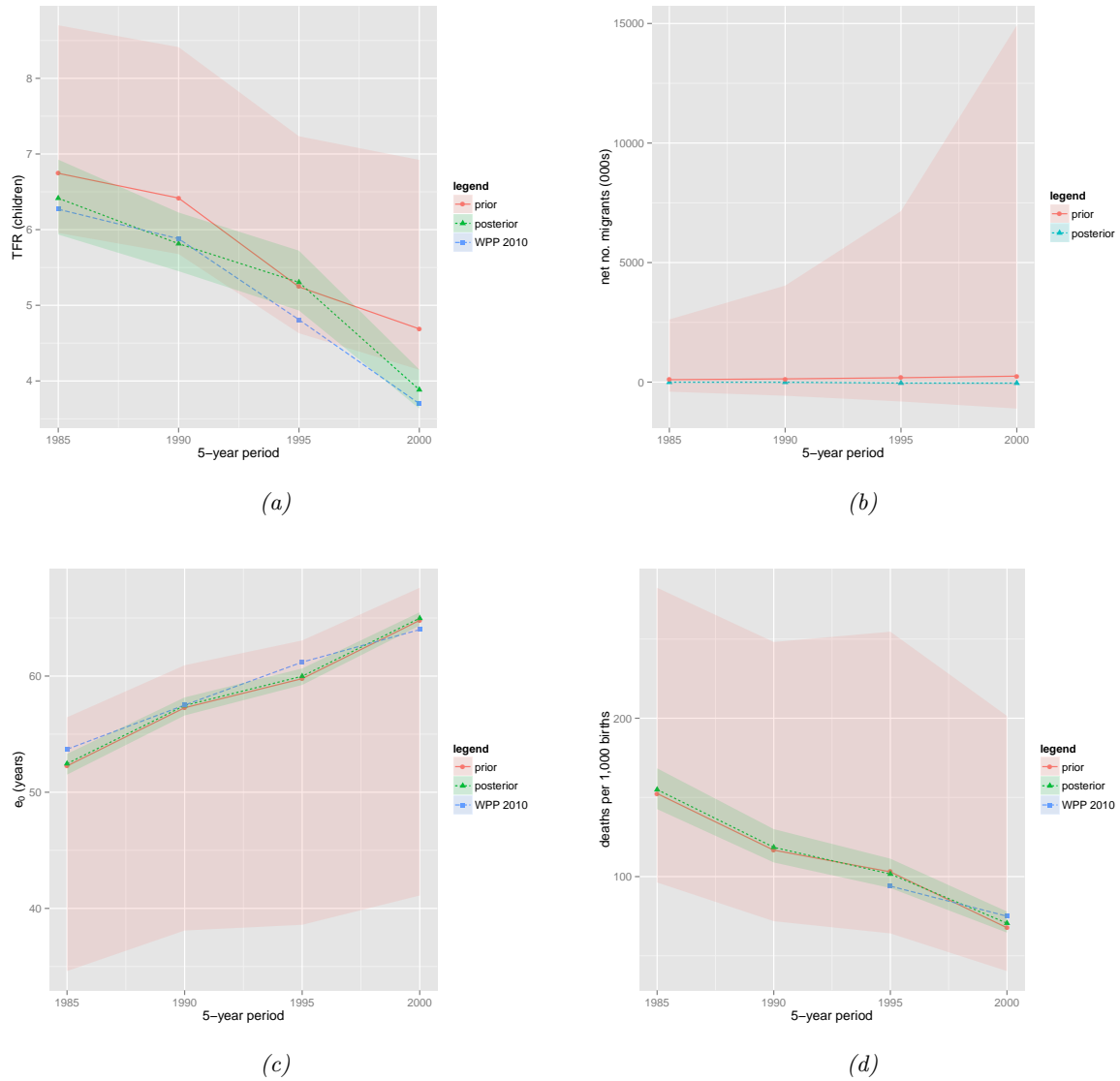


Figure 3.1. Prior and posterior medians and 95 percent credible intervals for selected parameters for the reconstructed female population of Laos, 1985–2005. Prior medians correspond to initial estimates. (a) Total fertility rate (TFR). (b) Total net number of female migrants (average annual). (c) Female life expectancy at birth ( $e_0$ ). (d) Female under-five mortality rate (U5MR) (deaths to 0–4 year olds per 1,000 live births).

### *Interpolation to Accommodate Irregular Census Intervals*

The method introduced in Chapter 2 assumed that censuses were taken at regular intervals but there is an irregular gap between the 1963 and 1971 censuses. Therefore, I propose interpolating the CCMPP outputs on the growth rate scale such that they coincide with the census years. I explain by way of an example.

Consider the number in the population aged  $[x, x + 5)$  for which I have a census-based estimate at 1963 and another census-based estimate at 1971. Initial estimates for vital rates are available at 1963, 1968, 1973, and at subsequent five-year increments. The CCMPP can be used with these data to derive projected counts for this age group in 1968 and 1973. To compare the CCMPP output with the census counts at 1971, I assume that the growth rate for this age group,  $r_{x,1968}$ , was constant between 1968 and 1973, and estimate it from the projected counts. The estimate is then used to interpolate the CCMPP output to 1971. Using a “hat” ( $\hat{\phantom{x}}$ ) to denote “estimate”, this is compactly expressed as:

$$\hat{r}_{x,1968} = \frac{1}{5} \log \left( \frac{n_{x,1973}}{n_{x,1968}} \right); \quad \hat{n}_{x,1971} = (n_{x,1968})e^{3\hat{r}_{x,1968}}.$$

I use a similar method to extrapolate the population counts from the 1953 census back to 1951 using the 1953–1963 growth rate. Interpolating in this manner is adequate for periods of length less than five years.

### *Results*

Posterior distributions for the demographic parameters are summarized in Figure 3.2. Detailed descriptions are given in Appendix 3.B.2 at the end of this chapter. The posterior estimates of mortality and migration agree closely with those of WPP 2010 and Luther et al. (1987). Applying Bayesian reconstruction suggests, however, that the sources upon which the initial estimates were based are inconsistent with intercensal changes in the number of births. The posterior estimates of TFR from Bayesian reconstruction differ noticeably from the initial estimates in the periods 1951–1956 and 1956–1961 (posterior intervals (5.09, 5.69) and (5.21, 5.93); initial estimates 5.01 and 5.03 children per woman, respectively). The method has automatically provided a correction which, in this case, yields results similar to the WPP 2010 estimates.

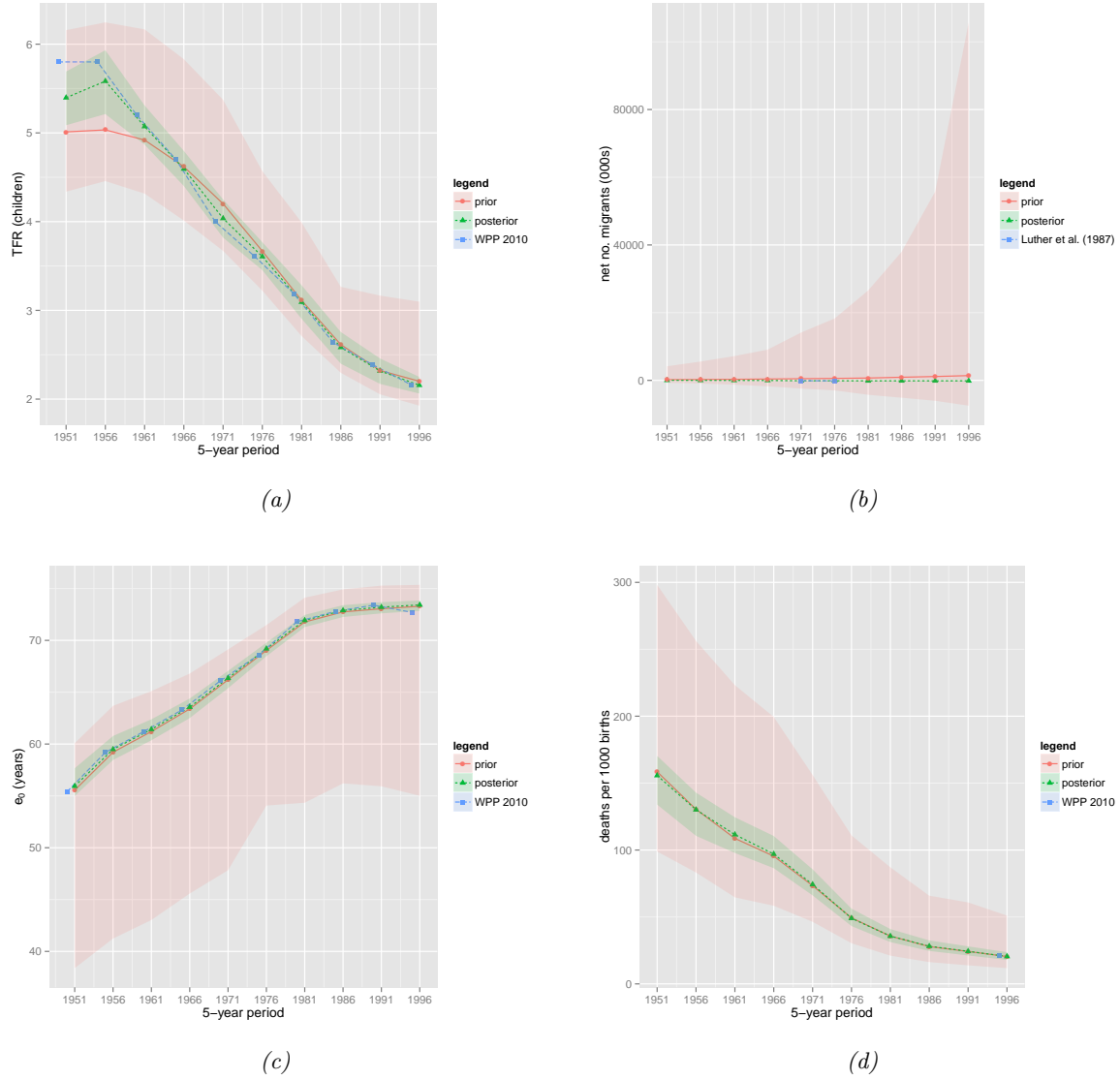


Figure 3.2. Prior and posterior medians and 95 percent credible intervals and WPP 2010 estimates of selected parameters for the reconstructed female population of Sri Lanka, 1951–2001. Prior medians correspond to initial estimates. (a) Total fertility rate (TFR). (b) Total net number of female migrants (average annual). (c) Female life expectancy at birth ( $e_0$ ). (d) Female under-five mortality rate (U5MR) (deaths to 0–4 year olds per 1000 live births).



### 3.3.3 New Zealand, 1961–2006

#### *Data and Initial Estimates*

Census counts came from national censuses conducted every five years between 1961 and 2006. Initial estimates of fertility rates were calculated from published ASFRs (Statistics New Zealand, 2011a) and numbers of births (Statistics New Zealand, 2012) by age group of mother by year. Initial estimates for survival proportions were calculated from New Zealand life tables (Statistics New Zealand, 2011b).

Information about the measurement errors of these parameters was available in the form of census post-enumeration surveys (PESs) and estimates of the coverage achieved by the birth and death registration systems. Elicited relative errors were based on this information and were set to 2.5 percent, one percent, and one percent for population counts, fertility and mortality, respectively.

Information about international migration is quite reliable given that New Zealand is a small island nation with a well-resourced official statistics system. The basis of my initial estimates of international migration are counts of permanent and long-term (PLT) migrants taken from arrivals and departures cards (Statistics New Zealand, 2010c). The largest source of error in these data as estimates of international migration is the discrepancy between the stated intentions and actual behavior of travelers. To reflect this, I set the elicited relative error of this parameter to five percent.

#### *Results*

The posterior distributions for TFR, total net number of migrants,  $e_0$  and U5MR are summarized in Figure 3.3. Detailed descriptions are in Appendix 3.B.3. The posterior estimates of mortality and fertility follow the initial estimates closely. This is not unexpected; the initial estimates were based on data of high quality and coverage. The least reliable data, *a priori*, were those for migration. The posterior intervals suggest small corrections in some time periods. The initial estimates for periods between 1961 and 1974 appear to be too high while those for periods between 1976 and 1989 are too low.

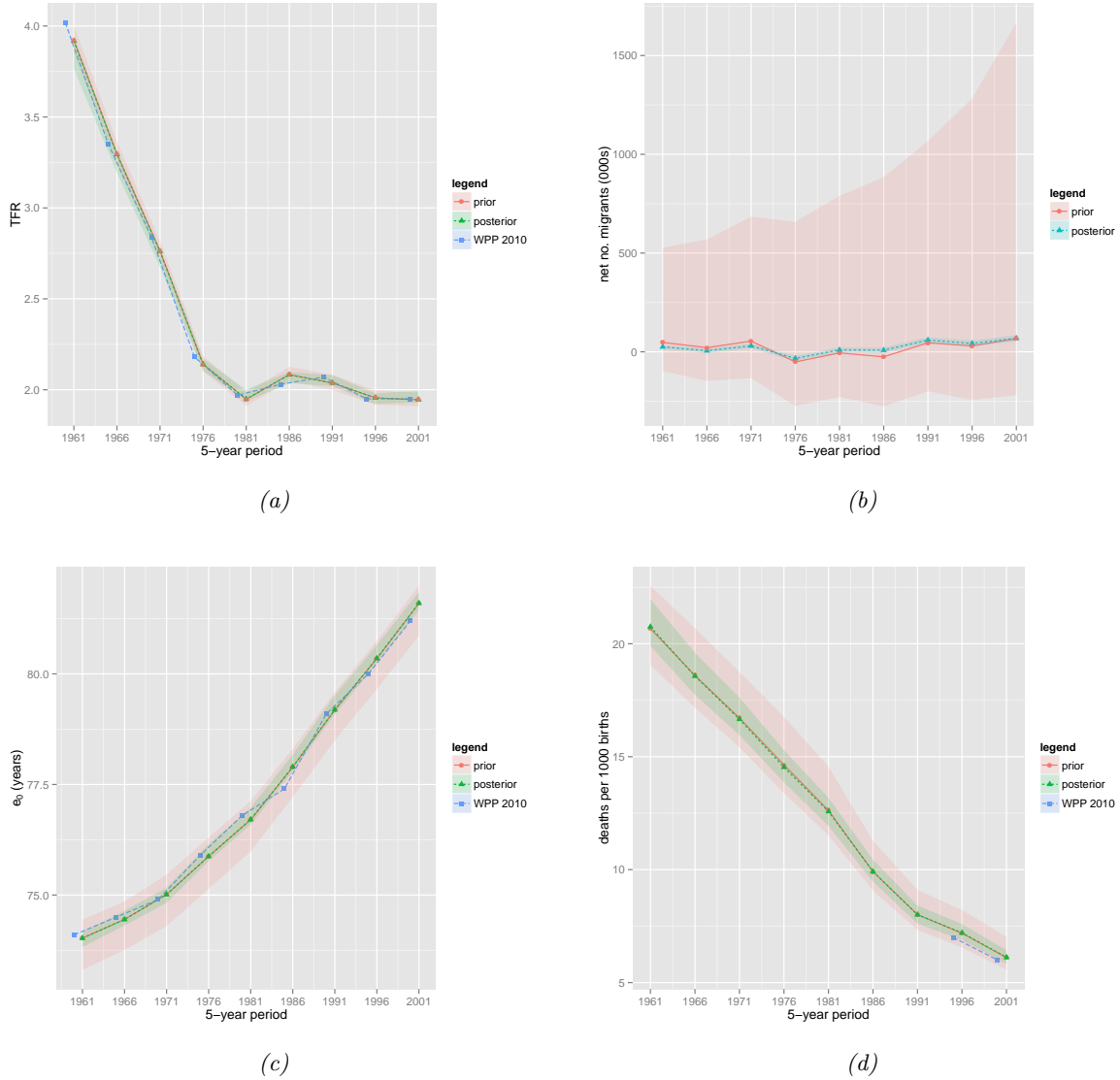


Figure 3.3. Prior and posterior medians and 95 percent credible intervals and WPP 2010 estimates of selected parameters for the reconstructed female population of New Zealand, 1961–2006. Prior medians correspond to initial estimates. (a) Total fertility rate (TFR). (b) Total net number of female migrants (average annual). (c) Female life expectancy at birth ( $e_0$ ). (d) Female under-five mortality rate (U5MR) (deaths to 0–4 year olds per 1000 live births).

### 3.4 *Choosing Between Alternative Initial Estimates of Mortality*

In the application to Laos I derived initial estimates of over-five mortality from the CD West model life table. This choice was made by UNPD analysts who drew on previous studies (Hartman, 1996a,b; United Nations, 2011b). However, other approaches are possible. Here, I compare the results above with those given by an alternative set of initial estimates of survival based on a different model life table, and use them to explain why the CD West model should be preferred. To do this, I look at the age-specific mortality rates, rather than  $e_0$ .

The posterior distribution of  $e_0$  in Figure 3.1c was computed from the posterior distribution of the age-specific survival proportions,  $s_{a,t}$ , which are output by Bayesian reconstruction (notation and parameter definitions are in Section 2.3.1). These were converted into age-specific annual mortality rates using the separation factors implicit in the CD West life table. Medians and the limits of 95 percent credible intervals for the marginal posterior distributions of these parameters are shown in Figure 3.4 on the log scale. Posterior uncertainty about these quantities is very low; the mean half-widths over age, within year, are all less than 0.065.

An alternative set of initial estimates for the  $s_{a,t}$  was generated from the same data on under-five mortality, but adult mortality was estimated using the Brass two-parameter relational logit model with the United Nations South Asian (UNSA) model life table,  $e_0 = 57.5$  years. Figure 3.5 gives the initial estimates and marginal posteriors of the survival proportions using these alternative survival estimates, but keeping the initial estimates of all other parameters the same. The posterior intervals are much wider under this set of initial estimates; the mean half-widths over age, within year, are between 1.1 and 1.3; a large increase on the log scale.

The wider intervals show that using the alternative initial estimates greatly increases posterior uncertainty. In addition, for many of the older age groups, the posterior medians are actually closer to the CD West initial point estimates than those used to fit the model. This suggests that the initial estimates based on the CD West life tables are much more consistent with the intercensal changes in population counts, given the initial estimates

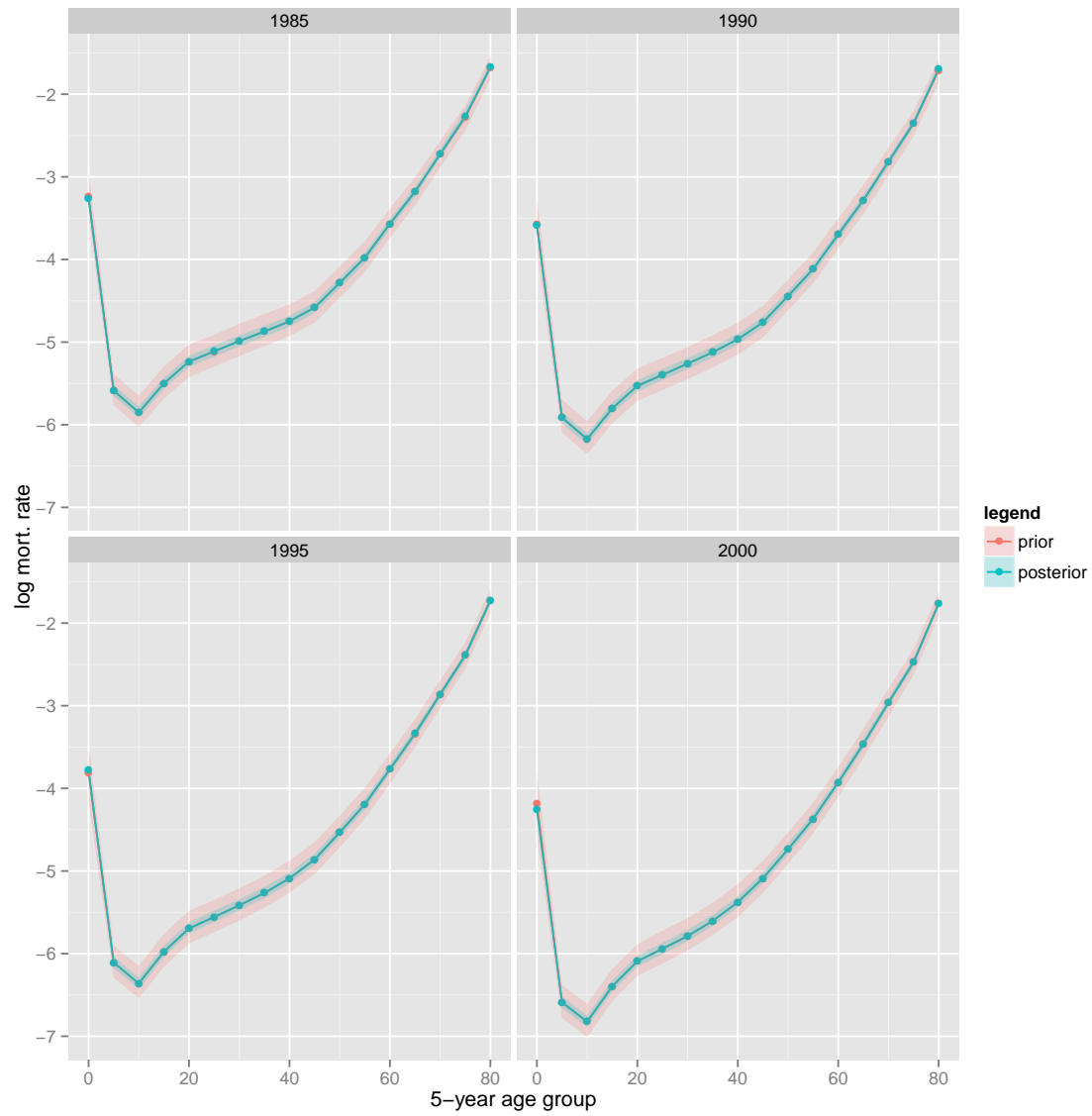
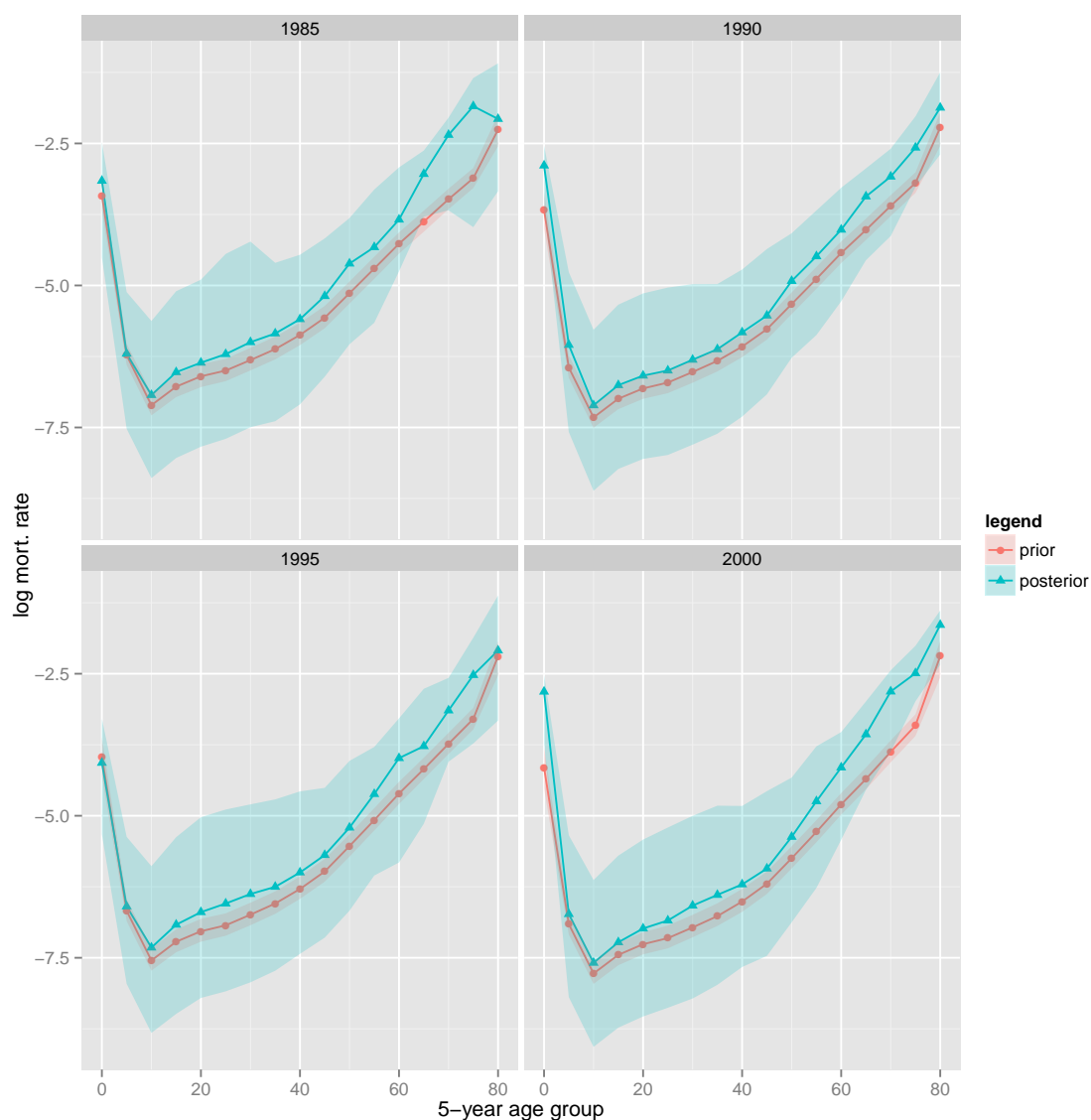


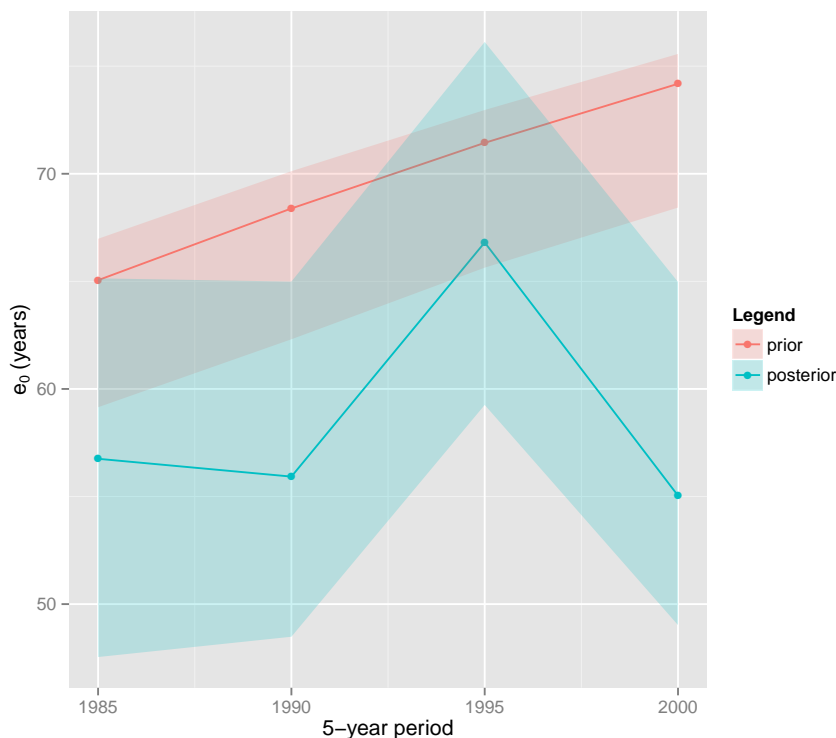
Figure 3.4. Prior and posterior medians and 95 percent credible intervals for the age-specific log mortality rate ( ${}_5m_x$ ) for the reconstructed female population of Laos, 1985–2005. Prior medians correspond to initial estimates which were calculated using the Coale and Demeny West (CD West) model life table.



*Figure 3.5.* Prior and posterior medians and 95 percent credible intervals for age-specific log mortality rate ( ${}_5m_x$ ) for the reconstructed female population of Laos, 1985–2005. Prior medians correspond to initial estimates. Initial estimates and posterior distributions were calculated using the United Nations South Asian (UNSA) model life table and the Brass two-parameter logit relational model.

for the other parameters, and that they should be preferred over the UNSA-derived initial estimates.

Looking at  $e_0$  in Figure 3.6 leads to the same conclusion. Again, uncertainty is much greater under the alternative set of initial estimates (cf. Figure 3.3c). The posterior distribution has shifted away from the initial estimates used to fit the model toward those derived from the CD West model life table. In fact, all CD West initial point estimates are contained within the 95 percent posterior intervals based on the alternative estimates while this is not the case for the initial estimates used to fit the model.



*Figure 3.6.* Prior and posterior medians and 95 percent credible intervals for life expectancy at birth ( $e_0$ ) for Laos females, 1985–2005, using the Brass two-parameter logit model and the United Nations South Asian (UNSA) model life table. This figure summarizes the same results shown in Figure 3.5.

I emphasize that my preferred set of initial estimates is that generated using the CD

West standard. The purpose here is not to advocate for the UNSA standard, or the Brass two-parameter logit model, but to present an alternative, plausible set of initial estimates which I can use to generate an alternative set of posterior estimates for use in a comparative analysis.

### 3.5 Discussion

In this chapter I have demonstrated and extended the method of reconstructing past, national-level population structures introduced in Chapter 2. This method embeds the standard CCMPP in a hierarchical statistical model which takes initial estimates of vital rates and population counts as inputs, together with expert opinion about their relative error (informed by data if available). International migration is handled in the same way as fertility and mortality, and the method yields fully probabilistic interval estimates for all of the inputs. The approach is Bayesian as the initial estimates serve as informative, but not restrictive, priors for population counts through the CCMPP, which are then updated using available census data over the period of reconstruction. Reconstruction can be undertaken for any period for which estimates of baseline population, vital rates and international migration are available. However, reconstruction beyond the year of the most recent census will be based on the initial estimates alone.

I presented 95 percent credible intervals for the marginal distributions of TFR, total net number of migrants,  $e_0$  and U5MR. Ninety-five percent intervals cover the range of most likely values. Results for TFR and age-specific fertility for Laos showed that the posterior intervals are not constrained to lie inside prior intervals, nor are they necessarily more narrow than prior intervals. My posterior estimates of TFR for Laos and Sri Lanka suggested that, in some years, the initial estimates based mainly on surveys were inconsistent with intercensal changes in the number of births and Bayesian reconstruction was able to provide an appropriate correction.

I showed that the method works well when applied to different countries spanning a wide range of data quality characteristics. For Laos, all mortality data are for ages five and below and come from surveys, while New Zealand has complete period life tables based on vital registration. Sri Lanka and Burkina Faso (analyzed in Chapter 2) lie between these

extremes. The posterior intervals for New Zealand were much more narrow than those for Sri Lanka and Laos, reflecting the greater accuracy and coverage of the New Zealand data. The greatest value of Bayesian reconstruction is likely to be for those countries without well-resourced statistical systems. Roughly half of all the countries and areas included in the WPP fall into this category ([United Nations, 2011a](#)).

The method as described in Chapter 2 was limited by the fact that it required census data at regular intervals. Here, I have relaxed this requirement by showing that linearly interpolating census counts on the growth rate scale produces good results.

I have also shown how Bayesian reconstruction might be used to help choose between two sets of initial mortality estimates. I compared the posterior distributions of age-specific mortality rates for Laos derived from initial estimates based on the CD West model life table and the Brass two-parameter relational logit with the UNSA model life table. In the latter case, the interval widths were much greater. This implies that the CD West based initial estimates agree much more closely with the data on fertility, mortality and population counts and they should be preferred.

Bias and measurement error variance are handled separately under Bayesian reconstruction. Existing demographic techniques, such as indirect estimation via  $P/F$  ratios and model life tables, are used to reduce bias in initial point estimates based on raw data collected from surveys, vital registration and censuses. The nature of bias varies greatly across parameters, time and country, hence I do not propose a general purpose method to replace the many existing techniques. Instead, the analyst is able to select the most appropriate technique for the data at hand. Measurement error variance is accounted for through the standard deviations of the initial point estimates. Expert opinion is used *a priori* to set reasonable ranges for measurement error uncertainty. The marginal posterior distributions are slightly sensitive to the elicited relative error (Appendix 3.C).

To ensure that uncertainty is not underestimated, census data should not be used to derive initial point estimates of vital rates and migration. If no reliable migration data are available, the default initial point estimates should be centered at zero with a large elicited relative error.

Bayesian reconstruction was developed and demonstrated here for female-only popula-



tions. In Chapter 4 I propose a method for the reconstruction of two-sex populations. A further potential refinement is to use single-year age groups and time periods.

A great deal of attention has already been directed at the estimation of uncertainty in demographic forecasts, as opposed to estimates about the past which I focus upon here. The study of stochastic models for forecasting dates back to at least Pollard (1966) and Sykes (1969). Further developments are reviewed by Booth (2006) with more recent additions in Hyndman and Booth (2008), Scherbov et al. (2011) and Alkema et al. (2011). One component of error in forecasts of population size is the error in estimates of population size and the vital rates prevailing at the jump-off time. While the ergodic theorems of Demography (Lotka and Sharpe, 1911; Lopez, 1961) imply that these become irrelevant if one forecasts far enough into the future, short term forecasts can be significantly affected (e.g., Keilman, 1998; National Research Council, Commission on Behavioral and Social Sciences and Education, 2000). It is possible, then, that Bayesian reconstructions could contribute to improved forecasting methods by providing important information about the uncertainty in estimates of jump-off populations.

The fact that official statistical estimates are imperfect is not disputed. The UNPD acknowledges this both explicitly (United Nations, 2011a) and implicitly in the fact that the WPP are revised biannually as new sources of data become available and methods are improved. Therefore, augmenting point estimates with quantitative estimates of their uncertainty is an important contribution. For many countries, the available data are fragmented and subject to bias and measurement error, thus the expert opinions of demographers are very valuable. A Bayesian approach is especially appropriate since this can be used in conjunction with the available data in a statistically coherent manner.

### ***Appendix 3.A Further Details About Data Sources and Initial Estimates***

#### *3.A.1 Laos, 1985–2005*

Initial estimates for females were the same as those used in Chapter 4 for the two-sex reconstruction of Laos; see Section 4.B.1 for details.

### 3.A.2 Sri Lanka, 1951–2001

#### *Population Counts*

Censuses were conducted in Sri Lanka in 1953, 1963, 1971, 1981 and 2001 so I reconstruct the female population between 1953 and 2001. I took population counts from WPP 2010 which were adjusted to account for underenumeration and set the elicited relative error to 10 percent.

#### *Fertility*

Data on ASFRs for Sri Lanka came from data on children ever born classified by age of mother collected in the 1971 census, maternity history and children ever born data from the 1975 Sri Lanka World Fertility Survey (WFS), the 1987, 1993 and 2000 Sri Lanka DHSs, maternity history data from the 2006–07 Sri Lanka DHS and recent births registered by the Department of Census and Statistics, Sri Lanka (DCS Sri Lanka) between 1972 and 2006.

A single series of age-specific initial estimates was derived in a manner similar to that used for Laos, although at the level of TFR I used *loess* (Cleveland et al., 1992; Cleveland, 1979) to smooth multiple data points across time period. Elicited relative error for this parameter was set at 10 percent.

The initial estimates obtained, and the original data points, are plotted in Figures 3.7–3.9 and 3.18.

#### *Mortality*

Official estimates of infant and child mortality from DCS Sri Lanka were adjusted upward to improve consistency with UN Inter-agency Group for Child Mortality Estimation (2010) estimates. These were based on maternity histories and children ever born data from the 1975 Sri Lanka WFS, the 1987, 1993, 2000 and 2006 Sri Lanka DHS and the 1971 Census, assuming that the age pattern of mortality followed that in the Coale-Demeny West model life table (Coale et al., 1983). These estimates were combined with registered deaths and population estimates to produce abridged national life tables at five yearly intervals over the period of reconstruction. The  ${}_nq_x$  for these life tables are shown in Figure 3.10. Age-specific

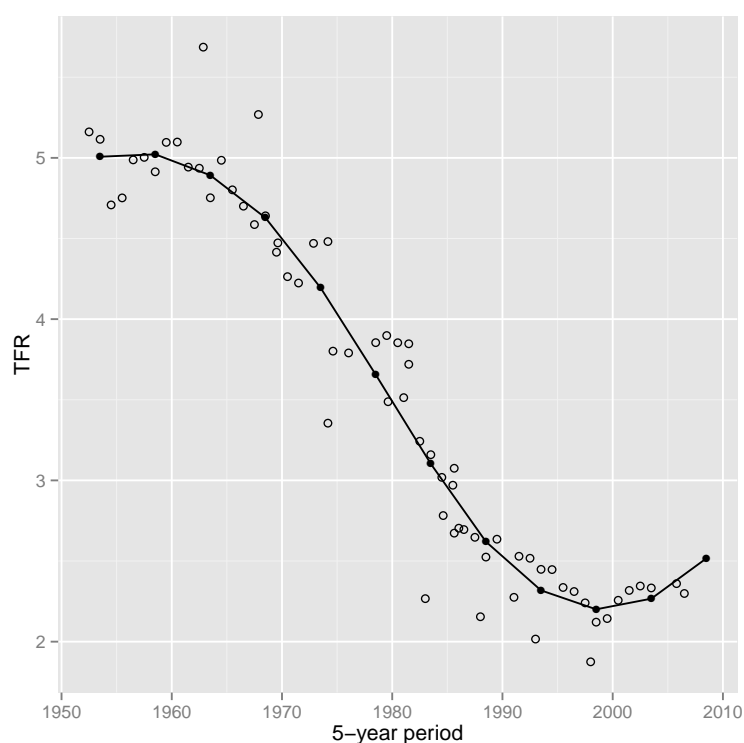
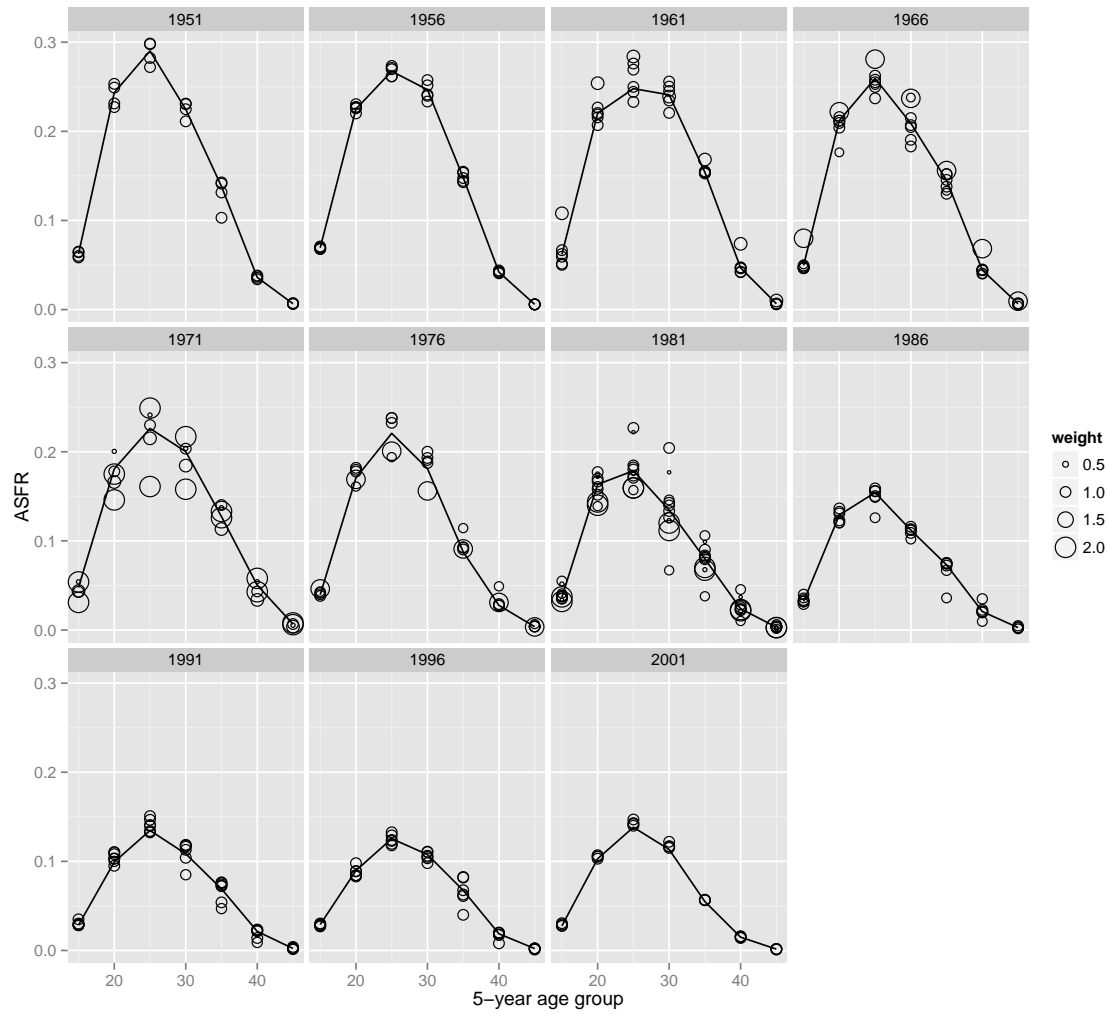


Figure 3.7. Data points (open circles) and initial estimates (solid circles, line) for total fertility rate (TFR) for the female population of Sri Lanka, 1951–2001. See text for sources.

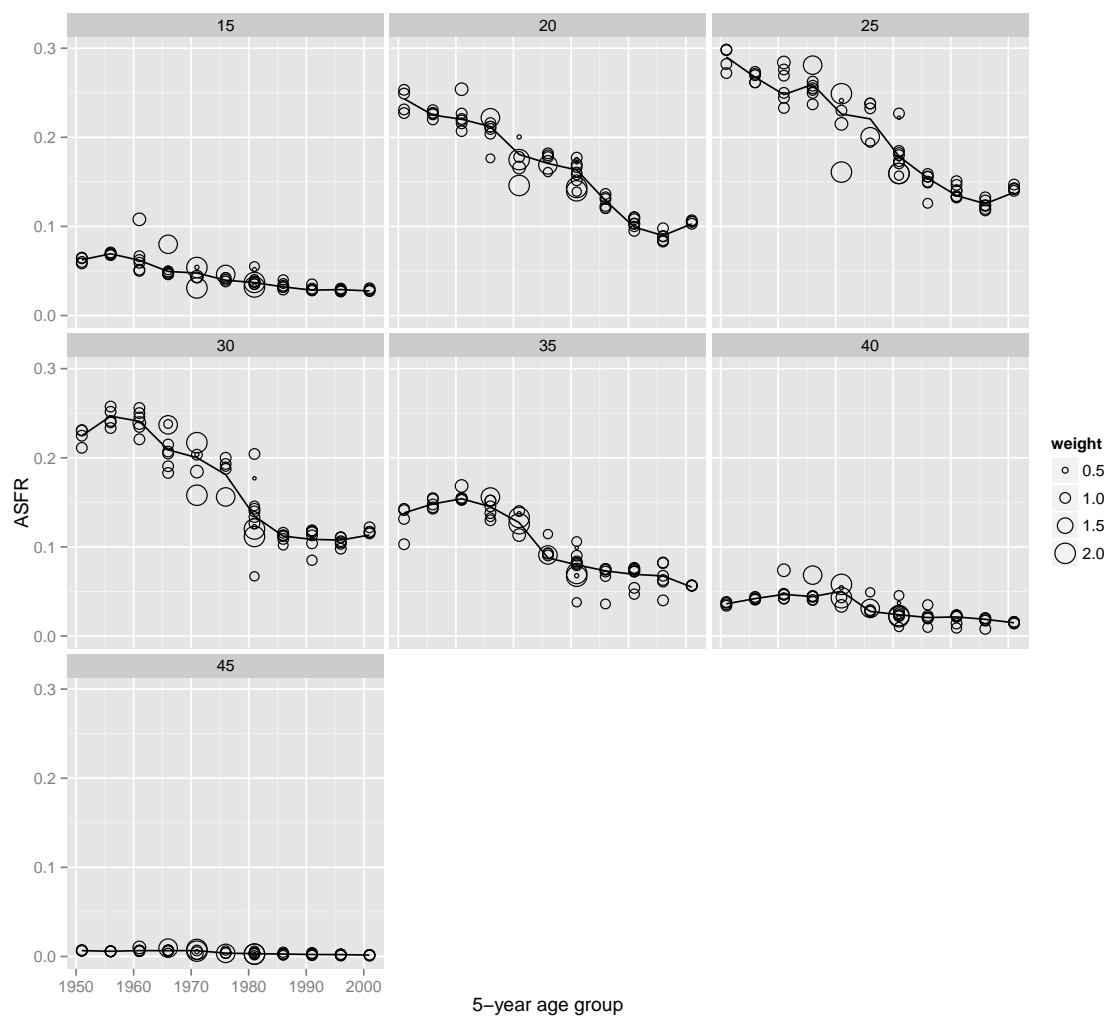
survival proportions for the five-year periods [1951, 1956), ..., [1996, 2001) were obtained by linearly interpolating the  ${}_n m_x$  and  ${}_n a_x$  values to the period midpoints. Initial estimates of age-specific survival proportions for five-year age groups ( ${}_5 s_x$ ) were calculated from these interpolated tables (Figure 3.19). Elicited relative error for this parameter was set at 10 percent.

### Migration

DCS Sri Lanka releases counts of international arrivals and departures which provide some information about international migration (e.g., [Department of Census and Statistics, Sri Lanka, 2010](#)). However, their accuracy as estimates of actual net migration was difficult to determine and counts by age were not available for most of the period of reconstruction.



*Figure 3.8.* Data points and initial estimates for age-specific fertility rate (ASFR) by time period for the female population of Sri Lanka, 1951–2001. See text for sources.



*Figure 3.9.* Data points and initial estimates for age-specific fertility rate (ASFR) by age group for the female population of Sri Lanka, 1951–2001. See text for sources.

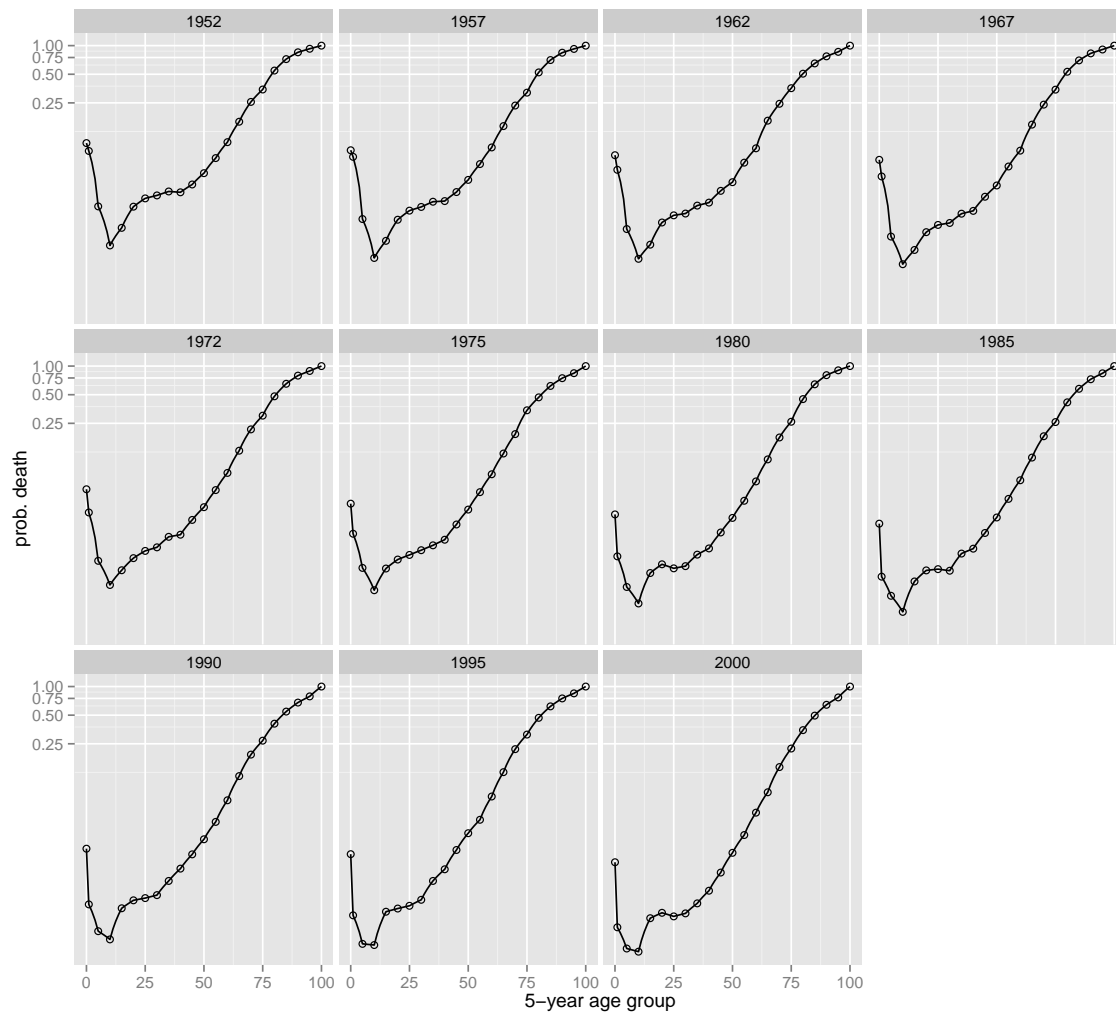


Figure 3.10. Adjusted Department of Census and Statistics, Sri Lanka (DCS Sri Lanka) age-specific probabilities of death ( ${}_nq_x$ ) by time period for the female population of Sri Lanka, 1952–2005. The vertical axis has been transformed to the log scale. See text for sources.

[Luther et al. \(1987\)](#) provide age-specific estimates for the periods 1971–1975 and 1976–1980 using census data as well as information about vital rates. Their results are not suitable as a basis for initial estimates because they were derived, in part, from census counts. Since intercensal changes are automatically accounted for by Bayesian reconstruction, incorporating census information into initial estimates would result in using the data twice and underestimate posterior uncertainty. Therefore, I used the same default initial estimate as for Laos and use [Luther et al.’s \(1987\)](#) results for comparison.

### *3.A.3 New Zealand, 1961–2006*

#### *Population Counts*

National censuses were conducted every five years from 1961 to 2001. I took the counts published in WPP 2010 and interpolated them to the census years on the growth rate scale. PESs were used to estimate undercount in the 1996 and 2001 censuses. The ninety-five percent credible intervals for the undercount of total population as estimated by these surveys are (1.4, 1.8) and (1.9, 2.5) percentage points for 1996 and 2001 respectively ([Statistics New Zealand, 2001](#)). Since PESs were not conducted for earlier censuses, I took a conservative approach to determining the distributions of the initial estimates and made them symmetric about the census counts. Elicited relative error was set at 2.5 percent under the assumption that undercount in 2001 is an upper bound on the measurement error for all previous censuses back to 1961.

#### *Fertility*

Initial estimates of fertility rates were calculated from published ASFRs, available from ([Statistics New Zealand, 2011a](#)), and numbers of births ([Statistics New Zealand, 2012](#)) by age group of mother by year. The denominators of the rates were inferred from these two tables. Age-specific rates for the five-year periods 1961–1965, . . . , 2001–2005 were calculated by binning the number of births and person-years lived into the five-year periods, summing and taking ratios. Initial estimates are shown in Figure [3.24](#).

In New Zealand, all births are recorded in a centralized birth register. Any inaccuracies

are primarily due to late registrations; that is, registrations made more than two years after the birth. These are excluded from the data used to estimate fertility. However, it is estimated that these late registrations make up no more than one percent of all eventually registered births ([Statistics New Zealand, 2010a](#)). Consequently, the initial estimates of fertility rates were deemed to have a very high level of reliability relative to the two previous case studies and elicited relative error was set to one percent.

### *Mortality*

Initial estimates for survival proportions were calculated from New Zealand life tables, available from ([Statistics New Zealand, 2011b](#)). These are tabulated for the periods 1960–1962, . . . , 2000–2002. To derive estimates for the five-year projection intervals [1961, 1965), . . . , [2001, 2005), tabulated mortality rates ( ${}_n m_x$ ) and  ${}_n a_x$  values were linearly interpolated. Initial estimates of survival proportions for five-year age groups were calculated from these tables (Figure 3.25).

Mortality information contained within these tables comes from the central death register. This register achieved high coverage of the whole population (including New Zealand Māori) from 1960 onward. Any inaccuracies are likely to be concentrated at very young ages, but these became negligible from 1961 ([Statistics New Zealand, 2006](#)). Therefore, as with fertility, initial estimates of survival were deemed to be highly reliable and elicited relative error was set to one percent.

### *Migration*

Since New Zealand is an island nation with a well resourced official statistics system, information about international migration is potentially quite reliable relative to other countries. The basis of my initial estimates of international migration are counts of PLT migrants taken from arrivals and departures cards required of all travelers. PLT migrants are those intending to remain present/absent for at least 12 months. ([Statistics New Zealand, 2010b](#)).

Net numbers of PLT migrants by five-year age group and sex for single years between 1979 and 2006 were taken from [Statistics New Zealand \(2010c\)](#). Only total counts are



available by single year between 1961 and 1979 (Statistics New Zealand, 2010d). These were disaggregated into age-specific female counts by multiplying the total counts by the 1979 age and sex pattern. Were counts by sex and age not available, a model age/sex pattern (e.g., Rogers and Castro, 1981) could have been used. The resulting set of net counts for females by five-year age group, single years, were then summed over the five-year periods 1961–1965, 1966–1970, ..., 2001–2005 and converted into average annual proportions by dividing by five times the population counts described in Section 3.A.3. Initial estimates are shown in Figure 3.27.

The largest source of error in these data as estimates of international migration is the discrepancy between stated and actual intentions. Some of those classified as PLT migrants according to their stated intentions may leave or return earlier than twelve months, some of those classified as short term migrants may leave or return later. This effect is not negligible and to reflect its effect on the initial estimates I set the elicited relative error of this parameter to five percent. This is lower than the elicited error in migration for Laos and Sri Lanka, but much higher than the error for New Zealand fertility and survival estimates.

### ***Appendix 3.B Further Results***

In this section I give detailed descriptions of the results in Section 3.3, marginal posterior distributions for all age-specific input parameters, some other outputs, and further information about MCMC sampling.

#### *3.B.1 Laos, 1985–2005*

##### *Detailed Description of Results in Section 3.3.1*

**TFR** Total fertility rate (Figure 3.1a) declined over the period of reconstruction, from (5.94, 6.93) to (3.63, 4.15). The mean half-width of the posterior 95 percent credible intervals is 0.38 children.

For most of the years, the posterior median moved away from the initial estimates toward the WPP 2010 estimates. No information about intercensal population changes was used in the initial estimates, whereas both the posterior and WPP 2010 do use this information.

The 95 percent credible interval contains the WPP 2010 estimate in all five-year periods except 1995–1999 where the estimate is (4.93, 5.72) compared with 4.81 in WPP 2010. These results also show that the posterior is not constrained to lie within the initial estimate (see the posterior intervals for the 1990–1994 and 2000–2004).

**Net Number of Migrants** The total net number of migrants (Figure 3.1b) changed from (−38,051, 32,249) women over the period 1985–1989 to (−103,984, 15,269) over 2000–2004. The 95 percent posterior intervals have a mean half-width of 47,331 and are considerably more narrow than the corresponding initial estimate intervals (mean half width 3,953,406). In this case, the only information about migration comes from intercensal changes that are not accounted for by fertility and mortality.

**Life Expectancy at Birth** Female life expectancy at birth (Figure 3.1c) increased consistently between 1985 and 2005, from (51.6, 53.1) years over the period 1985–1989 to (64.5, 65.4) over the period 2000–2004. The mean half-width of the intervals over the whole period of reconstruction is 0.61 years. The mean trend in the posterior agrees broadly with WPP 2010 but implies a lower  $e_0$  over the 1985–1989 and 1995–1999 periods and a higher  $e_0$  over the 2000–2004 period.

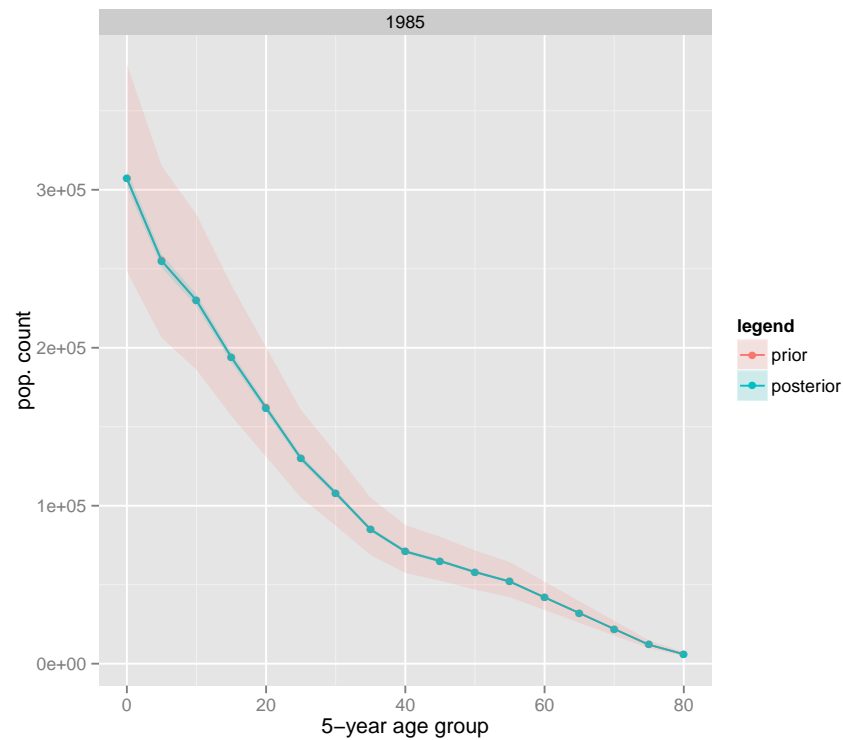
**Under-five Mortality** U5MR (Figure 3.1d) decreased consistently over the period of reconstruction from (143, 168) deaths per 1,000 live births over 1985–1989 to (64.6, 77.9) over 2000–2004. The latter of these contains the WPP 2010 estimate of 75. The 95 percent interval for 1995–1999 is (92.8, 111) which also contains the WPP 2010 estimate of 94. The mean half-width of the intervals is 9.84.

### *Additional Results*

**Population Counts** Census-based initial estimates and posterior quantiles for the size of the Laos female population are given in Table 3.1. Between 1985 and 2005, the posterior median estimate increased from 1.83 to 2.96 million, an average annual growth rate of 2.4 percent. Age-specific population counts in the baseline year, 1985, are in Figure 3.11.

*Table 3.1.* Initial estimates, posterior medians and 95 percent credible intervals for population count, Laos female population, 1985–2005, in millions.

Year	Posterior Percentile			Init. Est.
	2.5th	50th	97.5th	
1985	1.80	1.83	1.86	1.83
1990	2.01	2.10	2.19	
1995	2.37	2.41	2.44	2.41
2000	2.58	2.70	2.82	
2005	2.90	2.95	3.01	2.95



*Figure 3.11.* Prior and posterior medians and 95 percent credible intervals for age-specific population count for the reconstructed female population of Laos, 1985.

**Age-specific Fertility Rates** The posterior intervals for ASFRs are wider than the prior intervals in all years and ages (Figure 3.12). This is feasible under the statistical model and is a consequence of there being very little information about the age pattern of fertility in the other parameters.

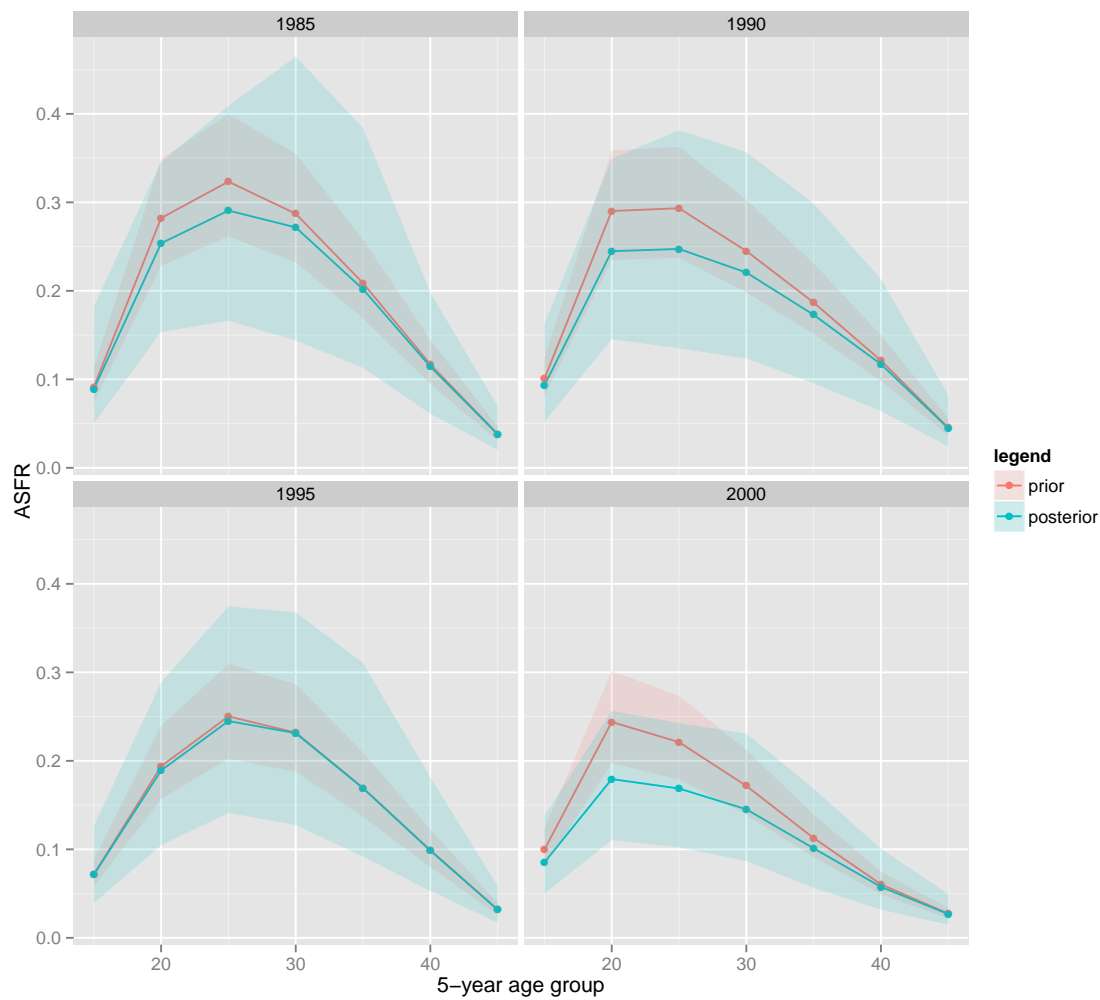


Figure 3.12. Prior and posterior medians and 95 percent credible intervals for age-specific fertility rate (ASFR) for the reconstructed female population of Laos, 1985–2005.

**Age-specific Survival, Mortality and Migration** See Figures 3.13–3.15.

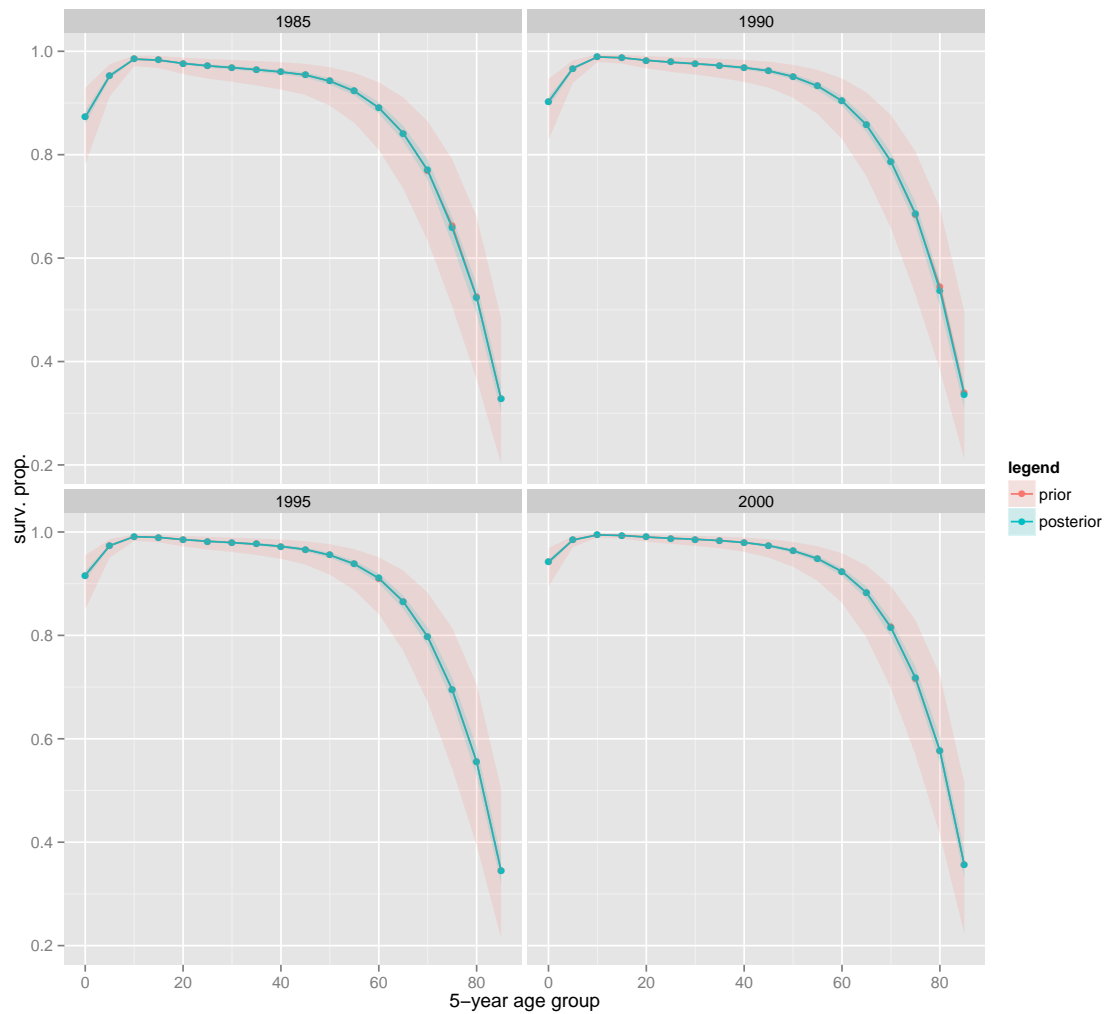


Figure 3.13. Prior and posterior medians and 95 percent credible intervals for age-specific survival proportion for the reconstructed female population of Laos, 1985–2005.

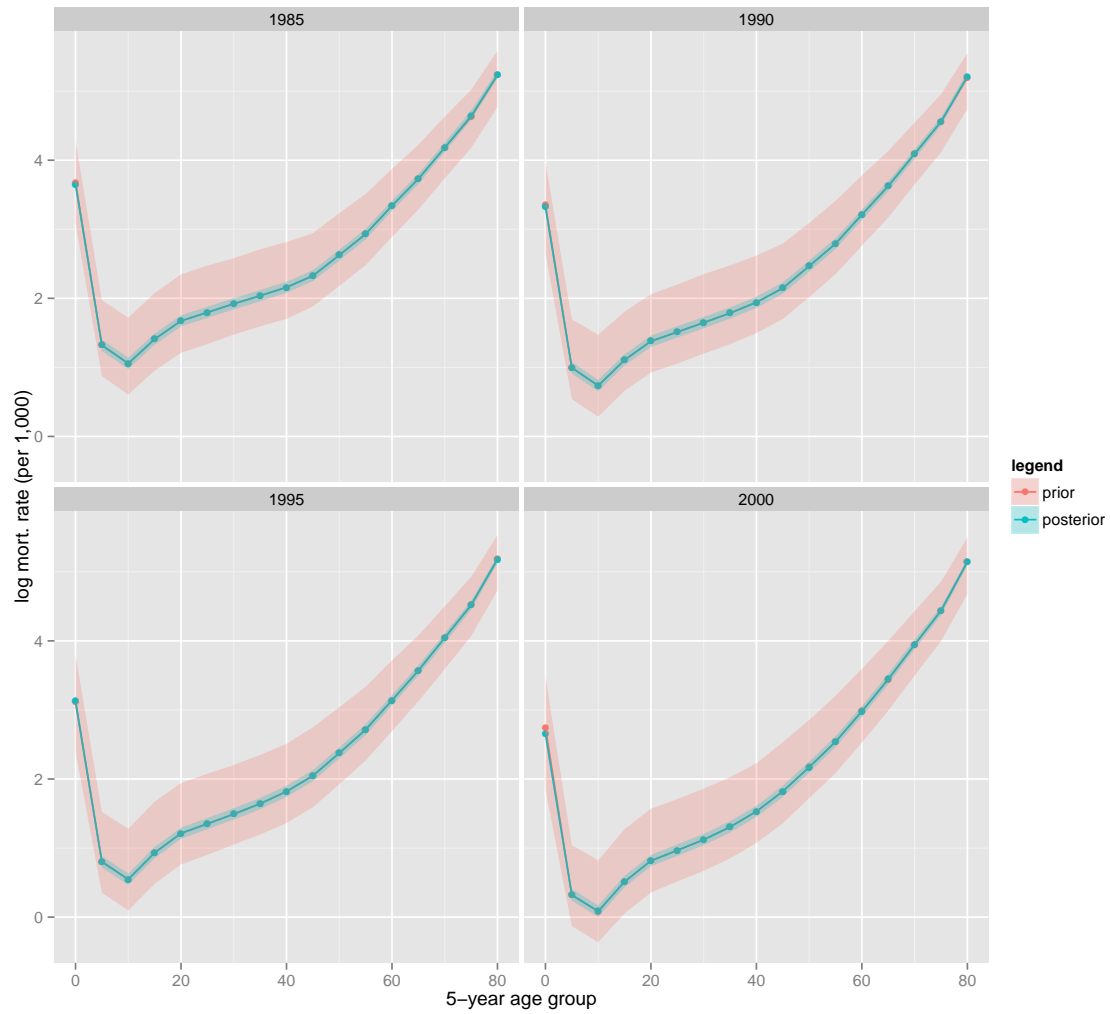
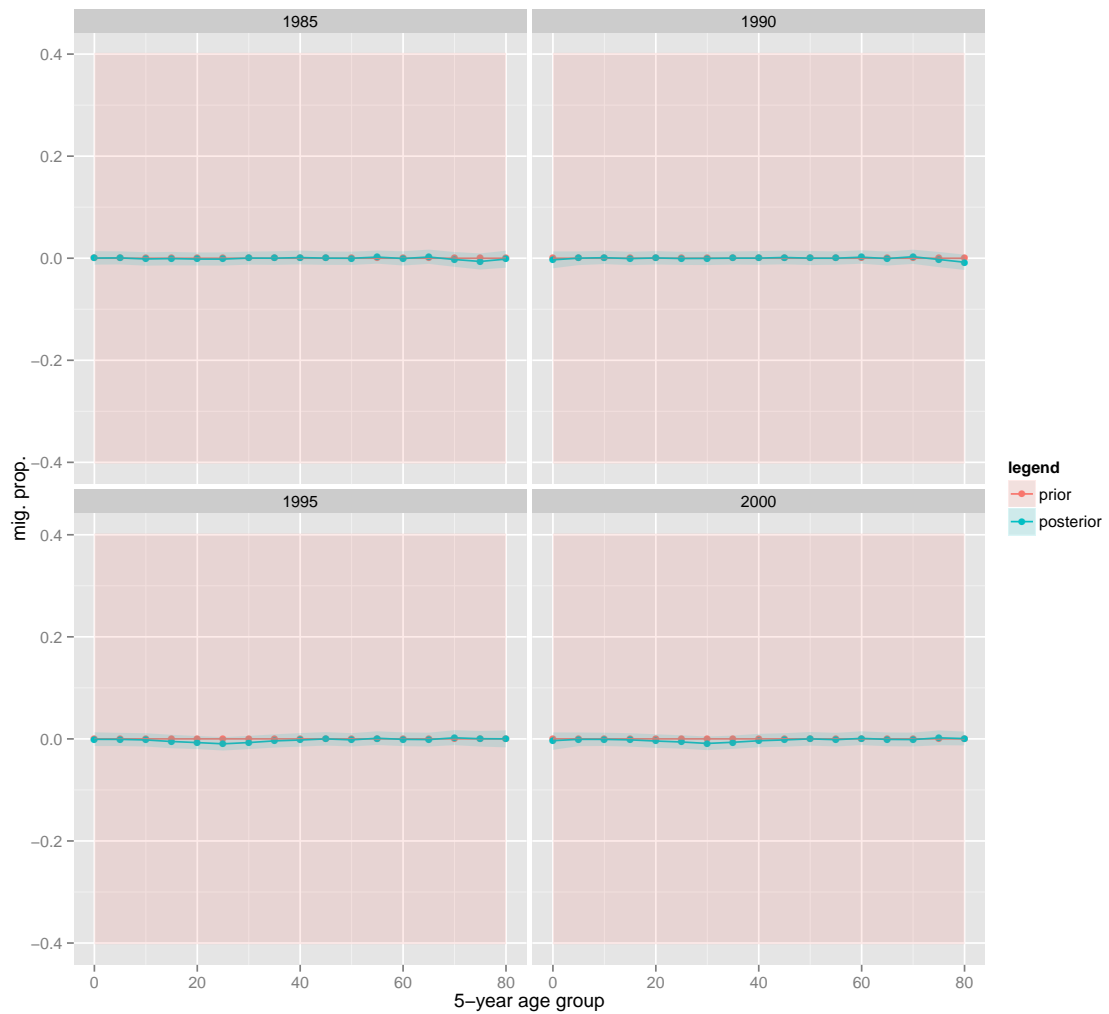


Figure 3.14. Prior and posterior medians and 95 percent credible intervals for age-specific mortality rate for the reconstructed female population of Laos, 1985–2005.



*Figure 3.15.* Prior and posterior medians and 95 percent credible intervals for age-specific migration proportion for the reconstructed female population of Laos, 1985–2005.

### *Prior and Posterior Density Estimates for Standard Deviation Parameters*

Prior and posterior kernel density estimates for the standard deviation parameters  $\sigma_v$ ,  $v = \{n, f, s, g\}$  are shown in Figure 3.16. The posterior for  $\sigma_f$  has a much higher mode than the prior indicating that overall uncertainty about ASFR is higher in the posterior than in the prior. Overall uncertainty for all other parameters has been reduced.

### *3.B.2 Sri Lanka, 1951–2001*

#### *Detailed Description of Results in Section 3.3.2*

**TFR** Fertility changed markedly in Sri Lanka over the fifty years between 1951 and 2000. The posterior estimates suggest that TFR (Figure 3.2a) declined from (5.09, 5.69) births per woman to (2.06, 2.25). The mean half-width of the posterior intervals is 0.206 children.

The initial point estimates of TFR for the periods 1951–1956 and 1956–1961 were 5.01 and 5.03, respectively, much lower than the corresponding medians of the posterior; 5.4 and 5.07 respectively. The WPP 2010 estimate is 5.8 births for both of the periods 1950–1954 and 1955–1959. This suggests that the sources upon which the initial estimates were based are inconsistent with intercensal changes in the number of births. The posterior estimates and those of the WPP 2010 account for this by adjusting the estimates upward over this ten year period.

**Net Number of Migrants** The average annual total net number of migrants (Figure 3.2b) changed from (−6,599, 18,682) during 1951–1955 to (−65,861, 13,077) between 1996 and 2001. The mean half-width of the posterior 95 percent intervals is 132,816.

The results indicate net out-migration from 1971 to 2001 but there is not enough information to determine the direction of the flow between 1951 and 1970. There is close agreement between my results and those of Luther et al. (1987). They estimated net migration from intercensal changes after accounting for changes due to fertility and mortality; their method does not provide an estimate of uncertainty.



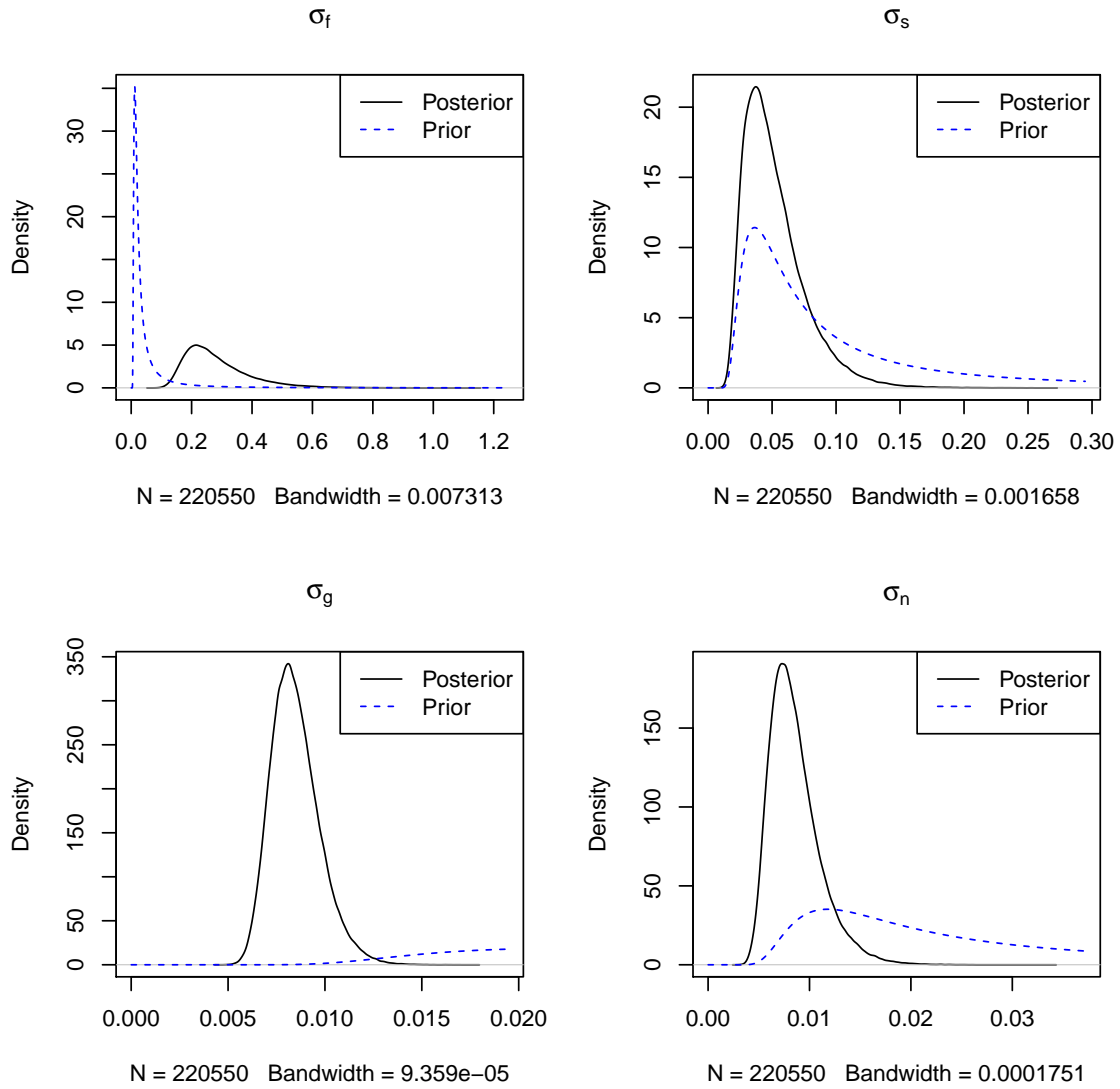


Figure 3.16. Prior and posterior densities of model standard deviation parameters,  $\sigma_v$ ,  $v = \{n, f, s, g\}$ . Posterior densities are kernel density estimates for the reconstructed female population of Laos, 1985–2005.

**Life Expectancy at Birth** Female life expectancy at birth (Figure 3.2c) increased between 1951 and 2001, from (55, 57.7) years to (72.8, 73.9). The mean half-width of the posterior 95 percent credible intervals is 0.815 years. My results are in close agreement with WPP 2010 estimates in all five-year periods except 1996–2000. The WPP 2010 estimate for 1995–1999 is 72.7, 0.3 years below the lower bound of the 95 percent interval for 1996–2000.

**Under-five Mortality** U5MR mortality (Figure 3.2d) decreased from (134, 170) deaths per 1,000 live births over 1951–1955 to (17.9, 23.7) over 1996–2001. The mean half-widths of the posterior intervals is 9.11. The WPP 2010 estimate of under five mortality over 1995–1999 is similar at 21 deaths per 1,000 live births.

#### *Additional Results*

**Population Counts** Posterior estimates of the size of the Sri Lanka female population are given in Table 3.2. Age-specific counts for 1951, the baseline year, are in Figure 3.17.

**Age-specific Fertility, Mortality, Survival and Migration** See Figures 3.18–3.21.

#### *Prior and Posterior Density Estimates for Standard Deviation Parameters*

Prior and posterior kernel density estimates for the variance parameters  $\sigma_v$ ,  $v = \{n, f, s, g\}$  are shown in Figure 3.22. The posterior for  $\sigma_f$  has a much higher mode than the prior indicating that overall uncertainty about ASFR is higher in the posterior than in the prior. Overall uncertainty about survival proportions also increased slightly in the posterior. It decreased for all other parameters.

#### *3.B.3 New Zealand, 1961–2006*

##### *Detailed Description of Results in Section 3.3.3*

**TFR** Fertility declined steeply in New Zealand. The posterior estimates for TFR over the 1961–1965 period (Figure 3.3a) are (3.77, 3.93) births per woman, declining to (1.93, 1.99) over 2001–2006. The mean half-width of the 95 percent posterior credible intervals is 0.04 children. My estimates are broadly similar to those in WPP 2010.

*Table 3.2.* Initial estimates and posterior medians and 95 percent credible intervals for population count for the reconstructed female population of Sri Lanka, 1951–2006, in millions.

Year	Posterior Percentile			Init. Est.
	2.5th	50th	97.5th	
1951	3.74	3.81	3.88	
1953				3.99
1956	4.12	4.27	4.42	
1961	4.73	4.88	5.04	
1963				5.13
1966	5.32	5.52	5.73	
1971	6.10	6.21	6.33	6.22
1976	6.53	6.83	7.15	
1981	7.37	7.51	7.65	7.51
1986	7.70	8.14	8.60	
1991	8.13	8.67	9.23	
1996	8.63	9.12	9.63	
2001	9.33	9.51	9.70	9.50
2006	9.48	10.16	10.87	

**Net Number of Migrants** I estimate that the total net number of migrants (Figure 3.3b) changed from (14,223, 35,570) during 1961–1965 to (53,092, 84,268) during 2001–2006. The mean half-width of the posterior 95 percent intervals is 12,836. This is much more narrow than the posterior intervals for both Laos and Sri Lanka, reflecting the relatively reliable migration information used to form the initial estimates.

**Life Expectancy at Birth** Female life expectancy at birth (Figure 3.3c) increased between 1961 and 2001, from (73.82, 74.16) years to (81.44, 81.85). The mean half-width of the posterior 95 percent credible intervals is 0.19 years. My results are broadly comparable with those in WPP 2010.

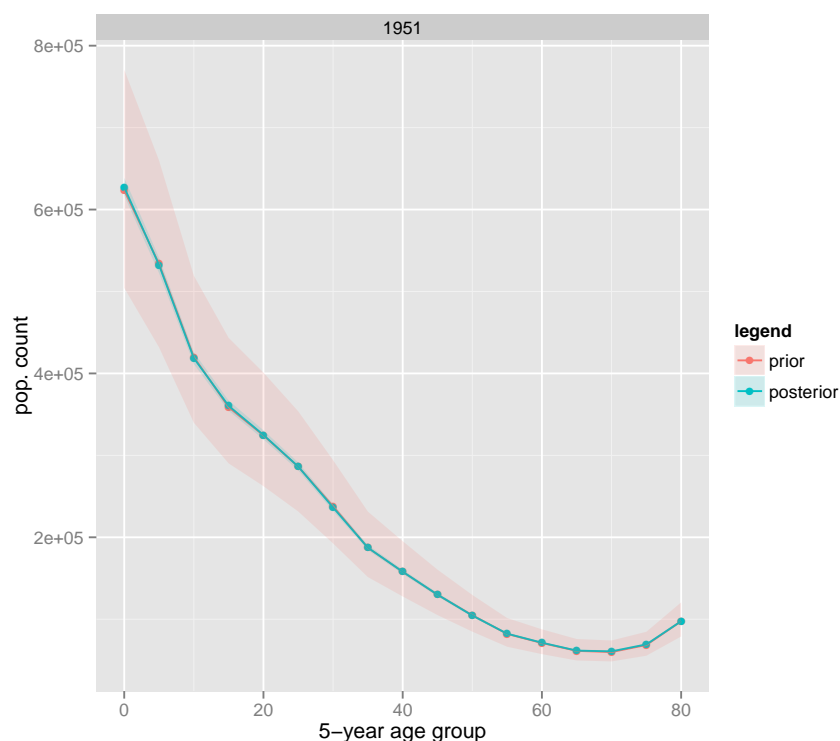


Figure 3.17. Prior and posterior medians and 95 percent credible intervals for age-specific population count for the reconstructed female population of Sri Lanka, 1951.

**Under-five Mortality** U5MR (Figure 3.3d) decreased from (19.9, 22) deaths per 1,000 live births over 1961–1965 to (6.88, 7.59) over 1996–2001. The mean half-widths of the posterior intervals is 0.633. The WPP 2010 estimates of under five mortality over 1995–1999, and 2000–2005 (7 and 6 deaths per 1,000 live births, respectively) are lower. However, at such small numbers it is possible that some of this discrepancy is due to rounding; the WPP 2010 results appear to be rounded to the nearest whole number.

#### *Additional Results*

**Population Counts** Posterior estimates of the size of the New Zealand female population are given in Table 3.3. Age-specific population counts in the baseline year are in Figure 3.23.

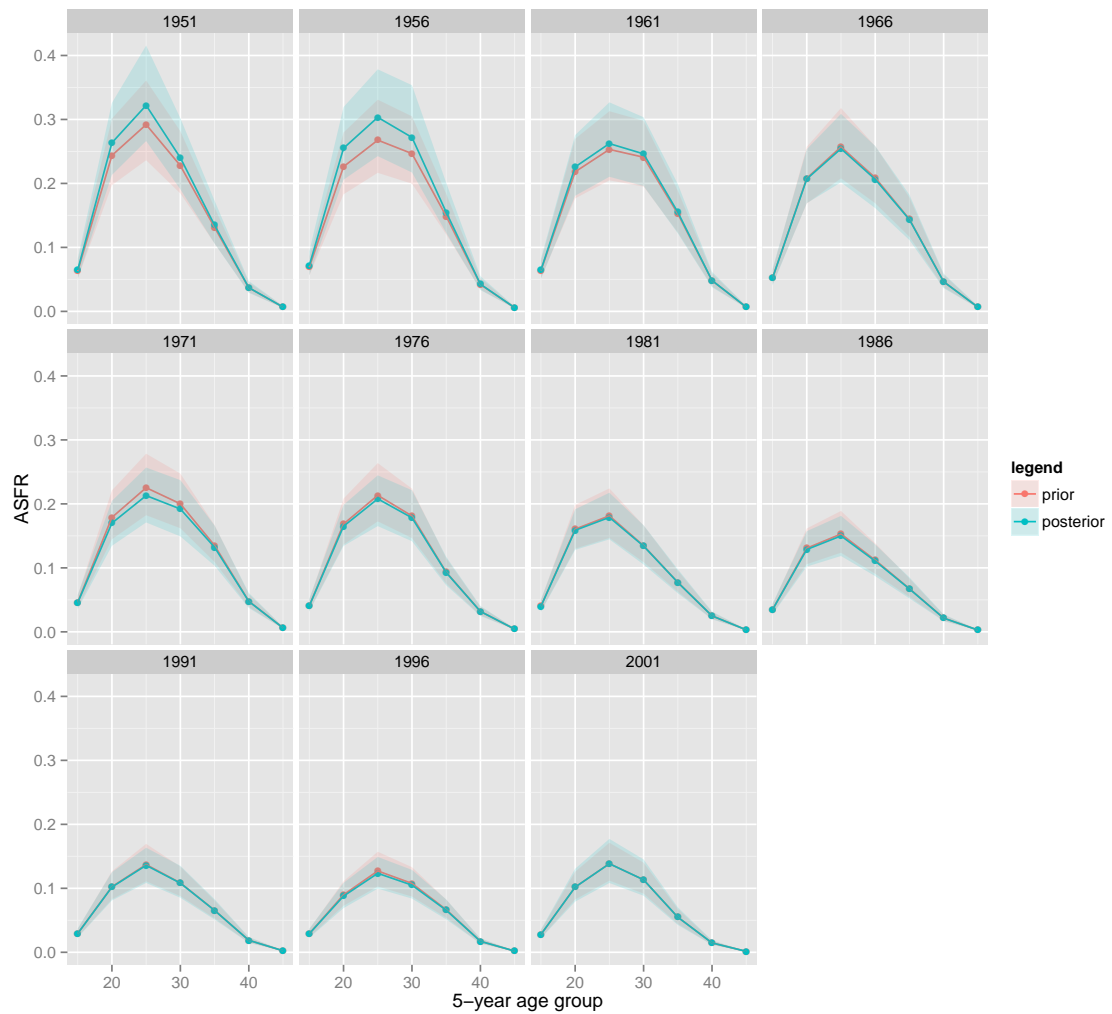
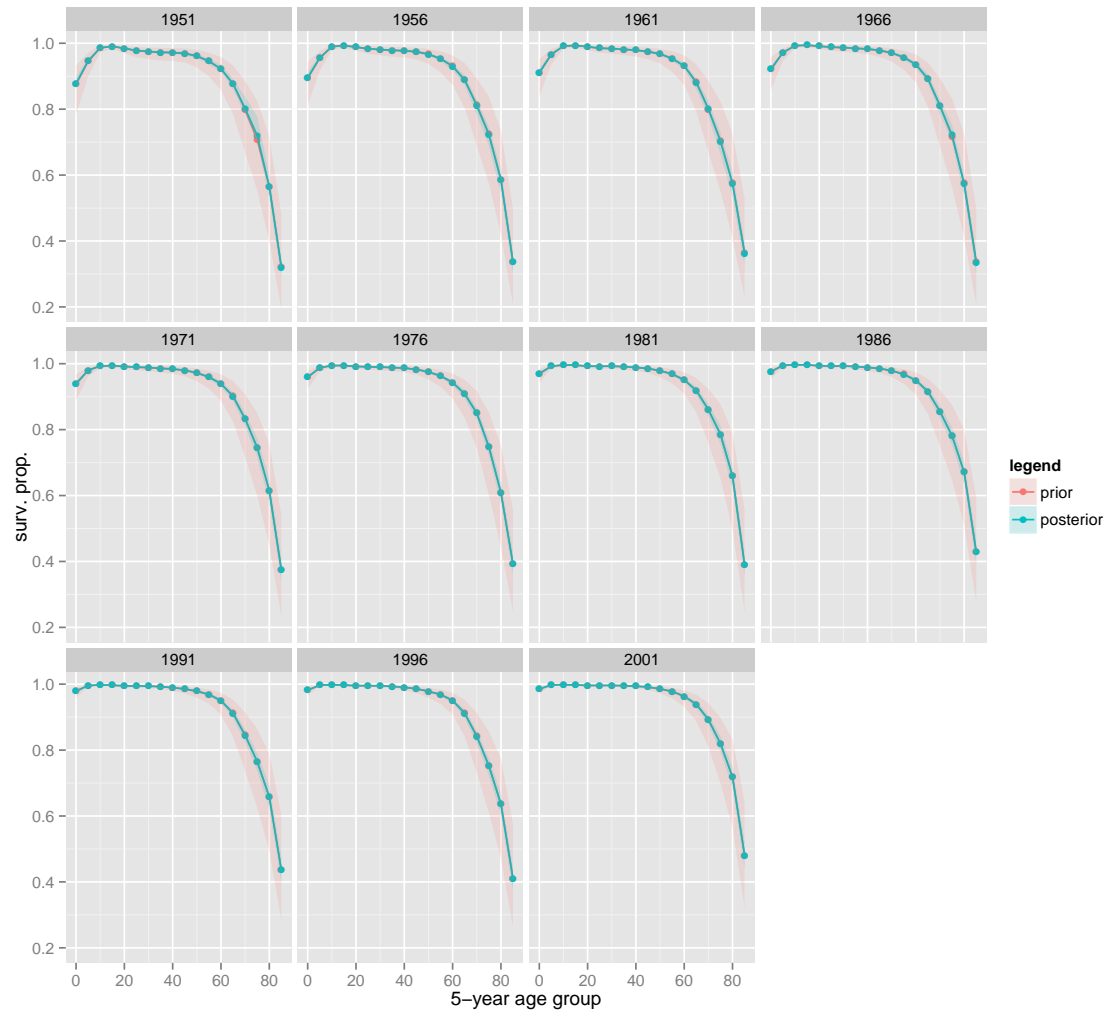
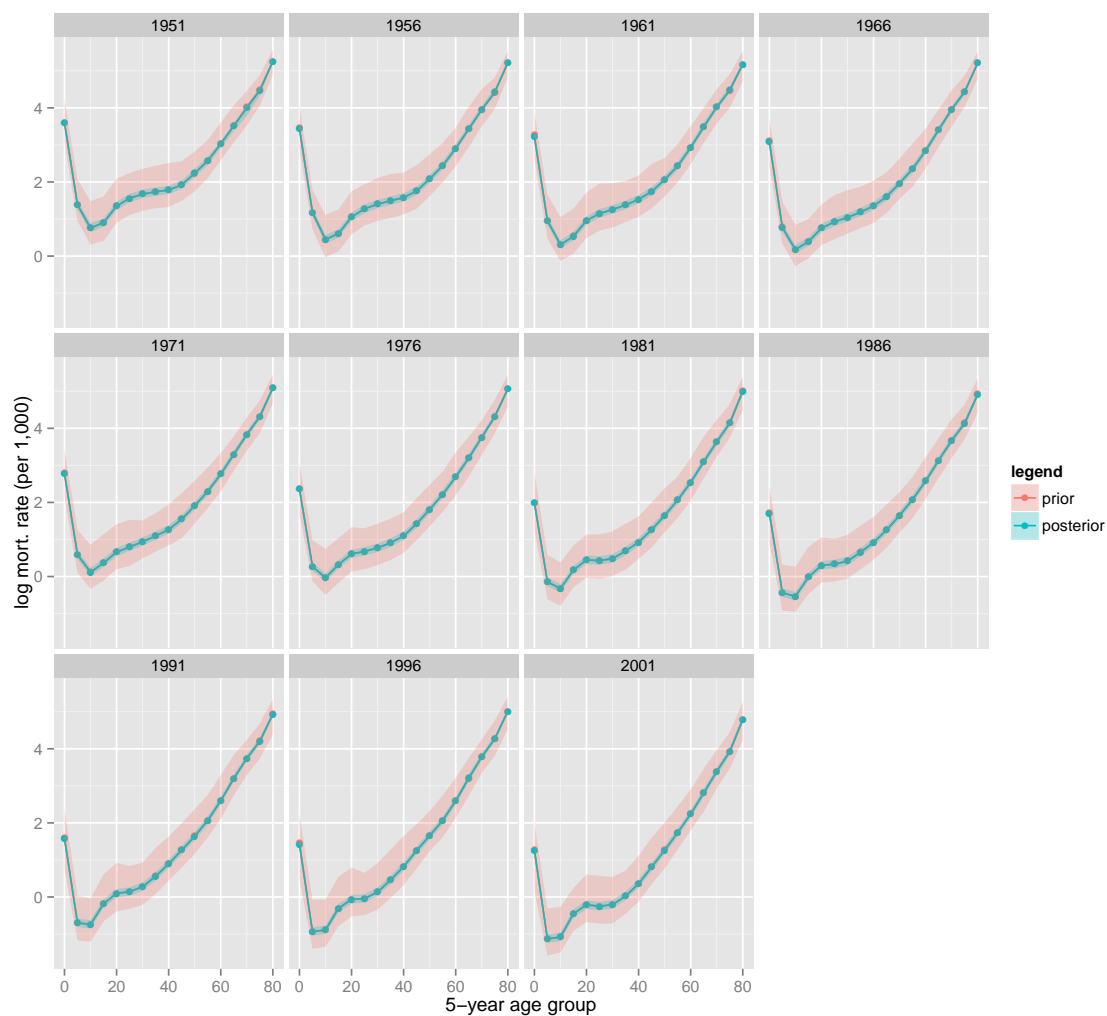


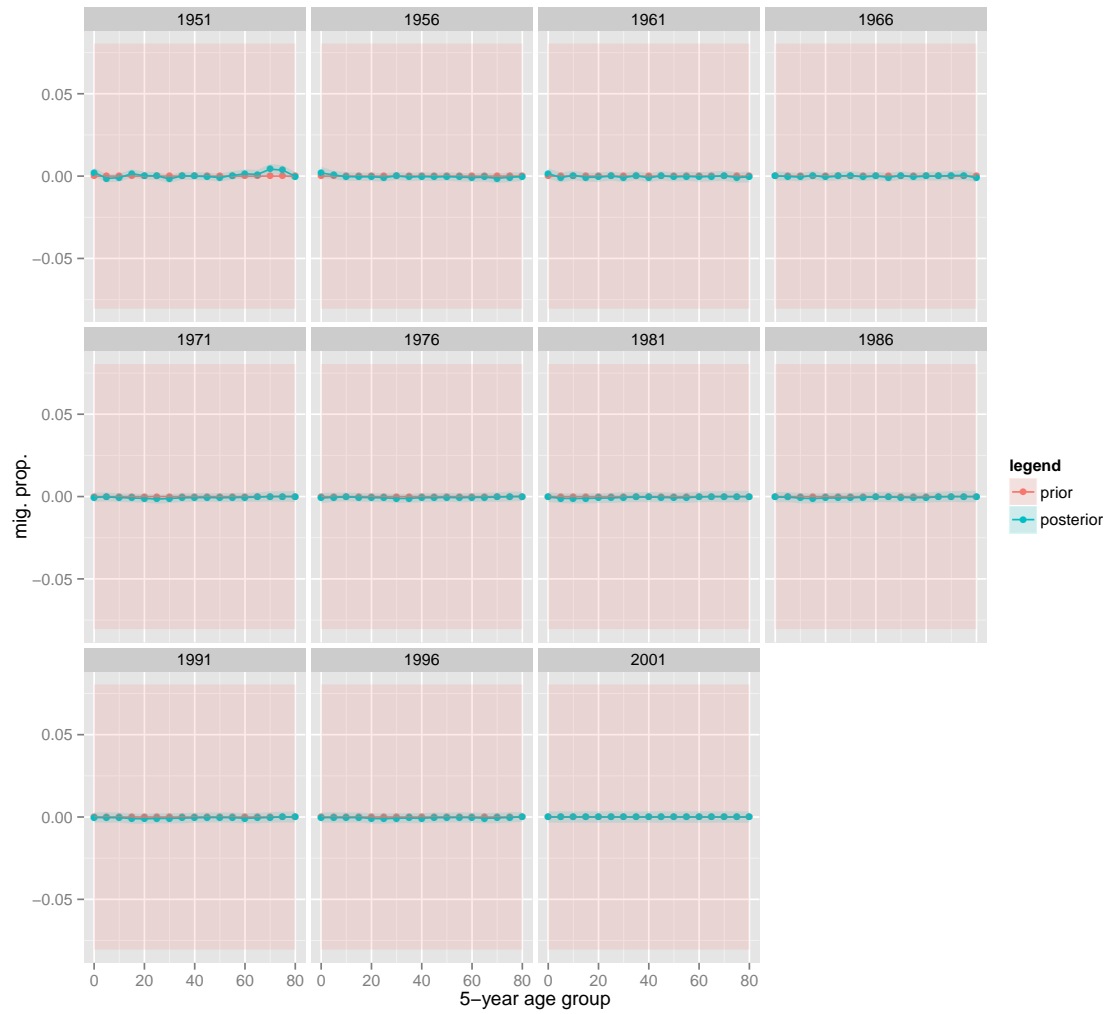
Figure 3.18. Prior and posterior medians and 95 percent credible intervals for age-specific fertility rate (ASFR) for the reconstructed female population of Sri Lanka, 1951–2001.



*Figure 3.19.* Prior and posterior medians and 95 percent credible intervals for age-specific survival proportion for the reconstructed female population of Sri Lanka, 1951–2001.



*Figure 3.20.* Prior and posterior medians and 95 percent credible intervals for age-specific mortality rate for the reconstructed female population of Sri Lanka, 1951–2001.



*Figure 3.21.* Prior and posterior medians and 95 percent credible intervals for age-specific migration proportion for the reconstructed female population of Sri Lanka, 1951–2001.



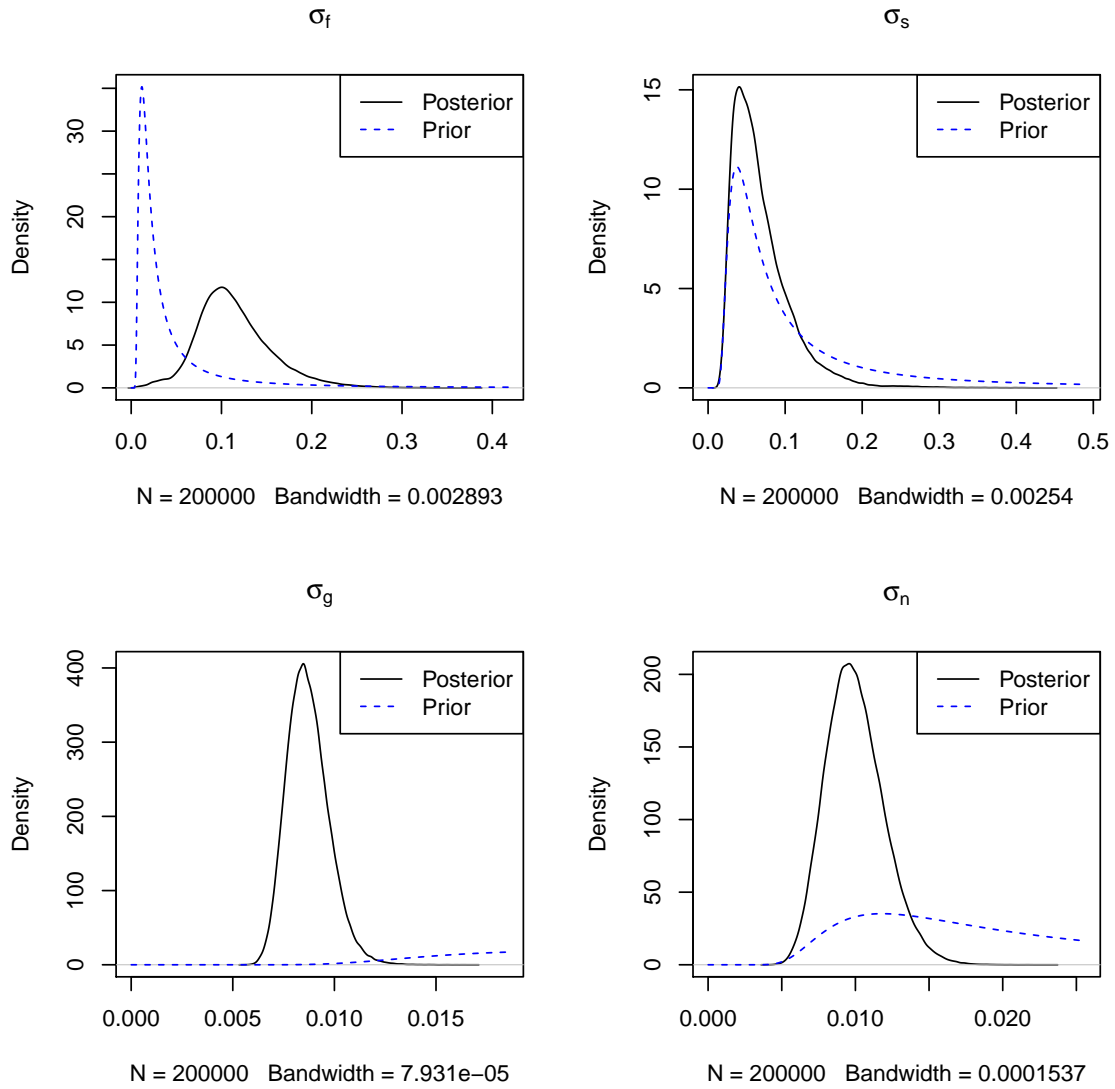


Figure 3.22. Prior and posterior densities of model standard deviation parameters,  $\sigma_v$ ,  $v = \{n, f, s, g\}$ . Posterior densities are kernel density estimates for the reconstructed female population of Sri Lanka, 1951–2001.

*Table 3.3.* Initial estimates and posterior medians and 95 percent credible intervals for population count for the reconstructed female population of New Zealand, 1961–2006, in millions.

Year	Posterior Percentile			Init. Est.
	2.5th	50th	97.5th	
1961	1.18	1.20	1.23	
1966	1.31	1.33	1.36	1.33
1971	1.41	1.44	1.46	1.44
1976	1.53	1.56	1.59	1.55
1981	1.56	1.59	1.63	1.59
1986	1.63	1.67	1.70	1.66
1991	1.72	1.75	1.78	1.75
1996	1.85	1.88	1.92	1.88
2001	1.95	1.99	2.03	1.99
2006	2.08	2.13	2.17	2.13

**Age-specific Fertility, Mortality, Survival and Migration** See Figures 3.24–3.27.

#### *Prior and Posterior Density Estimates for Standard Deviation Parameters*

Prior and posterior kernel density estimates for the variance parameters  $\sigma_v$ ,  $v = \{n, f, s, g\}$  are shown in Figure 3.28. The posterior for  $\sigma_n$  has a higher mode than the prior indicating that overall uncertainty about population counts is higher in the posterior than in the prior. Overall uncertainty about survival proportions also increased slightly in the posterior. It decreased for all other parameters.

#### **Appendix 3.C Sensitivity to Elicited Relative Errors: Laos**

A sensitivity analysis was performed to study the effect of different elicited relative errors on the results for the reconstruction of the female population of Laos, 1985–2005. The reconstruction was re-run three times, each time using elicited relative errors twice as large

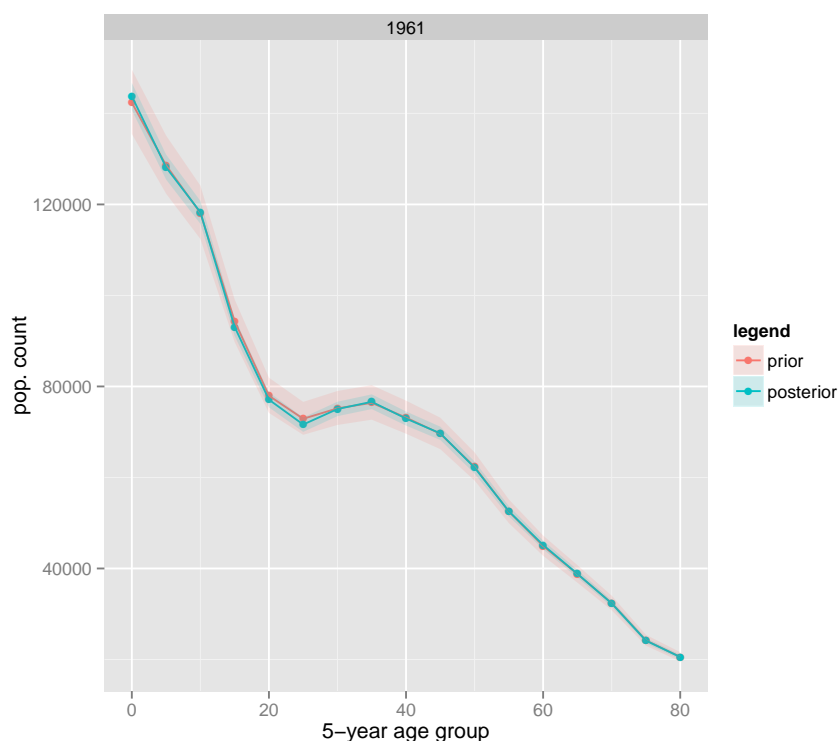


Figure 3.23. Prior and posterior medians and 95 percent credible intervals for age-specific population count for the reconstructed female population of New Zealand, 1961.

as those used in Section 3.3.1 for each of the following parameters, one parameter per re-run: ASFR, age-specific survival proportion and age-specific migration proportion.

### 3.C.1 Age-specific Fertility Rate

Figures 3.29 and 3.30 compare the ASFR and TFR results reported in Sections 3.B.1 and 3.3.1 with those obtained using an elicited relative error for ASFR of 20 percent. There is a difference in the width of the 95 percent credible intervals for these parameters, but it is slight. There is no discernible difference for age-specific survival and migration proportions, and  $e_0$  (not shown). This suggests a low degree of sensitivity to the elicited relative errors for ASFR in the range 10–20 percent.

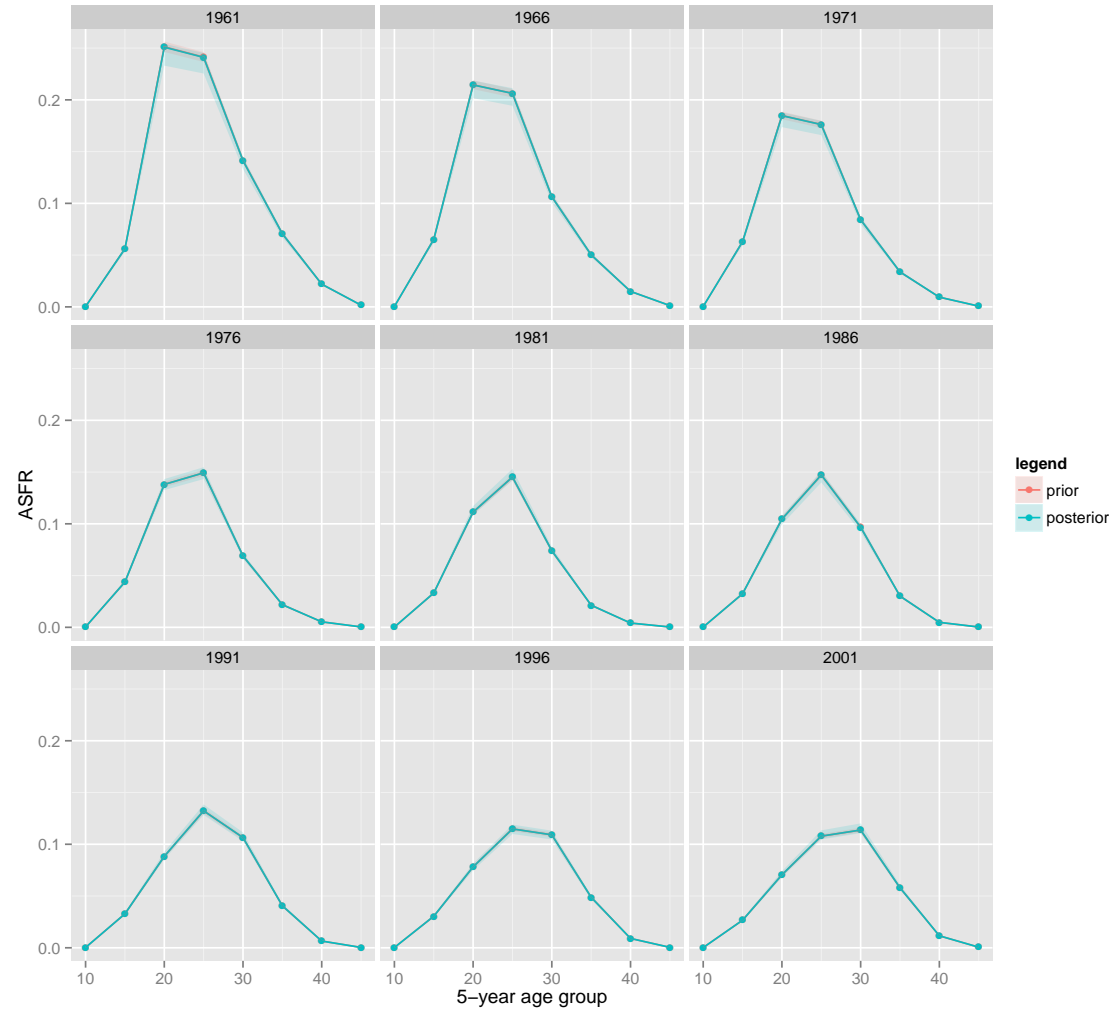
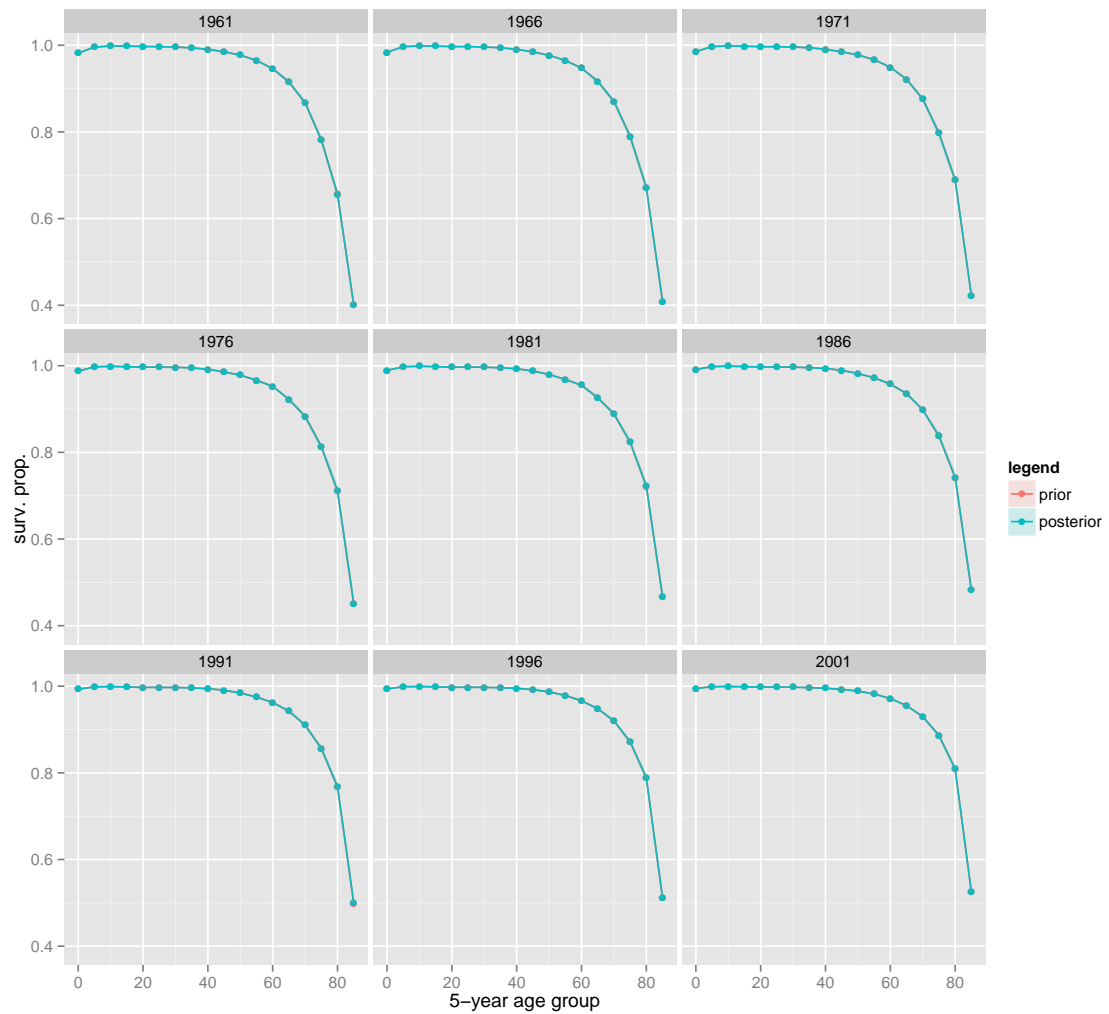
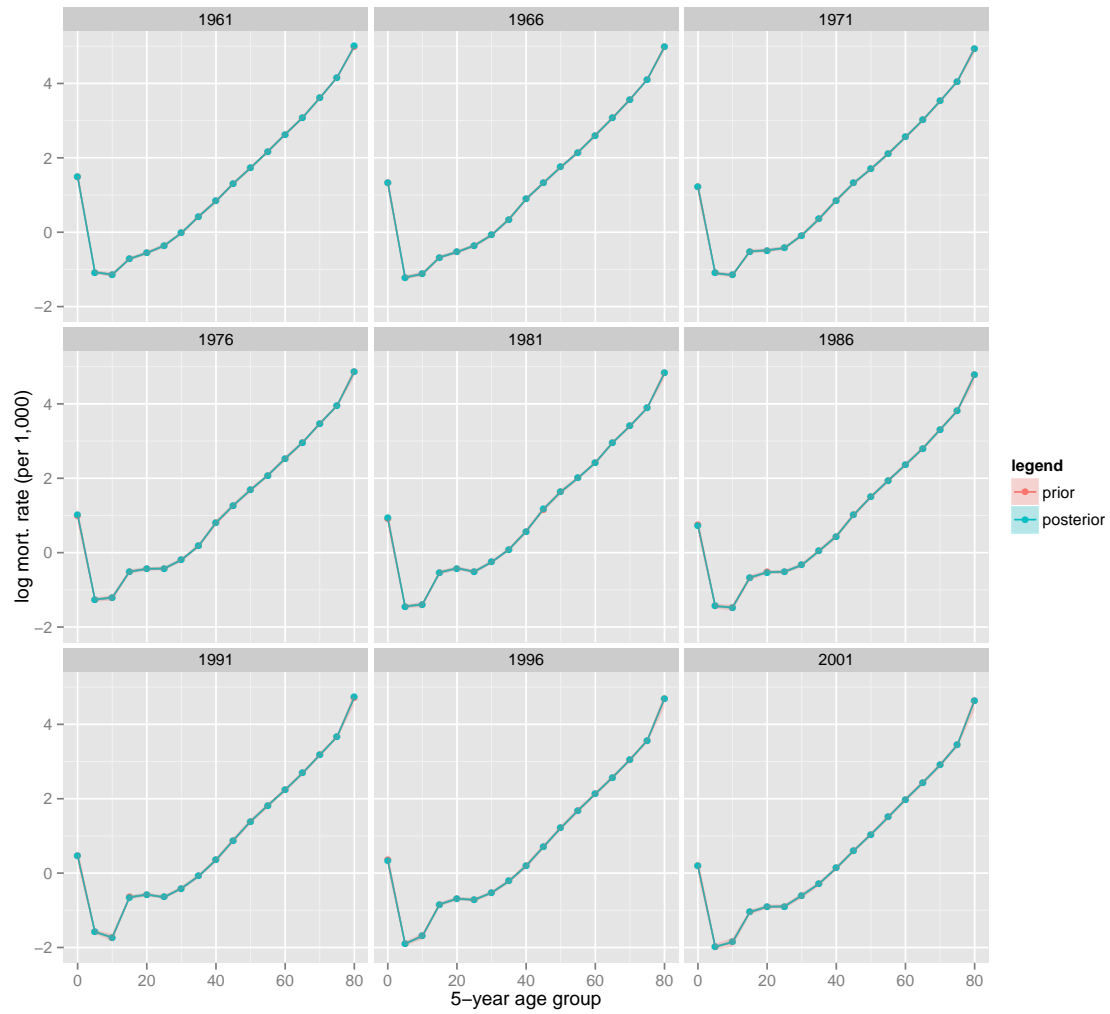


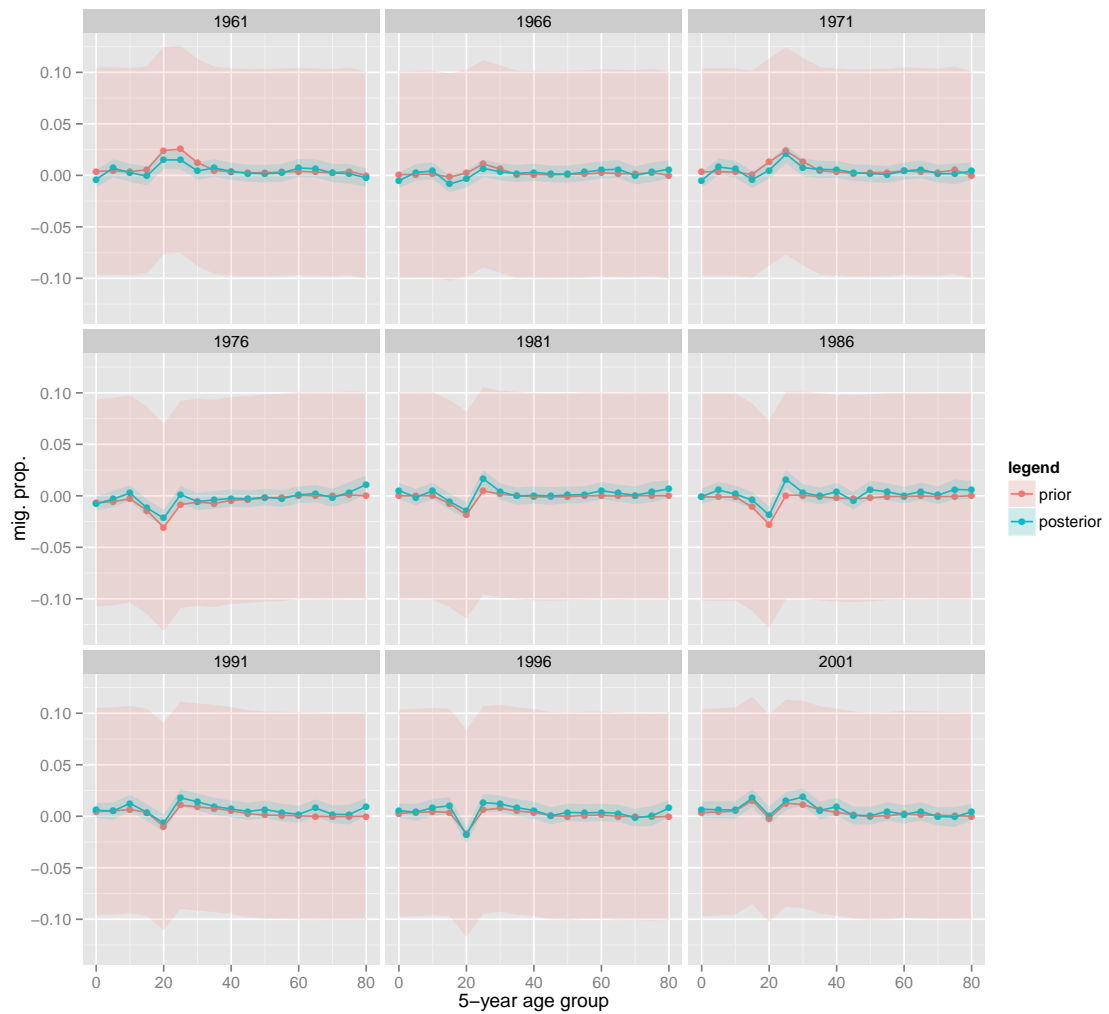
Figure 3.24. Prior and posterior medians and 95 percent credible intervals for age-specific fertility rate (ASFR) for the reconstructed female population of New Zealand, 1961–2006.



*Figure 3.25.* Prior and posterior medians and 95 percent credible intervals for age-specific survival proportion for the reconstructed female population of New Zealand, 1961–2006.



*Figure 3.26.* Prior and posterior medians and 95 percent credible intervals for age-specific mortality rate for the reconstructed female population of New Zealand, 1961–2006.



*Figure 3.27.* Prior and posterior medians and 95 percent credible intervals for age-specific migration proportion for the reconstructed female population of New Zealand, 1961–2006.

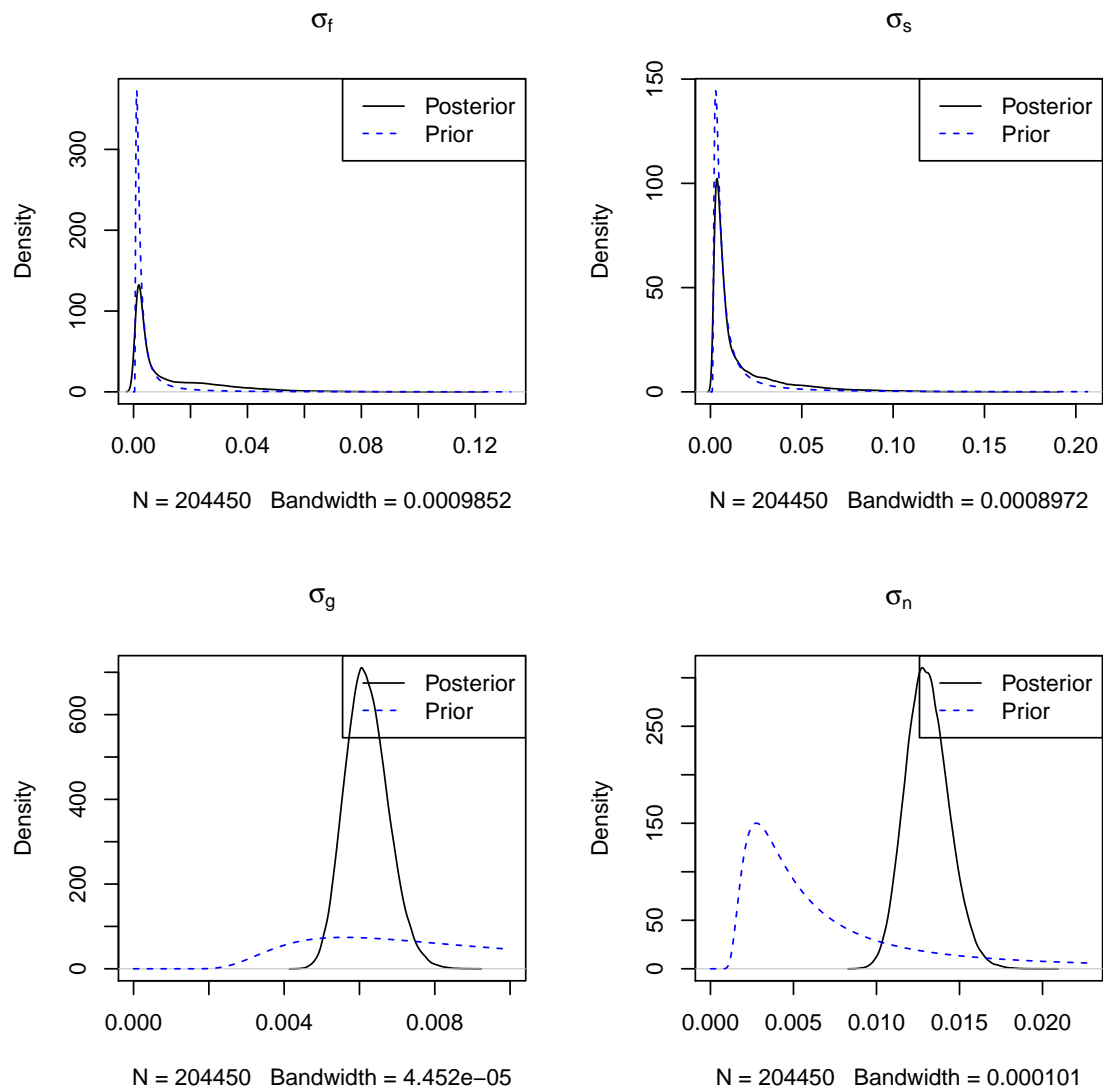
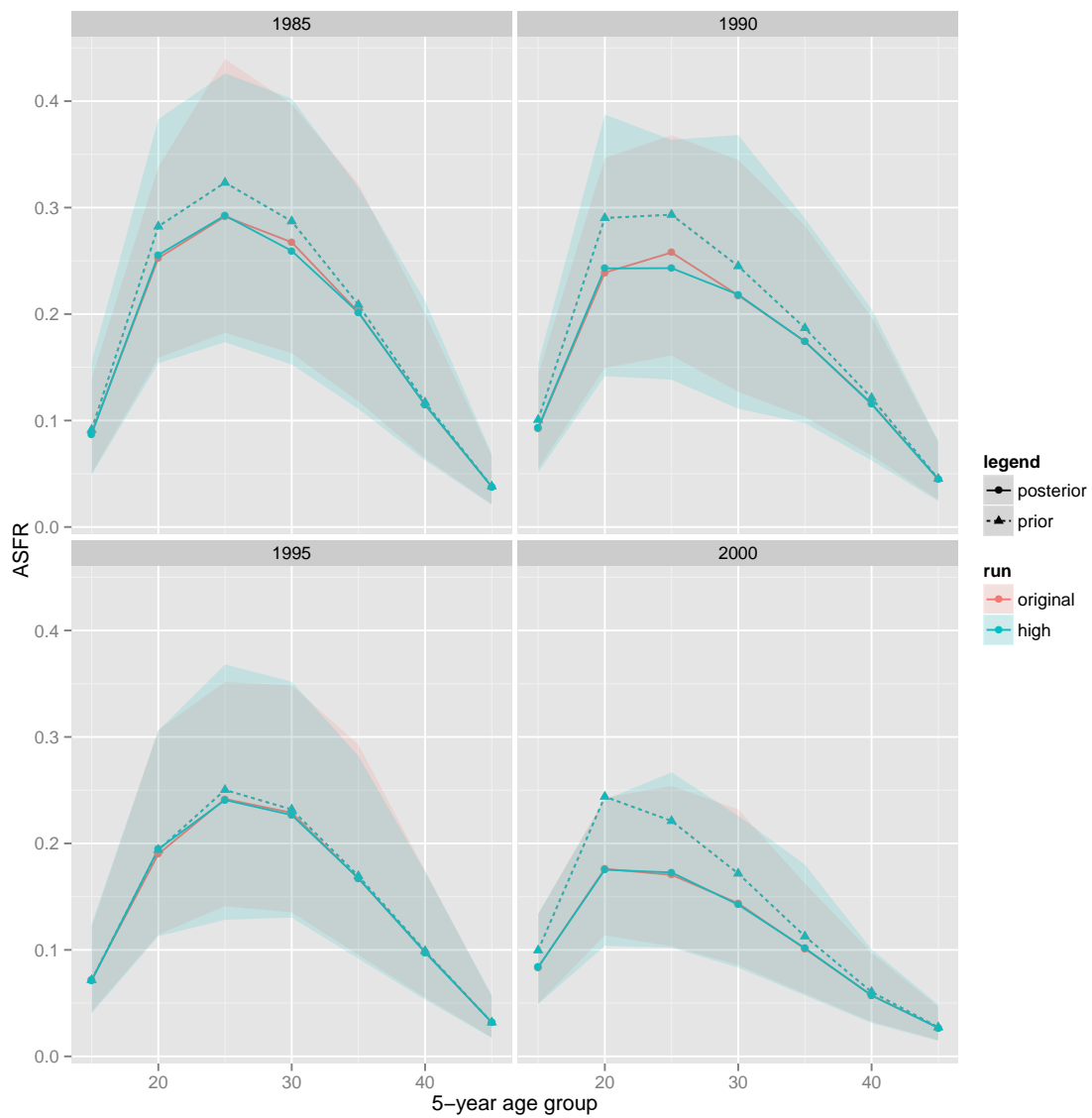


Figure 3.28. Prior and posterior densities of model standard deviation parameters,  $\sigma_v$ ,  $v = \{n, f, s, g\}$ . Posterior densities are kernel density estimates for the reconstructed female population of New Zealand, 1961–2006.





*Figure 3.29.* Prior and posterior medians and 95 percent credible intervals for age-specific fertility rate (ASFR) with elicited relative errors of 10 percent (“original”) and 20 percent (“high”) for ASFR, for the reconstructed female population of Laos, 1985–2005.

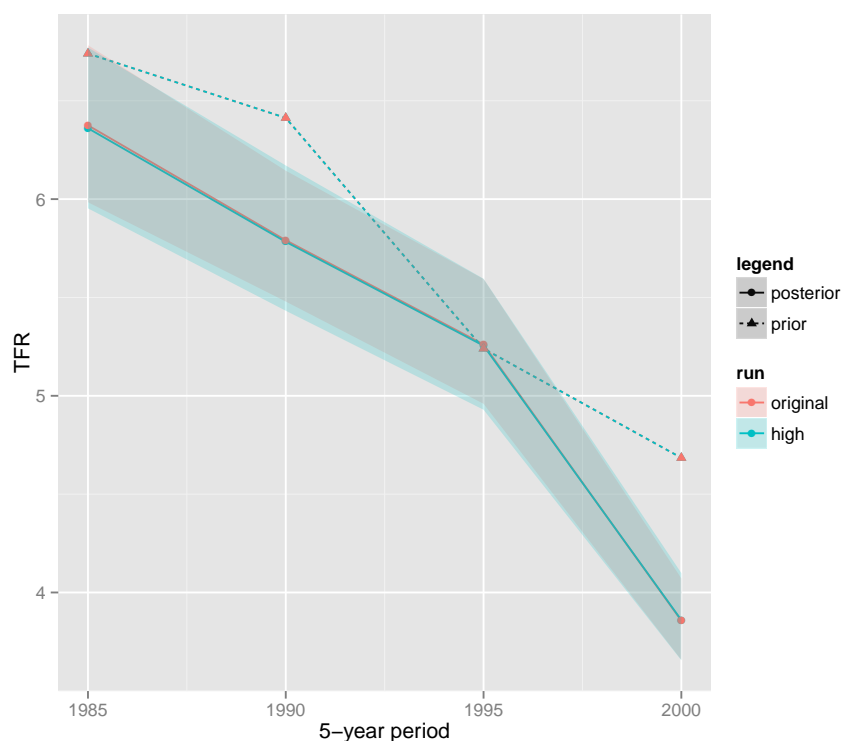


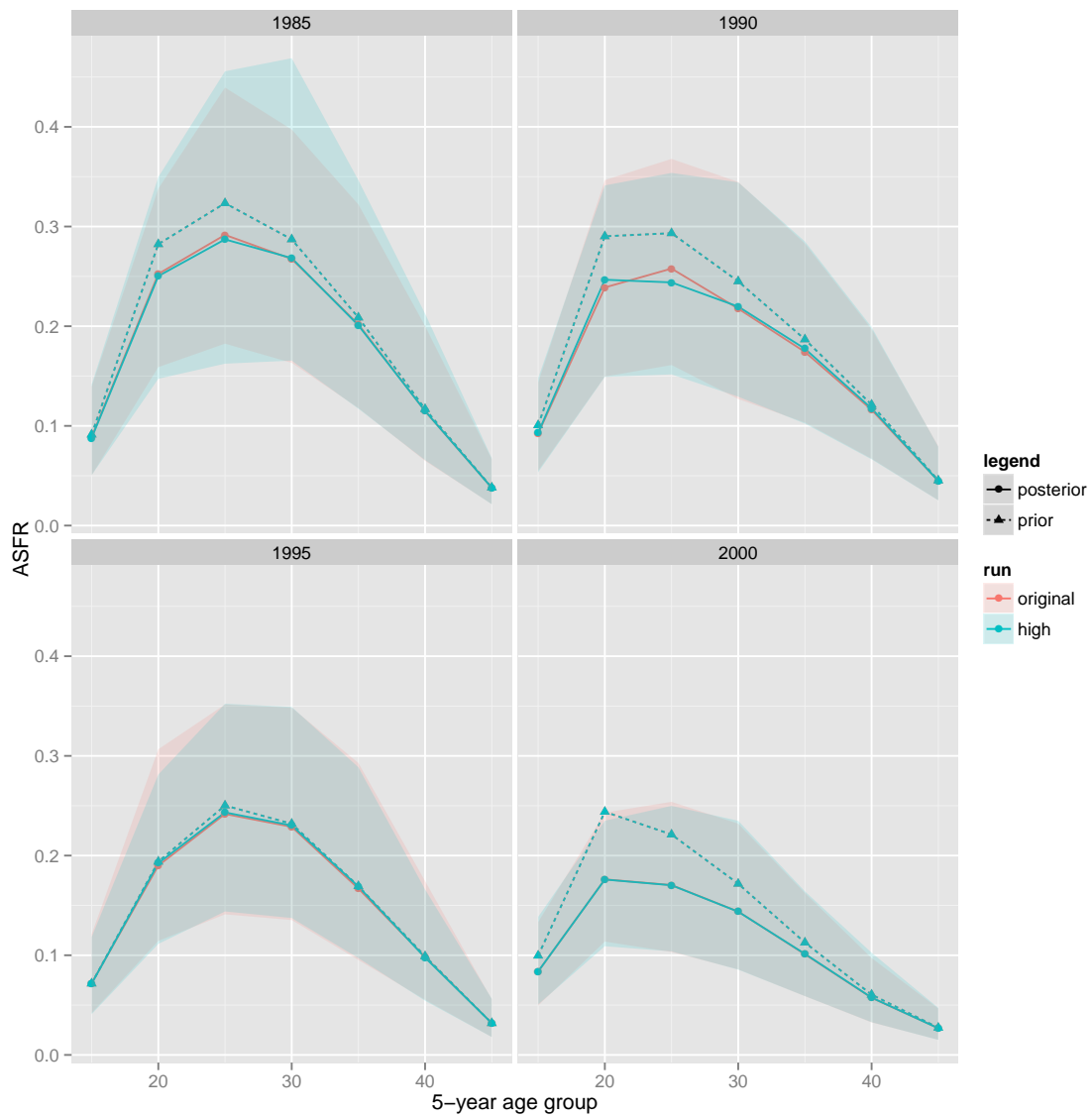
Figure 3.30. Prior and posterior medians and 95 percent credible intervals for total fertility rate (TFR) with elicited relative errors of 10 percent (“original”) and 20 percent (“high”) for age-specific fertility rate (ASFR), for the reconstructed female population of Laos, 1985–2005.

### 3.C.2 Age-specific Survival Proportion

Figures 3.31–3.34 compare the ASFR, TFR and  $e_0$  results reported in Sections 3.B.1 and 3.3.1 with those obtained using an elicited relative error for age-specific survival proportion of 20 percent. The larger elicited relative errors resulted in a small increase in the width of the credible intervals for fertility and survival parameters. There is no discernible difference for age-specific migration proportions (not shown).

### 3.C.3 Age-specific Migration Proportion

Results for ASFR, TFR and age-specific migration proportion under elicited relative errors for migration proportion of 20 and 40 percent are compared in Figures 3.35–3.37. There is



*Figure 3.31.* Prior and posterior medians and 95 percent credible intervals for age-specific fertility rate (ASFR) with elicited relative errors of 10 percent (“original”) and 20 percent (“high”) for age-specific survival proportion, for the reconstructed female population of Laos, 1985–2005.

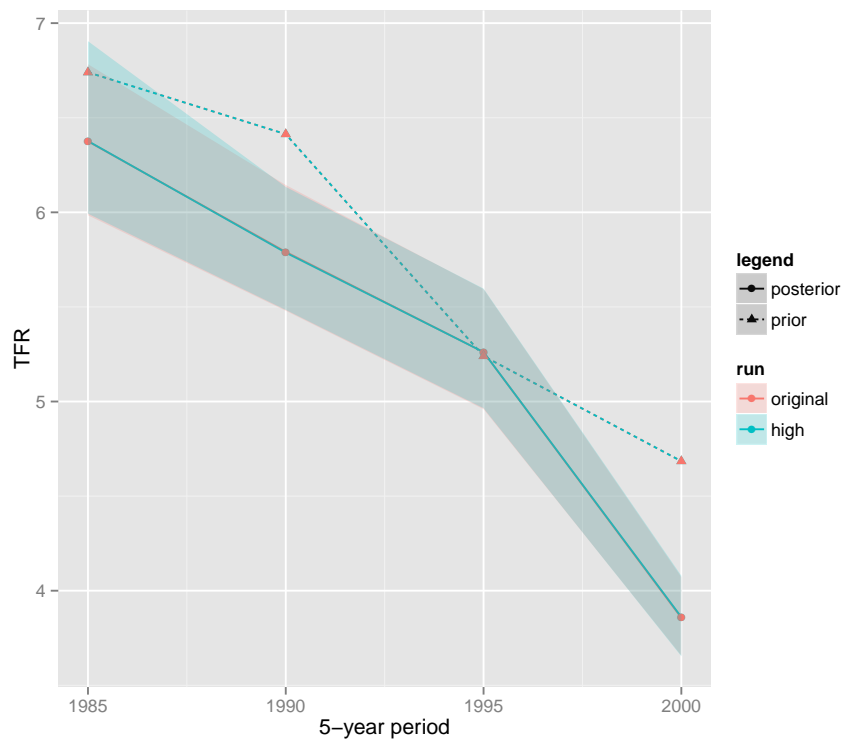
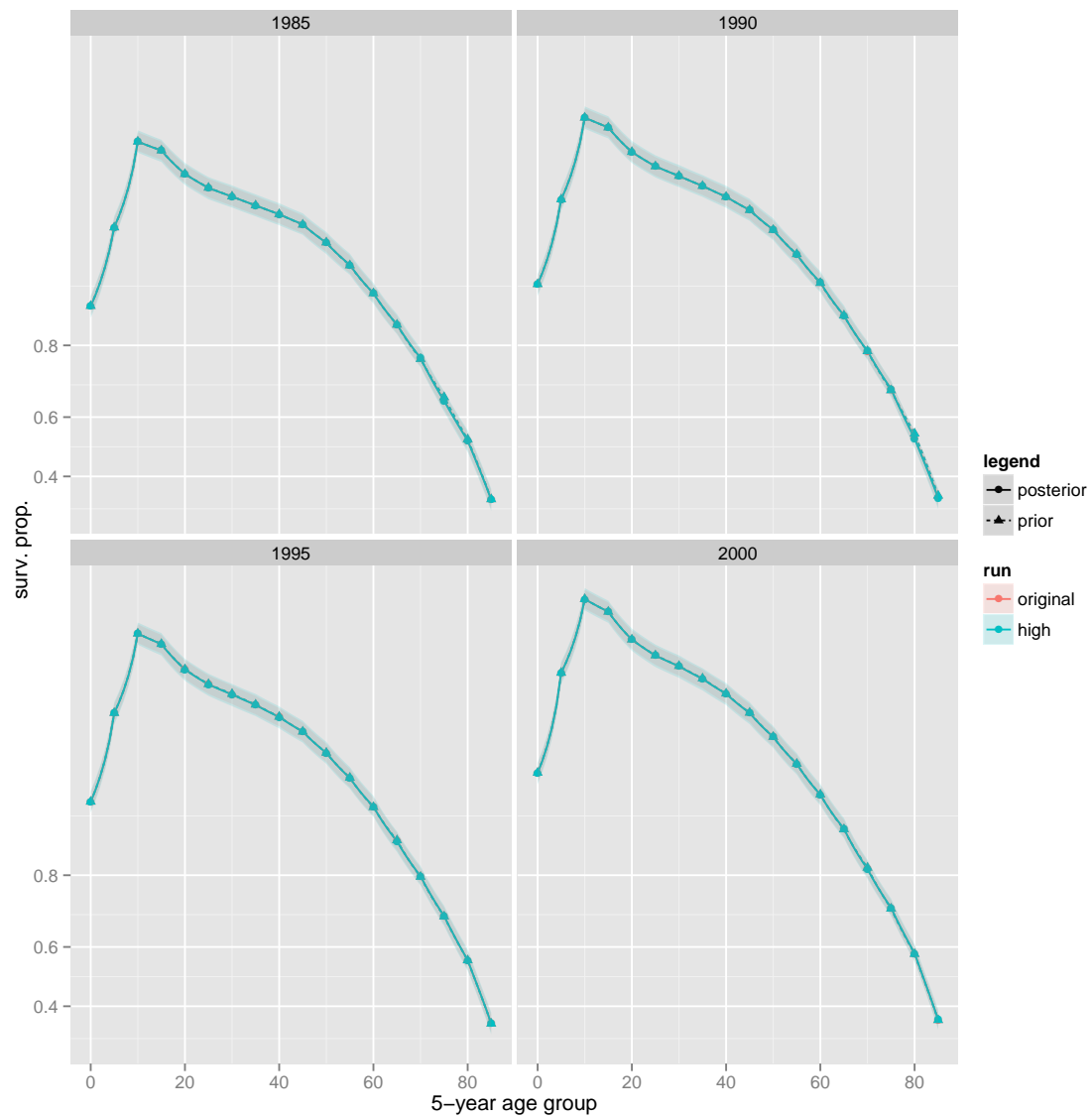


Figure 3.32. Prior and posterior medians and 95 percent credible intervals for total fertility rate (TFR) with elicited relative errors of 10 percent (“original”) and 20 percent (“high”) for age-specific survival proportion, for the reconstructed female population of Laos, 1985–2005.

an increase in the width of the credible intervals, but it is small relative to the change in elicited relative error. There is no discernible difference for the mortality parameters (not shown).

### 3.C.4 Discussion

Doubling the elicited relative errors for ASFR, age-specific survival, and age-specific migration proportions used in the reconstruction of the female population of Laos did result in an increase in the widths of credible intervals for these parameters. In each case, the credible intervals for the parameter with increased elicited relative error became wider. Moreover, the credible intervals for ASFR and TFR became wider, no matter which elicited relative



*Figure 3.33.* Prior and posterior medians and 95 percent credible intervals for age-specific survival proportion with elicited relative errors of 10 percent (“original”) and 20 percent (“high”) for age-specific survival proportion, for the reconstructed female population of Laos, 1985–2005. The vertical axis has been transformed to the logit scale.

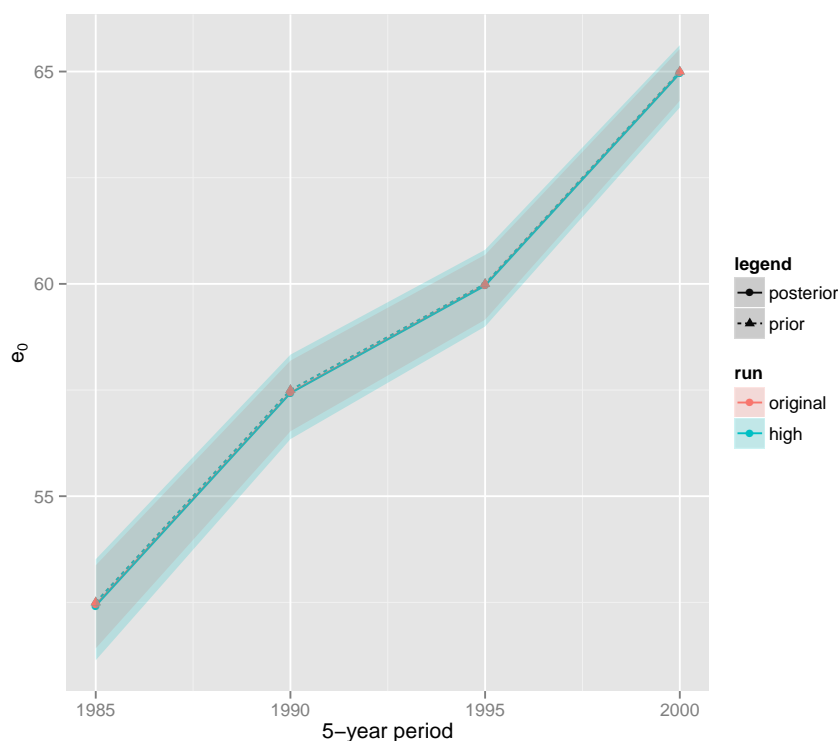
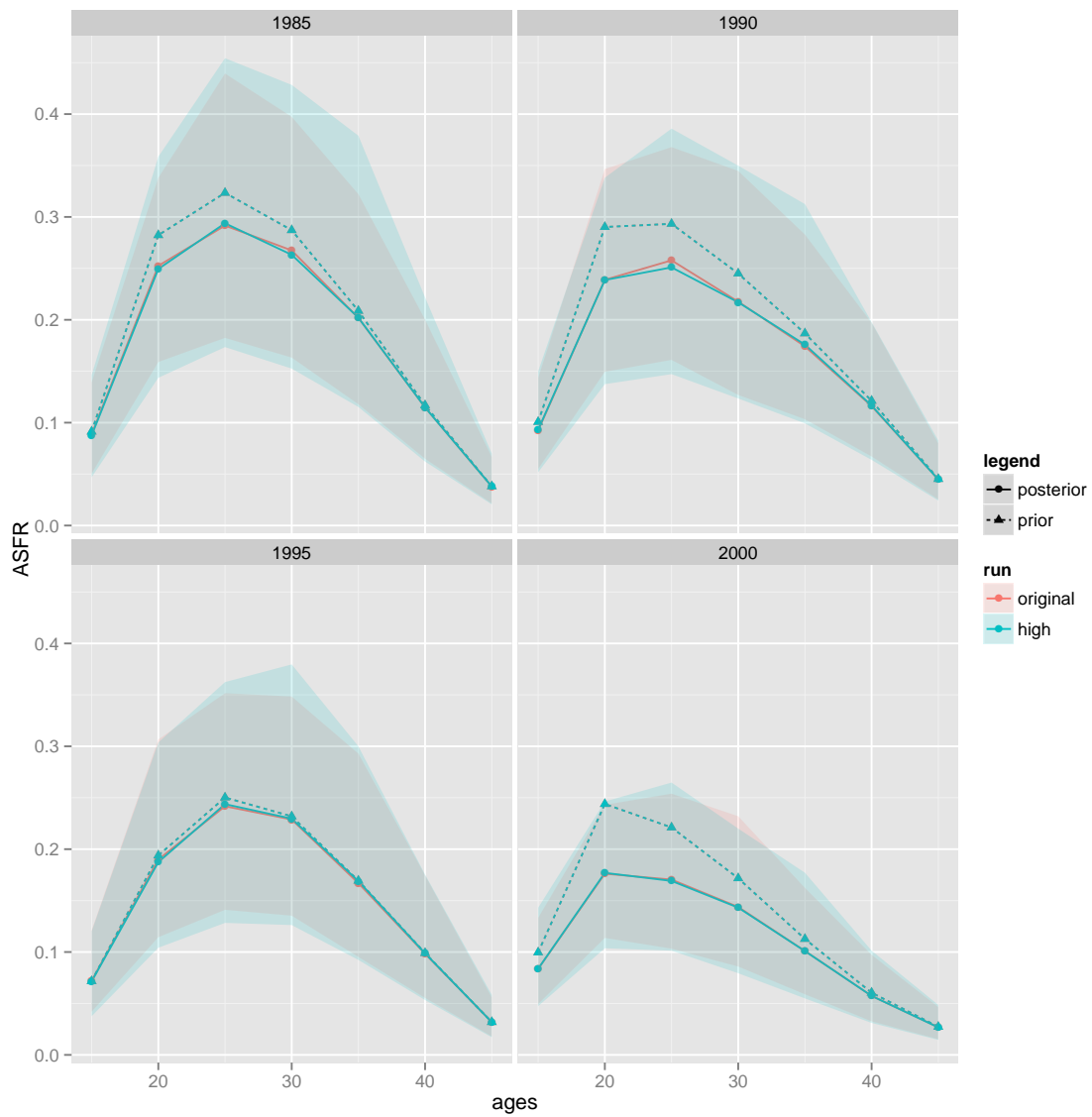


Figure 3.34. Prior and posterior medians and 95 percent credible intervals for life expectancy at birth ( $e_0$ ) with elicited relative errors of 10 percent (“original”) and 20 percent (“high”) for age-specific survival proportion, for the reconstructed female population of Laos, 1985–2005.

error was doubled. The increases were small relative to the changes made to the elicited relative errors, however. Therefore, posterior uncertainty about each vital rate parameter is slightly sensitive to the elicited relative error for that parameter. Posterior uncertainty about fertility is slightly sensitive to elicited relative errors for age-specific survival and migration proportion, as well as for ASFR.

### Appendix 3.D Sensitivity to Elicited Relative Errors: New Zealand

A sensitivity analysis was performed to study the effect of different elicited relative errors on the results for the reconstruction of the female population of New Zealand, 1961–2006. The reconstruction was re-run using the elicited relative errors used for the reconstruction



*Figure 3.35.* Prior and posterior medians and 95 percent credible intervals for age-specific fertility rate (ASFR) with elicited relative errors of 20 percent (“original”) and 40 percent (“high”) for age-specific migration proportion, for the reconstructed female population of Laos, 1985–2005.

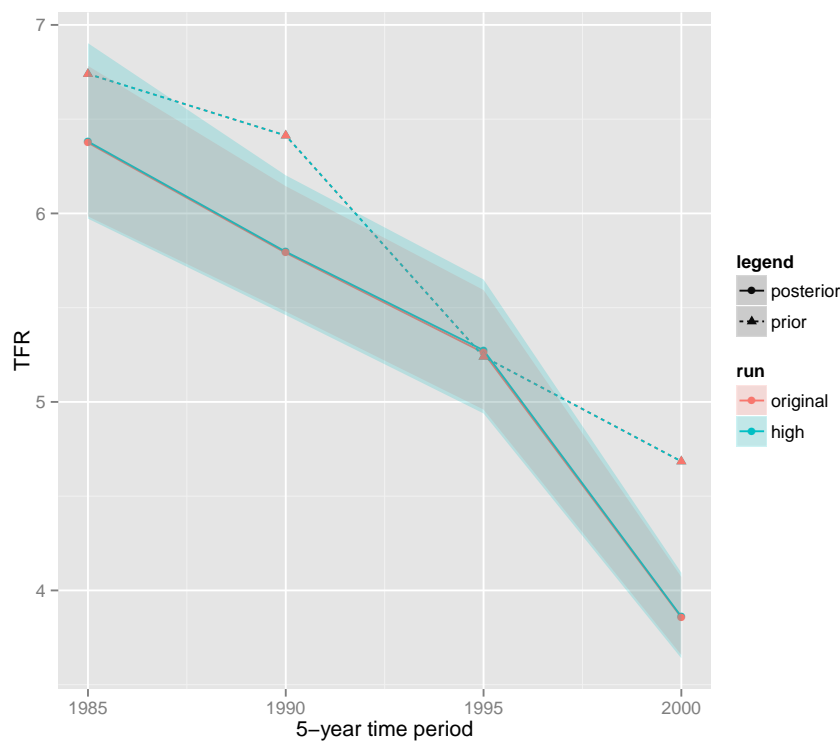


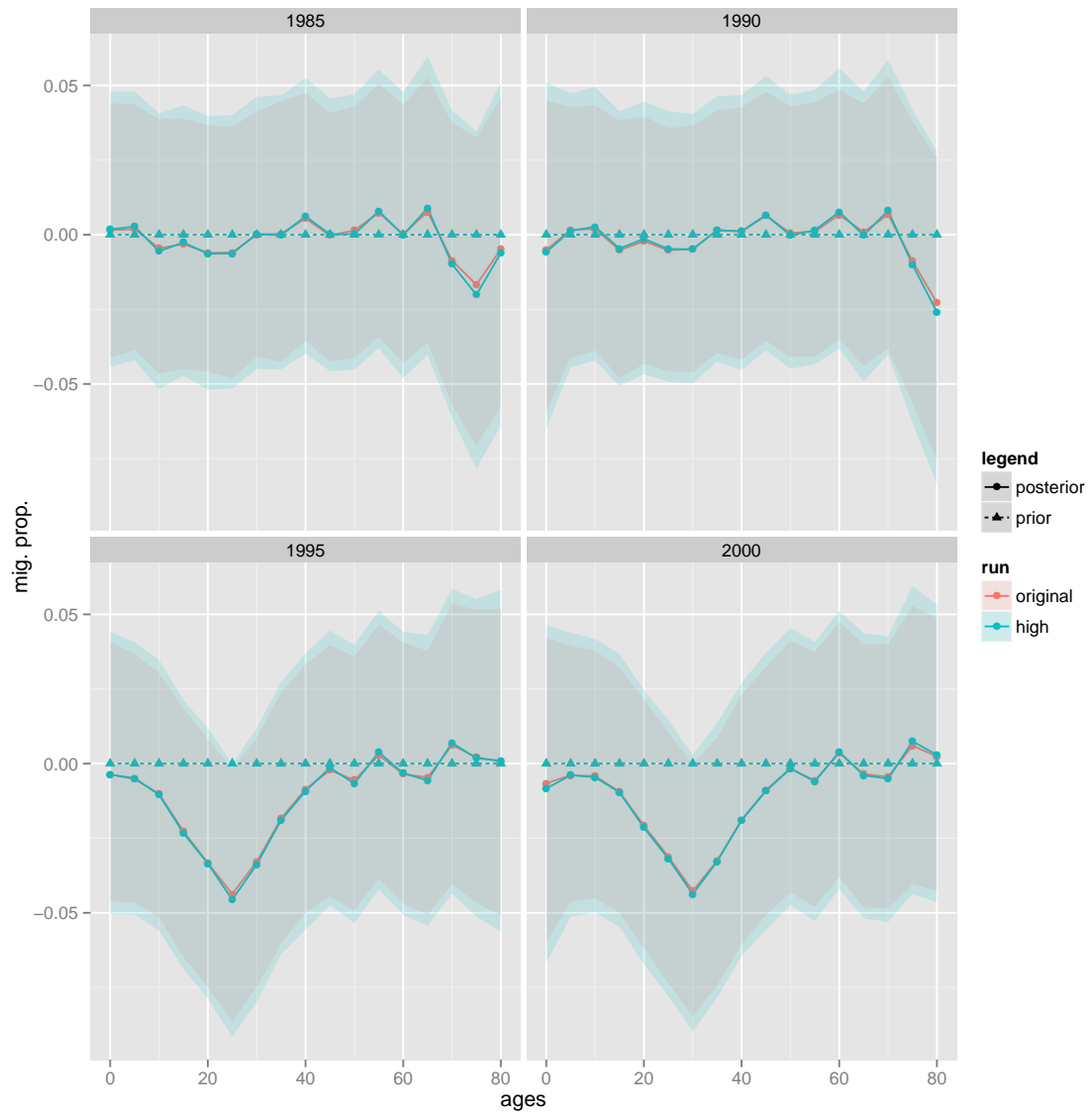
Figure 3.36. Prior and posterior medians and 95 percent credible intervals for total fertility rate (TFR) with elicited relative errors of 20 percent (“original”) and 40 percent (“high”) for age-specific migration proportion, for the reconstructed female population of Laos, 1985–2005.

of the female population of Laos (Section 3.3.1). This differs from the sensitivity analysis in Section 3.C because all elicited relative errors were increased under this alternative reconstruction; in Section 3.C there are several alternative reconstructions and in each alternative only the elicited relative errors for a subset of the parameters are increased.

### 3.D.1 Results

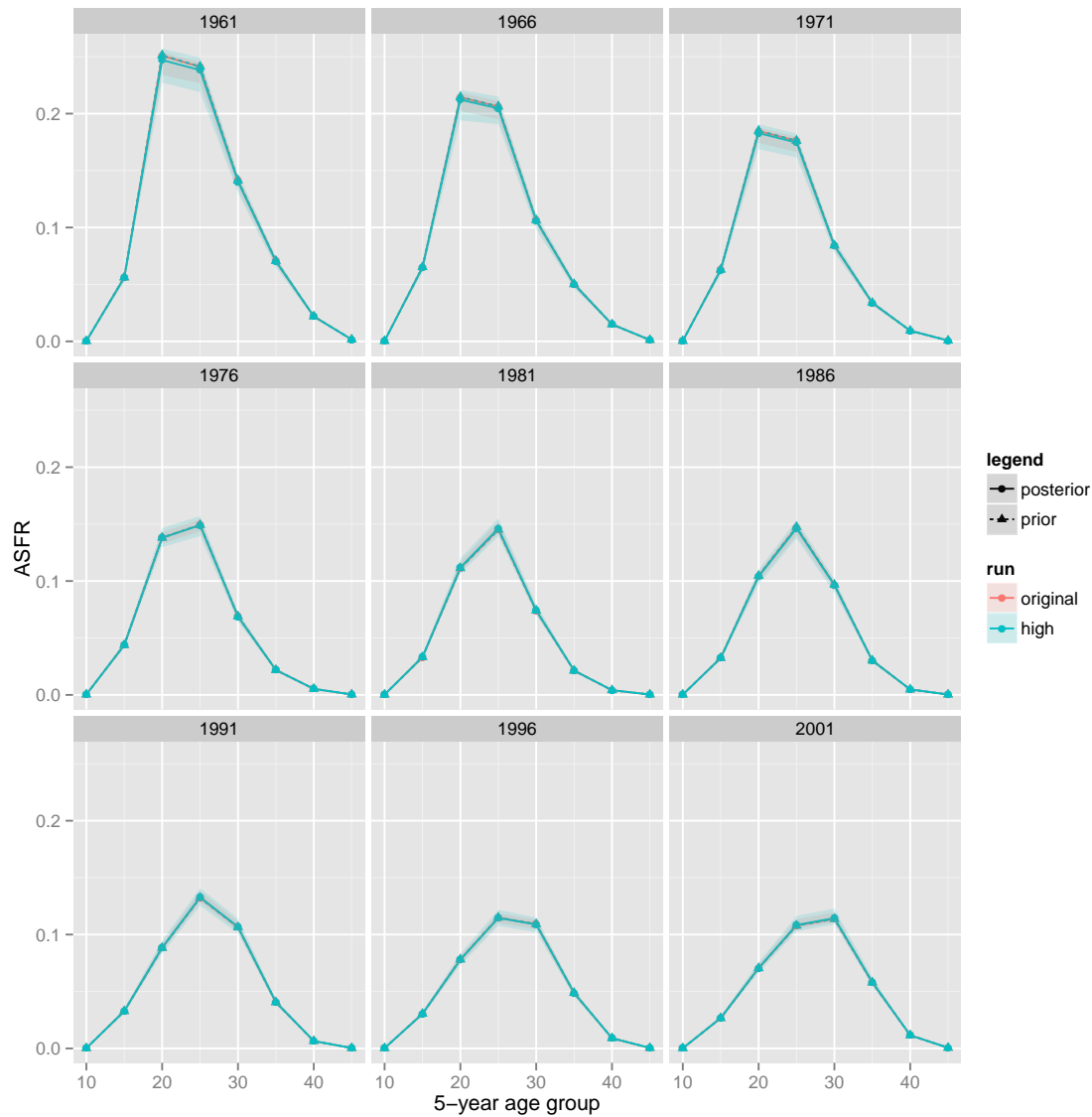
Results for ASFR and TFR are compared in Figures 3.38 and 3.39. The widths of the 95 percent credible intervals for ASFR are larger under the higher elicited relative errors for ages where ASFR is high. Posterior medians are also slightly different; for example, they are lower under higher elicited relative errors for age groups 20–24 and 25–29 in the 1961





*Figure 3.37.* Prior and posterior medians and 95 percent credible intervals for age-specific migration proportion with elicited relative errors of 20 percent (“original”) and 40 percent (“high”) for age-specific migration proportion, for the reconstructed female population of Laos, 1985–2005.

time period. Posterior intervals for TFR are also wider under the larger elicited relative errors and posterior medians are different in some time periods.



*Figure 3.38.* Prior and posterior medians and 95 percent credible intervals for age-specific fertility rate (ASFR) with elicited relative errors used in Section 3.3.3 (“original”) and elicited relative errors used for the reconstruction of Laos in Section 3.3.1 (“high”) for the reconstructed female population of New Zealand, 1961–2006.

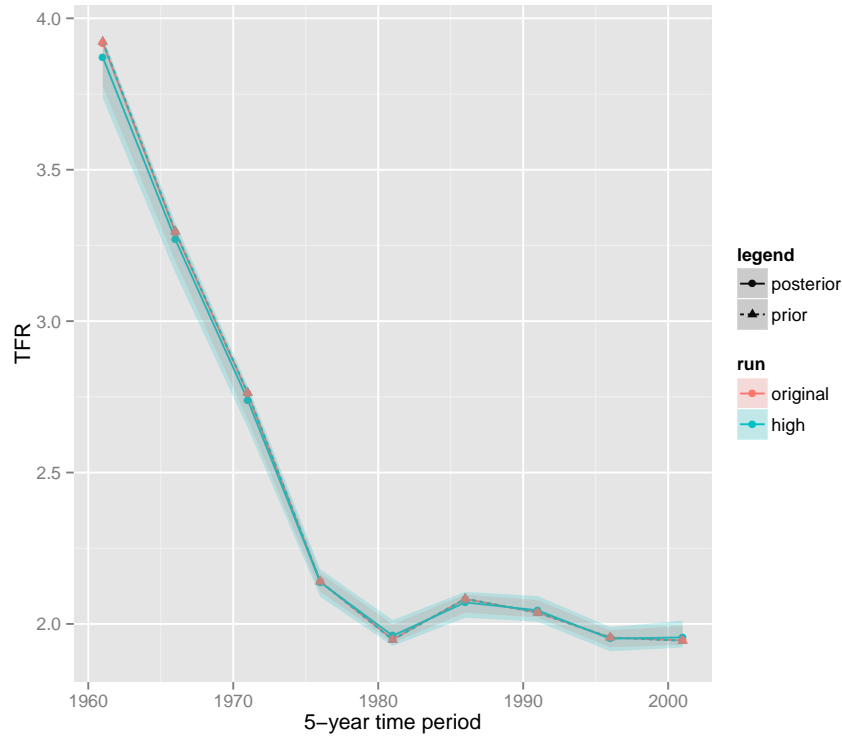
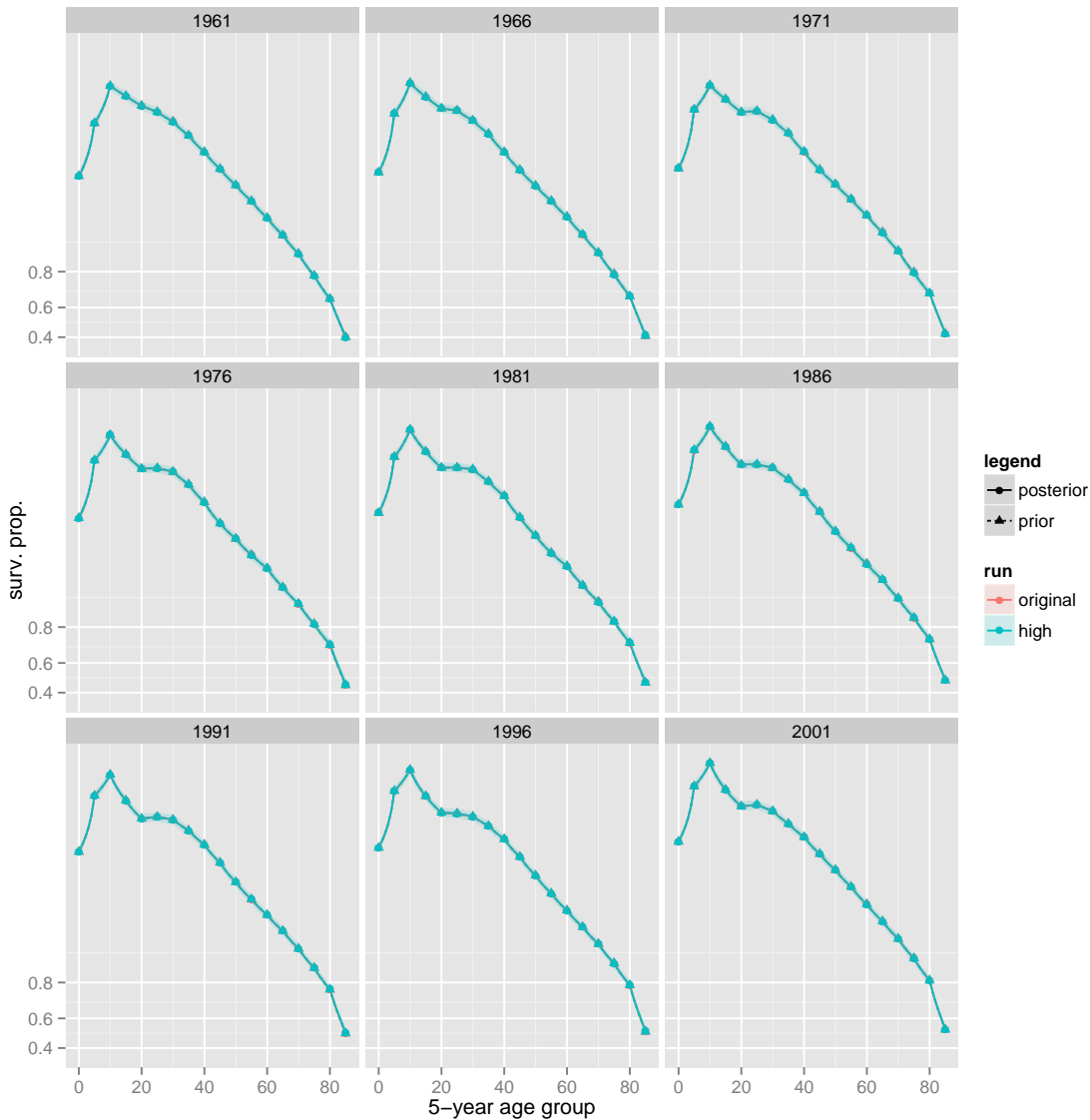


Figure 3.39. Prior and posterior medians and 95 percent credible intervals for total fertility rate (TFR) with elicited relative errors used in Section 3.3.3 (“original”) and elicited relative errors used for the reconstruction of Laos in Section 3.3.1 (“high”) for the reconstructed female population of New Zealand, 1961–2006.

Posterior uncertainty for age-specific survival (Figure 3.40) and  $e_0$  (Figure 3.41) is noticeably larger under the “high” elicited relative errors. Posterior medians for  $e_0$  changed slightly in some years.

Credible intervals for age-specific migration proportions are not consistently wider or more narrow under the “high” elicited relative errors (Figure 3.42). Poster medians differ in some time periods.

For the population count in the baseline year, increasing elicited relative errors appears to have made the credible intervals more narrow in many age groups (Figure 3.43). This is perhaps because the higher elicited relative errors for the vital rate parameters allowed



*Figure 3.40.* Prior and posterior medians and 95 percent credible intervals for age-specific survival proportion with elicited relative errors used in Section 3.3.3 (“original”) and elicited relative errors used for the reconstruction of Laos in Section 3.3.1 (“high”) for the reconstructed female population of New Zealand, 1961–2006. The vertical axis has been transformed to the logit scale.

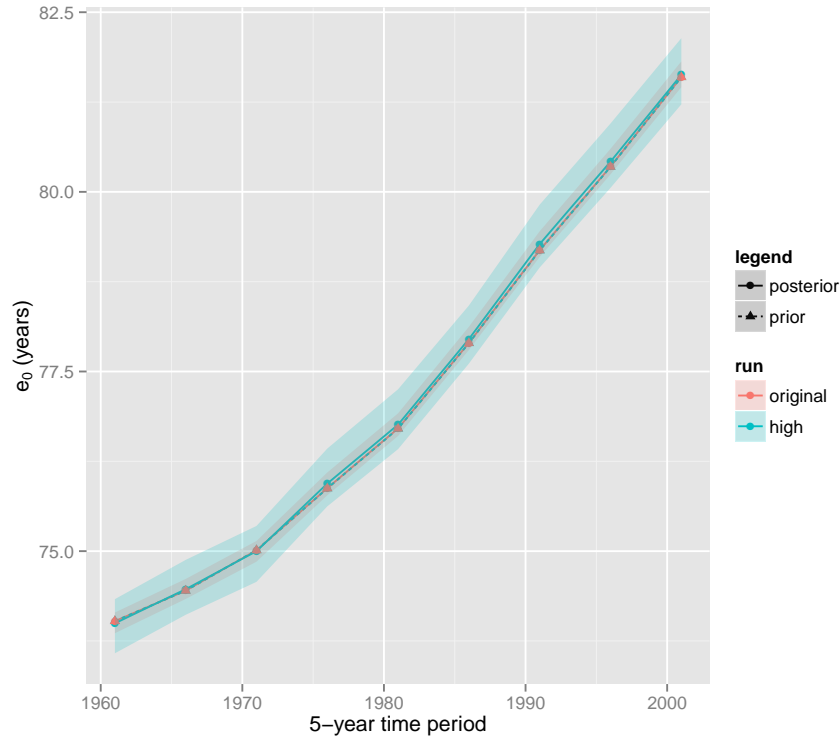
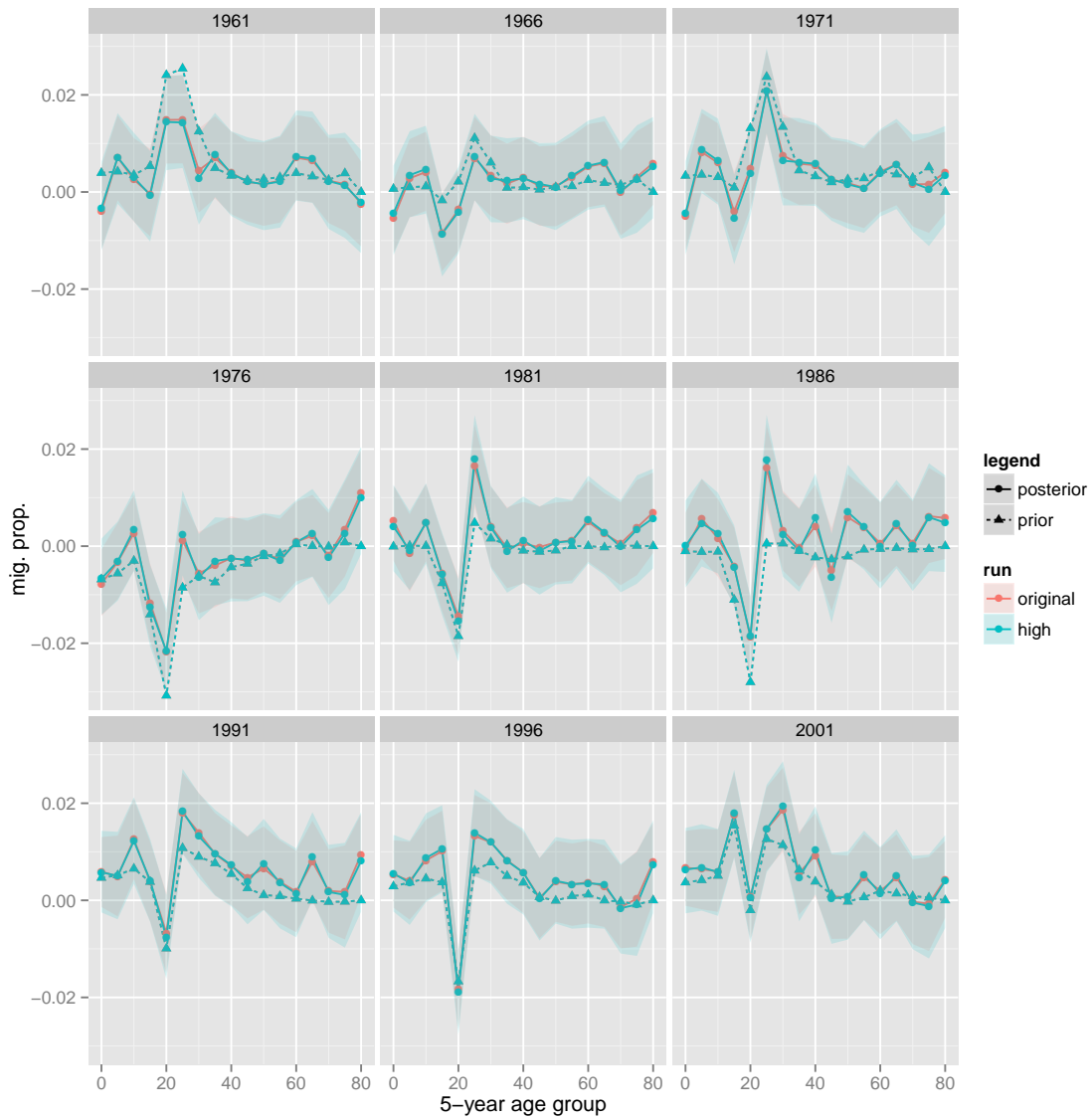


Figure 3.41. Prior and posterior medians and 95 percent credible intervals for life expectancy at birth ( $e_0$ ) with elicited relative errors used in Section 3.3.3 (“original”) and elicited relative errors used for the reconstruction of Laos in Section 3.3.1 (“high”) for the reconstructed female population of New Zealand, 1961–2006.

discrepancies between the adjusted census counts and the counts implied by the vital rate initial estimates to be compensated for in the posterior in a different way; higher uncertainty in the vital rates and shifted posterior medians under higher elicited relative errors compared with higher uncertainty about baseline population counts under the original run.

### 3.D.2 Discussion

Results for the reconstruction of the female population of New Zealand, 1961–2006, appear to be sensitive to the elicited relative errors. Using larger values increased the widths of the credible intervals for the fertility and survival parameters and led to changes in the posterior



*Figure 3.42.* Prior and posterior medians and 95 percent credible intervals for age-specific migration proportion with elicited relative errors used in Section 3.3.3 (“original”) and elicited relative errors used for the reconstruction of Laos in Section 3.3.1 (“high”) for the reconstructed female population of New Zealand, 1961–2006.

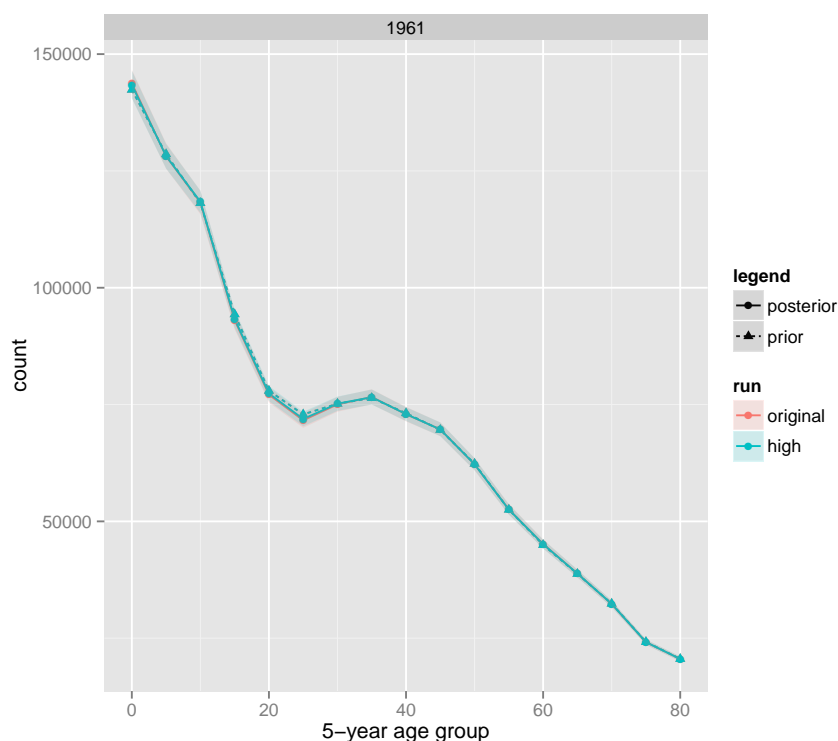


Figure 3.43. Prior and posterior medians and 95 percent credible intervals for age-specific population count with elicited relative errors used in Section 3.3.3 (“original”) and elicited relative errors used for the reconstruction of Laos in Section 3.3.1 (“high”) for the reconstructed female population of New Zealand, 1961.

medians for certain age groups and time periods. Note, however, that the relative errors used in Section 3.3.3 were based on data such as post-enumeration surveys and analyzes of the coverage of vital registration. Therefore, there is good reason to prefer the original results over the alternatives reported here.

### Appendix 3.E MCMC Diagnostics

Inference was based on a large sample drawn from the joint posterior distribution using an MCMC algorithm, implemented in the *R* package *popReconstruct*. Start values for the population counts, vital rates and migration proportions were set to the initial estimates.

Start values for the variances were arbitrarily set to 5. Further, related discussion can be found in Section 2.3.5 (Chapter 2) and Appendix 2.E.

### 3.E.1 The Raftery-Lewis Diagnostic

The method of Raftery and Lewis (1996) was used to choose chain lengths ( $q = 0.025, 0.975$ ,  $r = 0.0125$ ,  $s = 0.95$ ; the 0.025 and 0.975 quantiles are of interest since I report 95 percent credible intervals). The diagnostic was applied to the chains for each Level 4 (variance) parameter, each age- time-specific Level 3 (vital rate) parameter and the age- time-specific Level 2 parameters (the projected population counts,  $n_{a,t}$ ). Raftery and Lewis's (1996) method involves monitoring Metropolis acceptance proportions as well as the required chain length for a given degree of accuracy, to guard against using too few iterations and poor mixing. The number of burn-in iterations and the number used for inference in each case study are given in Table 3.4.

Table 3.4. Markov chain Monte Carlo (MCMC) chain lengths used for each case study.

Country	Burn-in	Used
Laos (CDWest)	10000	220550
Laos (UNSA)	12240	403263
Sri Lanka	10000	200000
New Zealand	6033	204450

### 3.E.2 Gelman-Rubin Diagnostic

The Gelman-Rubin diagnostic (Gelman and Rubin, 1992; Brooks and Gelman, 1998) is described in Appendix 2.E.2 (end of Chapter 2). It can be used to help identify when the MCMC chains for univariate parameters have not reached convergence and to study the impact of start values on the chains used for inference. As inputs, it requires several MCMC chains generated from the same algorithm but with different, very dispersed start values. Here, I apply it to the reconstruction of the female population of Laos and study



different start values for both Level 3 (vital rate) and Level 4 (variance) parameters. In Appendix 2.E.2 I applied it to chains with different start values for Level 4 (variance) in the reconstruction of the female population of Burkina Faso.

### *Different Start Values for Vital Rate (Level 3) Parameters*

Six additional chains, labeled “A”–“F”, were run using very dispersed start values for the vital rate (Level 3) parameters. These were generated using a simple scheme described in Table 3.5. The “high” and “low” values for each age- time-specific parameter are plotted in Figure 3.44. High and low values for ASFRs were 0.6 and 0.1, respectively, which correspond to TFRs of 21 and 3.5. High and low values for the age-specific survival proportions were derived by adding ten percent and subtracting fifty percent to/from the initial estimates on the logit scale. Using start values much more extreme than these resulted in chains that failed to move at all. High and low values for migration were set to 0.2 and -0.2, respectively; very extreme values for Laos. High and low values for the baseline count were 1.5 and 0.67 times the initial estimates. Start values for the variance parameters were arbitrarily set to 5.

The *gelman.diag* function in the *R* package *coda* was used to compute potential scale reduction factors (PSRFs). The chains were of length  $1.9 \times 10^5$  with a burn-in of  $1 \times 10^4$ . The function’s transform argument was used to improve the normal approximation used to calculate the credible intervals.

The upper 95 percent credible intervals for all age-specific vital rate parameters and variance parameters were found to be less than 1.02. All multivariate PSRFs were less than 1.01. Values less than 1.2 constitute a lack of evidence that *i*) the posterior based on samples after burn-in is overly dependent on start values; *ii*) that the chains are far from convergence (Brooks and Gelman, 1998). Evolution plots showing the value of the PSRF for increasing numbers of iterations were inspected to ensure that PSRF trajectories had settled down and were not still fluctuating. Examples where this appeared to be slowest are shown in Figures 3.45–3.47 (variance parameters) and Figures 3.48–3.50 (ASFRs for 1985–1990, age groups 15–30). PSRFs all settled down to values below 1.2 after about

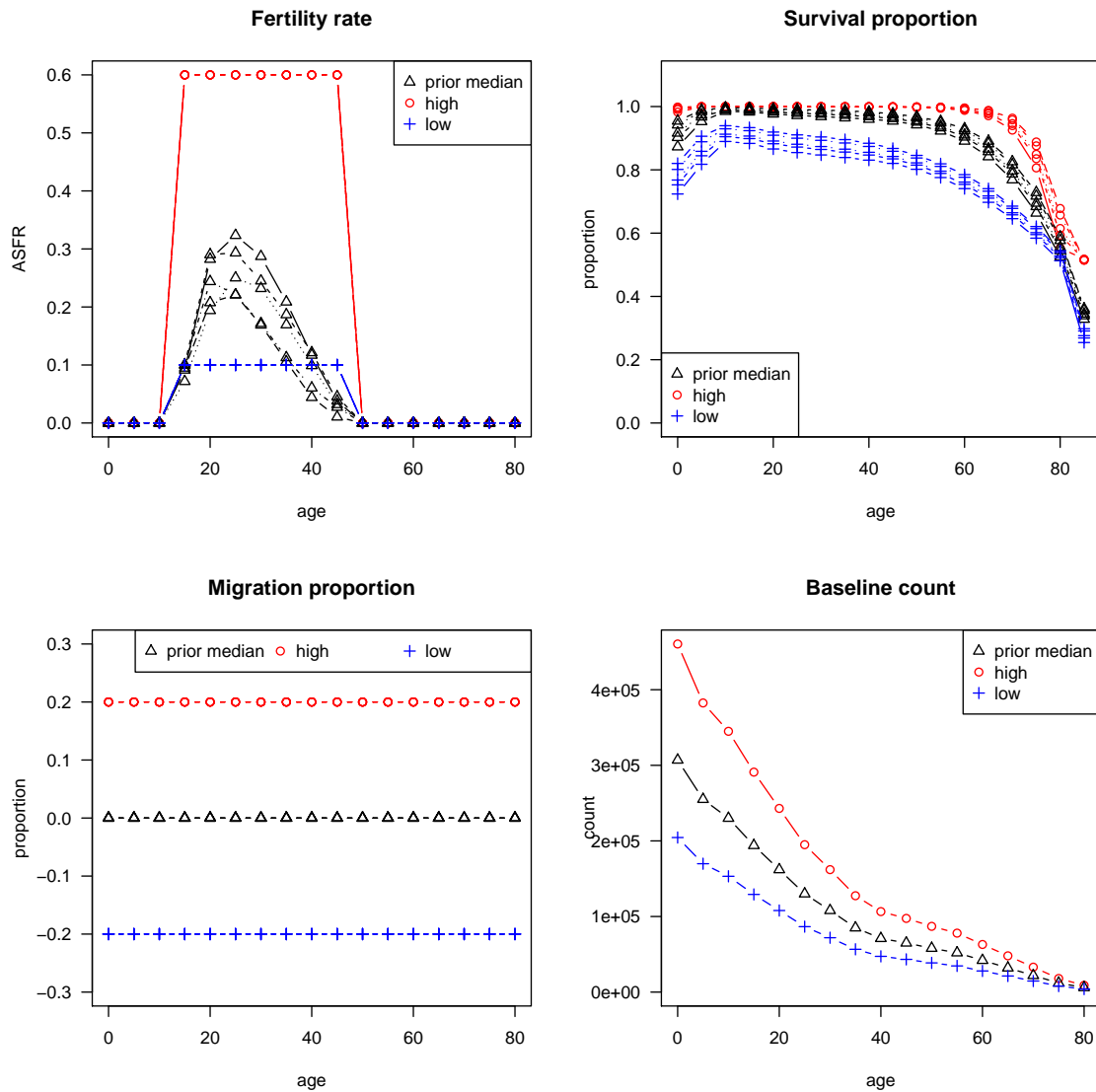


Figure 3.44. Start values for the multiple chains used as input to the Gelman-Rubin diagnostic for the reconstructed female population of Laos, 1985–2005. Each series (lines) gives the values for one of the five-year periods in the reconstruction.

*Table 3.5.* Scheme of Level 3 parameter start values used to generate multiple chains for the Gelman-Rubin diagnostic for the reconstructed female population of Laos, 1985–2005.

Series	Parameter			
	Fertility	Survival	Migration	Baseline
A	high	high	high	high
B	high	high	high	low
C	high	low	high	low
D	low	high	low	high
E	low	low	low	high
F	low	low	low	low

$1 \times 10^4$  iterations for these parameters, and much sooner for all the remaining ones. These results were interpreted as a lack of evidence against a bias due to the start values used in the chains used for inference, reported in Section [3.3.1](#).

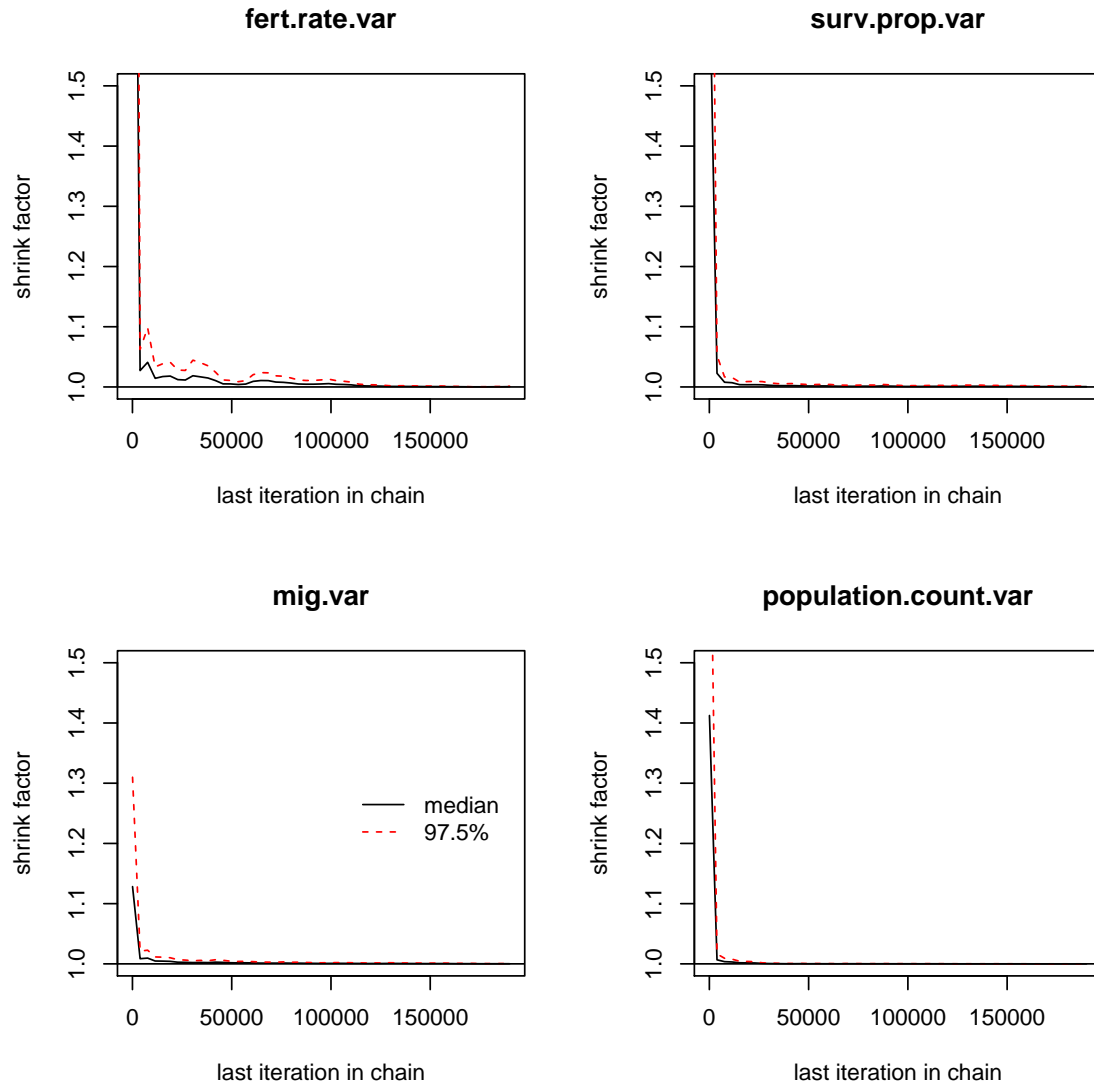


Figure 3.45. Potential scale reduction factor (PSRF) evolution plots for the Level 4 (variance) parameters from six chains (superimposed), each generated using different start values for the Level 3 (vital rate) parameters, for the reconstructed female population of Laos, 1985–2005 (“fert.rate.var”= $\sigma_f^2$ , “surv.prop.var”= $\sigma_s^2$ , “mig.prop.var”= $\sigma_g^2$ , “population.count.var”= $\sigma_n^2$ ).

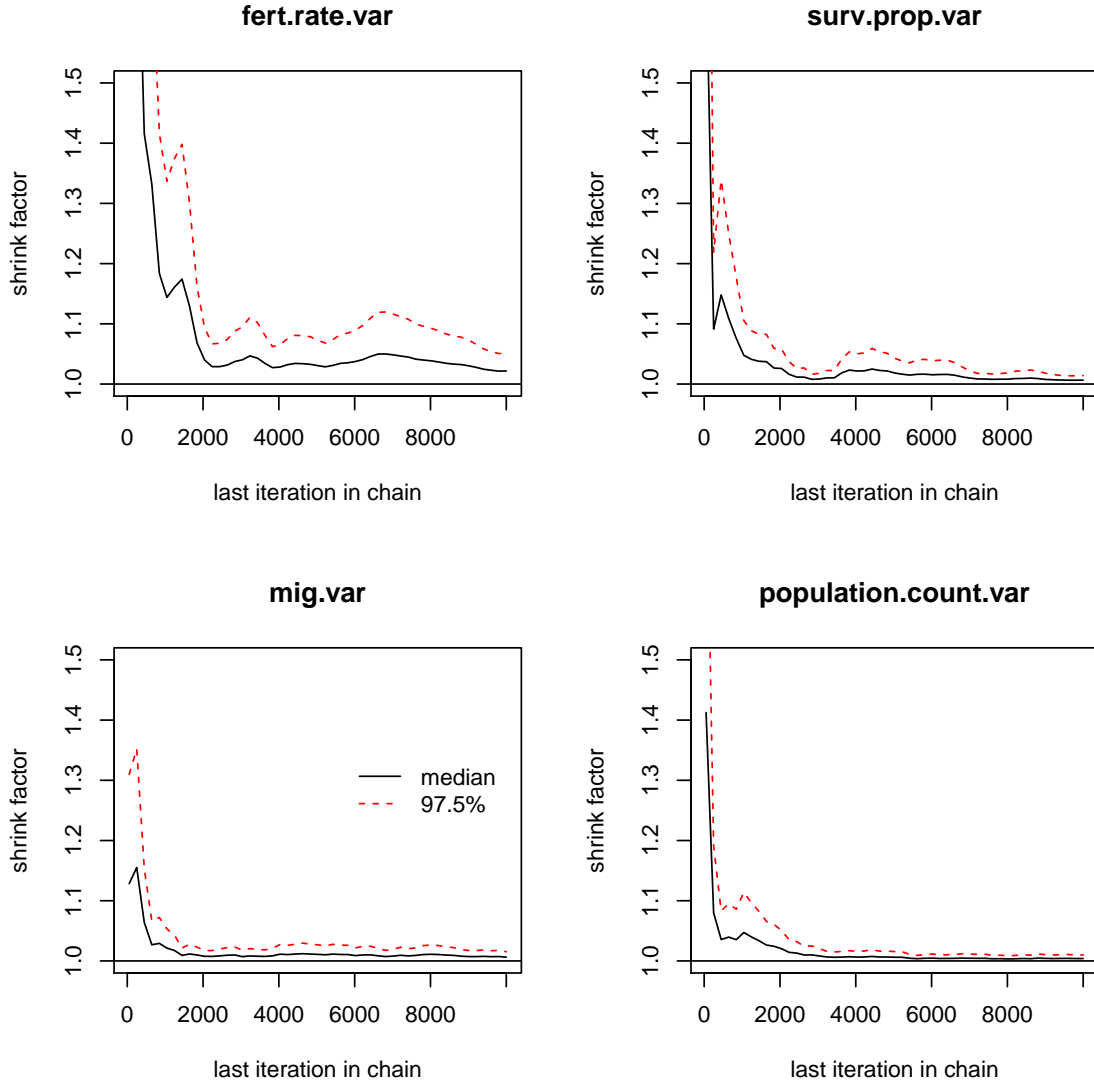


Figure 3.46. Potential scale reduction factor (PSRF) evolution plots for the Level 4 (variance) parameters from six chains (superimposed), each generated using different start values for the Level 3 (vital rate) parameters, for the reconstructed female population of Laos, 1985–2005, iterations 1–10000 only (“fert.rate.var”= $\sigma_f^2$ , “surv.prop.var”= $\sigma_s^2$ , “mig.prop.var”= $\sigma_g^2$ , “population.count.var”= $\sigma_n^2$ ).

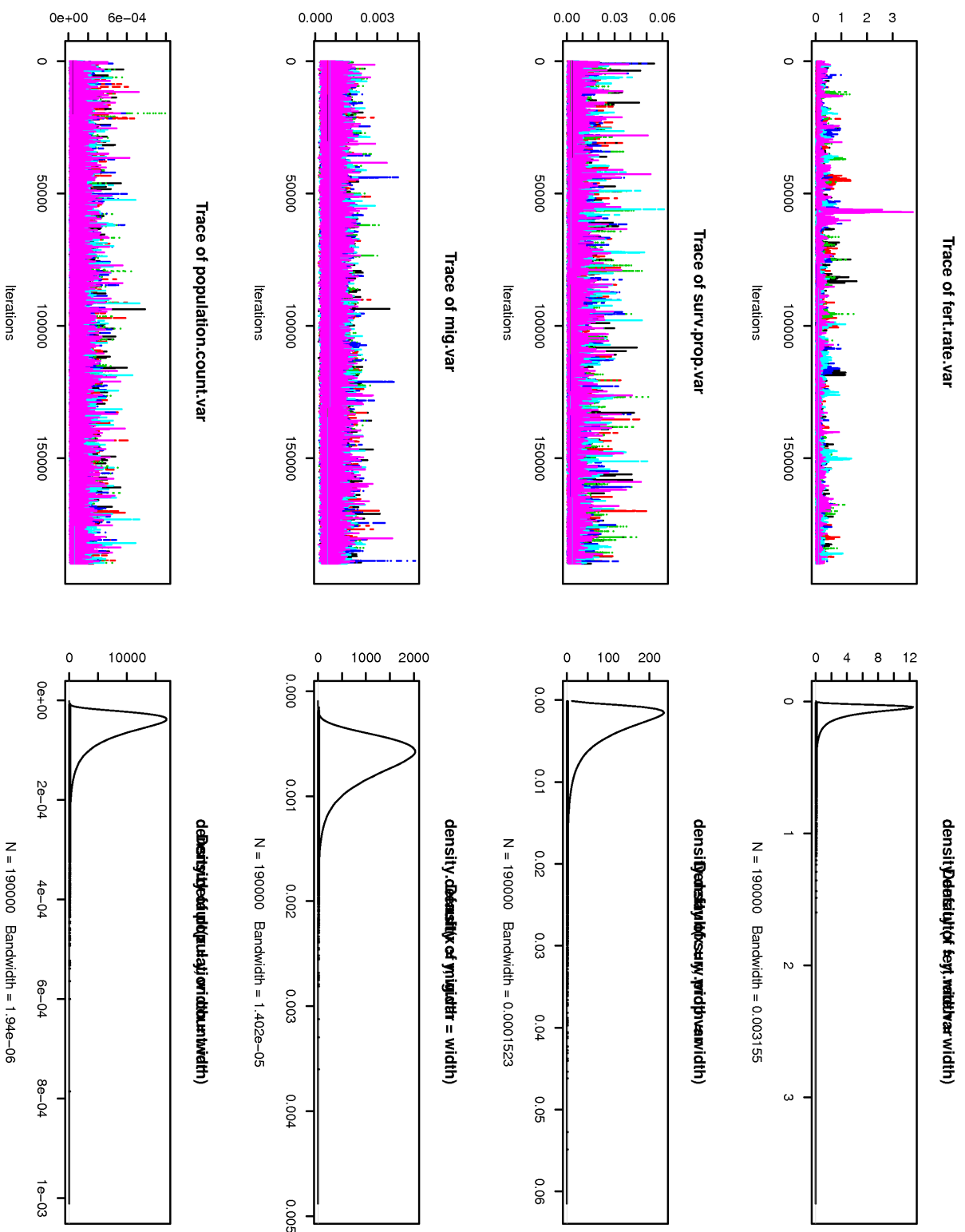
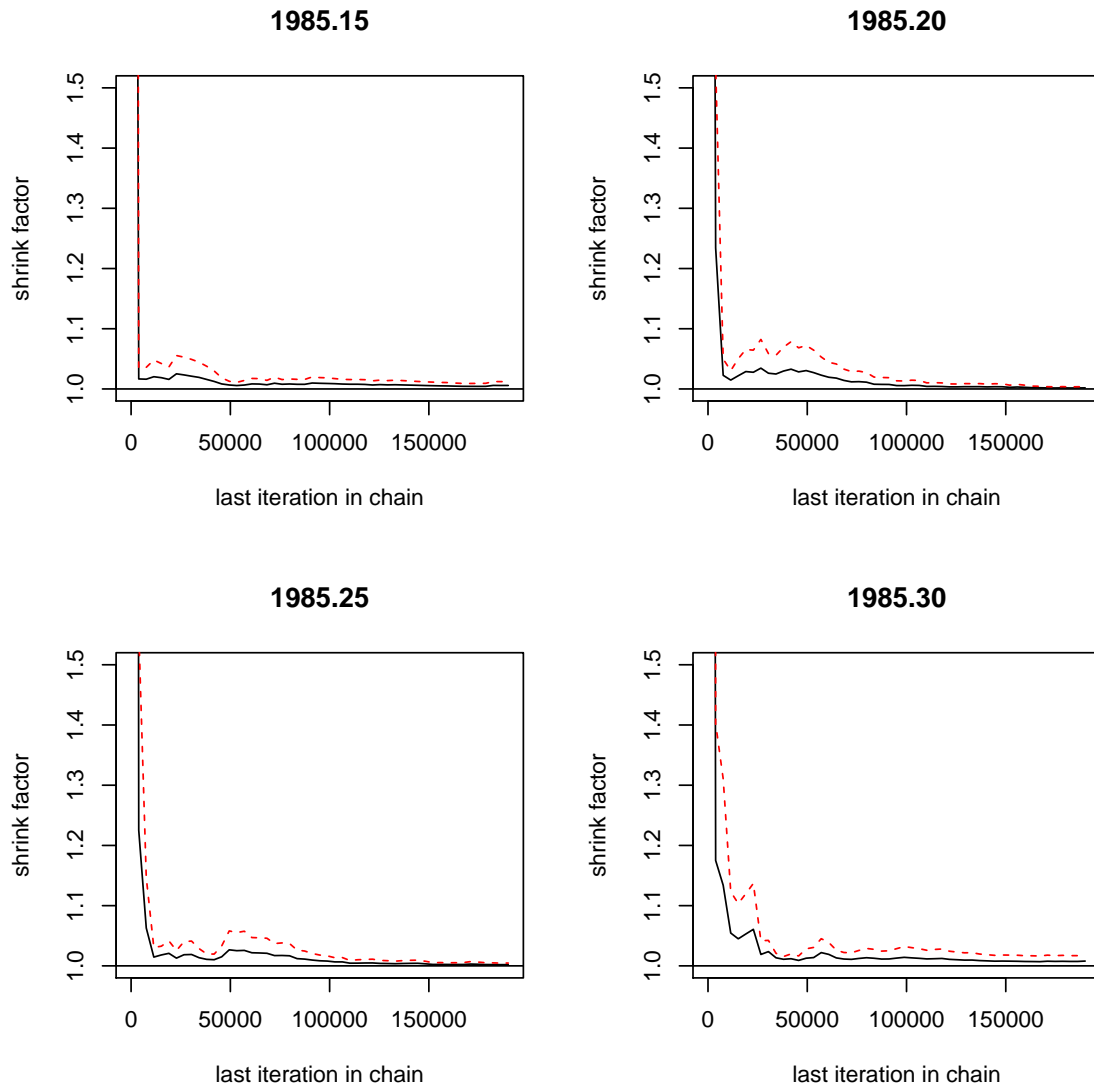
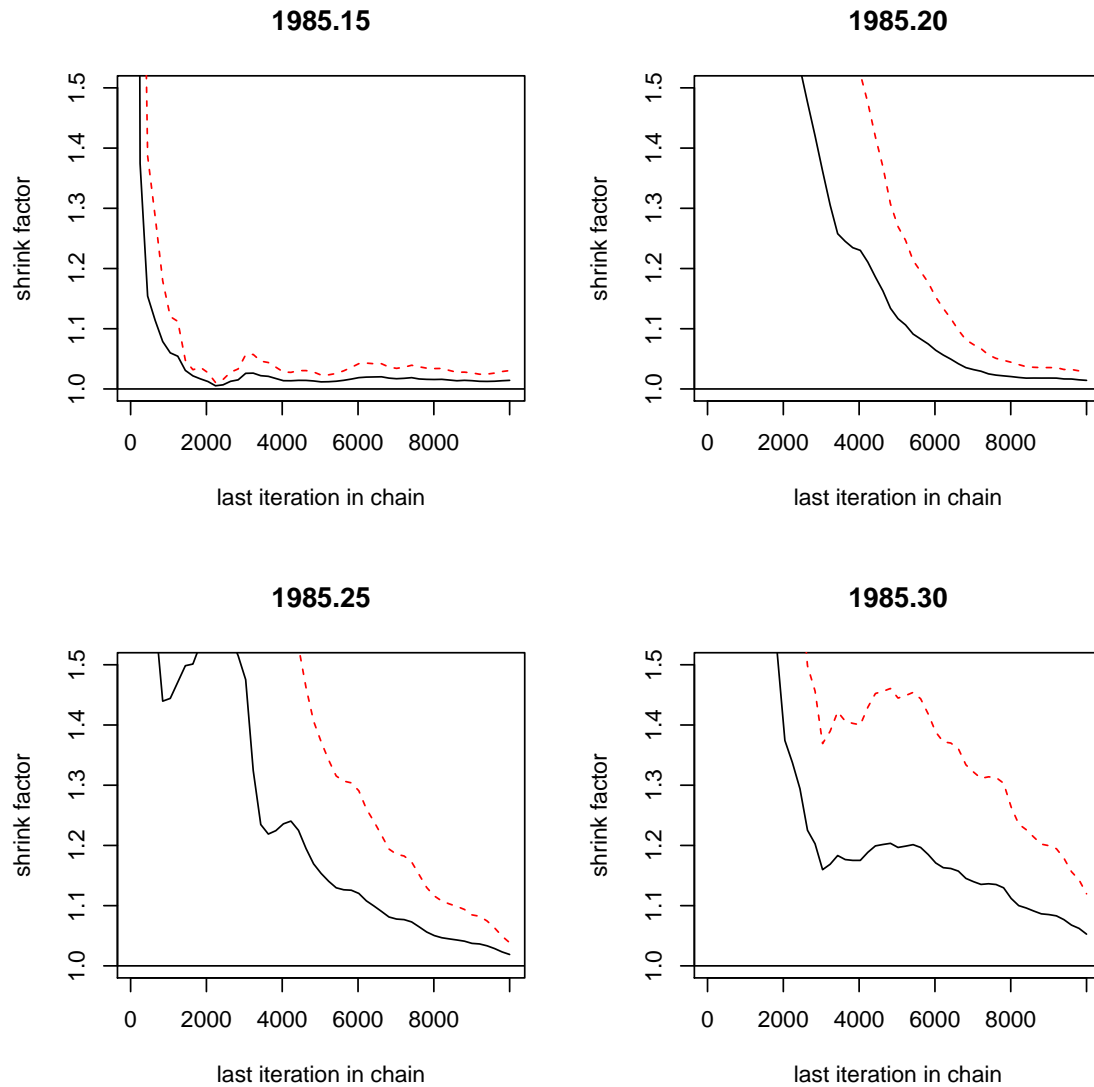


Figure 3.47. Traceplots and kernel density estimates for the Level 4 (variance) parameters from six chains (superimposed), each generated using different start values for the Level 3 (vital rate) parameters, for the reconstructed female population of Laos, 1985–2005 (“fert.rate.var”= $\sigma_f^2$ , “surv.prop.var”= $\sigma_s^2$ , “mig.prop.var”= $\sigma_g^2$ , “population.count.var”= $\sigma_n^2$ ).



*Figure 3.48.* Potential scale reduction factor (PSRF) evolution plots for age-specific fertility rates (ASFRs), 1985–1990, age groups 15–30, from six chains (superimposed), each generated using different start values for the Level 3 (vital rate) parameters, for the reconstructed female population of Laos, 1985–2005.



*Figure 3.49.* Potential scale reduction factor (PSRF) evolution plots for age-specific fertility rates (ASFRs), 1985–1990, age groups 15–30, from six chains (superimposed), each generated using different start values for the Level 3 (vital rate) parameters, for the reconstructed female population of Laos, 1985–2005, iterations 1–1000 only.



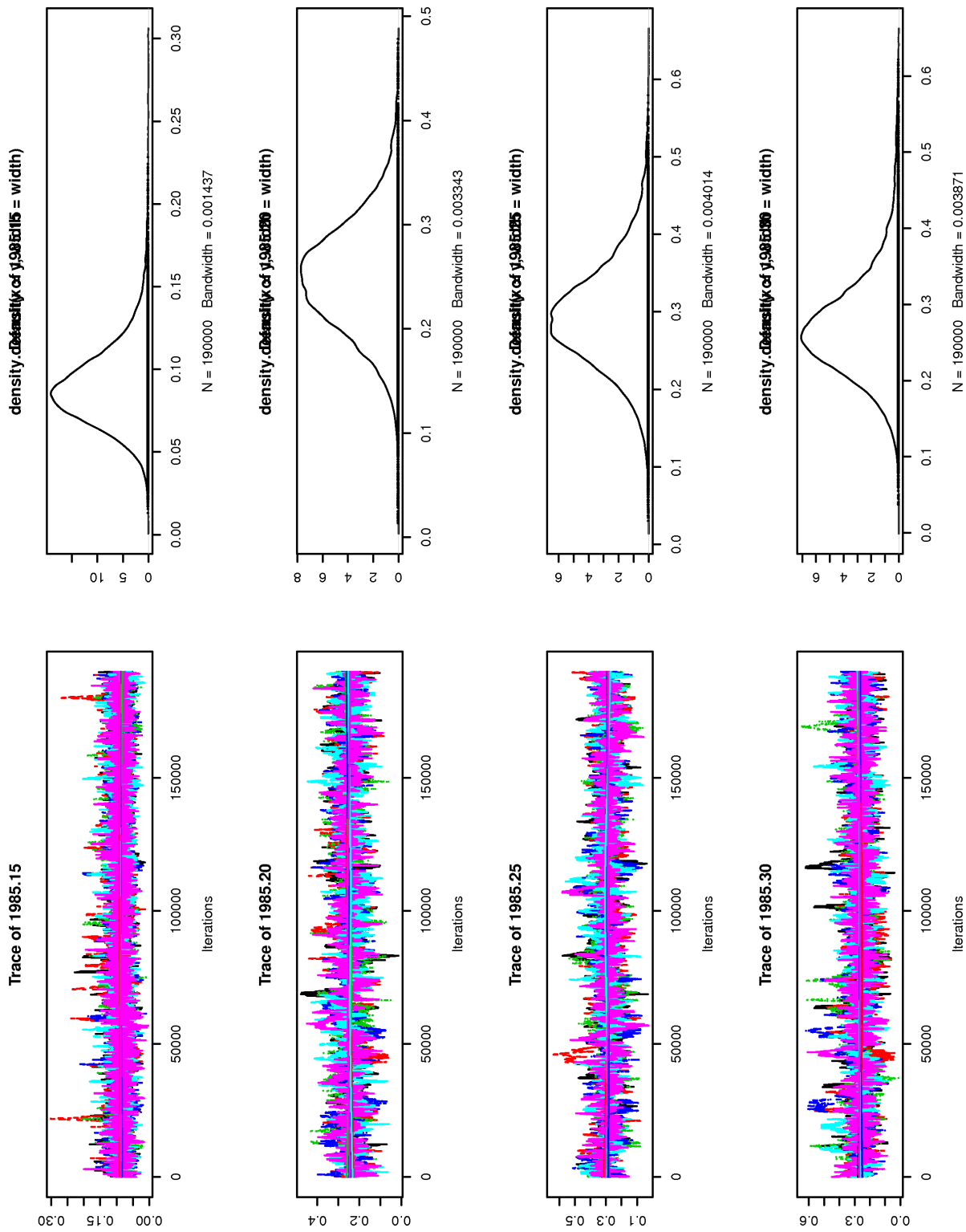


Figure 3.50. Traceplots and kernel density estimates for age-specific fertility rates (ASFRs), 1985–1990, age groups 15–30, from six chains (superimposed), each generated using different start values for the Level 3 (vital rate) parameters, for the reconstructed female population of Laos, 1985–2005.

*Different Start Values for Variance (Level 4) Parameters*

The effect of choosing different start values for the variance (Level 4) parameters was investigated using the Gelman-Rubin diagnostic and the same scheme of start values as those in Appendix 2.E.2 to Chapter 2. Six sets of start values were used (Table 3.6, copied for convenience).

*Table 3.6.* Scheme of Level 4 parameter start values used to generate multiple chains for the Gelman-Rubin diagnostic for the reconstructed female population of Laos, 1985–2005 (this is a copy of Table 2.6).

Series	Level 4 Parameter			
	$\sigma_f^2$	$\sigma_s^2$	$\sigma_g^2$	$\sigma_n^2$
A	5	5	5	5
B	5	5	5	0.001
C	5	0.001	5	0.001
D	0.001	5	0.001	5
E	0.001	0.001	0.001	5
F	0.001	0.001	0.001	0.001

The maximum of the upper limits of the 95 credible intervals for the PSRFs was 1, indicating a lack of evidence that the start values used for the Level 4 parameters led to bias in the inferences. PSRF evolution plots for the Level 4 parameters are in Figures 3.51 and 3.52 and trace plots are in Figure 3.53. None of these plots are cause for concern about lack of convergence or problems due to badly chosen start values.

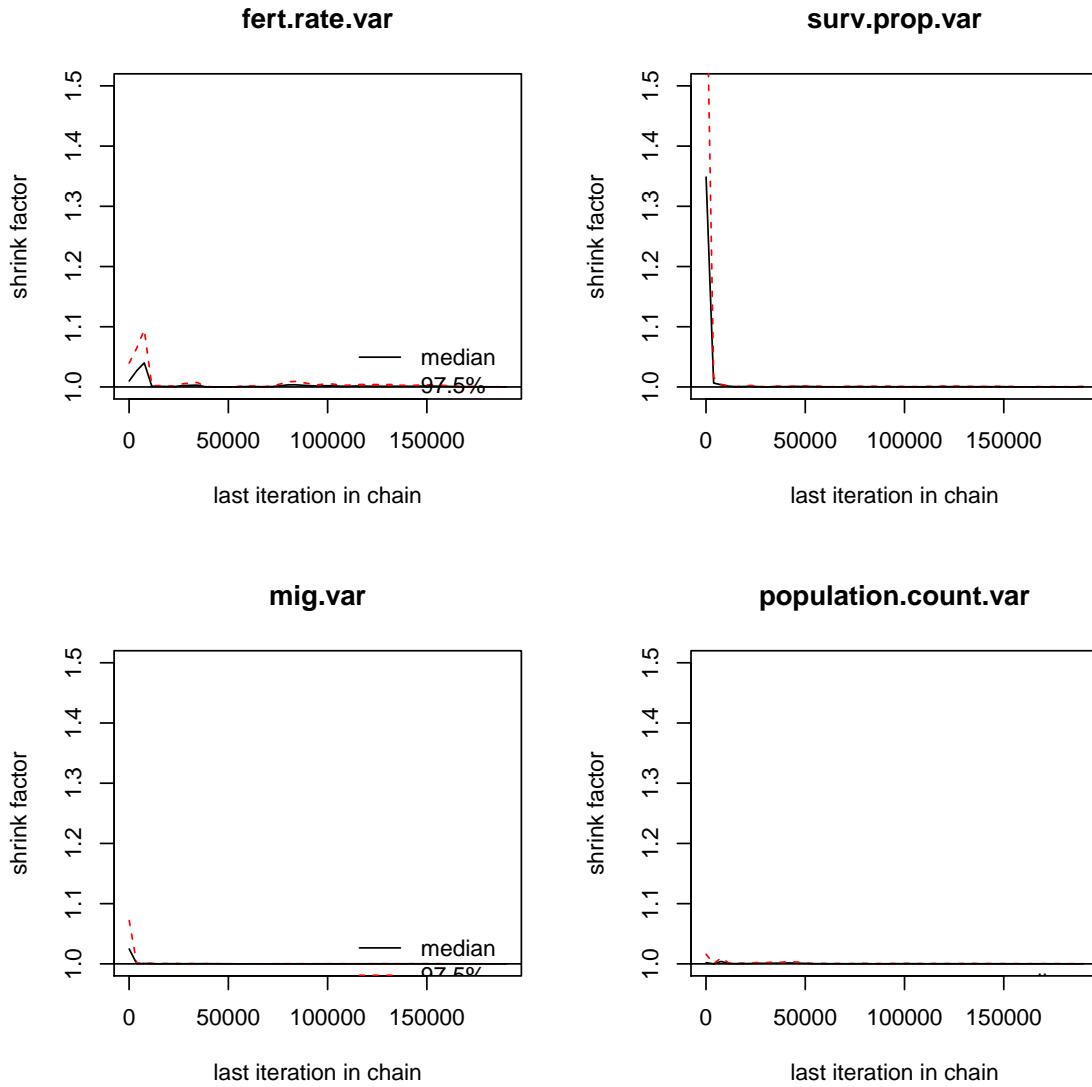


Figure 3.51. Potential scale reduction factors (PSRFs) for the Level 4 parameters calculated from six chains with dispersed start values for Level 4 (variance) parameters, for the reconstructed female population of Laos, 1985–2005 (“fert.rate.var”= $\sigma_f^2$ , “surv.prop.var”= $\sigma_s^2$ , “mig.prop.var”= $\sigma_g^2$ , “population.count.var”= $\sigma_n^2$ ).

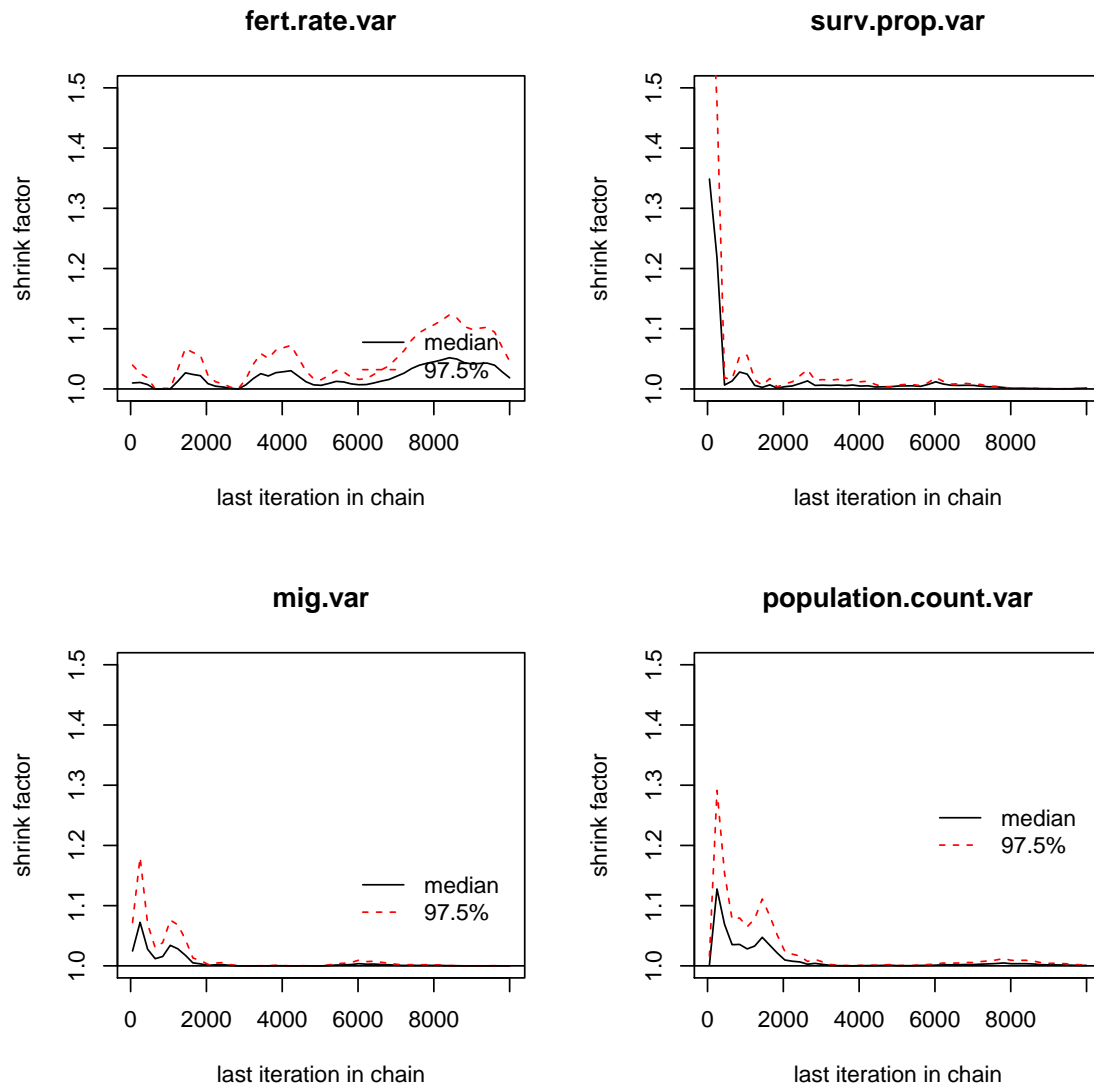


Figure 3.52. Potential scale reduction factors (PSRFs) for the Level 4 parameters calculated from six chains with dispersed start values for Level 4 (variance) parameters, for the reconstructed female population of Laos, 1985–2005, iterations 1–10000 only (“fert.rate.var”= $\sigma_f^2$ , “surv.prop.var”= $\sigma_s^2$ , “mig.prop.var”= $\sigma_g^2$ , “population.count.var”= $\sigma_n^2$ ).

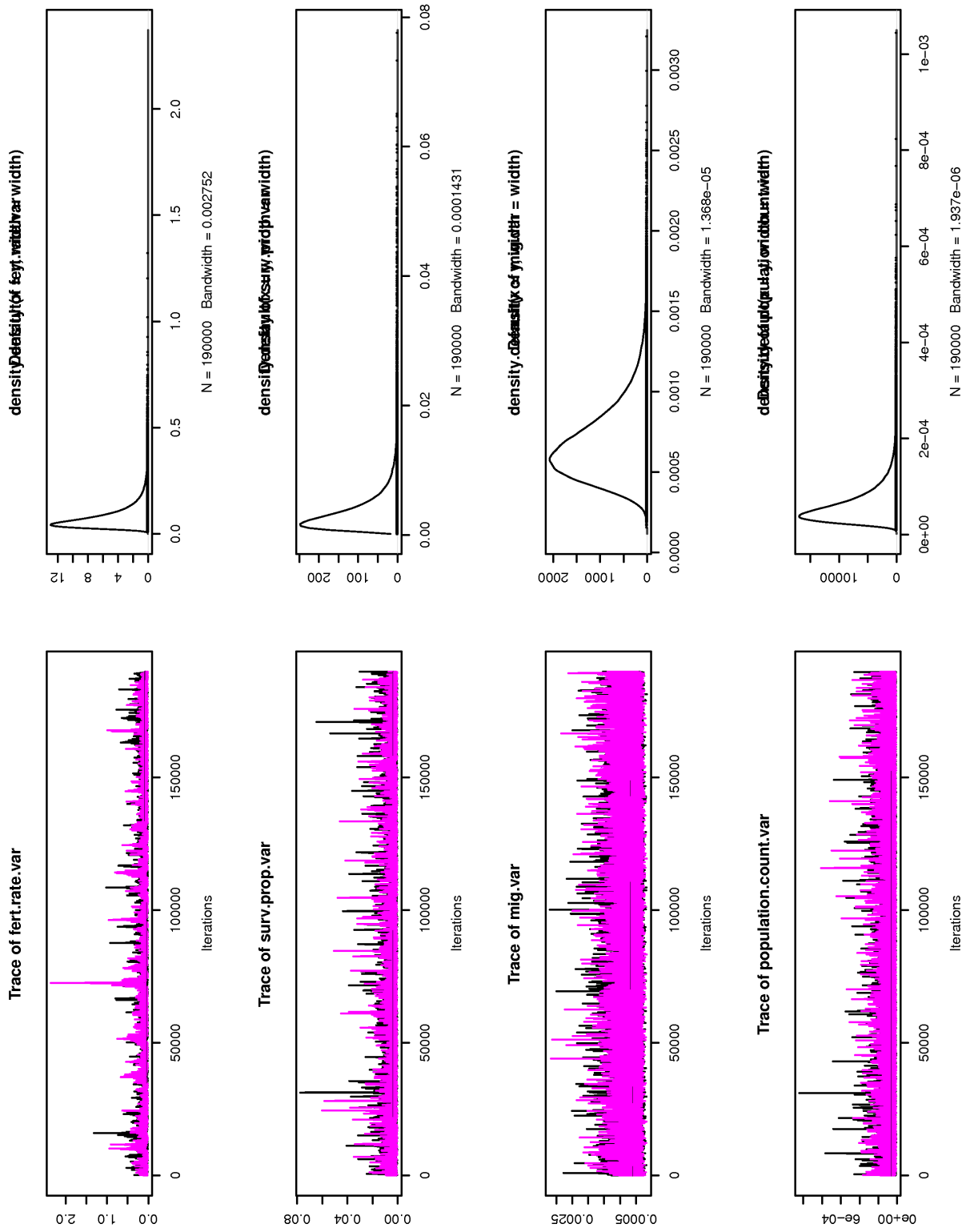


Figure 3.53. Traceplots and kernel density estimates for the six Level 4 chains (superimposed) used for the Gelman-Rubin diagnostic for the reconstructed female population of Laos, 1985–2005 (“fert.rate.var” =  $\sigma_f^2$ , “surv.prop.var” =  $\sigma_s^2$ , “mig.prop.var” =  $\sigma_g^2$ , “population.count.var” =  $\sigma_n^2$ ).

## Chapter 4

## SEX RATIOS AT BIRTH, SEX RATIOS OF MORTALITY, AND THE RECONSTRUCTION OF TWO-SEX POPULATIONS

**4.1 Introduction**

Bayesian reconstruction (Chapters 2 and 3) was proposed as a method of quantifying uncertainty in estimates of the key parameters driving human population dynamics. It is a method of simultaneously estimating population counts, fertility and mortality rates (vital rates) and net international migration at the country level, by age, together with uncertainty. The original formulation was able to reconstruct female-only populations. In this chapter, I further develop Bayesian reconstruction for two-sex populations. This allows us to estimate age- and time-specific indicators of fertility, mortality and migration separately for females and males and, importantly, sex ratios of these quantities, all with probabilistic measures of uncertainty. In addition, I also show how Bayesian reconstruction can be used to derive probabilities of change over time in these quantities. To demonstrate the method, I reconstruct the full populations of Laos from 1985–2005, Thailand from 1960–2000 and India from 1971–2001.

Bayesian reconstruction embeds standard demographic projection in a hierarchical statistical model. As inputs, it takes bias-reduced initial estimates of age-specific fertility rates (ASFRs), survival proportions (a measure of mortality), net international migration and census-based population counts. Also required is expert opinion about the measurement error of these quantities, informed by data if available. The output is a joint posterior probability distribution on the inputs, allowing all parameters to be estimated simultaneously, together with fully probabilistic posterior estimates of measurement error. In Chapter 2 described Bayesian reconstruction for female only populations at the national level. I showed that marginal credible intervals were well calibrated and reconstructed the female population of Burkina Faso from 1960 to 2000. In Chapter 3 I extended female-only Bayesian

reconstruction to countries with censuses at irregular intervals and showed that it works well across a wide range of data quality contexts by reconstructing the female populations of Laos, Sri Lanka, and New Zealand. Laos is a country with very little vital registration data where population estimation depends largely on surveys, Sri Lanka has some vital registration data, and New Zealand is a country with high-quality registration data. In this chapter, I propose a method for reconstructing full two-sex populations. In addition to producing estimates of population counts, mortality and migration for males, two-sex reconstruction allows estimation of sex ratios such as the sex ratio at birth (SRB), sex ratios of mortality and population sex ratios.

Global sex ratio in the total population (SRTP), defined as the ratio of the number of males per female, has risen slightly from about 1.00 in 1950 to 1.02 in 2010. There is a great deal of variation among country groups, however. For instance, SRTP in the more developed regions ranged from 0.91 to 0.95 over this period, while in the less developed regions it remained constant at about 1.04. In Eastern Asia, which includes China, and in Southern Asia, which includes India, SRTPs ranged from 1.05 to 1.06 and from 1.09 to 1.06, respectively (United Nations, 2011c). Guilmoto (2007c) claims that the population of Asia underwent “masculinization” during the latter half of the twentieth century, with one likely consequence being a “marriage squeeze” (Guilmoto, 2009, 2012) wherein many males will be unable to find a marriage partner. Imbalances in population sex ratios are caused by imbalances in SRBs and sex ratios of mortality (SRMs) (Guillot, 2002). These quantities have received considerable attention in the literature on the demography of Asia (e.g. Sen, 1990; Coale, 1991; Mayer, 1999; Bongaarts, 2001; Bhat, 2002b,c; Das Gupta, 2005; Guilmoto, 2009). Sawyer (2012) called for further work to quantify uncertainty in estimates of SRMs. Estimates of SRB are subject to a large amount of uncertainty, especially in India (Bhat, 2002b,c; Guillot, 2002; Guilmoto, 2009). Here, I aim to respond by quantifying uncertainty in these parameters.

The chapter is organized as follows. In the remainder of this section I provide some background on the demography of sex ratios in Asia. A review of existing methods of population reconstruction was given previously (Sections 1.2.2 and 2.2). In Section 4.2 I describe the two-sex version of Bayesian reconstruction. In Section 4.3 I present results

from the case studies of Laos, Thailand and India where I focus on posterior distributions of SRB, SRM and the population sex ratio. I end with a discussion in Section 4.4 which provides further demographic context and an overall conclusion. Selected mathematical derivations are given in the chapter appendices, as are further details about data sources and some additional results.

#### 4.1.1 *Estimating Sex Ratios*

Methods of reporting sex ratios are not standardized. Here I adopt the convention that all ratios are “male-per-female”; in the Indian literature the inverse is more common. Hence, SRTP is the total number of males per female in the population and SRB is the number of male births per female birth. The SRM can be expressed using various mortality indicators. I will use the under-five mortality rate (U5MR) exclusively (see Appendix 4.A.1 for a formal definition). A low SRM means that male mortality is lower than female mortality. All-age mortality is summarized by life expectancy at birth, for which the standard demographic abbreviation is  $e_0$ . Comparison of  $e_0$  by sex is more commonly done using the difference rather than the ratio and I adopt that convention here. Male  $e_0$  is subtracted from female  $e_0$  to obtain the difference.

SRBs for most countries are in the range 1.04–1.06 (United Nations Population Fund, 2010). Estimates of SRB in some regions in Asia are higher; the National Family Health Survey in India estimated SRB over 2000–2006 to be 1.09, for example (Guilmoto, 2009). For almost all countries,  $e_0$  is higher for females than males. This is thought to be due to a range of biological and environmental factors, with the relative contribution of each class of factor varying among countries (Waldron, 1985, 2009). Age-specific SRMs are more variable as they are affected by sex-specific causes of death such as those associated with child birth. The preferred way of estimating SRBs and SRMs at the national level is from counts of births and deaths recorded in official registers (vital registration) together with total population counts from censuses. In many countries where such registers are not kept, surveys such as the Demographic and Health Surveys (DHSs) and World Fertility Surveys (WFSs) must be used. These typically ask a sample of women about their birth



histories. Full birth histories collect information about the times of each birth and, if the child subsequently died, the time of the death. Summary birth histories ask only about the total number of births and child deaths the respondent has ever experienced ([United Nations, 1983](#); [Preston et al., 2001](#)).

Estimates based on both vital registration and surveys are susceptible to systematic biases and non-systematic measurement error. Counts of births or deaths from vital registration may be biased downwards by the omission of events from the register or under-coverage of the target population. Full birth histories are susceptible to biases caused by omission of births or misreporting the timing of events. Some omissions may be deliberate in order to avoid lengthy subsections of the survey ([Hill et al., 2012](#)). Fertility and mortality estimates from summary birth histories are derived using so-called indirect techniques such as the Brass  $P/F$  ratio method ([Brass, 1964](#); [United Nations, 1983](#); [Feeney, 1996](#)). In addition to the biases affecting full birth histories, estimates based on summary birth histories can also be affected when the assumptions behind the indirect methods are not satisfied. These assumptions concern the pattern of mortality by age and the association between mother and child mortality. They often do not hold, for example, in populations experiencing rapid mortality decline ([Silva, 2012](#)).

In the absence of vital registration, estimates of adult mortality may be based on reports of sibling survival histories collected in surveys. Often however, the only data available are on child mortality collected from surveys of women. In such cases, estimates of adult mortality are extrapolations based on model life tables ([United Nations, 1983](#); [Preston et al., 2001](#)). Model life tables are families of life tables generated from mortality data collected from a wide range of countries over a long period of time. They are indexed by a summary parameter such as  $e_0$  or U5MR and are grouped into regions. The Coale and Demeny system ([Coale et al., 1983](#); [Preston, 1976](#)) and the United Nations (UN) system for developing countries ([United Nations, 1982](#)) both have five families. Errors in estimates of adult mortality derived in this way come from errors in the survey-based estimates of under five mortality and the inability of the model life table family to capture the true mortality patterns in the population of interest.

Concerns about the accuracy of SRB estimates, particularly for periods between 1950

and 1970, have led some authors to suggest using age-specific population sex ratios as a proxy for SRBs. [Guilmoto \(2009\)](#) suggests the male-to-female ratio among those aged 0–4 (the “child sex ratio”) and [Bhat \(2002b\)](#) suggests the ratio among those aged 0–14 for India (the “juvenile sex ratio”). Such ratios must be estimated from census data which is probably more reliable than survey data, but still subject to age misreporting and underreporting of certain groups. For example, there appears to have been under counting of females in censuses of India ([Bhat, 2002b,c](#); [Guillot, 2002](#)).

Estimates of fertility, mortality, migration and population counts and the implied sex ratios for successive five-year periods are all related to one another via the demographic balancing equation that underlies the cohort component method of population projection (CCMPP). The estimates of these quantities published in *World Population Prospects* (WPP) must be “projection consistent” in that the age-specific population counts for year  $t$  must be the counts one gets by projecting the published counts for year  $t - 5$  forward using the published fertility, mortality and migration rates.

Under current UN procedure, all available, representative data sources are considered and techniques to reduce bias are applied where UN analysts deem them appropriate. Projection consistency is achieved through an iterative “project-and-adjust” process. Sex ratios are calculated on the final set of point estimates.

Bias reduction techniques are source- and parameter-specific. For birth history data, these might involve omitting responses of very old women, or responses pertaining to events in the distant past. In other cases, parametric models of life tables, or specially constructed life tables, may be used if available. For this reason I do not propose a generally applicable method of bias reduction, one which would work well for all parameters and data sources, since many specialized ones already exist (e.g., [United Nations, 1983](#); [Murray et al., 2010, 2003](#); [Alkema et al., 2012](#)). Bayesian reconstruction takes as input bias-reduced initial estimates of ASFRs and age- and sex-specific initial estimates of mortality, international migration and population counts. Measurement error is accounted for by modeling these quantities as probability distributions. Projection consistency is achieved by embedding the CCMPP in a Bayesian hierarchical model. Inference is based on the joint posterior distribution on the input parameters, which is sampled from using Markov chain Monte

Carlo (MCMC).

## 4.2 Method

### 4.2.1 Notation and Parameters

The parameters of interest are age- and time-specific vital rates, net international migration flows, population counts and SRB. I am concerned only with international migration which I will refer to as simply “migration”. The symbols  $n$ ,  $s$ ,  $g$  and  $f$  denote population counts, survival (a measure of mortality), net migration (immigrants minus emigrants) and fertility, respectively. All of these parameters will be indexed by five-year increments of age, denoted by  $a$ , and time, denoted by  $t$ . The parameters  $n$ ,  $s$  and  $g$  will also be indexed by sex, denoted by  $l = F, M$ , where  $F$  and  $M$  indicate female and male, respectively. SRB is defined as the number of male births for every female birth. It will be indexed by time. Reconstruction will be done over the time interval  $[t_0, T]$ . The age scale runs from 0 to  $A > 0$ ; in my applications  $A$  is 80. The total number of age groups/time periods is denoted  $K$ . To model fertility, I define  $a_L^{[\text{fert}]} \leq a_U^{[\text{fert}]}$  where fertility is assumed to be zero at ages outside the range  $[a_L^{[\text{fert}]}, a_U^{[\text{fert}]} + 5)$ . Throughout, a prime indicates vector transpose. I will use boldface for vectors and a “.” to indicate the indices whose entire range is contained therein. Multiple indices are stacked in the order  $a, t, l$ . For example,  $\mathbf{n}_{\cdot, t_0, F}$  is the vector of age-specific female population counts in exact year  $t_0$ ,  $[n_{0, t_0, F}, \dots, n_{A, t_0, F}]'$  and  $\mathbf{n}_{\cdot, \cdot, \cdot} = [n_{0, t_0, F}, \dots, n_{A, T, F}, \dots, n_{0, t_0, M}, \dots, n_{A, T, M}]'$ .

The parameters are the standard demographic parameters used for projection. The fertility parameters,  $f_{a, t}$ , are age-, time-specific occurrence/exposure rates. They give the ratio of the number of babies born over the period  $[t, t + 5)$  to the number of person-years lived over this period by women in the age range  $[a, a + 5)$ . If a woman survives for the whole five-year period she contributes five person-years to the denominator; if she survives only for the first year and a half she contributes 1.5 person-years, and so forth. The survival parameters,  $s_{a, t, l}$ , are age-, time-, and sex-specific proportions. They give the proportion of those alive at time  $t$  that survive for five years. The age subscript on the survival parameters indicates the age-range will survived *into*. For example, the number of females aged  $[15, 20)$

alive in 1965 would be the product  $(n_{10,1960,F})(s_{15,1960,F})$  (ignoring migration for clarity). It also means that  $s_{0,1960,F}$  is the proportion of female births born during 1960–1965 that are alive in 1965, hence aged 0–4. The oldest age group is open-ended and survival must be allowed for in this age group. Thus, the proportion aged  $[A, \infty)$  at time  $t$  that survives through the interval  $[t, t+5)$  is denoted  $s_{A+5,t,l}$ . Migration is also expressed as a proportion. The net number of migrants aged  $[a, a+5)$  over the interval  $[t, t+5)$  is  $(n_{a,t,l})(g_{a,t,l})$ .

#### 4.2.2 Projection of Two-Sex Populations

The CCMPP allows one to calculate the number alive by age and sex, at any time,  $t = t_0 + 5, \dots, T$  using  $\mathbf{n}_{\cdot,t_0,\cdot}$ , the vector of age- and sex-specific female and male population counts at baseline  $t_0$ , and the age-, time-, sex-specific vital rates and migration up to time  $t$ .  $\mathbf{n}_{\cdot,t,\cdot}$  is simply  $\mathbf{n}_{\cdot,t_0,\cdot}$  plus the intervening births, minus the deaths, plus net migration. Projection is a discrete time approximation to a continuous time process, and several adjustments are made to improve accuracy. The form I use has two-steps; projection is done first for those aged 5 and above,  $\mathbf{n}_{5+,t,l}$  and then for those under five,  $n_{0,t,l}$ . To this end, let us write

$$\mathbf{n}_{\cdot,t,\cdot} = \left[ \begin{array}{cc|cc} n_{0,t,F} & \mathbf{n}_{5+,t,F} & n_{0,t,M} & \mathbf{n}_{5+,t,M} \end{array} \right]', \quad (4.1)$$

where vectors and matrices are here partitioned according to sex.

The number alive at exact time  $t+5$  aged 5 and above is then given by the following matrix multiplication:

$$\left[ \begin{array}{c} \mathbf{n}_{5+,t+5,F} \\ \mathbf{n}_{5+,t+5,M} \end{array} \right] = \left[ \begin{array}{cc} \mathbf{Q}_{5+,t,F} & \mathbf{0} \\ \mathbf{0} & \mathbf{Q}_{5+,t,M} \end{array} \right] \left[ \begin{array}{c} \mathbf{n}_{\cdot,t,F} + \mathbf{n}_{\cdot,t,F} \circ (\mathbf{g}_{\cdot,t,F})/2 \\ \mathbf{n}_{\cdot,t,M} + \mathbf{n}_{\cdot,t,M} \circ (\mathbf{g}_{\cdot,t,M})/2 \end{array} \right] + \left[ \begin{array}{c} (\mathbf{g}_{5+,t,F})/2 \\ (\mathbf{g}_{5+,t,M})/2 \end{array} \right]. \quad (4.2)$$

The symbol “ $\circ$ ” indicates element-wise product;  $\mathbf{n}_{5+,t,l}$ ,  $l = F, M$ , are  $(K-1) \times 1$  vectors containing the age-specific female and male population counts at exact time  $t$ ; and  $\mathbf{g}_{5+,t,l}$ ,  $l = F, M$ , are  $(K-1) \times 1$  vectors of age-specific female and male net migration expressed as a proportion of the population.  $\mathbf{Q}_{5+,t,F}$  and  $\mathbf{Q}_{5+,t,M}$  are  $(K-1) \times K$  matrices of survival proportions for females and males at ages 5 and above, and  $\mathbf{0}$  is a  $(K-1) \times K$  matrix of

zeros. The female and male survival matrices have the same form:

$$\mathbf{Q}_{5+,t,l} = \begin{bmatrix} s_{5,t,l} & 0 & \cdots & 0 & 0 \\ 0 & s_{10,t,l} & \ddots & 0 & 0 \\ 0 & 0 & \cdots & 0 & 0 \\ 0 & 0 & \cdots & s_{A,t,l} & s_{A+5,t,l} \end{bmatrix}, \quad l = F, M \quad (4.3)$$

Splitting migration in half and adding the first half at the beginning of the projection interval and the second half at the end is a standard method of improving the accuracy of this discrete time approximation to the underlying continuous time process (Preston et al., 2001).

The number of females and males alive aged  $[0, 5)$  in exact year  $t + 5$  is derived from the total number of births over the interval,  $b_t$ , where

$$b_t = \sum_{a=a_L^{[\text{fert}]} }^{a_U^{[\text{fert}]}} 5f_{a,t} \left\{ \frac{n_{a,t,F} + (n_{a-5,t,F})(s_{a,t,F})}{2} \right\} \quad (4.4)$$

The term in braces is an approximation to the number of person-years lived by women of child-bearing age over the projection interval. The total number of each sex aged  $[0, 5)$  alive at the end of the interval is computed from  $b_t$  using under five mortality, migration and SRB:

$$n_{0,t+5,F} = b_t \frac{1}{1 + \text{SRB}_t} \{s_{0,t,F} (1 + (g_{0,t,F})/2) + (g_{0,t,F})/2\} \quad (4.5)$$

$$n_{0,t+5,M} = b_t \frac{\text{SRB}_t}{1 + \text{SRB}_t} \{s_{0,t,M} (1 + (g_{0,t,M})/2) + (g_{0,t,M})/2\}. \quad (4.6)$$

Note that the  $f_{a,t}$  in (4.4) have only two subscripts; they are the age-specific (female) fertility rates introduced above. Thus the total number of births in the projection interval is a function of the number of females of reproductive age, but not the number of males of any age, or females of other ages. This is called “female dominant projection”. This approach is preferred to alternatives, such as basing fertility on the number of male person-years lived, because survey-based fertility data is often collected by interviewing mothers, not fathers. All-sex births are computed first and then decomposed because SRB is often a parameter of interest to demographers, as it is to us here (Preston et al., 2001).

### 4.2.3 Modeling Uncertainty

In many countries, the available data on vital rates and migration are fragmentary and subject to systematic biases and non-systematic measurement error. In Chapter 2 I proposed Bayesian reconstruction as a way of estimating past vital rates, migration and population counts for a single-sex population which accounts for measurement error. Systematic biases are treated in a pre-processing step which yields a set of bias-reduced “initial estimates” for each age-, time-specific fertility rate, survival and migration proportion and population count. I use an asterisk (“\*”) to denote initial estimates. Hence  $f_{a,t}^*$  is the initial estimate of  $f_{a,t}$ . At the heart of Bayesian reconstruction is a hierarchical model which takes the initial estimates as inputs. Here, I develop the model given in Chapter 2 to the case of two-sex populations.

Take  $t_0$  and  $T$  to be the years for which the earliest and most recent bias adjusted census-based population counts are available (henceforth, I refer to these simply as census counts). Years following  $t_0$  for which census counts are also available are denoted  $t_0 < t_L^{[\text{cen}]}, \dots, t_U^{[\text{cen}]} \leq T$ . Let  $\boldsymbol{\theta}$  be the vector of all age-, time- and sex-specific fertility rates, survival and migration proportions over the period  $[t_0, T)$ , the SRBs, and the age- and sex-specific census counts in year  $t_0$ . These are the inputs required by the CCMPP. I abbreviate CCMPP by  $M(\cdot)$ . Let  $\boldsymbol{\psi}_t$  be the components of  $\boldsymbol{\theta}$  corresponding to time  $t$ , excluding  $\mathbf{n}_{t_0}$ . Therefore,  $\boldsymbol{\theta} = [\mathbf{n}'_{\cdot, t_0, \cdot}, \mathbf{f}'_{\cdot, \cdot, \cdot}, \mathbf{s}'_{\cdot, \cdot, \cdot}, \mathbf{g}'_{\cdot, \cdot, \cdot}, \mathbf{SRB}'_{\cdot}]'$  and  $\boldsymbol{\psi}_t = [\mathbf{f}'_{\cdot, t, \cdot}, \mathbf{s}'_{\cdot, t, \cdot}, \mathbf{g}'_{\cdot, t, \cdot}, \mathbf{SRB}'_t]'$ ,  $t \neq t_0$ . Reconstruction requires estimation of  $\boldsymbol{\theta}$  which I do using the following hierarchical model:

$$\begin{aligned} \text{Level 1 :} \quad & \log n_{a,t,l}^* | n_{a,t,l}, \sigma_n^2 \sim \text{Normal}(\log n_{a,t,l}, \sigma_n^2) \\ & t = t_L^{[\text{cen}]}, \dots, t_U^{[\text{cen}]} \end{aligned} \tag{4.7}$$

$$\begin{aligned} \text{Level 2 :} \quad & n_{a,t,l} | \mathbf{n}_{\cdot, t-5, \cdot}, \boldsymbol{\psi}_{t-5} = M(\mathbf{n}_{\cdot, t-5, \cdot}, \boldsymbol{\psi}_{t-5}) \\ & t = t_0 + 5, \dots, T \end{aligned} \tag{4.8}$$

$$\text{Level 3 :} \quad \log \text{SRB}_t | \text{SRB}_t^*, \sigma_{\text{SRB}}^2 \sim \text{Normal}(\log \text{SRB}_t^*, \sigma_{\text{SRB}}^2) \tag{4.9}$$

$$\log f_{a,t} | f_{a,t}^*, \sigma_f^2 \sim \begin{cases} \text{Normal}(\log f_{a,t}^*, \sigma_f^2), & a = a_L^{[\text{fert}]}, \dots, a_U^{[\text{fert}]} \\ \text{undefined}, & \text{otherwise} \end{cases} \tag{4.10}$$

$$\log n_{a,t_0,l} \mid n_{a,t_0,l}^*, \sigma_n^2 \sim \text{Normal}(\log n_{a,t_0,l}^*, \sigma_n^2) \quad (4.11)$$

$$\text{logit } s_{a,t,l} \mid s_{a,t,l}^*, \sigma_s^2 \sim \text{Normal}(\text{logit } s_{a,t,l}^*, \sigma_s^2), \quad a = 0, 5, \dots, A + 5 \quad (4.12)$$

$$g_{a,t,l} \mid g_{a,t,l}^*, \sigma_g^2 \sim \text{Normal}(g_{a,t,l}^*, \sigma_g^2) \quad (4.13)$$

(where  $a = 0, 5, \dots, A$ ;  $t = t_0, t_0 + 5, \dots, T$ ;  $l = F, M$  in (4.7)–(4.13) unless otherwise specified)

$$\text{Level 4 :} \quad \sigma_v^2 \sim \text{InvGamma}(\alpha_v, \beta_v), \quad v = n, f, s, g, SRB. \quad (4.14)$$

For  $x < 0 < 1$ ,  $\text{logit}(x) \equiv \log(x/(1-x))$ . The joint prior at time  $t$  is multiplied by

$$I\{M(\mathbf{n}_t, \boldsymbol{\psi}_t) > 0\} \equiv \begin{cases} 1 & \text{if, for all } a = 0, \dots, A, A + 5, l = F, M, n_{a,t+5,l} \geq 0 \\ 0 & \text{otherwise.} \end{cases} \quad (4.15)$$

to ensure a non-negative population. In Chapter 2, the female-only model had  $SRB$  fixed at 1.05 and  $l = F$ .  $SRB$  can be interpreted as the odds that a birth is male, so (4.9) is a model for the log-odds that a birth is male.

The parameters  $\alpha_v, \beta_v$ ,  $v = n, f, s, g, SRB$ , define the distribution of the standard deviation parameters that represent measurement error in the initial estimates. I set these parameters using the expert opinion of United Nations Population Division (UNPD) analysts by eliciting liberal, but realistic, estimates of initial estimate accuracy as described in Section 3.2.3. These elicitations are called “elicited relative errors”.

Bayesian reconstruction defines a joint prior distribution over the input parameters (4.9)–(4.15) which induces a prior on the population counts after the baseline via CCMPP. This is updated using the census counts for which a likelihood is given in (4.7). Some methods of estimating migration rely on “residual” counts; projected counts based only on vital rates are compared with census counts and the difference attributed to international migration. Methods of adjusting vital rates and census counts to ensure mutual consistency have also been proposed that use a similar approach (e.g., Luther and Retherford, 1988; Luther et al., 1986). Initial estimates of  $f_{a,t}^*$ ,  $s_{a,t,l}^*$ ,  $g_{a,t,l}^*$  should not be based on such methods since

this would amount to using the data twice and uncertainty will be underestimated in the posterior. Inference is based on a large sample drawn from the joint posterior via an MCMC algorithm as described in Section 2.3.5.

### 4.3 Application

I apply two-sex Bayesian reconstruction to the populations of Laos from 1985–2005, Thailand from 1960–2000 and India from 1971–2001. The periods of reconstruction are determined by the available data. Laos has no vital registration data. Initial estimates of fertility are based on surveys of women and the only mortality estimates are for ages under five derived from these same surveys. Thailand and India have acceptable vital registration data which provide information about fertility and mortality at all ages. Nevertheless adjustments are necessary to reduce bias due to undercount of certain groups. Vital registration is thought to have underestimated U5MR in Thailand, for example (Hill et al., 2007) and in India 50–60 percent of children are born at home which increases the likelihood of omission from the register (United Nations Population Fund, 2010).

Estimates of population sex ratios in India have been relatively high throughout the twentieth century. Prior to the late 1970s, these were thought to have been caused by an excess of female mortality (high SRMs), and from the late 1970s onwards by high SRBs. Both of these phenomena have been linked to cultural preferences for sons over daughters which were intensified by a rapid fall in fertility rates (Visaria, 1971; Bhat, 2002b,c; Das Gupta, 2005; Guilmoto, 2007a). Concern over the accuracy of some estimates of SRB has led some authors to suggest using the SRTP and sex ratios for young age groups as proxies for SRB and SRMs (Bhat, 2002b,c; Guilmoto, 2009). I use Bayesian reconstruction to derive posterior intervals for the SRB, SRMs, and also the SRTP and the sex ratio among those aged 0–4.

Thai families appear to desire girls and boys about equally and SRBs are believed to have been mostly within the typical range despite Thailand experiencing an even more rapid fertility decline than India (Kamnuansilpa et al., 1982; Knodel et al., 1996; Guilmoto, 2009). Fertility rates in Laos have fallen but remain high relative to other Asian countries. Very little has been written about sex ratios for this country (but see Frisen, 1991).



In the remainder of this section, I briefly describe the data sources for each country and the method used to derive initial estimates. I focus on key details and the most interesting outputs; further results, including those for migration, can be found in the appendices to this chapter. All computations were done using the *R* environment for statistical computing (R Development Core Team, 2012). Bayesian reconstruction is implemented in the package *popReconstruct*. The method of Raftery and Lewis (1996) was used to select the length of MCMC chains ( $q = 0.025$ ,  $0.975$ ,  $r = 0.0125$ ,  $s = 0.95$ ).

#### 4.3.1 Data Sources

##### *Laos, 1985–2005*

National censuses were conducted in 1985, 1995 and 2005, hence I reconstruct the whole population between 1985 and 2005. I used the same initial estimates of fertility, female mortality, migration and population counts as in Chapter 3. In these, migration was centred at zero for all sexes, ages and time periods, with a large relative error of 20 percent. Initial estimates for males were derived in an analogous manner. There was very little information about the SRB, so initial estimates were set at 1.05, a demographic convention (Preston et al., 2001), with a large elicited relative error of 50 percent. Initial estimates for certain parameters are plotted along with the results (Section 4.3.2). Further details on data sources are in Appendix 4.B.

##### *Thailand, 1960–2000*

Censuses were conducted in 1960, 1970, 1980, 1990 and 2000. I used the counts in WPP 2010 which were adjusted for known biases such as undercount. Initial estimates of SRB were taken directly from current fertility based on vital registration. No smoothing was done. The elicited relative error was set to 50 percent. Initial estimates of age-specific fertility were based on direct and indirect estimates of current fertility and children ever born (CEB) based on the available data including surveys and vital registration. Each data series was normalized to give the age pattern and summed to give total fertility rate (TFR). These were smoothed separately using weighted cubic splines and the resulting estimates

combined to yield a single series of initial estimates of ASFRs. The weights were determined by UN analysts based on their expert judgment about the relative reliability of each source. Initial estimates of survival for both sexes were based on life tables calculated from vital registration, adjusted for undercount using data from surveys. The elicited relative error for fertility and survival was set to 10 percent. I used the same initial estimates of international migration as for Laos. Initial estimates for certain parameters are plotted along with the results (Section 4.3.2). Further details on data sources are in Appendix 4.B.2.

### *India, 1971–2001*

Censuses have been taken roughly every 10 years in India since 1872. I begin the period of reconstruction with 1971. This is the first census year for which vital rate data independent of the census are available, collected by the Indian Sample Registration System (SRS). Subsequent censuses were taken in 1981, 1991 and 2001. I used the counts in WPP 2010 which were adjusted for slight undercount in some age groups. Estimates of SRB, fertility and survival were based on data from the SRS ([Office of The Registrar General & Census Commissioner, 2011](#)), the National Family Health Surveys conducted between 1992 and 2006 ([International Institute for Population Sciences, 2009](#)) and the 2002–04 Reproductive Child Health Survey. Weighted cubic splines were used to smooth estimates of SRB and fertility in the same manner as for Thailand. The UN South-Asian model life table was used for survival estimates. The same initial estimates for migration were used for India as for Laos and Thailand and the elicited relative errors were also the same. The elicited relative error of 10 percent for the vital rates is consistent with independent assessments of the coverage of the SRS ([Bhat, 2002a](#); [Mahapatra, 2010](#)). The elicited relative error of 50 percent for SRB results in a marginal prior with 90th percentile approximately equal to 1.60. This is comparable to the highest reported estimates of SRB which were between 1.30 and 1.50 in some states ([Guilmoto, 2009](#)).

Initial estimates for certain parameters are plotted along with the results (Section 4.3.2). Further details on data sources are in Appendix 4.B.3.

### 4.3.2 Results

Key results are given by country; more results are presented in Appendix 4.C. I show the limits of 95 percent credible intervals for the marginal prior and posterior distributions of selected parameters. The magnitude of uncertainty will be summarized using half-widths of these intervals, averaged over sex and time. I compare my results to those published in WPP 2010 for years with comparable estimates. WPP 2010 was based on a different procedure but the same data, therefore the comparison is useful.

#### *Laos, 1985–2005*

Medians and prior and posterior probability intervals for TFR and SRB are shown in Figure 4.1. The initial estimate of SRB was fixed at 1.05, a demographic convention (Preston et al., 2001), due to lack of data. The posterior median deviates very little from this value, although the uncertainty has been considerably reduced; the mean of the half-widths of the 95 percent credible intervals is 0.052 compared with 0.96 for the prior (Figure 4.1b). In Chapter 3 I reconstructed the female-only population and fixed SRB at 1.05. The posterior intervals for SRB in this two-sex reconstruction are centered at this same value and the posterior for TFR obtained here (Figure 4.1a) is very similar that obtained in Chapter 3.

The results for  $e_0$  and U5MR are shown in Figures 4.2 and 4.3. The posterior estimates differ slightly from those in WPP 2010 but there is general agreement on the overall trend;  $e_0$  increased while U5MR decreased consistently over the period of reconstruction. There is strong evidence that female  $e_0$  was higher from 1990 through 2005 since the posterior intervals for the difference lie completely above zero for this period (Figure 4.2c). The mean half-width for the difference is 1.3 years. There appears to be very little evidence for a sex difference between 1985 and 1990, however. The posterior intervals for U5MR straddle one for the entire period of reconstruction (Figure 4.3c), again providing only weak evidence of a sex difference. The mean half-width for the sex ratio of U5MR is 0.17.

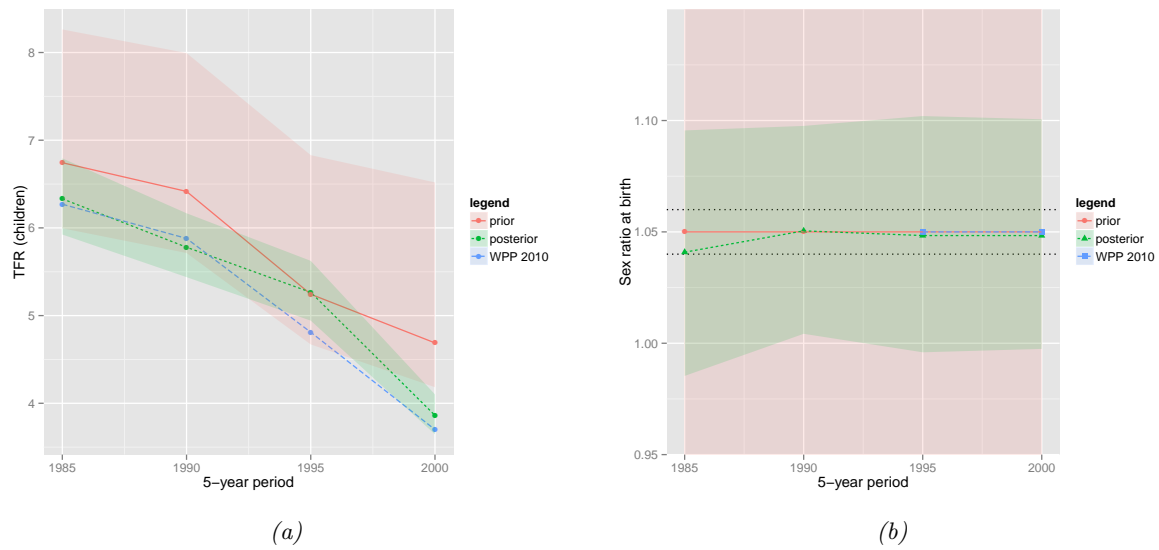


Figure 4.1. Prior and posterior medians and 95 percent credible intervals for the reconstructed population of Laos, 1985–2005: (a) total fertility rate (TFR); (b) sex ratio at birth (SRB).

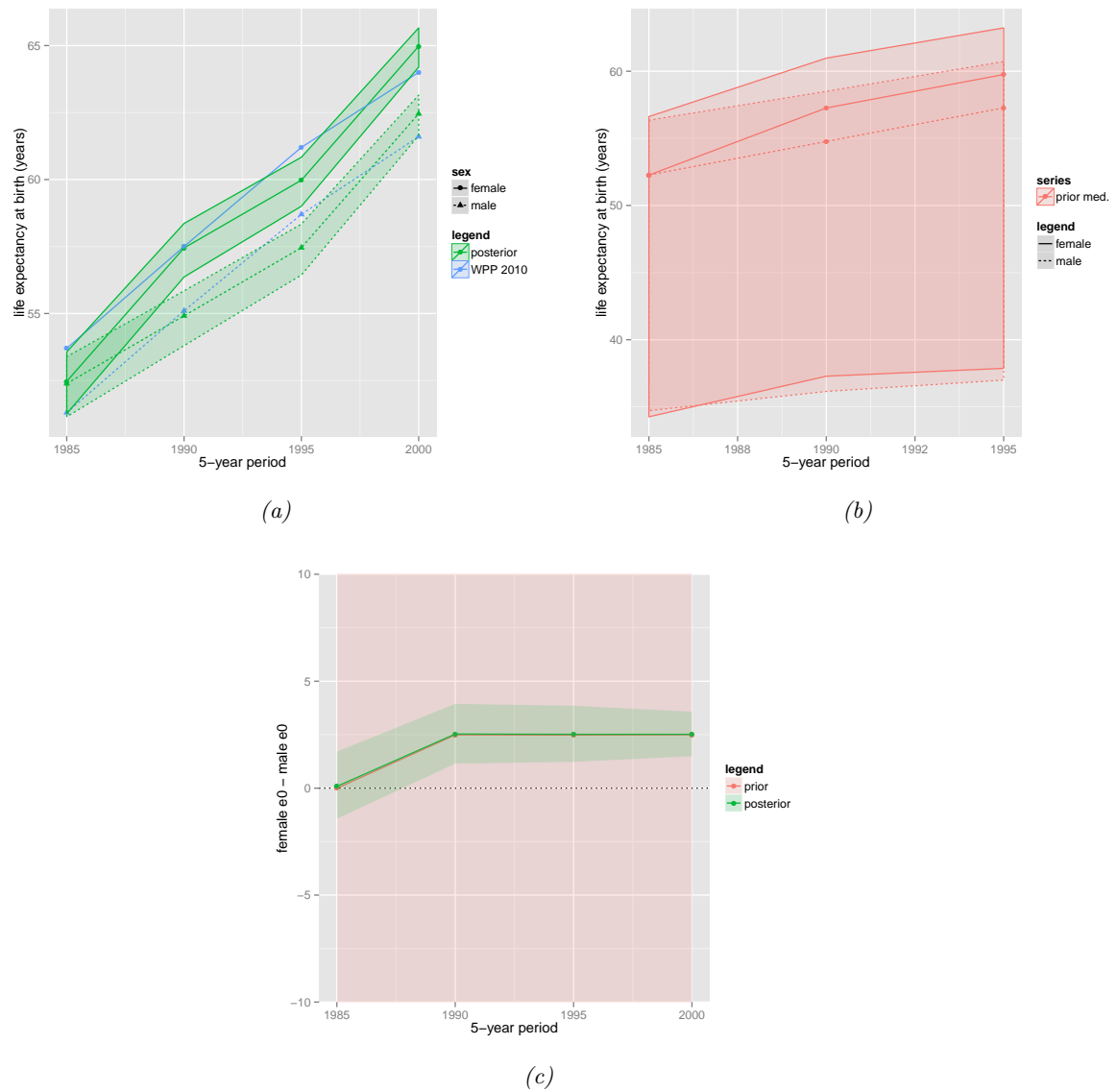


Figure 4.2. Prior and posterior medians and 95 percent credible intervals for life expectancy at birth ( $e_0$ ) for the reconstructed population of Laos, 1985–2005: (a) female and male posterior quantiles with *World Population Prospects* (WPP) 2010 estimates; (b) female and male prior quantiles only; (c) male-to-female difference.

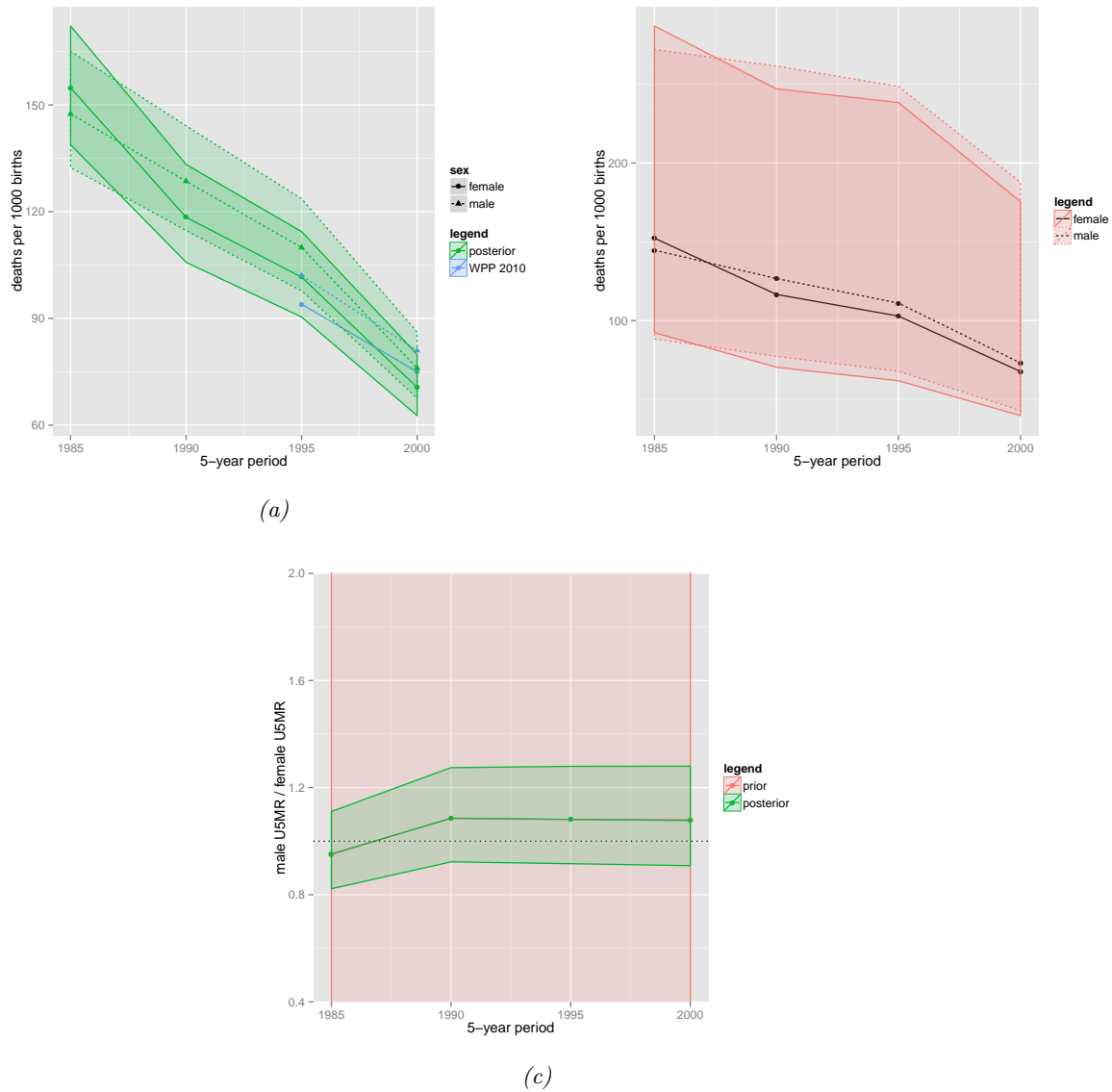


Figure 4.3. Prior and posterior medians and 95 percent credible intervals for under-five mortality rate (U5MR) for the reconstructed population of Laos, 1985–2005. (a) female and male posterior quantiles and *World Population Prospects* (WPP) 2010 estimates; (b) female and male prior quantiles only; (c) male-to-female ratio.

*Thailand, 1960–2000*

Results for TFR and SRB are shown in Figure 4.4. TFR fell very steeply in Thailand from 1960–2000 (Figure 4.4a). Posterior uncertainty about this parameter is small; the mean half-width of the posterior intervals is 0.07 children per woman. The WPP 2010 estimates all fall within the posterior intervals. In contrast, uncertainty about SRB is high. The posterior medians are lower than the initial estimates for the first five-year time-periods and the posterior intervals contain the typical range of 1.04–1.06. The probabilities that SRB was above 1.06 in each time period are in Table 4.1. These decrease from 1960–1985 and then increase through 2000.

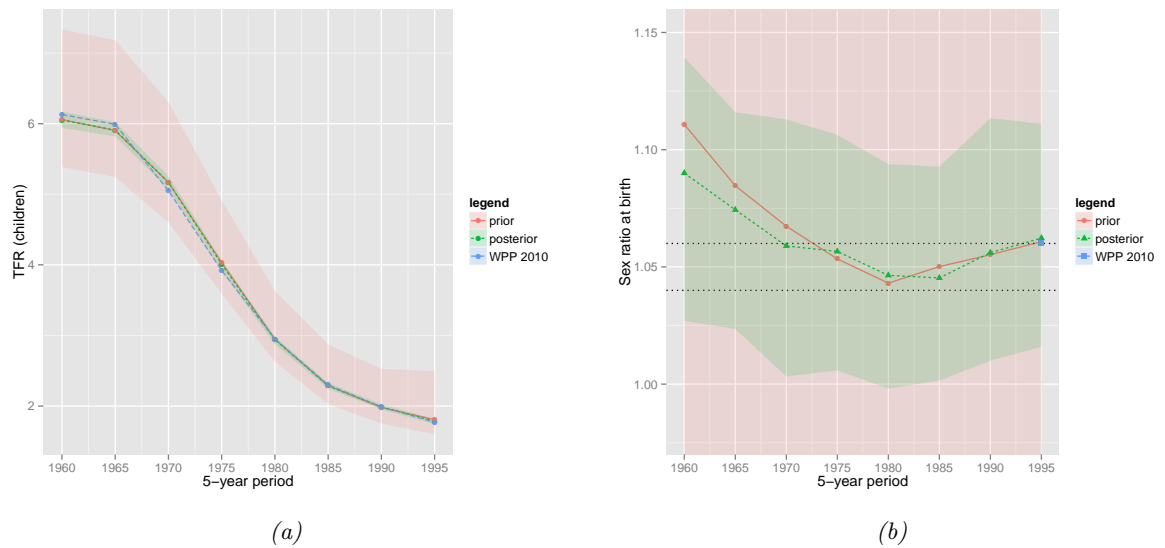


Figure 4.4. Prior and posterior medians and 95 percent credible intervals for the reconstructed population of Thailand, 1960–2000: (a) total fertility rate (TFR); (b) sex ratio at birth (SRB).

Results for mortality are shown in Figures 4.5 and 4.6. The mean half-width for  $e_0$  is 1.7 years and the posterior intervals contain the WPP 2010 estimates in all but two cases. The posterior intervals for the difference in  $e_0$  lie above zero in each five-year period, suggesting that female longevity was greater than that of males in Thailand from 1960–2000. The mean half-width is 2.5 years. The posterior for the sex ratio of U5MR is centered at or above 1 in all time periods, although 1 is within the limits of the 95 percent credible intervals. The

*Table 4.1.* Probability that sex ratio at birth (SRB) was greater than 1.06 in each time period for the reconstructed population of Thailand, 1960–2000.

1960	1965	1970	1975	1980	1985	1990	1995
0.82	0.71	0.48	0.45	0.28	0.26	0.44	0.54

mean half-width of the intervals for this ratio is 0.5.



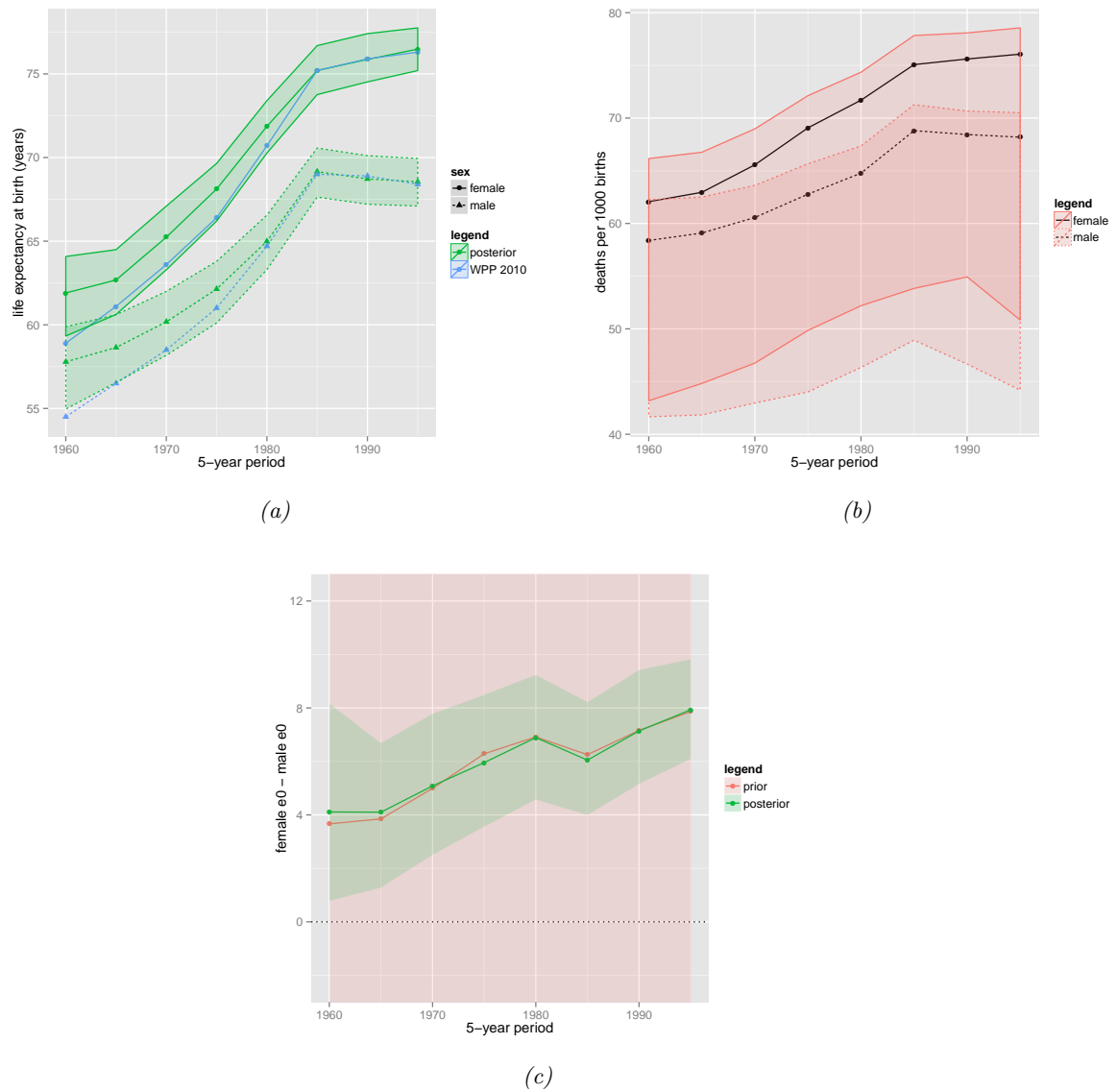


Figure 4.5. Prior and posterior medians and 95 percent credible intervals for life expectancy at birth ( $e_0$ ) for the reconstructed population of Thailand, 1960–2000. (a) female and male posterior quantiles with *World Population Prospects* (WPP) 2010 estimates; (b) female and male prior quantiles only; (c) male-to-female difference.

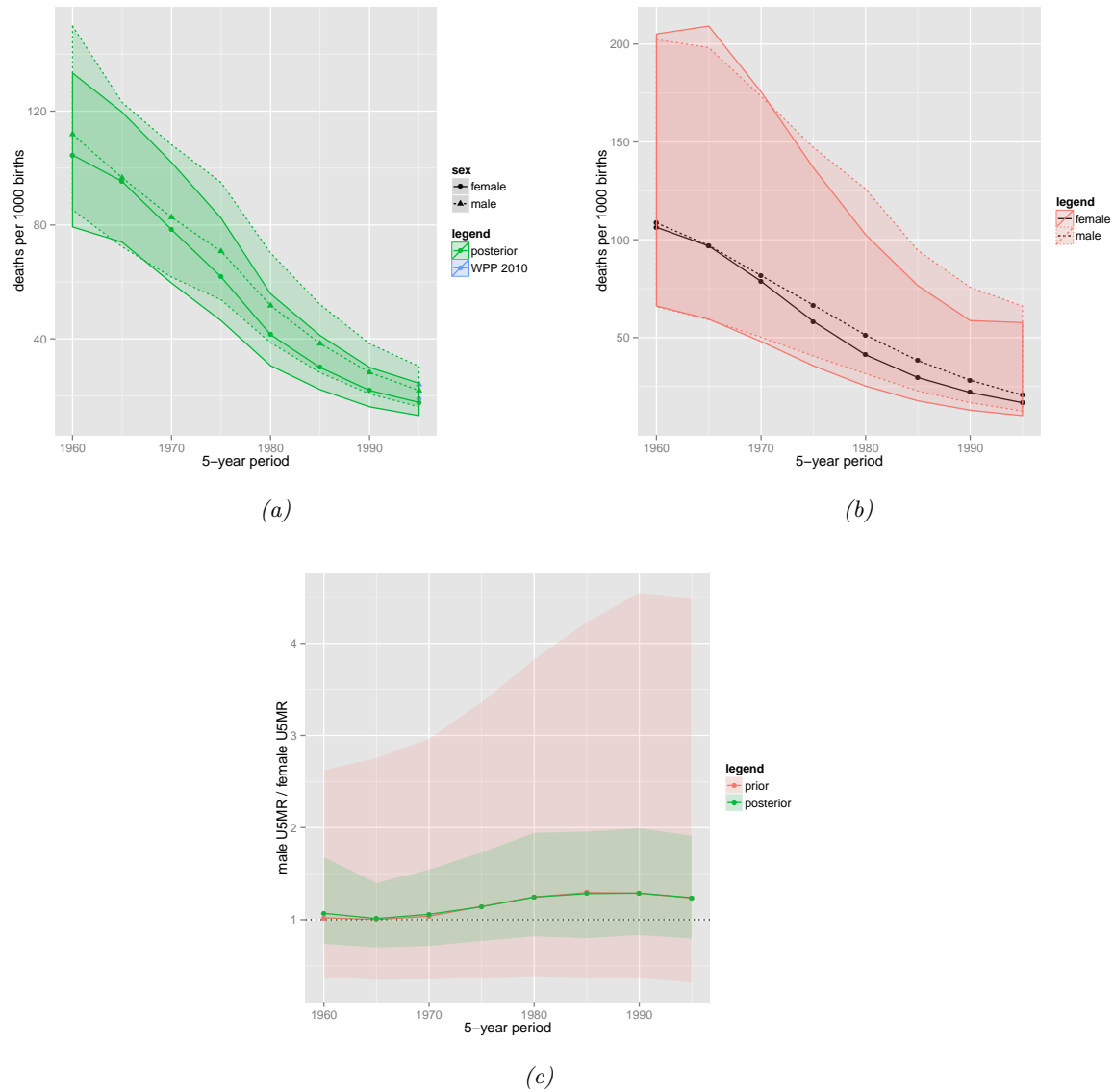


Figure 4.6. Prior and posterior medians and 95 percent credible intervals for under-five mortality rate (U5MR) for the reconstructed population of Thailand, 1960–2000 (a) female and male posterior quantiles and *World Population Prospects* (WPP) 2010 estimates; (b) female and male prior quantiles only; (c) male-to-female ratio.

*India, 1971–2001*

Figures 4.7 and 4.8 show posterior 95 percent credible intervals for TFR and SRB for India. TFR decreased consistently. The posterior intervals have half-width 0.11 children per woman. The marginal posterior for SRB is centered above the range 1.04–1.06 from 1976–2001 but the posterior uncertainty is high. The probabilities that SRB was above 1.06 in each time period are in Table 4.1. These, along with Figure 4.8, suggest that SRB increased over the period of reconstruction. To investigate this further I looked at the posterior distributions of two measures of increase: 1) the difference between SRBs in the first and last five-year time-periods; 2) the slope coefficient in the ordinary least squares (OLS) regression of SRB on time. Each quantity was calculated separately for each SRB trajectory in the posterior sample. Some actual trajectories are also shown in Figure 4.8. The probability that the difference was greater than zero is 0.76 and the same for the slope coefficient is 0.79 (Table 4.3).

*Table 4.2.* Probability that sex ratio at birth (SRB) was greater than 1.06 in each time period for the reconstructed population of India, 1971–2001.

1971	1976	1981	1986	1991	1996
0.45	0.55	0.61	0.77	0.78	0.84

*Table 4.3.* Probability of an increase in sex ratio at birth (SRB) in India, 1971–2001, measured by the difference in SRB at the start and end of the period of reconstruction and the slope coefficient in the ordinary least squares (OLS) regression of SRB on year.

Statistic	95% CI	Prob > 0
$\text{SRB}_{[1996,2001)} - \text{SRB}_{[1971,1976)}$	$[-0.037, 0.077]$	0.76
OLS slope ( $\text{SRB} \sim \text{time}$ )	$[-0.0012, 0.003]$	0.79

Results for the mortality indicators are shown in Figures 4.9 and 4.10. In contrast with Laos and Thailand, the plot for the sex difference in  $e_0$  does not suggest that female  $e_0$  is

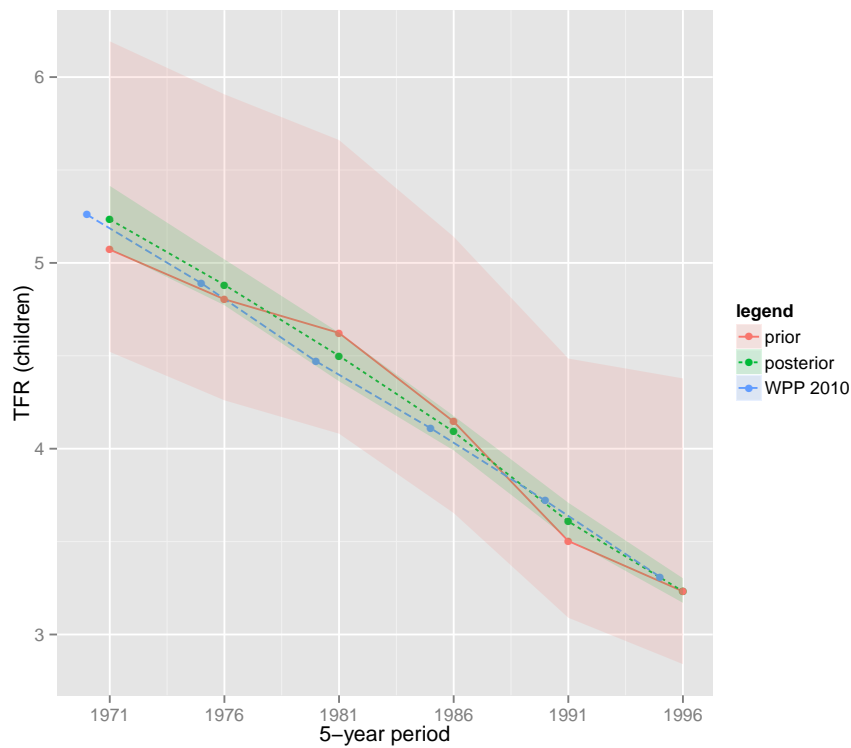
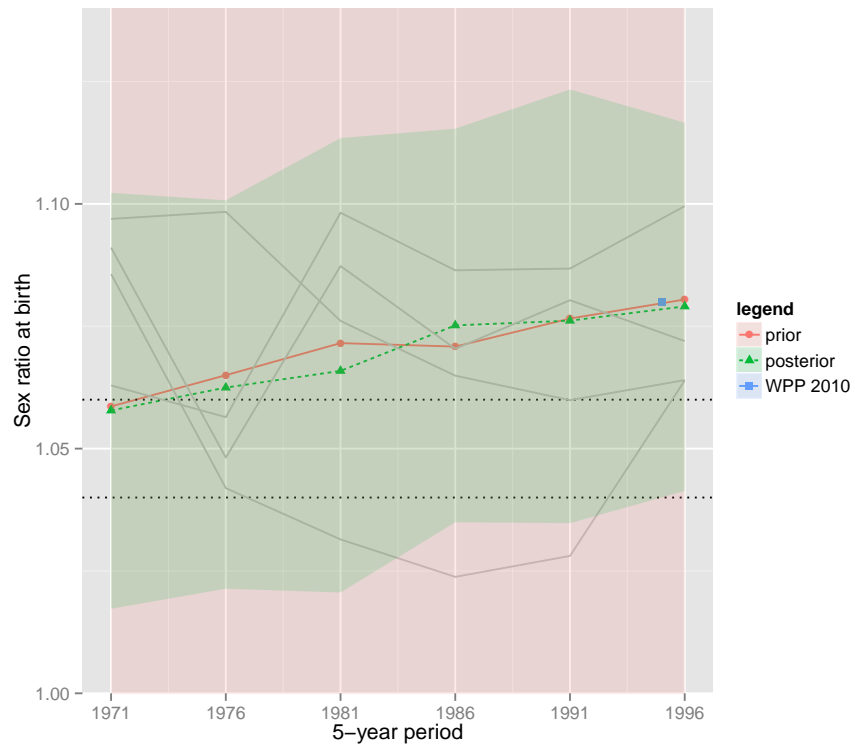


Figure 4.7. Prior and posterior medians and 95 percent credible intervals for total fertility rate (TFR) for the reconstructed population of India, 1971–2001.

typically higher than male  $e_0$  over the period of reconstruction (Figure 4.9c). The mean interval half-width for the sex difference in life expectancies is 1.9 years. The probabilities that female  $e_0$  was lower than male  $e_0$  are in Table 4.4. The possibility of a decrease in this difference was investigated using the same method applied to SRB. The probability of a simple decrease between 1971 and 2001 is 0.97 and the probability that the slope is less than zero is 0.96 (Table 4.5). Thus there is strong evidence that the difference decreased over the period of reconstruction.

Posterior medians of Indian U5MR for males are lower than those for females. The sex ratio in U5MR is centered below one but the posterior intervals contain it. The mean half-width of the intervals for this parameter is 0.19. The probability that the male-to-female ratios of U5MR was less than one (female U5MR higher than male) are in Table 4.4.



*Figure 4.8.* Prior and posterior medians and 95 percent credible intervals for sex ratio at birth (SRB) for the reconstructed population of India, 1971–2001. Four trajectories from the Markov chain Monte Carlo (MCMC) sample are also shown.

Probabilities of a linear decrease are in Table 4.5.

Population sex ratios are shown in Figure 4.11a. The posterior median SRTP declined more steeply than the ratio in the WPP census counts, which are contained within the posterior credible intervals. Sex ratios for the population aged 0–4 increased in the WPP census counts, but the posterior median remained relatively constant after an initial decline. Mean half-widths of the intervals for these two parameters are 0.012 and 0.035 respectively. Uncertainty is higher in years without a census.

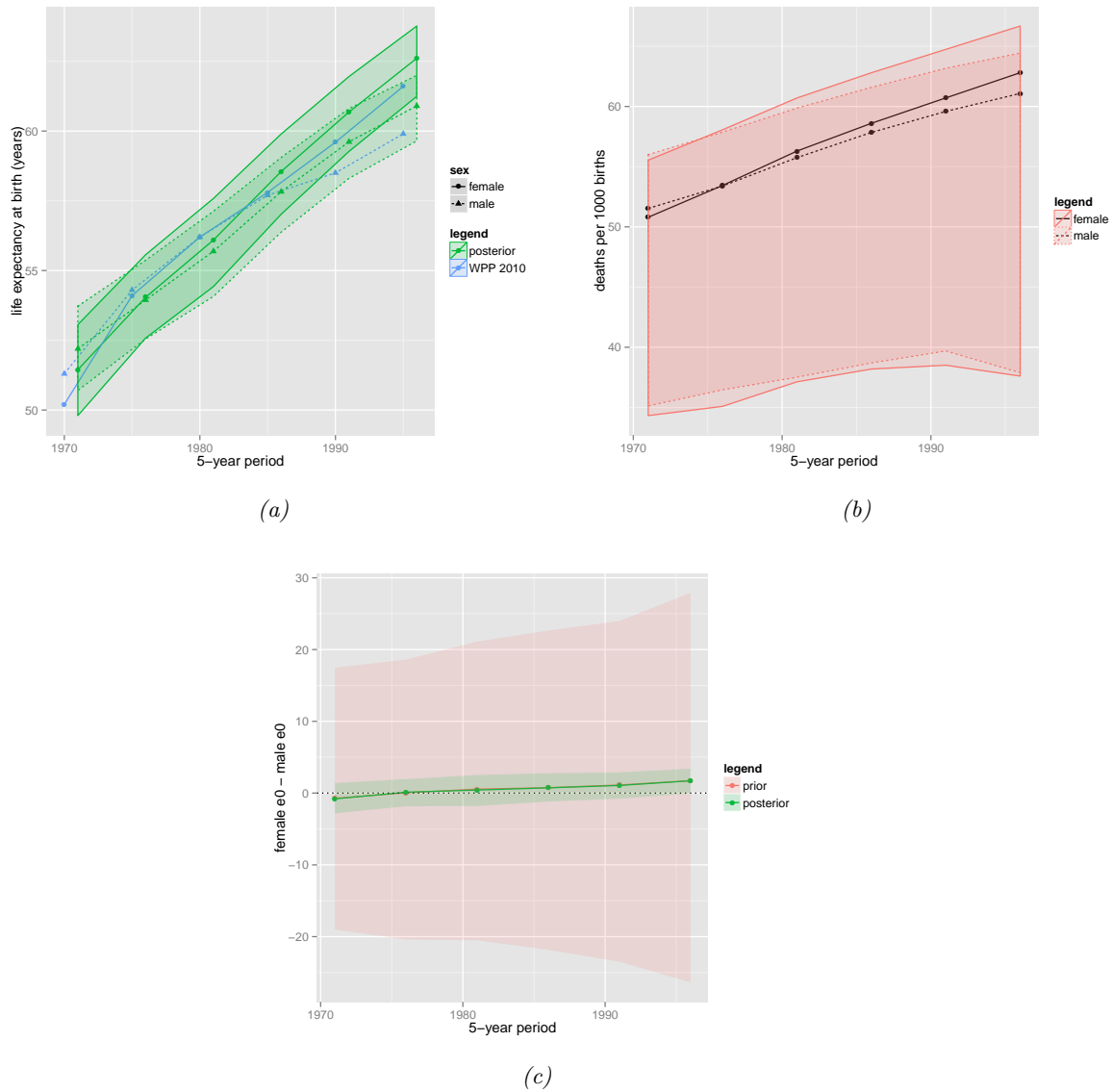


Figure 4.9. Prior and posterior medians and 95 percent credible intervals for life expectancy at birth ( $e_0$ ) for the reconstructed population of India, 1971–2001. (a) female and male posterior quantiles with *World Population Prospects* (WPP) 2010 estimates; (b) female and male prior quantiles only; (c) male-to-female difference.

*Table 4.4.* Probabilities that the difference between female and male  $e_0$  was greater than zero (female  $e_0$  higher than male) and probabilities that the sex ratio of U5MR was less than 1 (female U5MR higher than male), in each time period, for the reconstructed population of India, 1971–2001.

	1971	1976	1981	1986	1991	1996
$\Pr(\text{female } e_0 - \text{male } e_0) > 0$	0.78	0.45	0.34	0.24	0.11	0.03
$\Pr(\text{male U5MR} / \text{female U5MR}) < 1$	0.83	0.77	0.76	0.75	0.86	0.87

*Table 4.5.* Probability of an increasing linear trend for the male-to-female difference in life expectancy at birth ( $e_0$ ) and under-five mortality rate (U5MR) in India, 1971–2001, measured by the difference in sex ratio at birth (SRB) at the start and end of the period of reconstruction and the slope coefficient in the ordinary least squares (OLS) regression of SRB on year.

Statistic	95% CI	Prob > 0
life expectancy at birth ( $e_0$ )		
$e_{0[1996,2001]} - e_{0[1971,1976]}$	$[-0.15, 5.2]$	0.97
OLS slope ( $e_0 \sim \text{time}$ )	$[-0.00015, 0.0031]$	0.96
Under-five Mortality (U5MR)		
$\text{U5MR}_{[1996,2001]} - \text{U5MR}_{[1971,1976]}$	$[-0.25, 0.3]$	0.62
OLS slope ( $\text{U5MR} \sim \text{time}$ )	$[-0.011, 0.0074]$	0.34

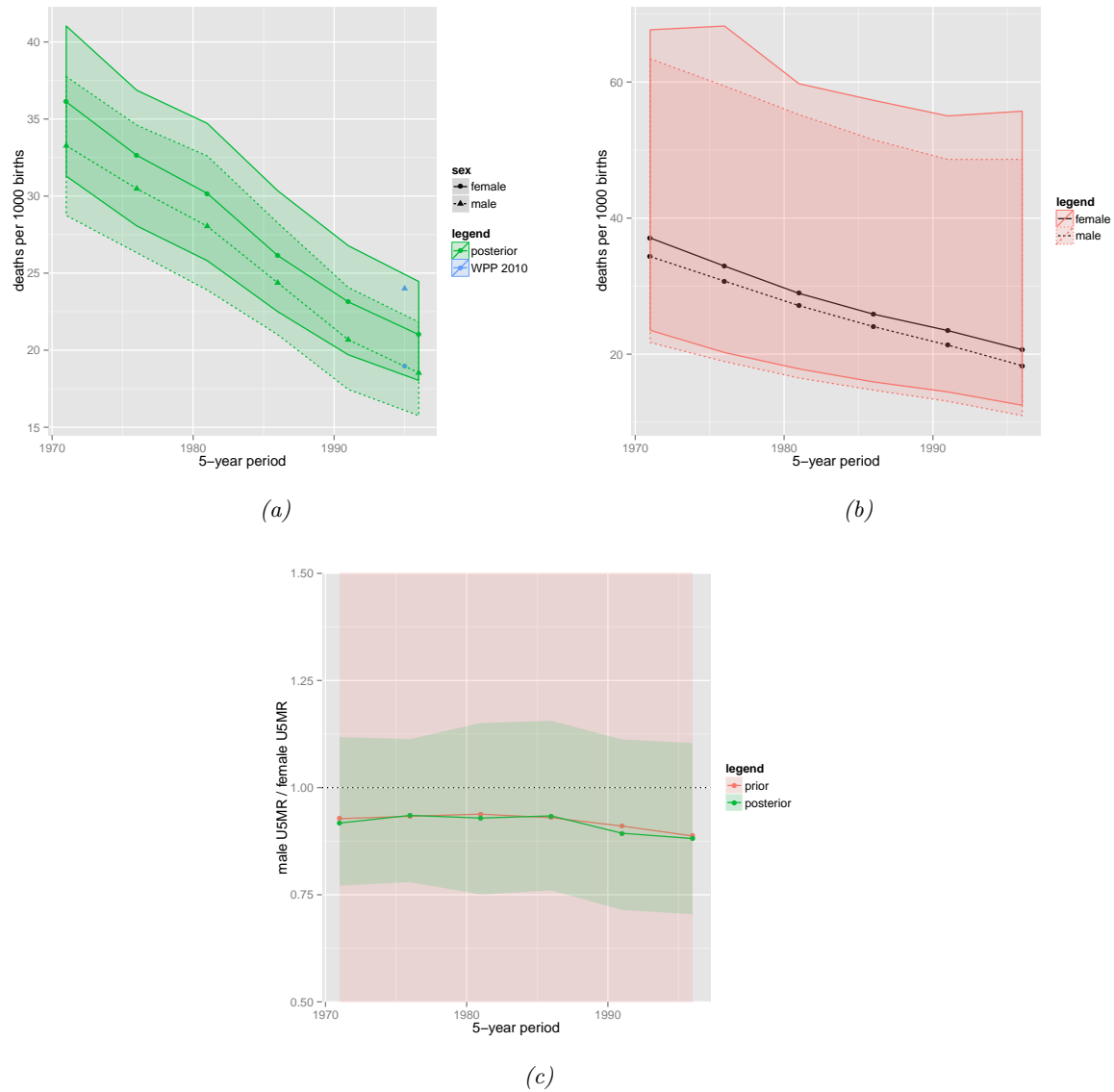


Figure 4.10. Prior and posterior medians and 95 percent credible intervals for under-five mortality rate (U5MR) for the reconstructed population of India, 1971–2001: (a) female and male posterior quantiles and *World Population Prospects* (WPP) 2010 estimates; (b) female and male prior quantiles only; (c) male-to-female ratio.



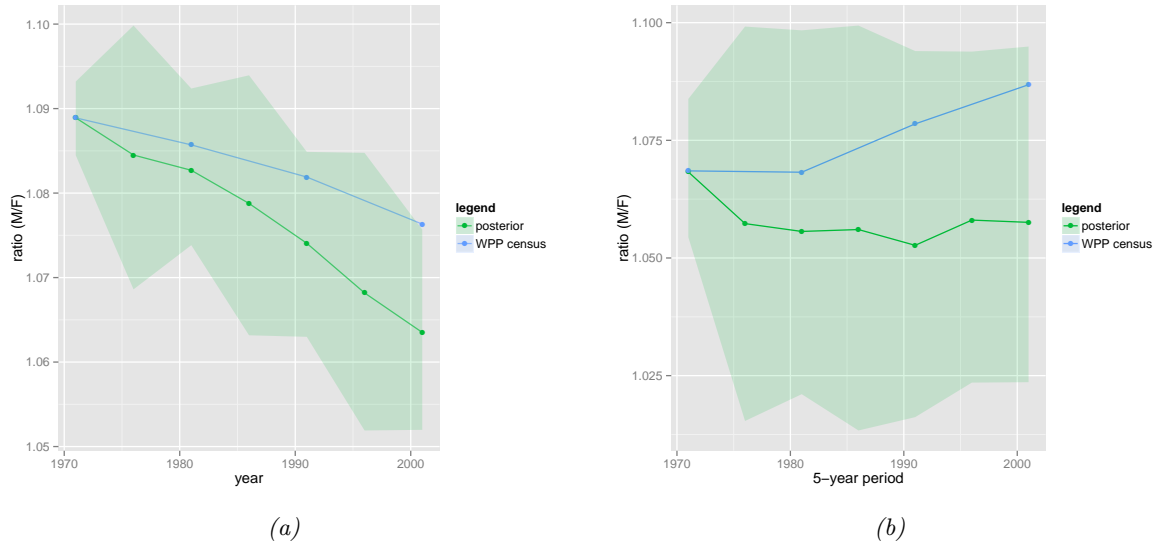


Figure 4.11. Prior and posterior medians and 95 percent credible intervals for sex ratios in the reconstructed population of India, 1971–2001: (a) sex ratio in the total population (SRTP); (b) population aged 0–4.

#### 4.4 Discussion

In its original formulation, Bayesian reconstruction was for female-only populations; here I show how two-sex populations can be reconstructed using the same framework. The method takes a set of data-derived, bias-reduced initial estimates of ASFRs, and age-sex-specific survival proportions, migration proportions and population counts from censuses, together with expert opinion on the measurement error informed by data if available. Bayesian reconstruction updates initial estimates using adjusted census counts via a Bayesian hierarchical model. The periods of reconstruction used in the applications begin in the earliest census year for which non-census vital rate data were available, and end with the year of the most recent census. Reconstruction can be done further ahead, but without a census the results are based purely on the initial estimates.

I reconstructed the populations of Laos from 1985–2005, Thailand from 1960–2000 and India from 1971–2001. My results suggest that, after accounting for measurement error, the probability SRB increased between 1971 and 2001 in India is about 0.76. Female  $e_0$  was

higher than that of males in Laos and Thailand over most of the periods of reconstruction, but not in India. However, the probability that the sex difference in Indian  $e_0$  increased between 1971 and 2001 was about 0.97.

Previous methods of population reconstruction were purely deterministic, were not designed to work with the type of data commonly available for many countries over the last sixty years or did not account for measurement error (e.g., [Lee, 1971, 1974](#); [Wrigley and Schofield, 1981](#); [Bertino and Sonnino, 2003](#)). [Daponte et al. \(1997\)](#) used a Bayesian approach to construct a counterfactual population, but age patterns of fertility were held fixed and mortality varied only through infant mortality. Bayesian reconstruction does not impose fixed age-patterns and mortality can vary at each age. Moreover, international migration is estimated in the same way as fertility and mortality.

I considered sex ratios of births and mortality because these are of interest to demographers. I compared mortality between sexes using the ratio of U5MRs and the difference of  $e_0$ s because these are the scales demographers are used to. I have not studied the associations among U5MR ratios,  $e_0$  differences and population sex ratios. The SRTP is a function of life-time cohort mortality but the U5MR and  $e_0$  presented here are period measures for which the relationship used by [Guillot \(2002\)](#) does not hold. My results add to previous work on SRMs, especially that of [Sawyer \(2012\)](#) who studied sex ratios of U5MR and called for further work to quantify its uncertainty. [Sawyer \(2012\)](#) decomposed U5MR into mortality between ages 0 and 1 (infant mortality) and mortality between ages 1 and 5 (child mortality). I reconstructed populations in age- time-intervals of width five because these are the intervals for which data is most widely available across all countries.

Many methods of adjusting vital registration using census data have been proposed (e.g., [Bennett and Horiuchi, 1981](#); [Hill, 1987](#); [Luther and Retherford, 1988](#)). [Luther et al. \(1986\)](#) and [Hill et al. \(2007\)](#) applied these methods to Thailand to estimate under-counts. The aim of these methods is to produce improved point estimates of vital rates. I have not used any census data to derive the initial estimates and Bayesian reconstruction does not produce improved point estimates. For example, initial estimates of survival were not based on inter-censal cohort survival and initial estimates of migration were not based on “residual” counts. Doing so would have amounted to using the census data twice and under-

estimated the uncertainty. The outputs of Bayesian reconstruction are interval estimates which quantify uncertainty probabilistically.

#### *4.4.1 Sex Ratios in Asia*

The SRTP is a crude measure of the balance of sexes in a population since it is not age-specific; sex ratios may be quite different among age groups, for example. Nevertheless, there is a large literature devoted to estimating SRTPs and exploring the causes and consequences, especially in Asia where SRTPs are the highest in the world ([United Nations, 2011c](#)). A persistently high sex ratio among younger cohorts will probably lead to a “marriage squeeze” in which a large number of young males may not be able to marry due to a lack of eligible females ([Guilmoto, 2012](#)). Formally, high SRTPs are the result of high SRBs and life-time sex ratios of cohort mortality ([Guillot, 2002](#)). The relative effects of these two factors may vary by time and country.

The typical range for SRB is believed to be 1.04–1.06 ([United Nations Population Fund, 2010](#)); on average, slightly more than half of all newborns are male. Concerns about quality, or a complete lack of data, have made it difficult to accurately estimate SRBs in many Asian countries.

With very few exceptions, country-level  $e_0$ s for females exceed those of males. The only countries for which this is not true are in South and Central Asia (e.g., India) and countries in Africa with generalized HIV epidemics ([United Nations, 2011c](#)). The reasons for a female advantage are diverse. Biological factors include advantages due to a superior female immune system, possibly related to the extra X chromosome, while environmental and behavioral factors include a lower prevalence of harmful activities among women, such as smoking, consumption of alcohol, and risky behavior leading to accidental death. Age-specific SRMs vary by country and age, especially in places with high maternal mortality ([Waldron, 1985, 2009; Lalic, 2011](#)).

*Laos*

Fertility in Laos remained high relative to its neighbors. For example, the estimated TFR between 1985 and 1990 is comparable to TFR in Thailand between 1960 and 1965 ([Frisen, 1991](#)). Posterior uncertainty about SRB is high and the results provide no evidence to suggest levels were atypical between 1985 and 2005. All-age mortality as summarized by  $e_0$  does appear to have been lower for females from 1990 onward. Uncertainty about sex ratios of U5MR (male / female) was such that the posterior 95 percent interval contained one in all time periods, although it was centered above one from 1990 onward.

*Thailand*

Like other parts of Asia, Thailand experienced rapid economic growth and a rapid fall in TFR from 1960. Posterior uncertainty about TFR is very low. The TFR decline was accompanied by an increase in the widespread use of modern contraceptive methods made available through government supported, voluntary family planning programs ([Kamnuan-silpa et al., 1982](#); [Knodel, 1987](#); [Knodel et al., 1996](#)).

Unlike India, Thailand is not considered to have had a high SRB ([Guilmoto, 2009](#)). Several surveys have found that the most commonly desired family configuration in Thailand is for small families of two or three children consisting of at least one boy and one girl. There is evidence that the TFR decline in Thailand intensified the existing preference for at least one child of each sex. This preferences may be related to the fact that women play important social and economic roles in Thailand, such as providing care for family members in old-age ([Knodel and Prachuabmoh, 1976](#); [Knodel et al., 1996](#)). Despite this, my posterior estimates imply that the probability SRB was above 1.06 is 0.82 between 1960 and 1965, and 0.71 between 1965 and 1970. The probabilities for subsequent time periods were lower.

Posterior intervals for sex ratios of mortality in Thailand reflect the typical pattern which is one of higher female life expectancy. As with Laos, the 95 percent posterior interval for U5MR was centered above one (male U5MR higher), but contained it for all time periods.

### *India*

The SRTP in India has received considerable attention, particularly as an indicator of discrimination against women (United Nations Population Fund, 2010). Griffiths et al. (2000) showed that only slightly elevated SRBs and SRMs at young ages are sufficient to produce the observed SRTP in India, if they persist for a long period of time. The relative contribution of these two factors may have varied over time. Bhat (2002c) and Guilmoto (2007a, 2009) argue that India experienced a transition in the 1970s whereby high SRB replaced low SRM as the cause of the high SRTPs observed throughout the period (a low SRM is a result of lower male mortality). Evidence suggested that low SRMs were due to female neglect and infanticide. In the 1970s, these practices gave way to sex selective abortion which raised the SRB instead.

The transition hypothesis is based on several pieces of evidence. Data suggested a possible rise in SRB in India above the typical range of 1.04–1.06 in the mid 1980s (Guilmoto, 2007a). In the 1970s, amniocentesis started to become available as a method for determining the sex of a foetus and abortion was legalized. Ultrasonography, a less invasive way of determining foetal sex, started to become available in many parts of India in the 1980s. In certain regions, such as the northern states and highly urbanized areas, there is a long standing tradition of preference for sons over daughters (Mayer, 1999; Bongaarts, 2001). The arrival of these new technologies in this context appears to have led to an increase in sex selective abortions in India (Bhat, 2002c; Guilmoto, 2007b; Jha et al., 2006b; United Nations Population Fund, 2010). The steep decline in Indian TFR, which began in the early 1970s, appears to have contributed to this phenomenon. Several studies have found evidence that SRB is higher at higher parities (birth orders), both in India (Das Gupta and Bhat, 1997; Bhat, 2002c; Jha et al., 2006a) and other Asian countries (Das Gupta, 2005). The increase appears to be greater if none of the earlier births were male. As family sizes decrease with TFR, the risk of having no sons increases (Guilmoto, 2009). Therefore, in cultures where sons play important economic and social functions, or where families benefit materially much more from the marriage of a son than of a daughter, the incentive to use sex selective abortion increases (Mayer, 1999; Guilmoto, 2009). After combining all available

data and including uncertainty, I found that the probability SRB was above 1.06 is 0.45 between 1971 and 1976, and 0.55 between 1996 and 2001. The probability that there was a linear increase between 1971 and 2001 is 0.76 under one measure and 0.79 under the other.

Overall mortality decreased rapidly in India from about 1950 as infectious diseases were brought under control, food security increased and health services became more widely available (Bhat, 2002c). My results suggest that, after taking account of uncertainty, there was an increase in  $e_0$  and a decrease in U5MR between 1971 and 2001 for both sexes. Using SRS data, (Bhat, 2002c) noted that the decrease was greater for females than males and the analysis of the change in the sex difference of  $e_0$  supports this; I found that the probability that the difference increased over the period of reconstruction is above 0.95. The same is not true for U5MR, however. The probability that the male-to-female U5MR ratio was higher in the 1996–2001 period than 1971–1976 was 0.62.

In the total population, the posterior median sex ratio decreases from 1971–2001 while that for the sex ratio in the age group 0–5 remains relatively constant. These trends are not inconsistent with the strong evidence for a decline in the male advantage in  $e_0$  but weaker evidence that the SRB has increased and sex ratio in U5MR declined. Uncertainty in posterior estimates of the population sex ratios is large, however, and they are not formally a function of life expectancies of U5MRs (Guillot, 2002).

India’s large population makes it a very important case for the study of sex ratios in Asia (Guilmoto, 2007a) and, like other authors (e.g., Guillot, 2002; United Nations, 2011c), I have focused on country level estimates only. However, available data suggest that there are large regional variations in SRBs and population sex ratios, with estimates for urban areas and northern states being much higher than other areas (Bhat, 2002c; Guilmoto, 2009). Currently, Bayesian reconstruction is not able to produce sub-national estimates, but could be extended to do so in the future.

#### 4.4.2 *Further Work and Extensions*

The prior distributions were constructed from initial point estimates of the CCMP input parameters, together with information about measurement error. In the examples given

here, this was based on expert opinion. In cases where good data on measurement error are available, they can be used. For example, in Chapter 3 I used information from post-enumeration surveys (PESs) to estimate the accuracy of New Zealand censuses. Data of this kind are rarely available in developing countries for either census or vital rate data. Nevertheless, some surveys come with a substantial amount of meta-data which could be used to model accuracy. This approach was taken by [Alkema et al. \(2012\)](#) who developed a method for estimating the quality of survey-based TFR estimates in west Africa by modeling bias and measurement error variance as a function of selected “data quality covariates”. I used these results in the reconstruction of the female population of Burkina Faso in Chapter 2. Extending [Alkema et al.’s \(2012\)](#) work to more countries could provide a source of initial estimates together with uncertainty that could be used as inputs to Bayesian Reconstruction.

Posterior uncertainty in estimates of U5MR is high and this led to ambiguous results for SRMs; it was not clear in any of the examples that U5MR was higher or lower for females relative to males. U5MR is under-identified in the model because the only census count it affects, that for ages 0–5, is also dependent on SRB and TFR. Recent work by the UN Interagency Group for Child Mortality Estimation (IGME) has focused on producing probabilistic estimates of U5MR ([Hill et al., 2012](#)). It might be possible to improve identifiability of the U5MR in Bayesian reconstruction by splitting the variance parameter  $\sigma^2$  into  $\sigma_{0-5}^2$  and  $\sigma_{5+}^2$ , say, and setting  $\sigma_{0-5}^2$  to IGME estimates of uncertainty, or using them to directly inform a prior on it.  $\sigma_{5+}^2$  would be treated in the same way as  $\sigma_s^2$ .

The prior distributions for international migration were centered at zero with large variances. This is a sensible default when accurate data are not available. Further work could investigate the possibility of using stocks of foreign-born, often collected in censuses, to provide more accurate initial estimates. Data on refugee movements is another source that could be investigated where relevant.

I have reconstructed national level populations only, principally because this is the level at which the UN operate. I have already mentioned that sub-national reconstructions might be of interest (Chapter 2). Subnational reconstructions could be done without any modifications to the method if the requisite data are available; national level initial estimates

and population counts would just be replaced with their subnational equivalents and the method applied as above. Reconstructing adjacent regions, or regions between which there is likely to be a lot of migration is not advisable, however, as dependencies between the two regions might not be adequately accounted for using the current approach.

A further possibility is to take the opposite direction and reconstruct the populations of several countries simultaneously. Similar concerns about migration would need to be overcome, but a multi-country version could bring advantages. For example, if the variance parameters were kept constant across countries, information about uncertainty in the Level 3 parameters could be shared among countries. If this is too restrictive the variances could be pre-multiplied by a country specific coefficient to increase flexibility.

The reconstructions reported here were done using age groups and time periods of width five years. Reducing these to intervals of width one year should be straightforward, but if data are not available at this level of detail the benefit will probably be small.

#### ***Appendix 4.A Derivation of Demographic Indicators***

TFR and  $e_0$  are defined in Chapter 2.

##### *4.A.1 Under-five Mortality Rate (U5MR)*

The U5MR is constructed in the same way as the standard “Infant Mortality Rate” (e.g., [Preston et al., 2001](#), Ch. 2), except it is for the age interval  $[0,5)$  in this case. It is defined as follows:

$$U5MR_t \equiv \frac{\text{No. deaths to those aged } [0,5) \text{ in the interval } [t, t+5)}{\text{No. births in the interval } [t, t+5)}.$$

It is neither a true demographic rate nor a probability but, nevertheless, is commonly used.



## **Appendix 4.B Further Details About Data Sources**

### *4.B.1 Laos, 1985–2005*

#### *Population Counts*

National censuses were conducted in 1985, 1995 and 2005. I used the census year counts in WPP 2010; there were no post-enumeration surveys, but these counts were adjusted to compensate for undercount in certain age groups.

#### *Fertility*

Direct and indirect estimates were based on CEB and recent births (preceding 12 and 24 months), all by age of mother, collected by the 1993 Laos Social Indicator Survey, the 1995 and 2005 censuses, the 1994 Fertility and Birth Spacing Survey, the 2000 and 2005 Lao Reproductive Health Surveys, the 1986–1988 multi-round survey and the 2006 MICS3 survey. Zaba’s (1981) Relational Gompertz Model, Arriaga’s (1983) method, the  $P/F$  method (Brass et al., 1968), Arriaga’s (1983) modified  $P/F$  method and the Brass fertility polynomial (Brass, 1960; Brass and CELADE, 1975) were used to derive indirect estimates.

Age patterns of fertility were estimated by taking medians across all available data points within the five-year intervals 1985–1990, . . . , 2000–2005. TFR was estimated separately by converting each age-specific data series into series of TFR by summing. Medians within five-year interval were then taken. The final initial estimates of the age-specific rates was obtained by multiplying the median age-patterns by the median TFRs. Data points were not weighted. The elicited relative error was set to 10 percent.

The initial estimates obtained, and the original data points, are plotted in Figures 4.12–4.14.

#### *Mortality*

Direct and indirect estimates of infant and under-five mortality ( ${}_1q_0$ ,  ${}_5q_0$ ) came from maternity histories and CEB and surviving data collected by the 1993 Laos Social Indicator Survey, the 1994 Fertility and Birth Spacing Survey, the 1995 and 2000 censuses and the

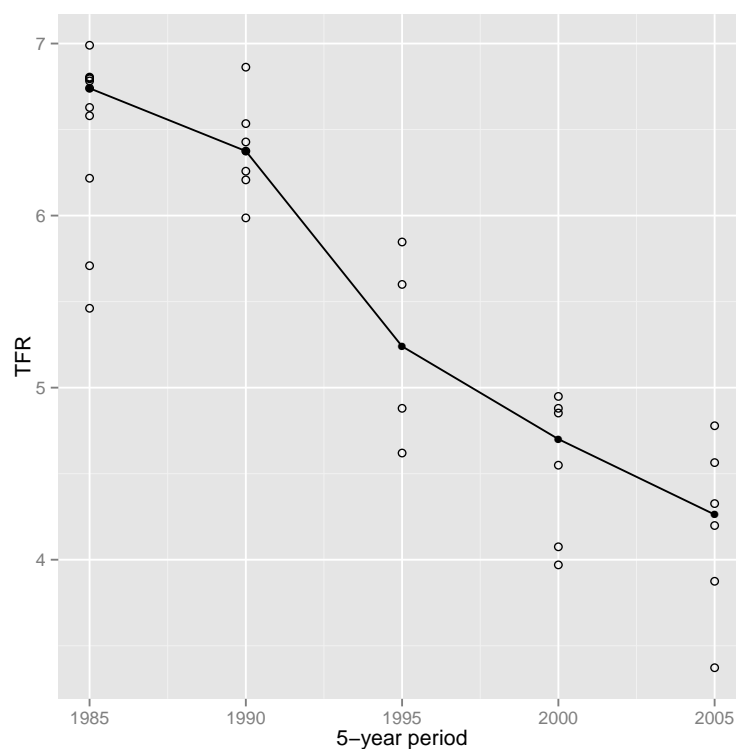


Figure 4.12. Data points (open circles) and initial estimates (solid circles, lines) for total fertility rate (TFR) for Laos, 1985–2005. See text for sources.

2000 and 2005 Lao Reproductive Health Surveys. These were smoothed using weighted cubic smoothing splines to produce single initial point estimates of the average  ${}_1q_0$  and  ${}_5q_0$  over each five-year interval during the period of reconstruction. Intercensal survival estimates were not used.

There are no direct estimates of mortality over age five. Initial estimates for these older ages were derived using the the Coale and Demeny (1983) West (CD West) family of model life tables in the following way. For each five year period, two CD West life tables were found; one with  ${}_1q_0$  closest to that produced by the smoothing procedure and one with  ${}_5q_0$  closest. Within each pair, the  $e_0$ s in these two tables were averaged. Age-specific survival proportions calculated from the CD West table with  $e_0$  closest to this average were then taken as the initial estimates of mortality at all ages. The elicited relative error of these

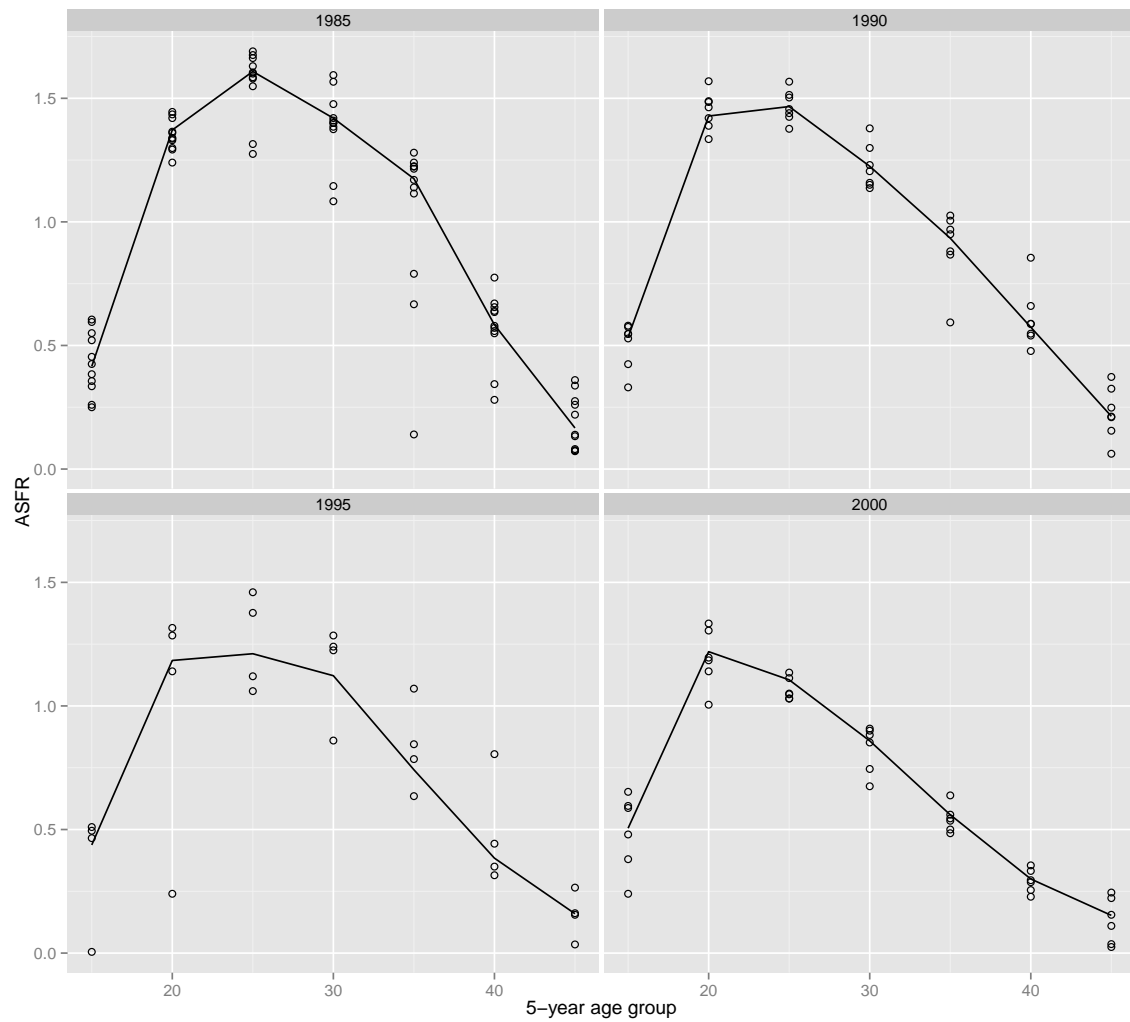


Figure 4.13. Data points (open circles) and initial estimates (lines) for age-specific fertility rate (ASFR) by time period for the population of Laos, 1985–2005.

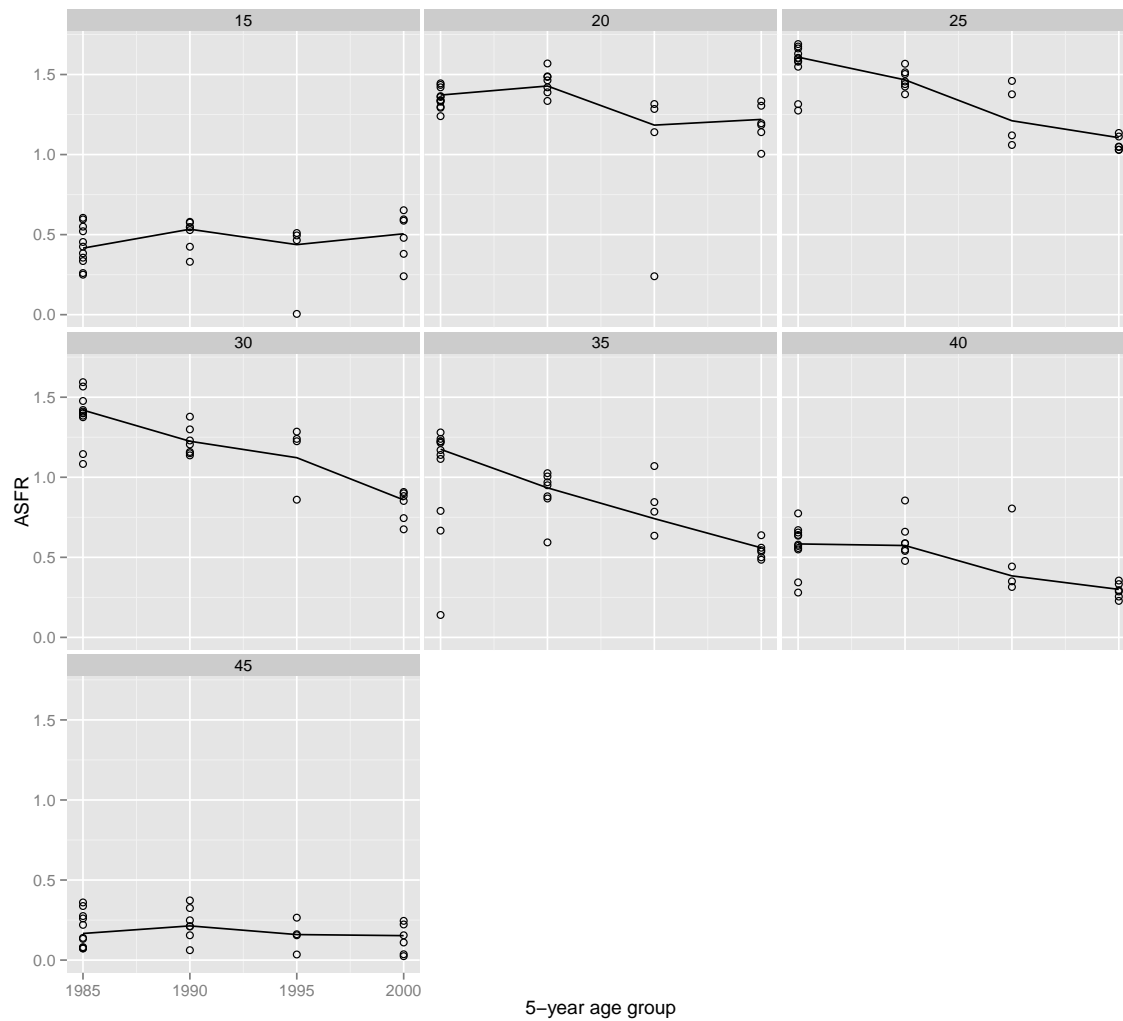


Figure 4.14. Data points (open circles) and initial estimates (lines) for age-specific fertility rate (ASFR) by age group for the population of Laos, 1985–2005. These are the same data and initial estimates as in Figure 4.13.

initial point estimates was set to 10 percent.

Figure 4.15 shows the values of  ${}_5q_0$  produced by the smoothing procedure and the abridged life table chosen from the CD West family. Initial estimates of survival proportions derived from these tables are shown in Figures 4.31 and 4.32.

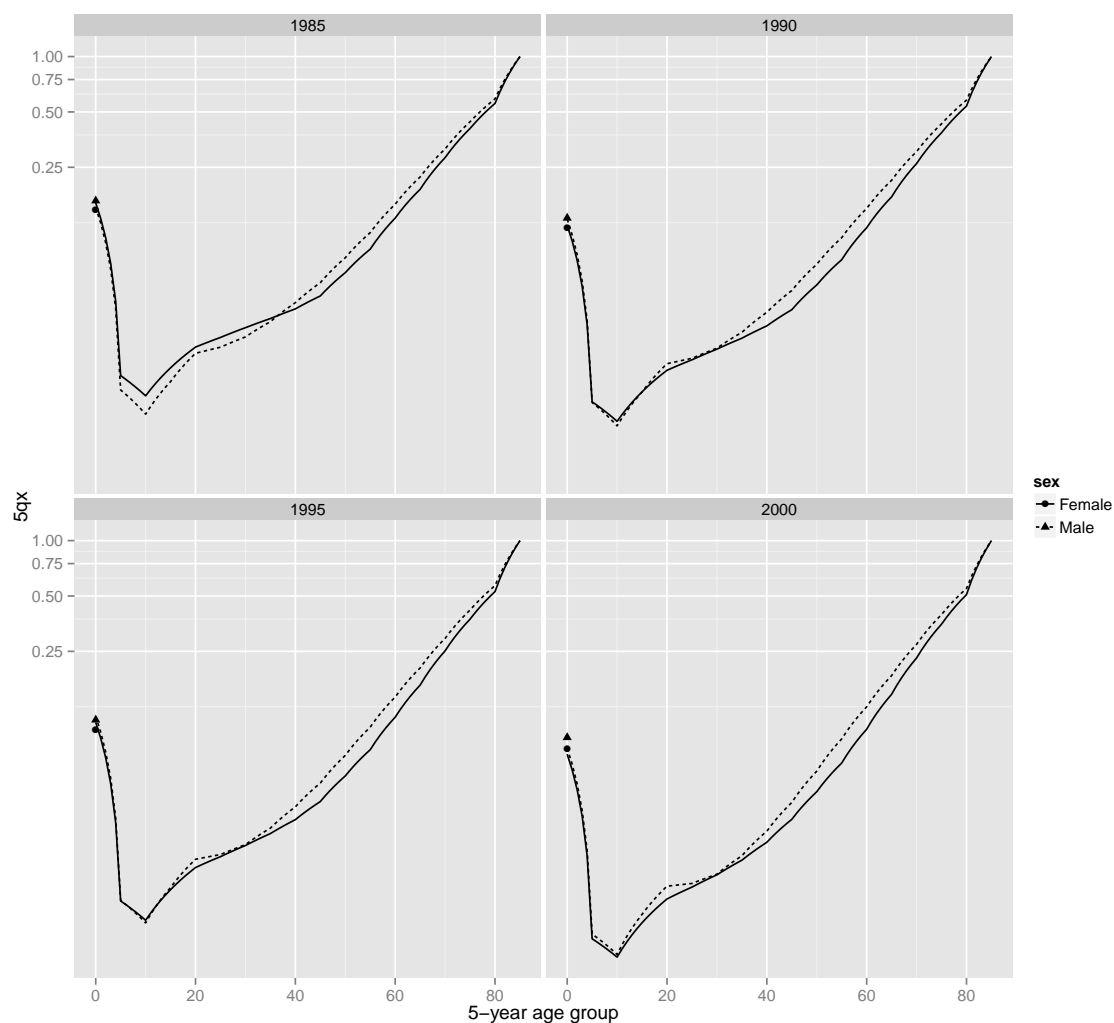


Figure 4.15. Initial estimates of age-, sex-specific probabilities of death ( ${}_nq_x$ ) for Laos females and males, 1985–2005 by five-year age group and five-year time period. Points indicate the values derived from smoothing available survey data; lines indicate the values from the Coale and Demeny West (CD West) model life table. The vertical axis has been transformed to the log scale. See text for sources.

### *Migration*

There is not much information about migration. Political upheaval resulted in significant levels of migration between 1975 and 1985 as refugees left the country. By 1985, however, these flows had become small ([U.S. Department of State, 2011](#)). No information about the age pattern or sex distribution is available. To model this, I set initial point estimates to zero for all ages and time periods, but used a large elicited relative error of 20 percent.

#### *4.B.2 Thailand, 1960–2000*

### *Fertility*

Initial estimates of age-specific fertility were based on direct and indirect estimates of current fertility and CEB taken from the Surveys of Population Change conducted between 1964 and 1996 ([The National Statistical Office of Thailand, 1970, 1977, 1992, 1997](#); see also [Vallin, 1976](#)), the WFSs ([United Nations, 1993](#)), the Thai Longitudinal Study of Economic, Social and Demographic Change ([Knodel and Pitaktepsombati, 1975](#)), the 1968–1972 Longitudinal Study of Economic, Social and Demographic Change ([National Research Council Panel on Thailand, 1980](#)), the 1978 and 1996 National Contraceptive Prevalence Surveys ([Suvanajata and Kamnuansilpa, 1979](#); [Chamrathirithong et al., 1997](#)), the 1987 DHS, and vital registration.

As for Laos, age patterns and levels of fertility were estimated separately from the available data. The available data were smoothed within age and within year using weighted splines. The weights were determined by UN analysts based on their expert judgment about the relative reliability of each source. Estimates of TFR, based on summed age-specific estimates, were obtained similarly ([Figure 4.16](#)). The final set of initial estimates was obtained by multiplying the smoothed TFRs by the smoothed age patterns ([Figures 4.17 and 4.18](#)). Elicited relative error for this parameter was set at 10 percent.

### *Mortality*

Initial estimates of mortality for both sexes were based on life tables calculated from vital registration. Vital registration is thought to have underestimated U5MR ([Hill et al., 2007](#)) so

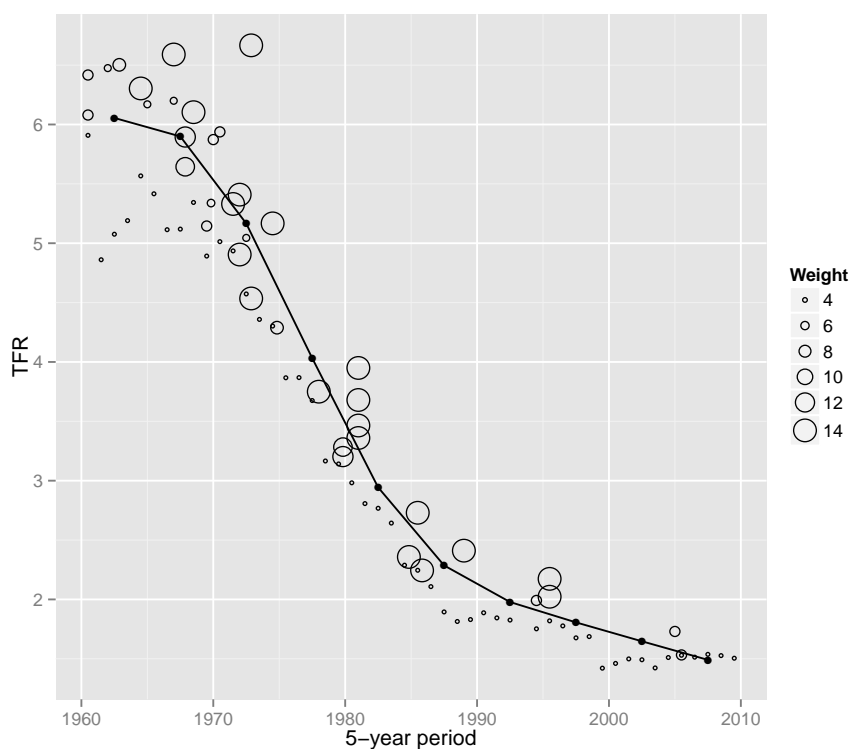


Figure 4.16. Data points (open circles) and initial estimates (solid circles, line) for total fertility rate (TFR) for Thailand, 1960–2000. See text for sources.

the following additional sources were used to derive initial estimates of under five mortality: (a) the 1974–1976, 1984–86, 1989, 1991, 1995–1996, Surveys of Population Change ([The National Statistical Office of Thailand, 1970, 1977, 1992, 1997](#)), (b) maternity-history data from the 1975 WFS and 1987 DHS, (c) data on children ever born and surviving from these surveys, the 1981–1986 Contraceptive Prevalence Surveys (CPSs). All available non-census data on  ${}_5q_x$  from these sources were weighted by UN analysts who used their expert judgment about potential biases and smoothed over time using cubic splines (Figure 4.19). The splines were evaluated at 1962.5, 1968.5, . . . 1998.5 and the values substituted for the  ${}_5q_x$ s in the life tables based solely on vital registration. The final tables are in Figure 4.20. Survival proportions were derived from these “spliced” life tables (see Figures 4.43 and 4.44).

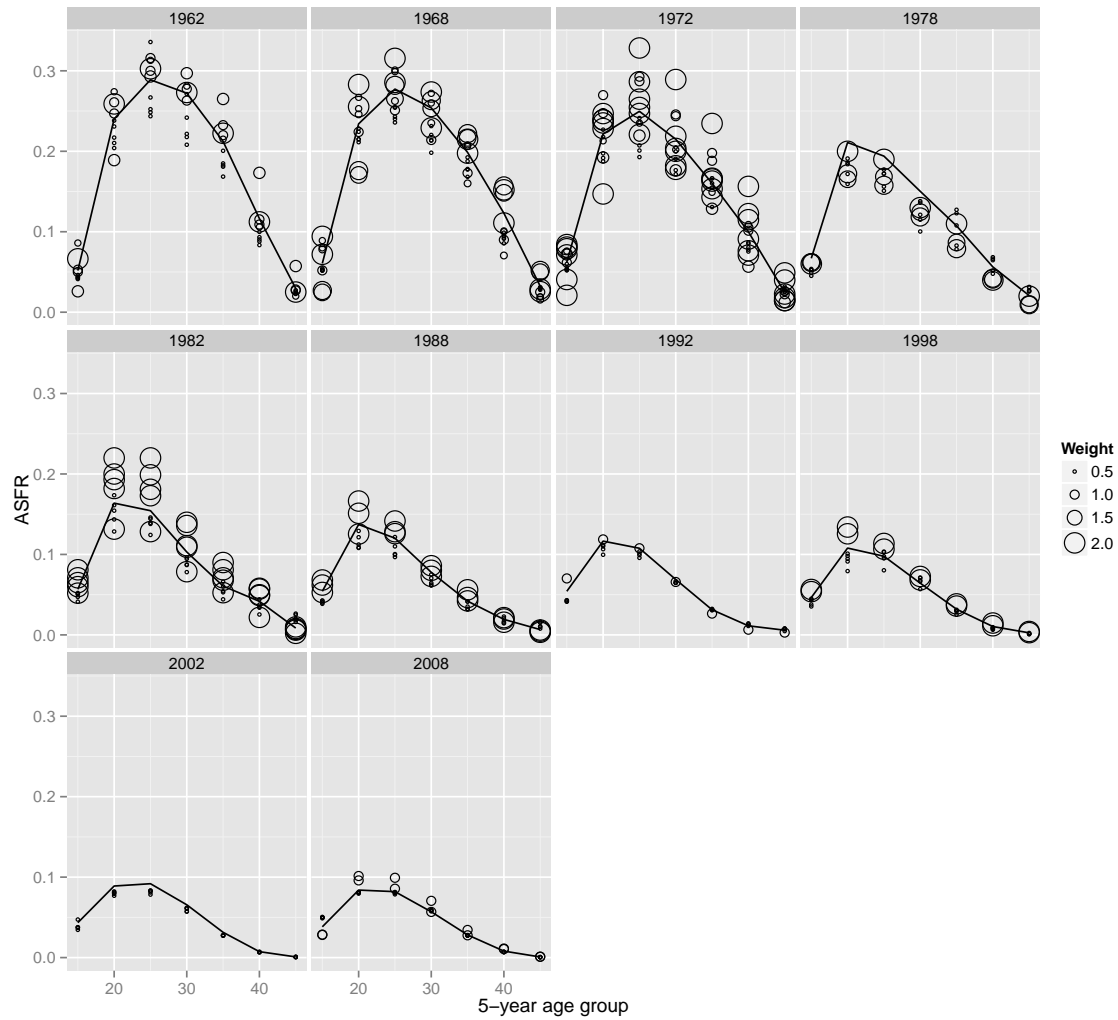


Figure 4.17. Data points (open circles) and initial estimates (lines) for age-specific fertility rate (ASFR) Thailand, 1960–2000. See text for sources.



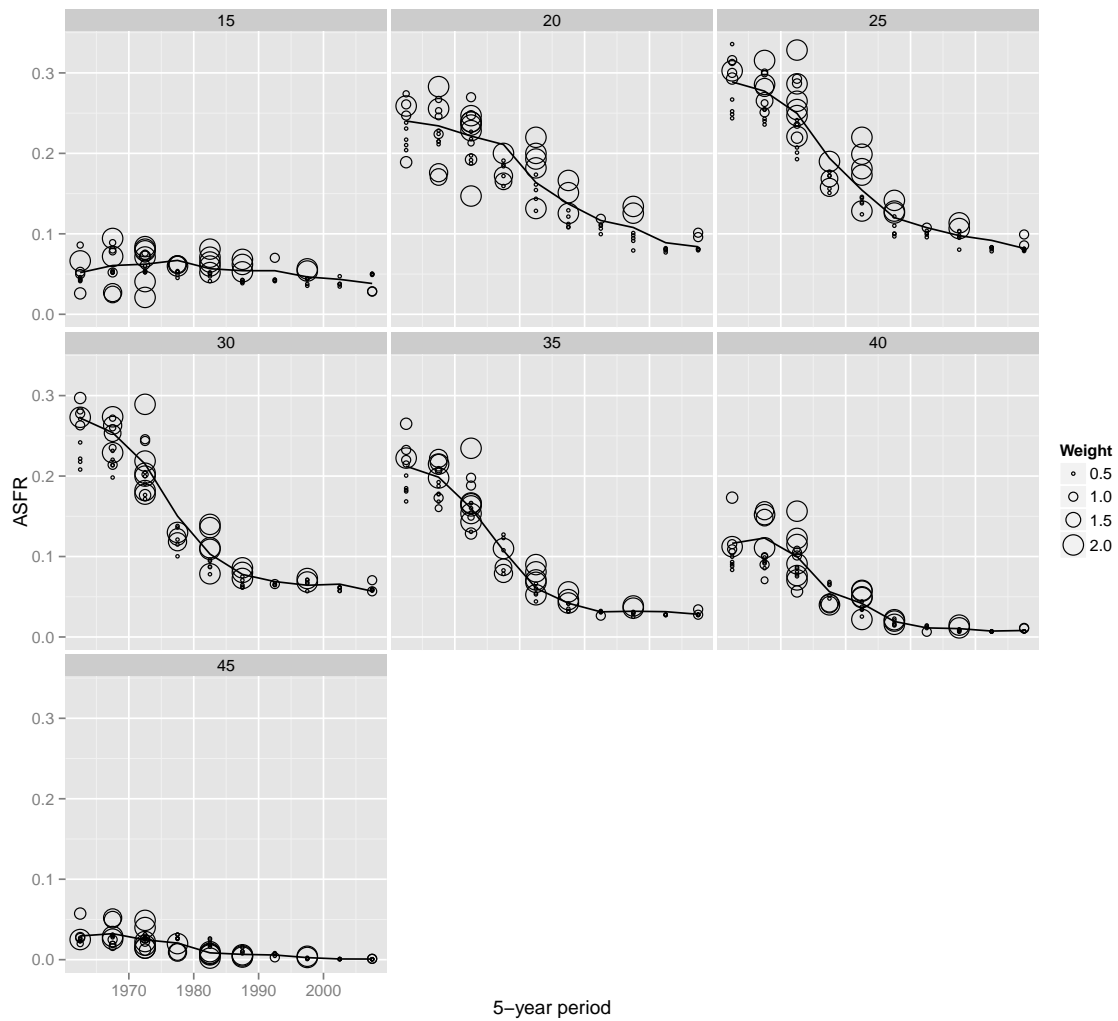


Figure 4.18. Data points (open circles) and initial estimates (lines) for age-specific fertility rate (ASFR) by age group for the population of Thailand, 1960–2000. These are the same data and initial estimates as in Figure 4.17. See text for sources.

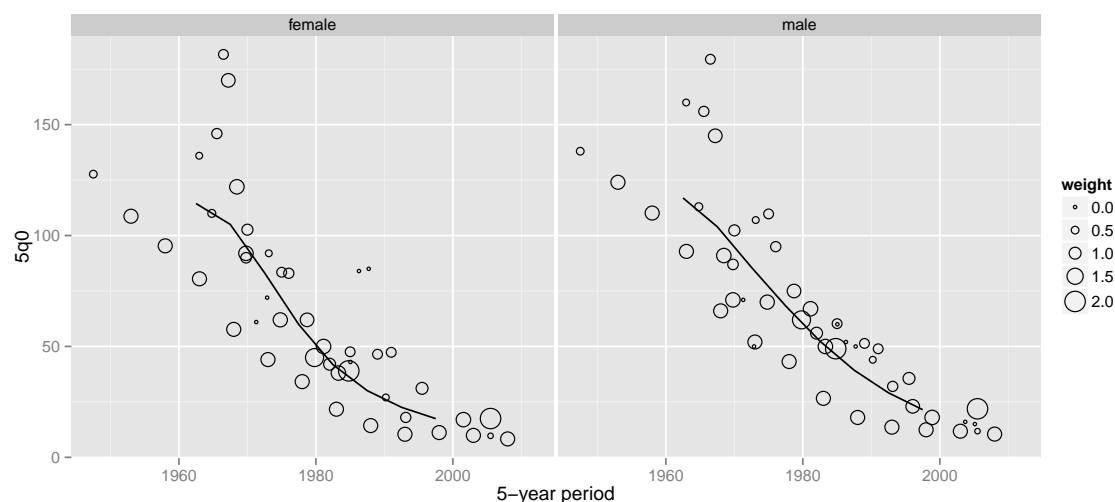


Figure 4.19. Data points (open circles) and weighted cubic smoothing splines (lines) for the probability of death before age five ( ${}_5q_0$ ), by sex, for the population of Thailand, 1960–2000. See text for sources.

#### 4.B.3 India, 1971–2001

##### *Sex Ratio at Birth*

Data on sex ratio at birth came from the same sources as data on age-specific fertility. A weighted cubic spline was used to smooth the available data and initial estimates were derived by evaluating the spline at the mid-points of the intervals 1971–1976, ..., 1996–2001. Elicited relative error for this parameter was set at 50 percent. The data points and initial estimates obtained are plotted in Figure 4.21.

##### *Fertility*

Initial estimates of age-specific fertility were based on data from the Indian SRS ([Office of The Registrar General & Census Commissioner, 2011](#)) and National Family Health Surveys (NFHSs) conducted between 1992 and 2006 ([International Institute for Population Sciences, 2009](#)). These were weighted and smoothed using the same procedure as for Thailand. Elicited relative error for this parameter was set at 10 percent. The initial estimates obtained

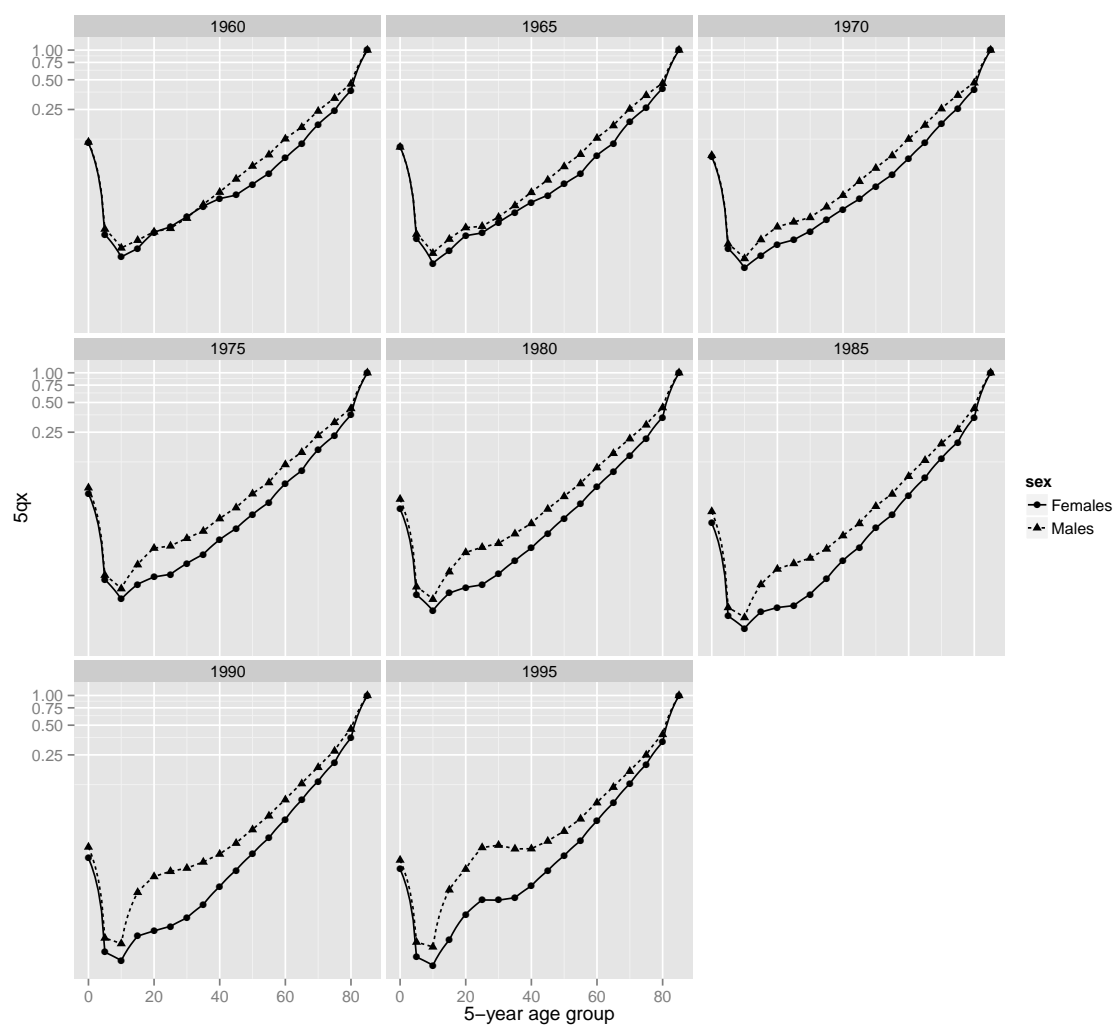


Figure 4.20. Initial estimates for the probability of death ( $5q_x$ ) by time period for the population of Thailand, 1960–2000. The vertical axis has been transformed to the log scale. See text for sources.

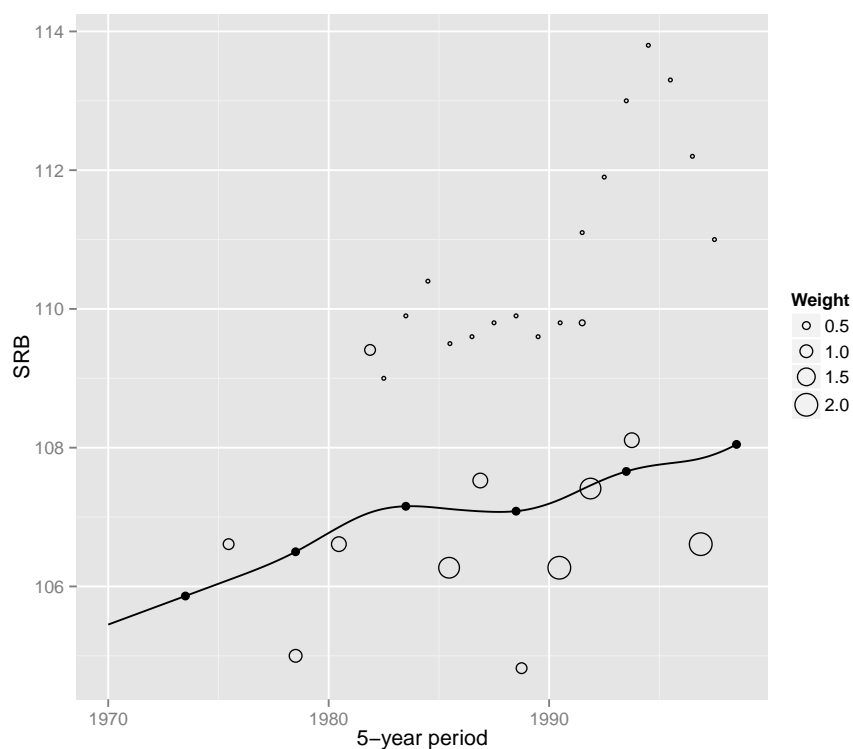


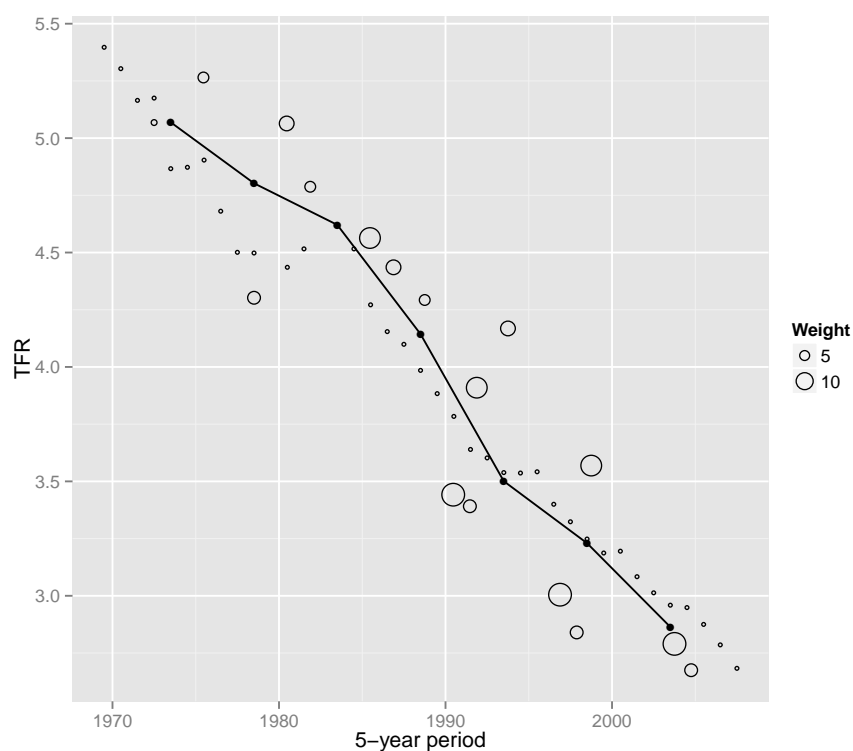
Figure 4.21. Data points (open circles) and initial estimates (solid circles, line) for sex ratio at birth (SRB) for the population of India, 1971–2001. See text for sources.

and the original data points are plotted in Figure 4.22 (TFR) and Figures 4.23 and 4.24 (ASFRs).

### *Mortality*

Initial estimates of survival proportions were calculated from abridged life tables based on data from the SRS from 1968–1969 through 2008. The average numbers of person-years lived in each interval ( ${}_n a_{xs}$ ) were computed using Greville's (1943) formula from age 15 and above. Values for ages under 5 are based on the formulas of Coale et al. (1983) using the West pattern. All other values were set to 2.5 (see also United Nations, 1982, Ch. 6).

Additional sources were used for infant and child mortality: data on births and deaths



*Figure 4.22.* Data points (open circles) and initial estimates (solid circles, lines) for total fertility rate (TFR) for the population of India, 1971–2001. See text for sources.

under-five were calculated from maternity-history data from the NFHSs conducted between 1992 and 2006 and data on children ever-born and surviving classified by age of mother (and the South-Asian model of the UN Model Life Tables) from these surveys and earlier ones as well as from the 2002–04 Reproductive and Child Health Survey (RCHS). Some sex-specific data were available but the majority were for all-sex mortality. For greater robustness, sex-specific initial estimates of the level of under-five mortality were derived by first smoothing available data on all-sex mortality using weighted cubic smoothing splines (Patrick Gerland, pers. comm.). Data for  $1q_0$  and  $5q_0$  were smoothed separately (Figure 4.25). The available sex-specific data were converted into data on the male-to-all-sex ratio which were also smoothed with weighted cubic smoothing splines (Figure 4.26). The smoothed level and sex-ratio values were combined to produce initial estimates of sex-specific  $1q_0$  and  $5q_0$ . From

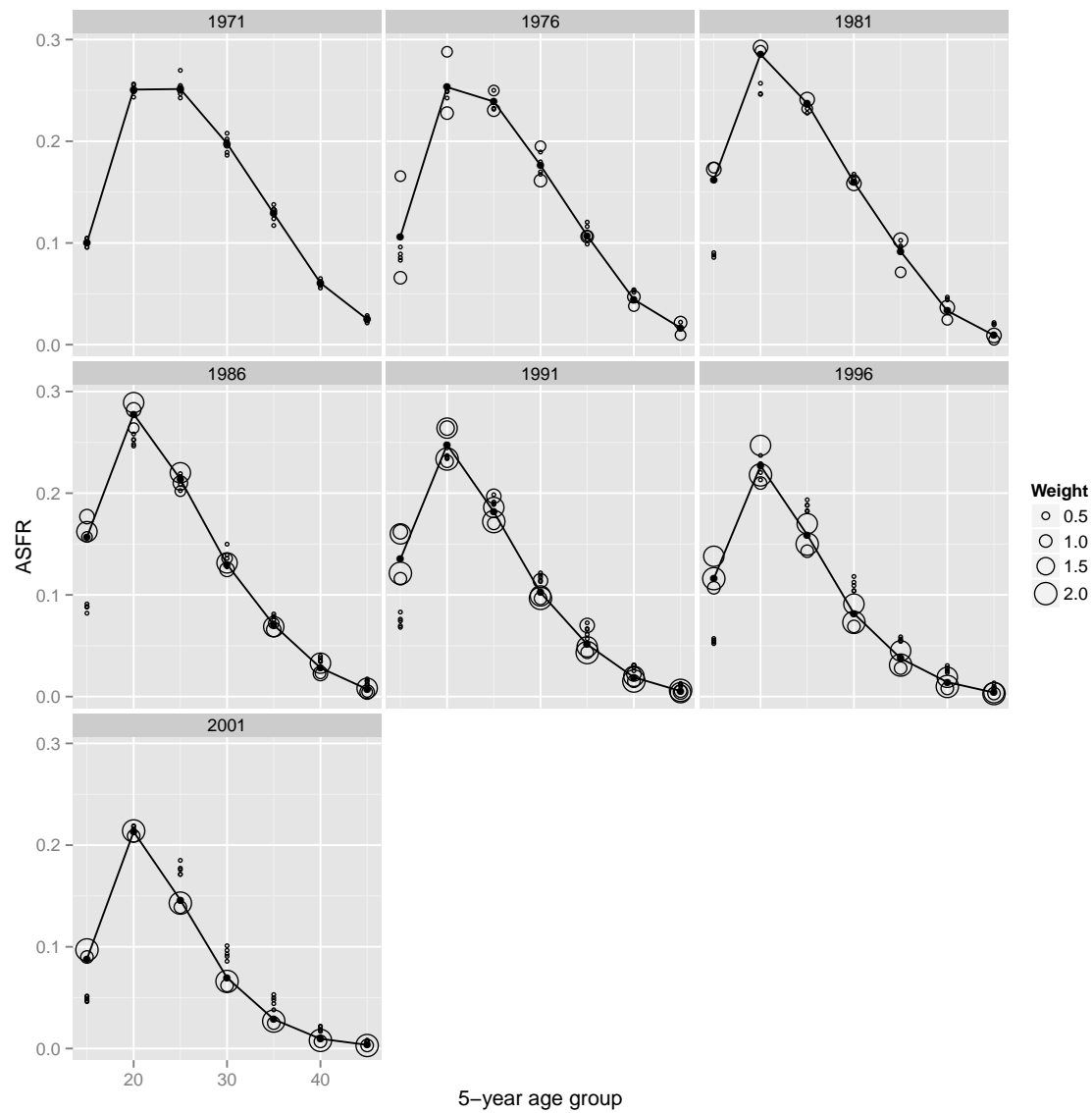


Figure 4.23. Data points (open circles) and initial estimates (solid circles, lines) by time period for age-specific fertility rate (ASFR) for the population of India, 1971–2001. See text for sources.

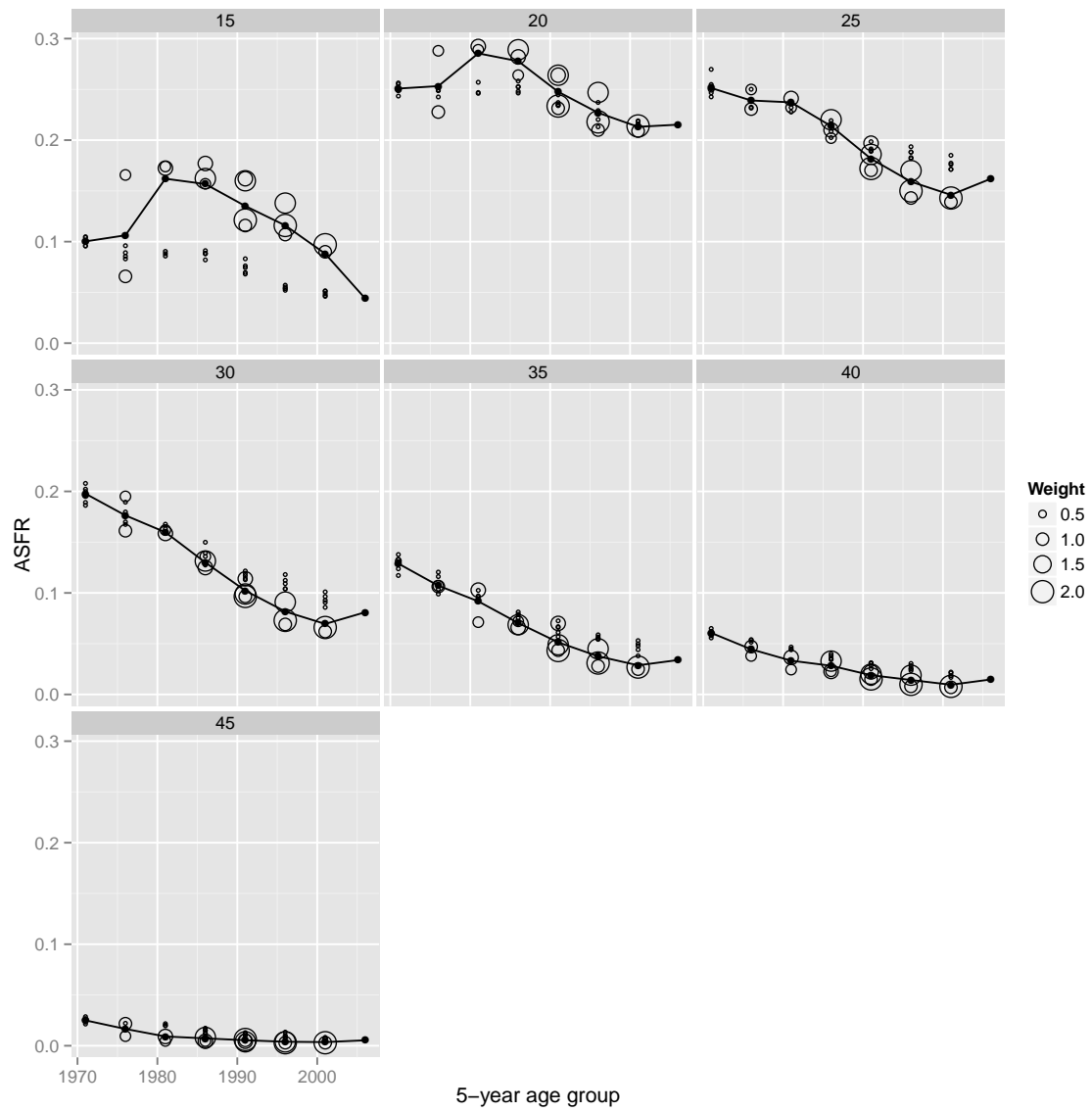


Figure 4.24. Data points (open circles) and initial estimates for age-specific fertility rate (ASFR) by age group for the population of India, 1971–2001. These are the same data and initial estimates as in Figure 4.23. See text for sources.

these, initial estimates of  ${}_4q_1$  were obtained via the identity  ${}_4q_1 = 1 - (1 - {}_5q_0)/(1 - {}_1q_0)$ .

The  ${}_1q_0$  and  ${}_4q_1$  were combined with mortality estimates at older ages from the SRS to obtain abridged life tables. This approach allowed us to use all available data since some sources provided information only on  ${}_1q_0$ . All weights were determined by UN analysts based on their expert judgment about the relative reliability of each source. The final set of initial estimates for probabilities of death are shown in Figure 4.27. Elicited relative error was set to 10 percent.

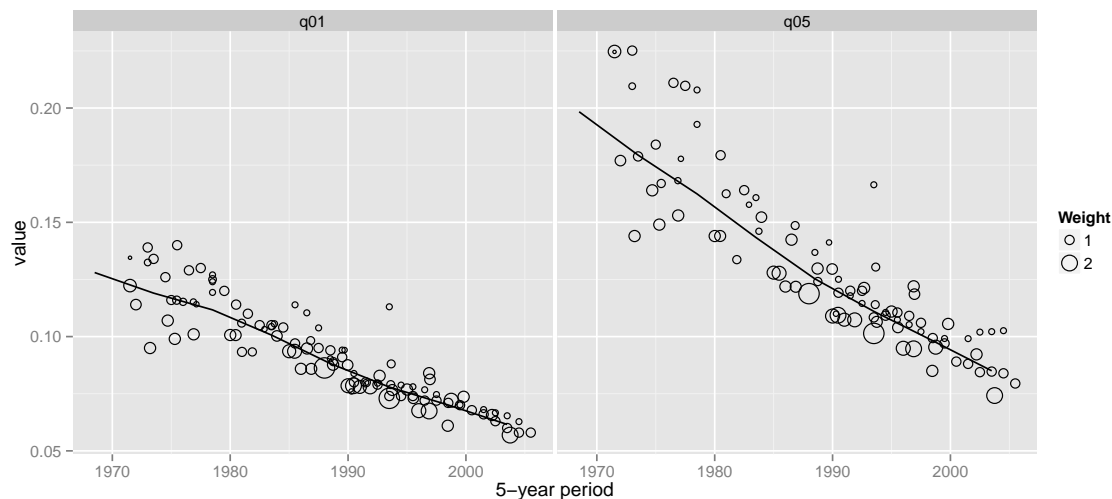


Figure 4.25. All-sex data points for the probability of death between ages 0 and 1 ( ${}_1q_0$ ) and between ages 0 and 5 ( ${}_5q_0$ ) with weighted cubic smoothing splines, for the population of India, 1971–2001. See text for sources.

### Migration

I used the same initial estimates for international migration as for Laos.



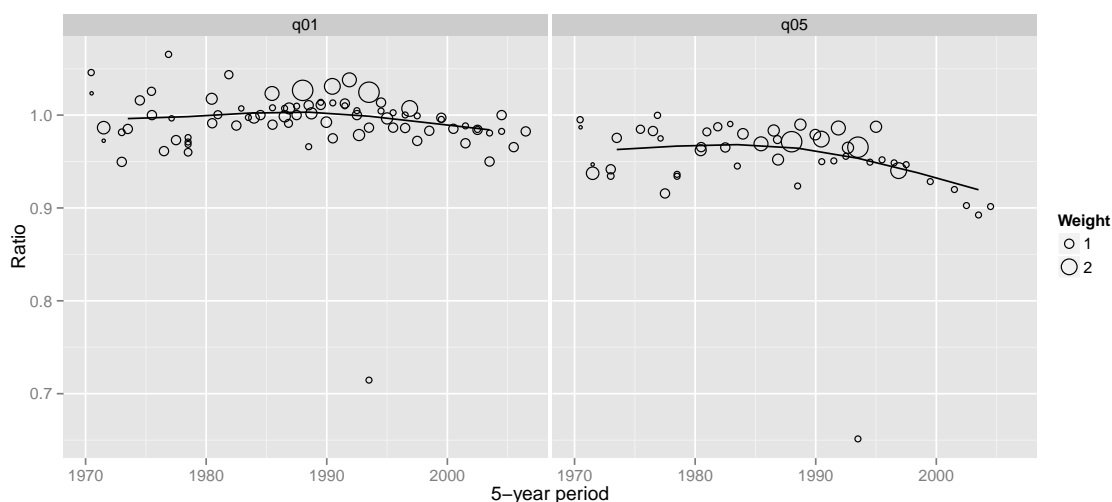


Figure 4.26. Data for the ratios of male probabilities of death to all-sex probabilities of death, for the probabilities of death between ages 0 and 1 ( ${}_1q_0$ ) and between ages 0 and 5 ( ${}_5q_0$ ), with weighted cubic smoothing splines, for the population of India, 1971–2001. See text for sources.

## Appendix 4.C Further Results

### 4.C.1 Laos, 1985–2005

#### Population Counts

Age-specific counts for 1985, the baseline year, are in Figures 4.28 and 4.29. Total population counts are in Tables 4.6 and 4.7.

#### Age-specific Fertility Rates

Results for age-specific fertility rates for the full-population reconstruction of Laos are in Figure 4.30.

#### Age-specific Survival Proportions

Results for age-specific survival proportions are in Figures 4.31 and 4.32.

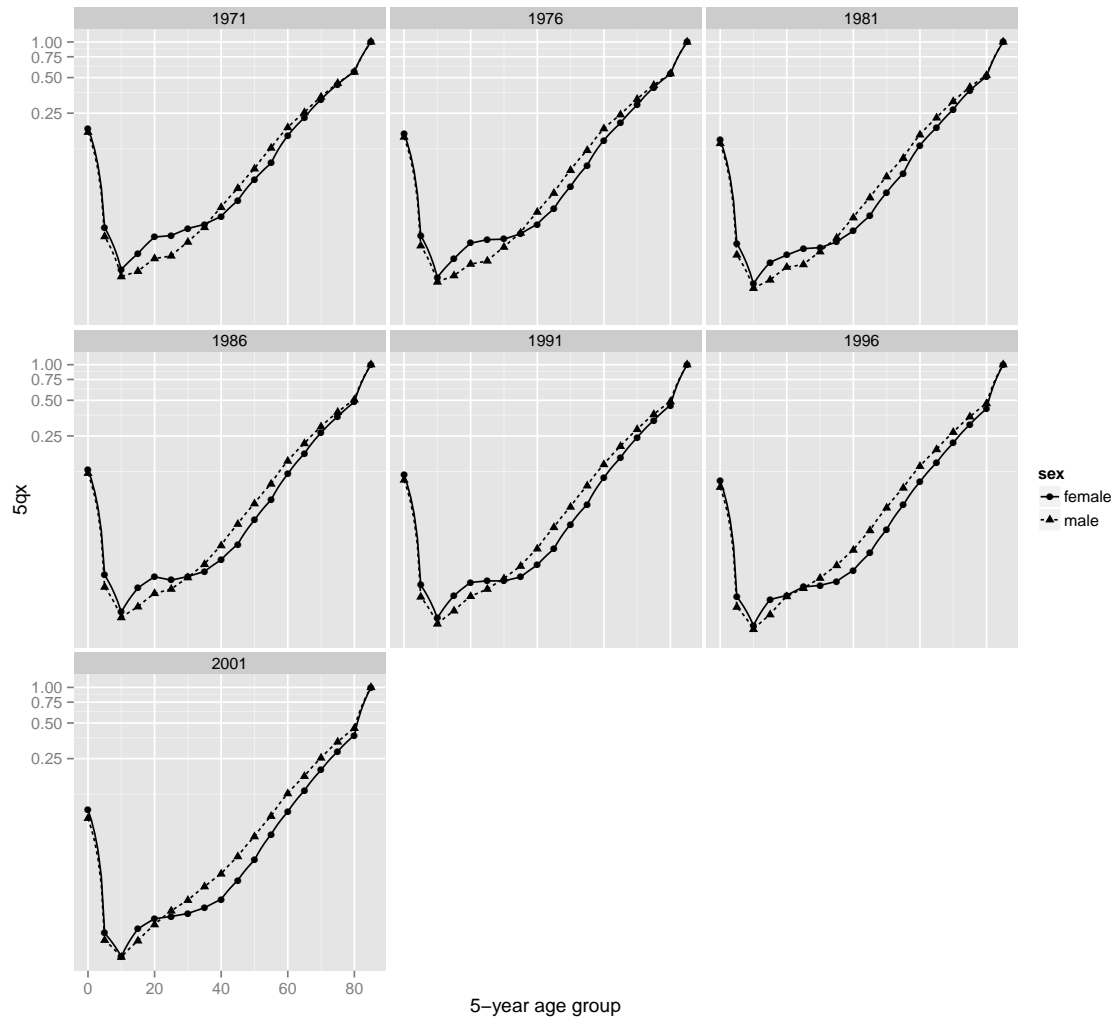


Figure 4.27. Initial estimates of age-specific probability of death ( $5q_x$ ) for the population of India, 1971–2001. The vertical axis has been transformed to the log scale. See text for sources.

*Table 4.6.* Initial estimates, posterior medians and 95 percent credible intervals for population count for the reconstructed female population of Laos, 1985–2005, in millions.

Year	Posterior Percentile			Init. Est.
	2.5th	50th	97.5th	
1985	1.81	1.83	1.86	1.83
1990	2.01	2.09	2.18	
1995	2.36	2.40	2.45	
2000	2.58	2.69	2.81	
2005	2.89	2.95	3.01	

*Table 4.7.* Initial estimates, posterior medians and 95 percent credible intervals for population count for the reconstructed male population of Laos, 1985–2005, in millions.

Year	Posterior Percentile			Init. Est.
	2.5th	50th	97.5th	
1985	1.80	1.82	1.85	1.82
1990	2.01	2.10	2.19	
1995	2.36	2.40	2.44	
2000	2.57	2.68	2.81	
2005	2.87	2.93	3.00	

### *Age-specific Mortality Rates*

Results for age-specific mortality rates on the log scale are in Figures 4.33 and 4.34.

### *Age-specific Migration Proportions*

Age-specific migration proportions are in Figures 4.35 and 4.36.

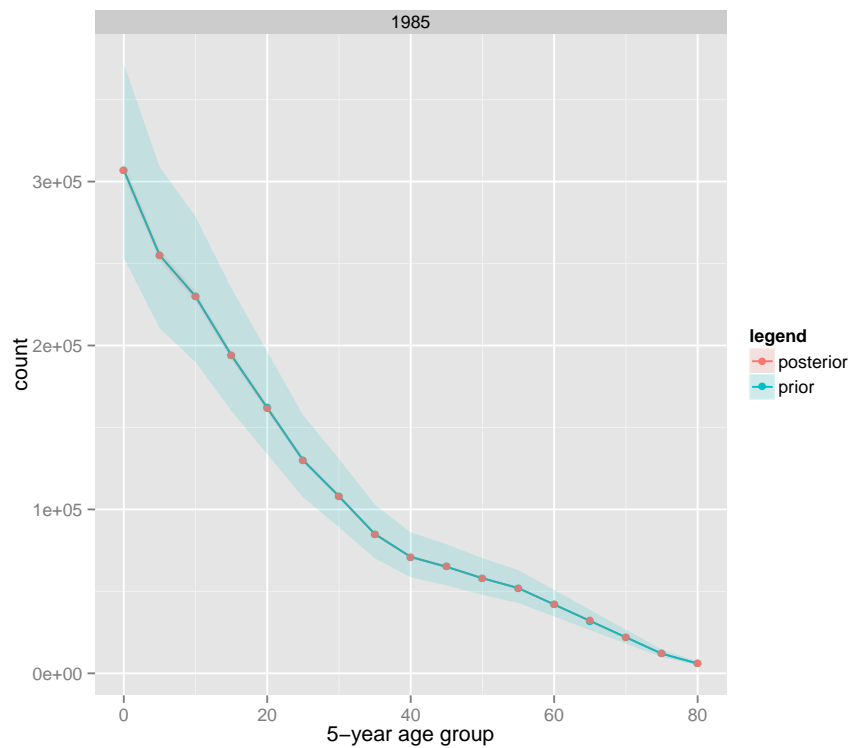


Figure 4.28. Prior and posterior medians and 95 percent credible intervals for age-specific population count for the reconstructed female population of Laos, 1985.

### *Total Net Number of Migrants*

Posterior distributions for the average annual net number of migrants are shown in Figure 4.37. Posterior uncertainty is high. Posterior medians indicate out-migration for most of the period of reconstruction. For 1995–2005, posterior intervals for males fall completely below zero.

### *Population Sex Ratios*

Posterior intervals for population sex ratios are in Figure 4.38. Posterior medians are reasonably similar to the ratios in the WPP census counts and uncertainty is high.

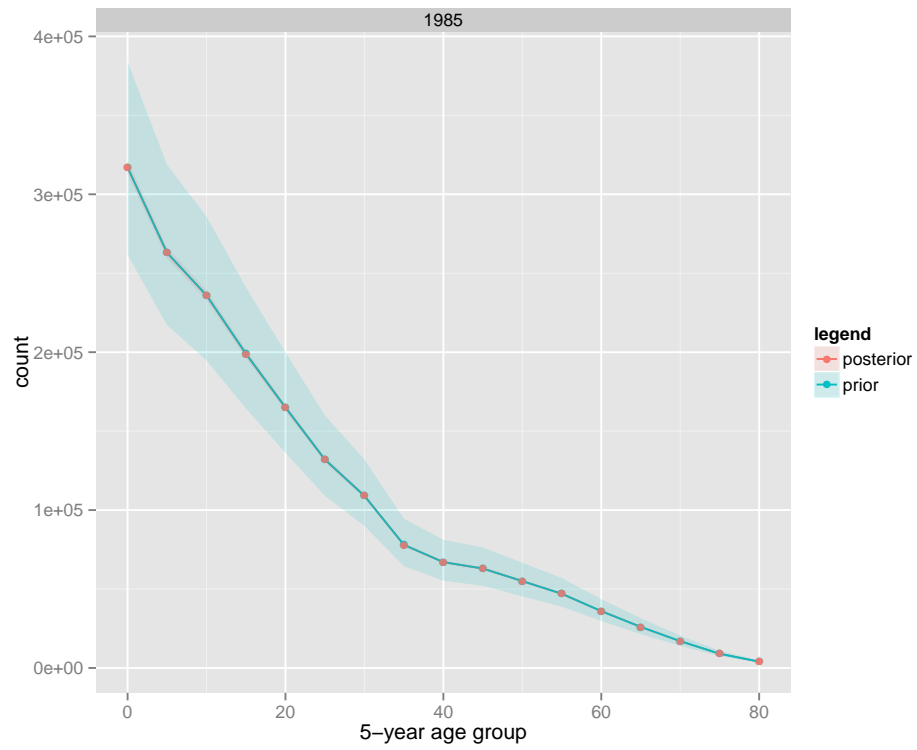


Figure 4.29. Prior and posterior medians and 95 percent credible intervals for age-specific population count for the reconstructed male population of Laos, 1985.

#### *Prior and Posterior Density Estimates for Variance Parameters*

Prior and posterior kernel density estimates for the standard deviation parameters  $\sigma_v$ ,  $v = \{n, f, s, g\}$  are shown in Figure 4.39.

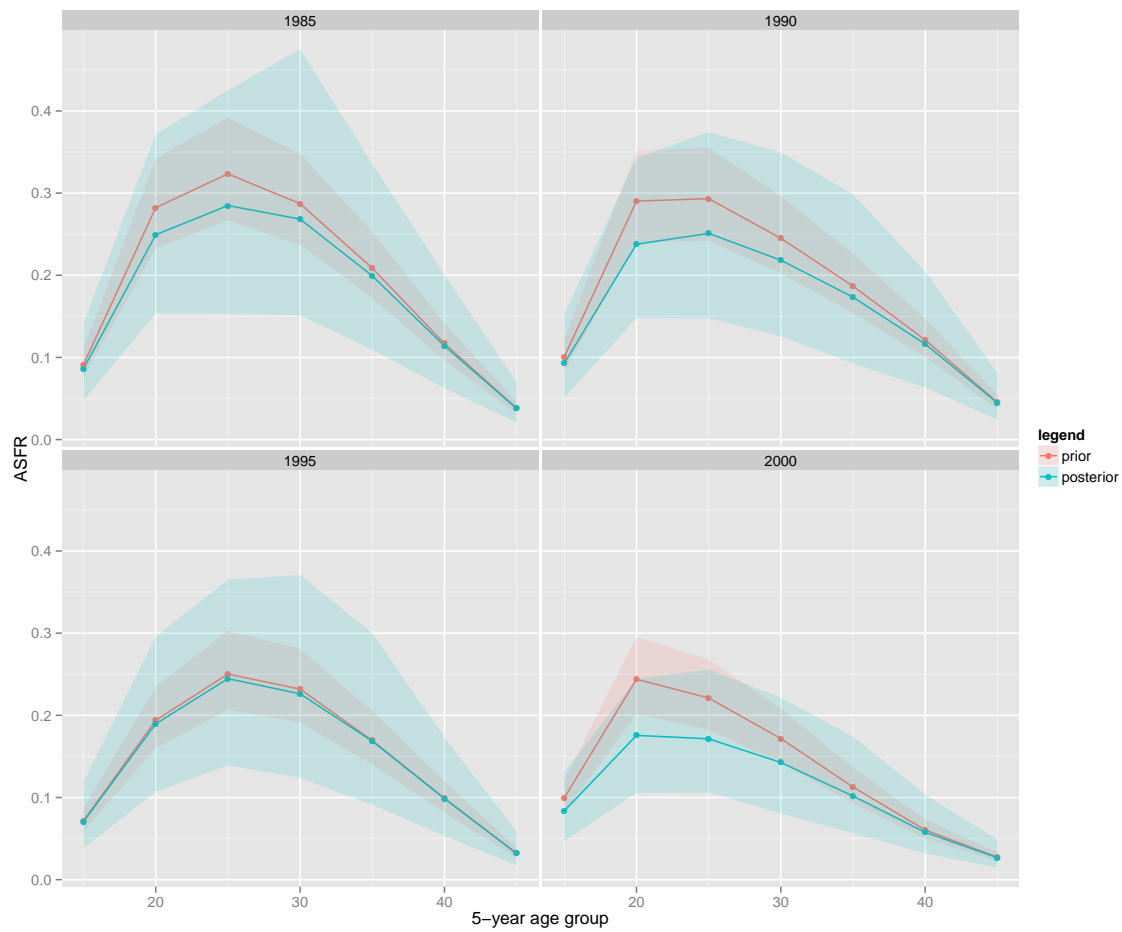


Figure 4.30. Prior and posterior medians and 95 percent credible intervals for age-specific fertility rates (ASFRs) for the reconstructed population of Laos, 1985–2005.

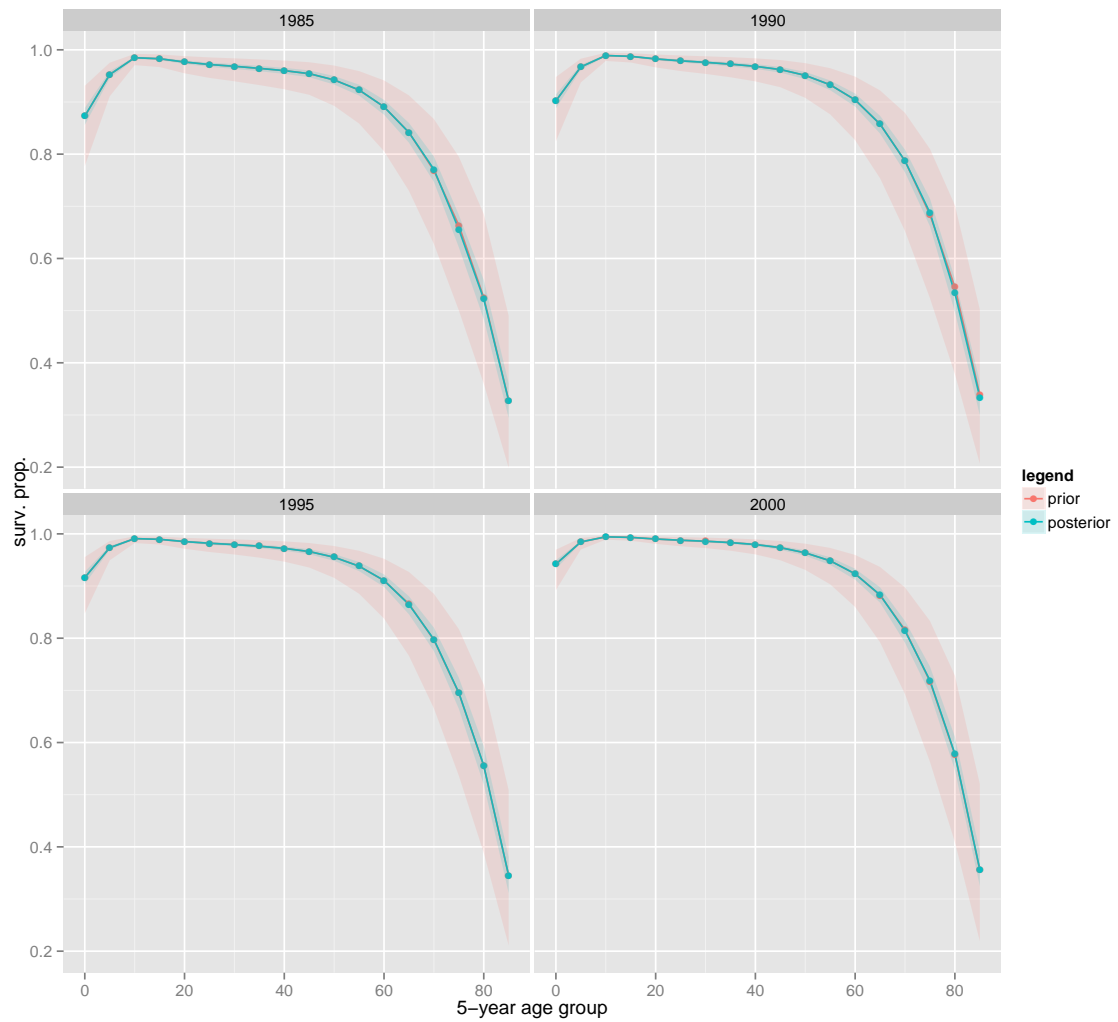


Figure 4.31. Prior and posterior medians and 95 percent credible intervals for age-specific female survival proportion for the reconstructed population of Laos, 1985–2005.

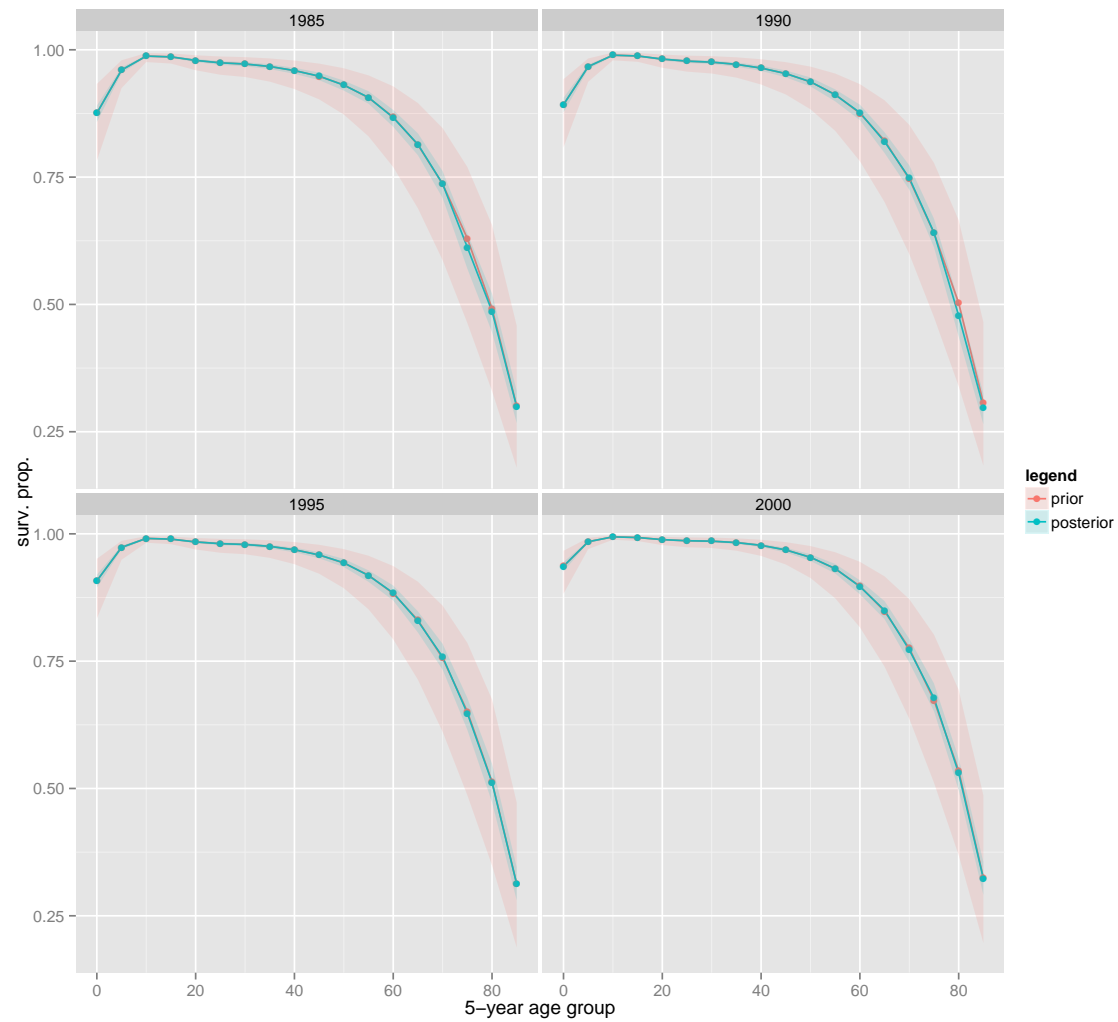


Figure 4.32. Prior and posterior medians and 95 percent credible intervals for age-specific male survival proportion for the reconstructed population of Laos, 1985–2005.



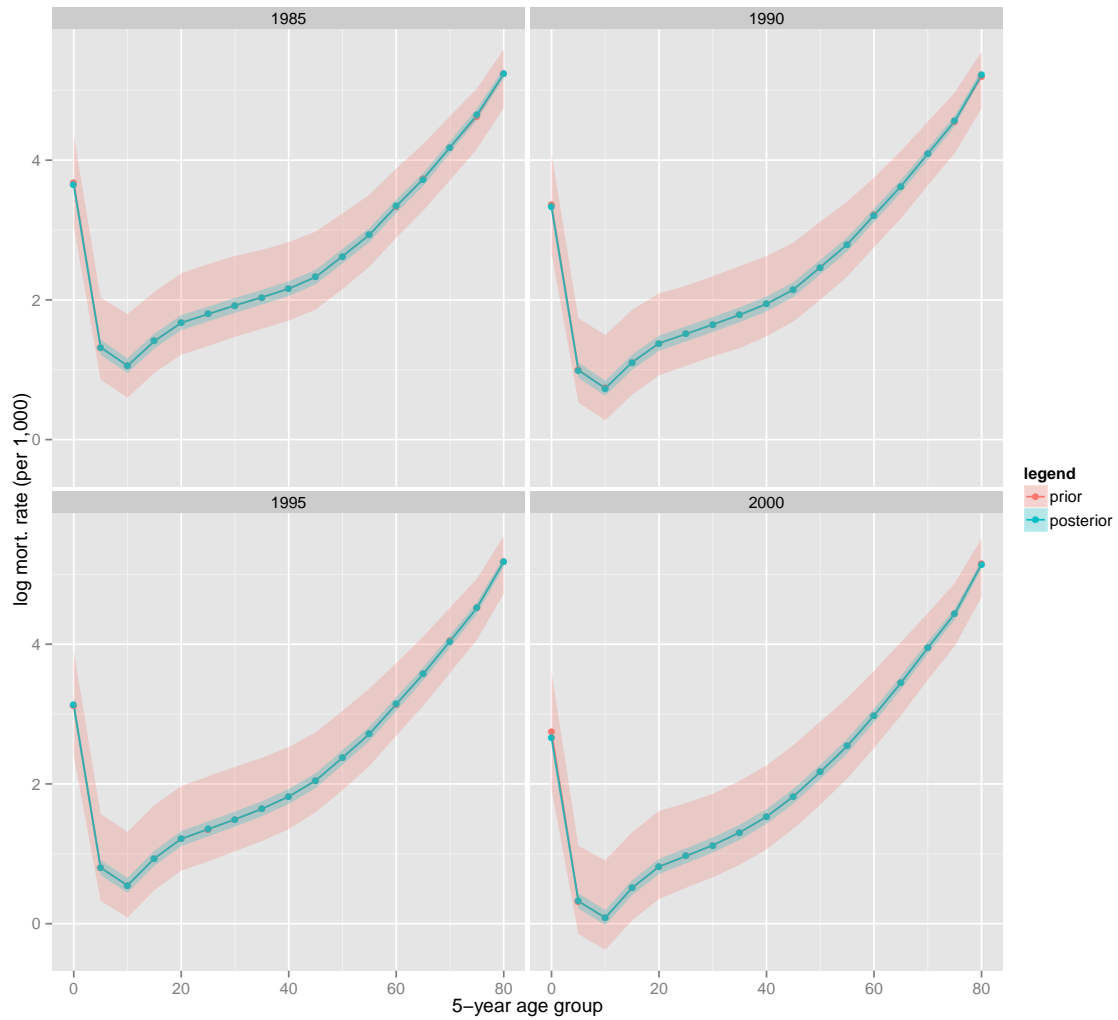


Figure 4.33. Prior and posterior medians and 95 percent credible intervals for age-specific female log mortality rate for the reconstructed population of Laos, 1985–2005.

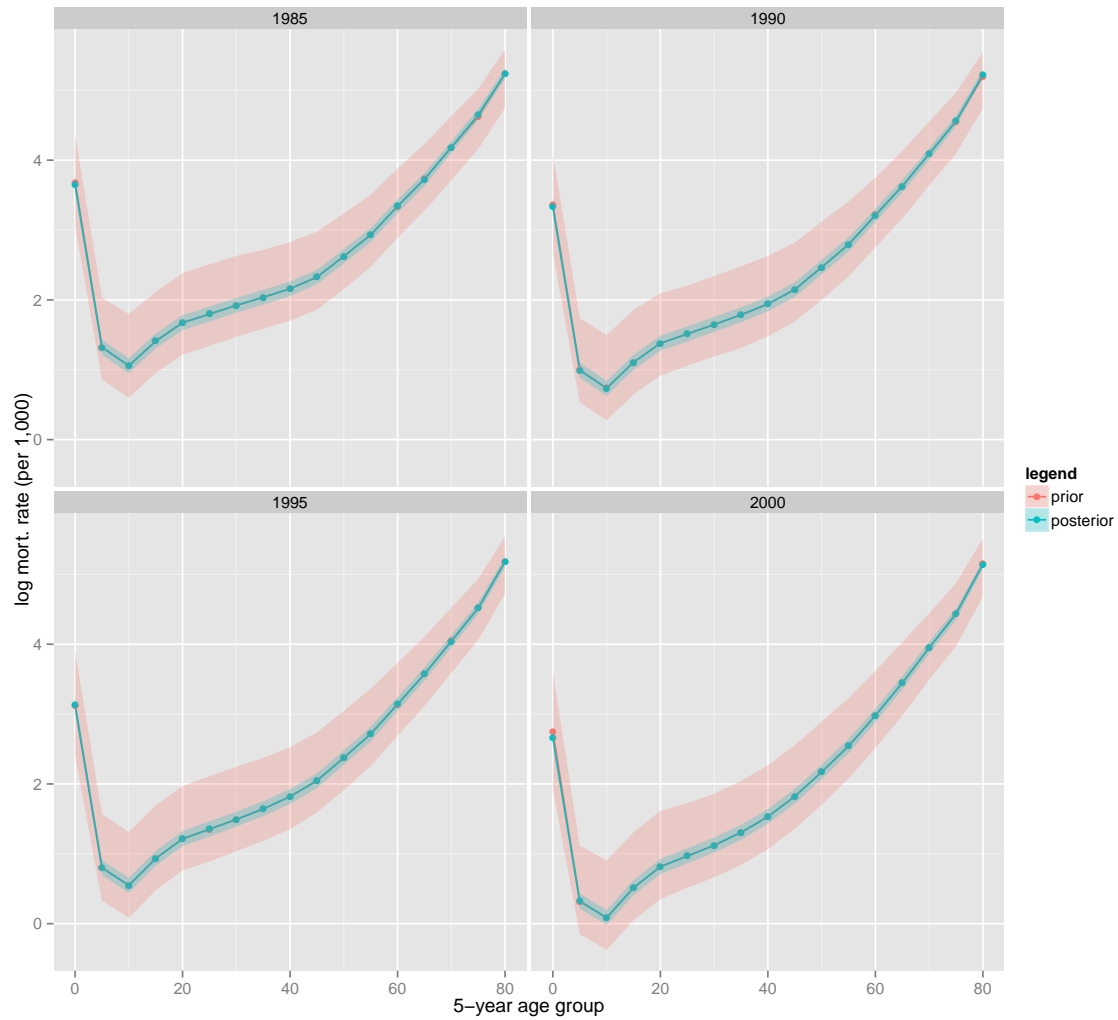
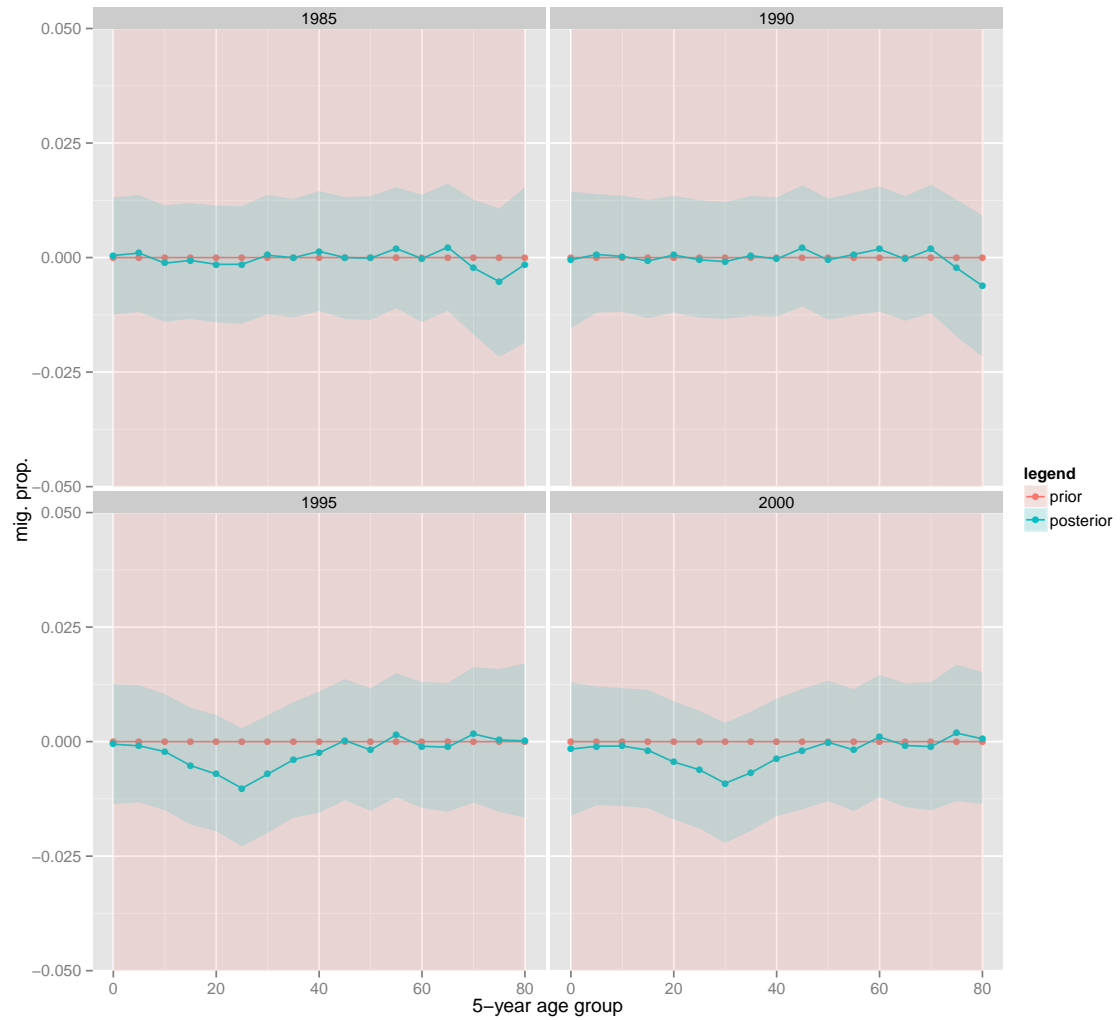


Figure 4.34. Prior and posterior medians and 95 percent credible intervals for age-specific male log mortality rate for the reconstructed population of Laos, 1985–2005.



*Figure 4.35.* Prior and posterior medians and 95 percent credible intervals for age-specific female migration proportion for the reconstructed population of Laos, 1985–2005.

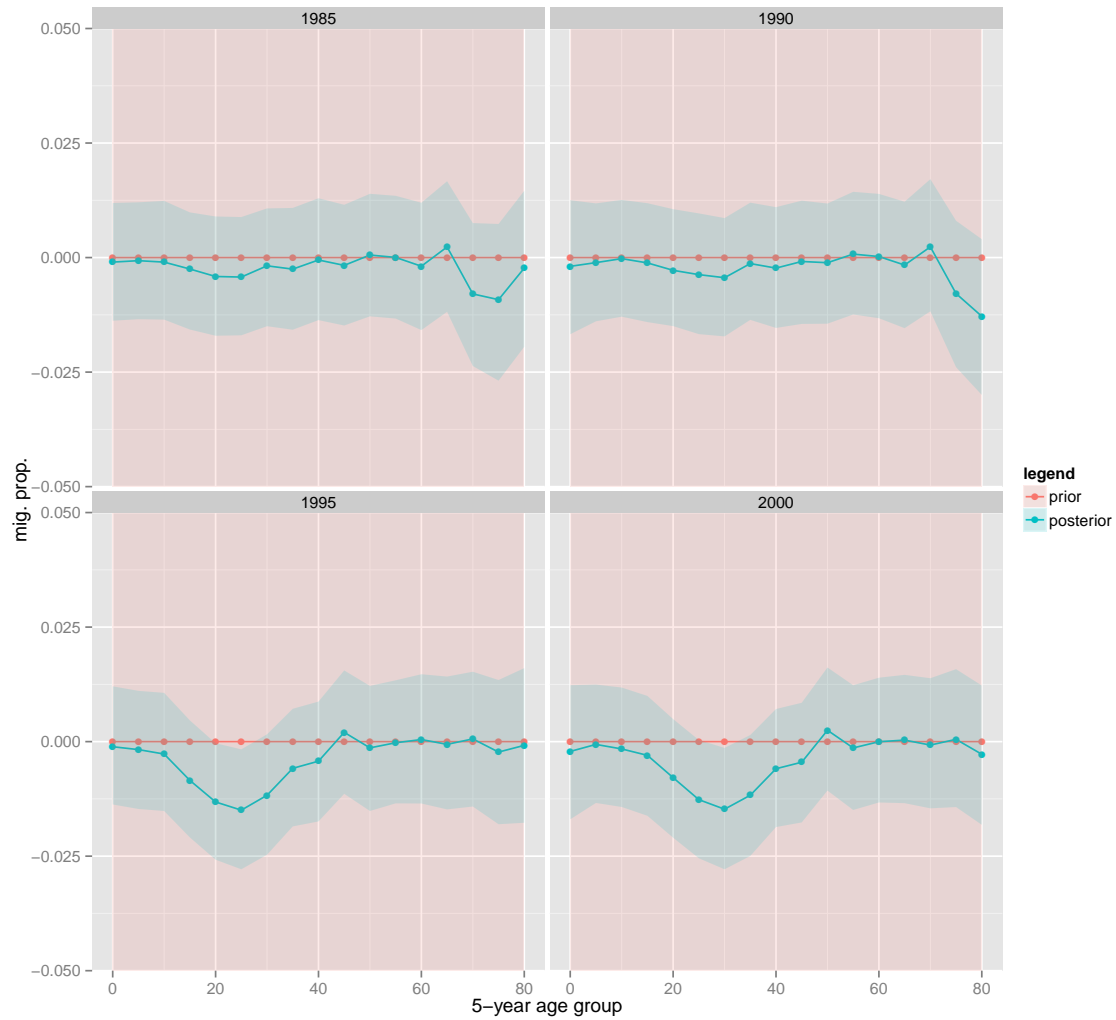


Figure 4.36. Prior and posterior medians and 95 percent credible intervals for age-specific male migration proportion for the reconstructed population of Laos, 1985–2005.

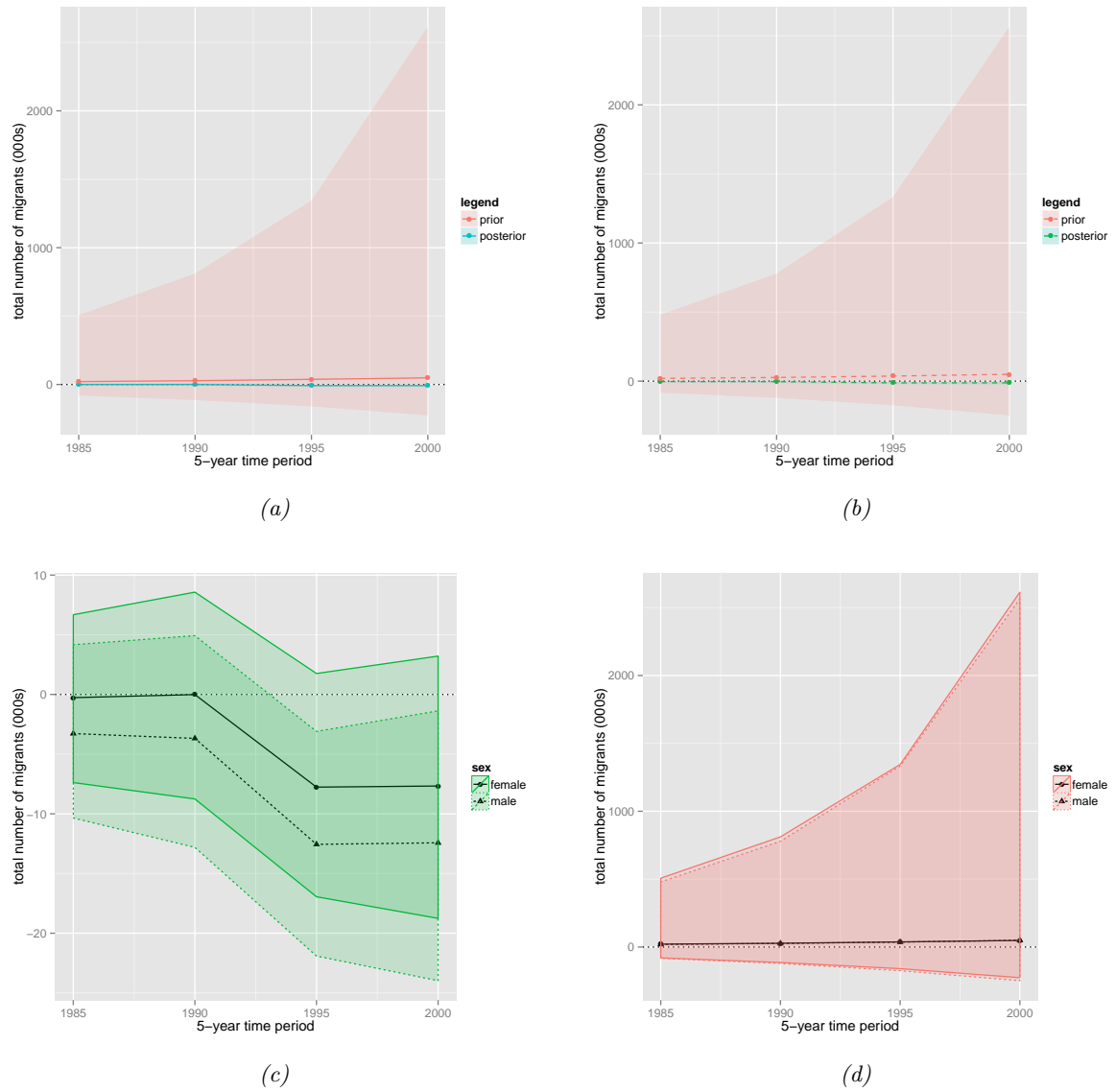


Figure 4.37. Prior and posterior medians and 95 percent credible intervals for the average annual net number of migrants for the reconstructed population of Laos, 1985–2005: (a) females; (b) males; (c) female and male posterior quantiles only; (d) female and male prior quantiles only.

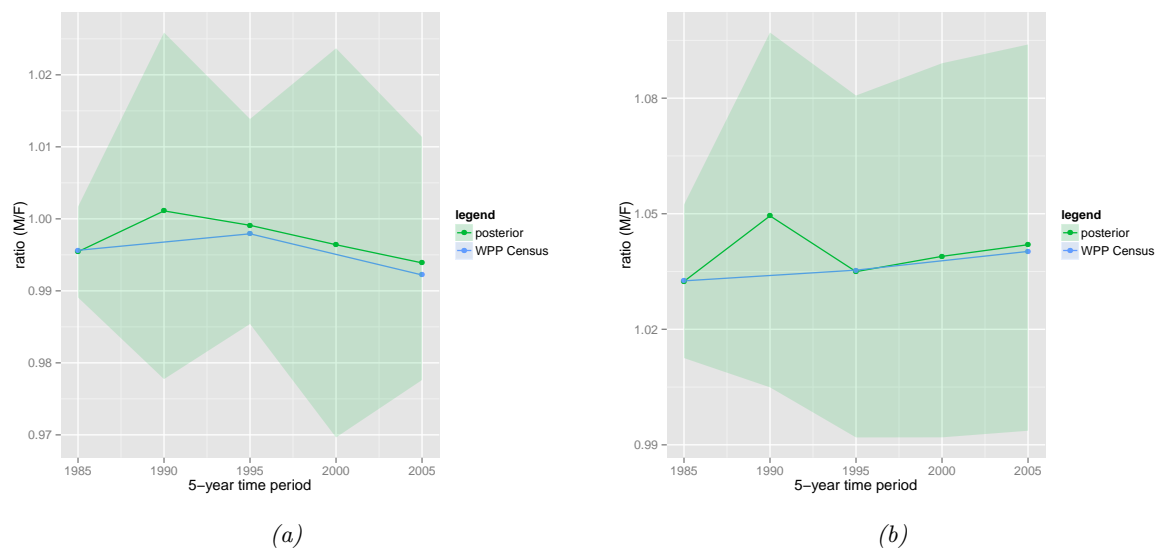


Figure 4.38. Prior and posterior medians and 95 percent credible intervals for the reconstructed population of Laos, 1985–2005: (a) sex ratio in the total population (SRTP); (b) population aged 0–4.

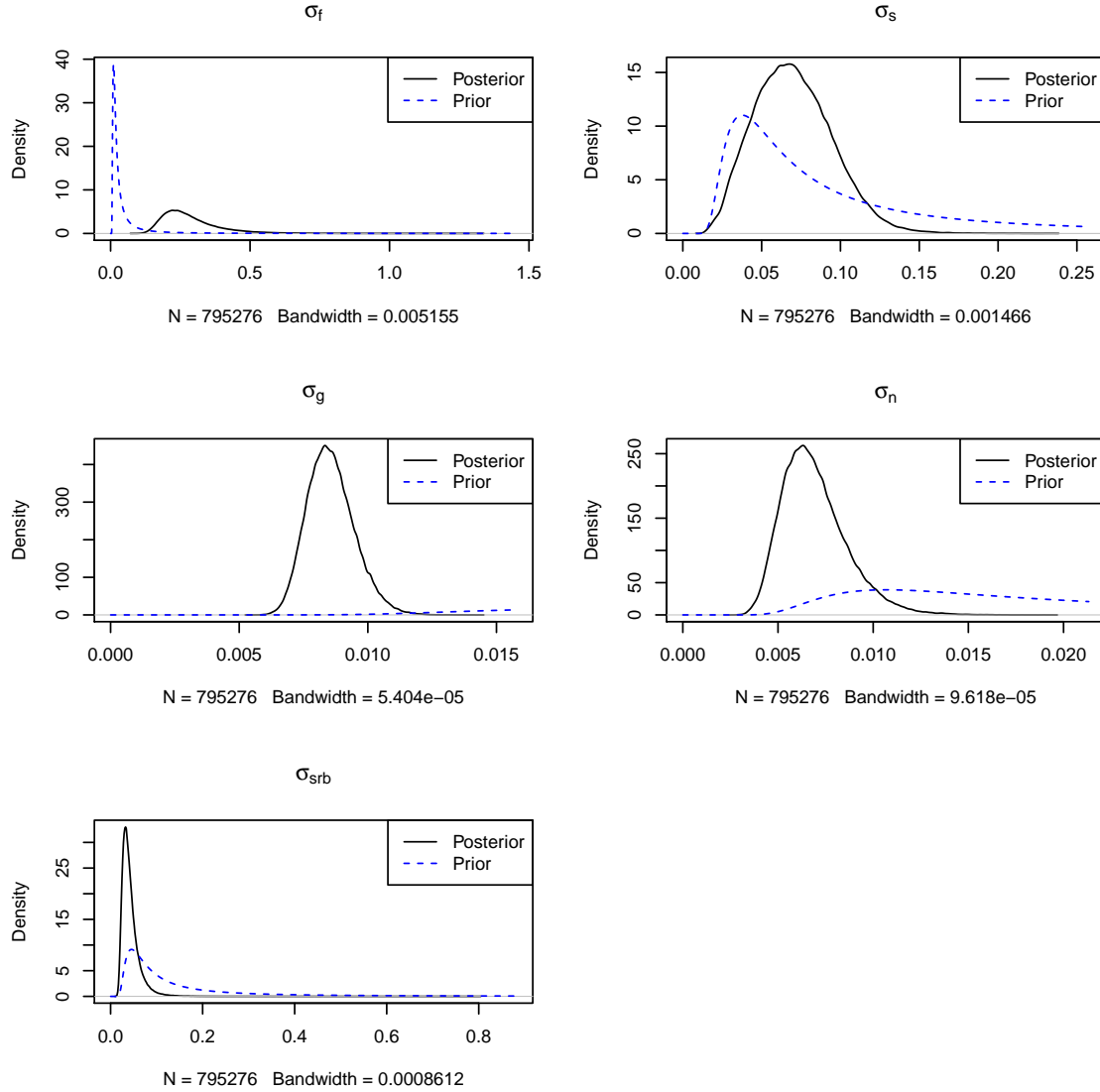


Figure 4.39. Prior and posterior densities of model standard deviation parameters,  $\sigma_v$ ,  $v = \{n, f, s, g\}$  for the reconstructed population of Laos, 1985–2005. Posterior densities are kernel density estimates.

#### 4.C.2 Thailand, 1960–2000

##### *Population Counts*

Age-specific counts for 1985, the baseline year, are in Figures 4.40 and 4.41. Total population counts are in Tables 4.8 and 4.9.

*Table 4.8.* Initial estimates, posterior medians and 95 percent credible intervals for population count for the reconstructed female population of Thailand, 1960–2000, in millions.

Year	Posterior Percentile			Init. Est.
	2.5th	50th	97.5th	
1960	13.5	13.6	13.8	13.6
1965	15.2	15.8	16.5	
1970	18.2	18.5	18.7	18.4
1975	20.2	21.2	22.1	
1980	23.3	23.8	24.2	23.6
1985	25.2	26.4	27.6	
1990	28.3	28.9	29.4	28.7
1995	29.2	30.6	32.1	
2000	31.5	32.3	33.0	32.1

##### *Age-specific Fertility Rates*

Results for age-specific fertility rates are in Figure 4.42.

##### *Age-specific Survival Proportions*

Results for age-specific survival proportions are in Figures 4.43 and 4.44.

##### *Age-specific Mortality Rates*

Results for age-specific mortality rates on the log scale are in Figures 4.45 and 4.46.



*Table 4.9.* Initial estimates, posterior medians and 95 percent credible intervals for population count for the reconstructed male population of Thailand, 1960–2000, in millions.

Year	Posterior Percentile			Init. Est.
	2.5th	50th	97.5th	
1960	13.6	13.7	13.9	13.7
1965	15.3	16.0	16.7	
1970	18.2	18.5	18.8	18.6
1975	20.3	21.2	22.2	
1980	23.3	23.7	24.2	23.8
1985	24.9	26.0	27.3	
1990	27.7	28.3	28.9	28.3
1995	28.5	29.9	31.4	
2000	30.4	31.1	31.8	31.1

#### *Age-specific Migration Proportions*

Posterior estimates for the age-specific migration proportions are in Figures 4.47 and 4.48.

#### *Total Net Number of Migrants*

Results for the average annual net number of migrants are in Figure 4.49. Uncertainty is large and the mean half-width is 82,199.

#### *Population Sex Ratios*

Population sex ratios are shown in Figure 4.50. Posterior medians follow the ratios in the WPP counts relatively closely.

#### *Prior and Posterior Density Estimates for Variance Parameters*

Prior and posterior kernel density estimates for the standard deviation parameters  $\sigma_v$ ,  $v = \{n, f, s, g\}$  are shown in Figure 4.51.

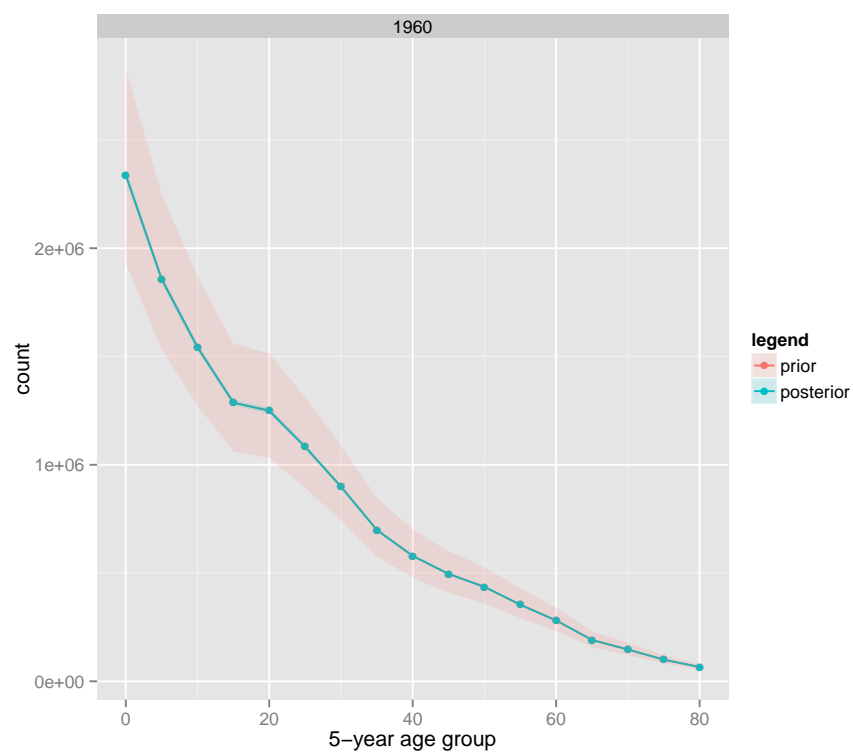


Figure 4.40. Prior and posterior medians and 95 percent credible intervals for age-specific population count for the reconstructed female population of Thailand, 1960.

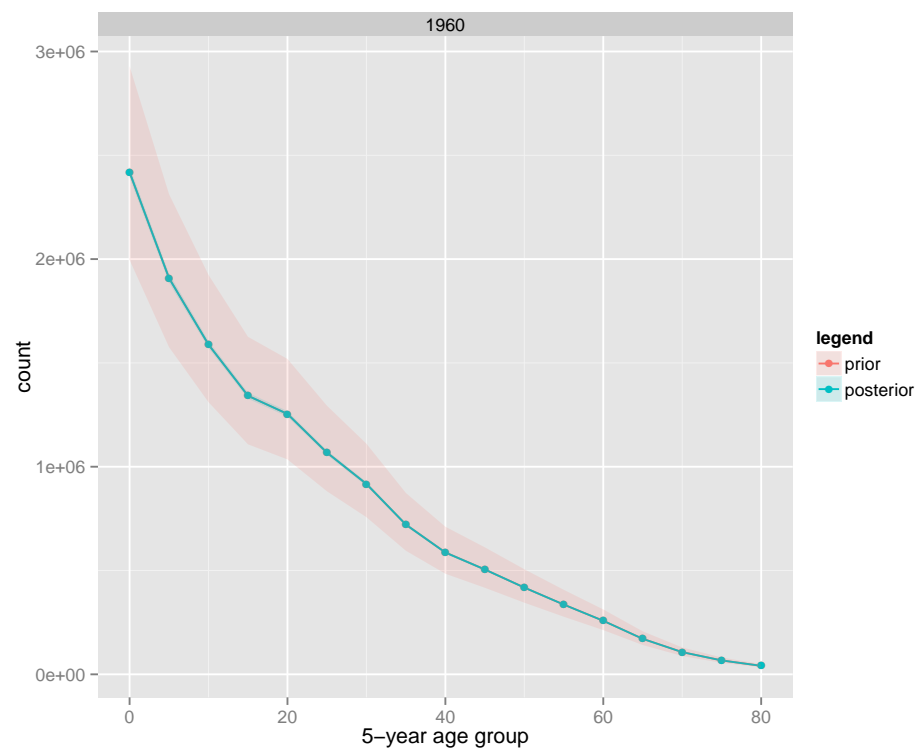


Figure 4.41. Prior and posterior medians and 95 percent credible intervals for age-specific population count for the reconstructed male population of Thailand, 1960.

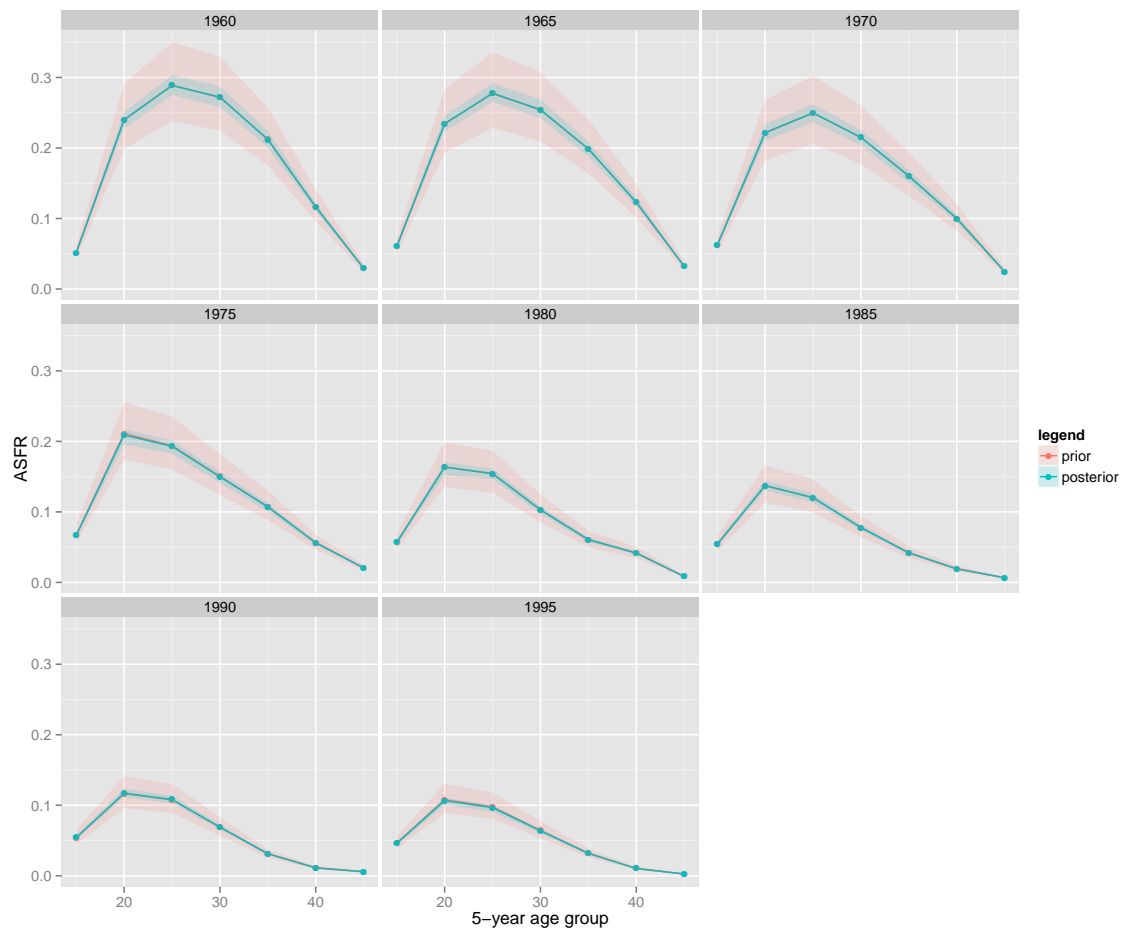


Figure 4.42. Prior and posterior medians and 95 percent credible intervals for age-specific fertility rates (ASFRs) for the reconstructed population of Thailand, 1960–2000.

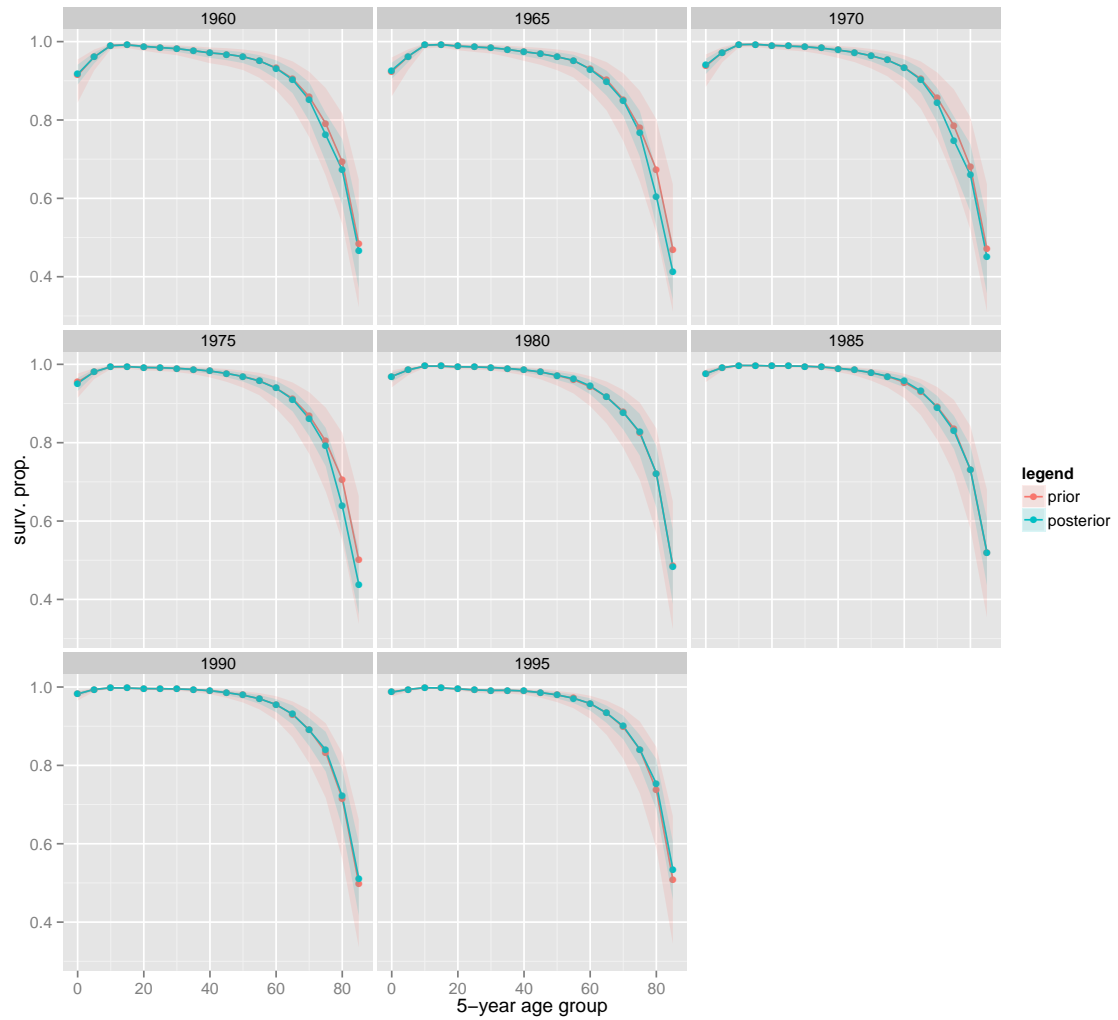


Figure 4.43. Prior and posterior medians and 95 percent credible intervals for age-specific female survival proportion for the reconstructed population of Thailand, 1960–2000.

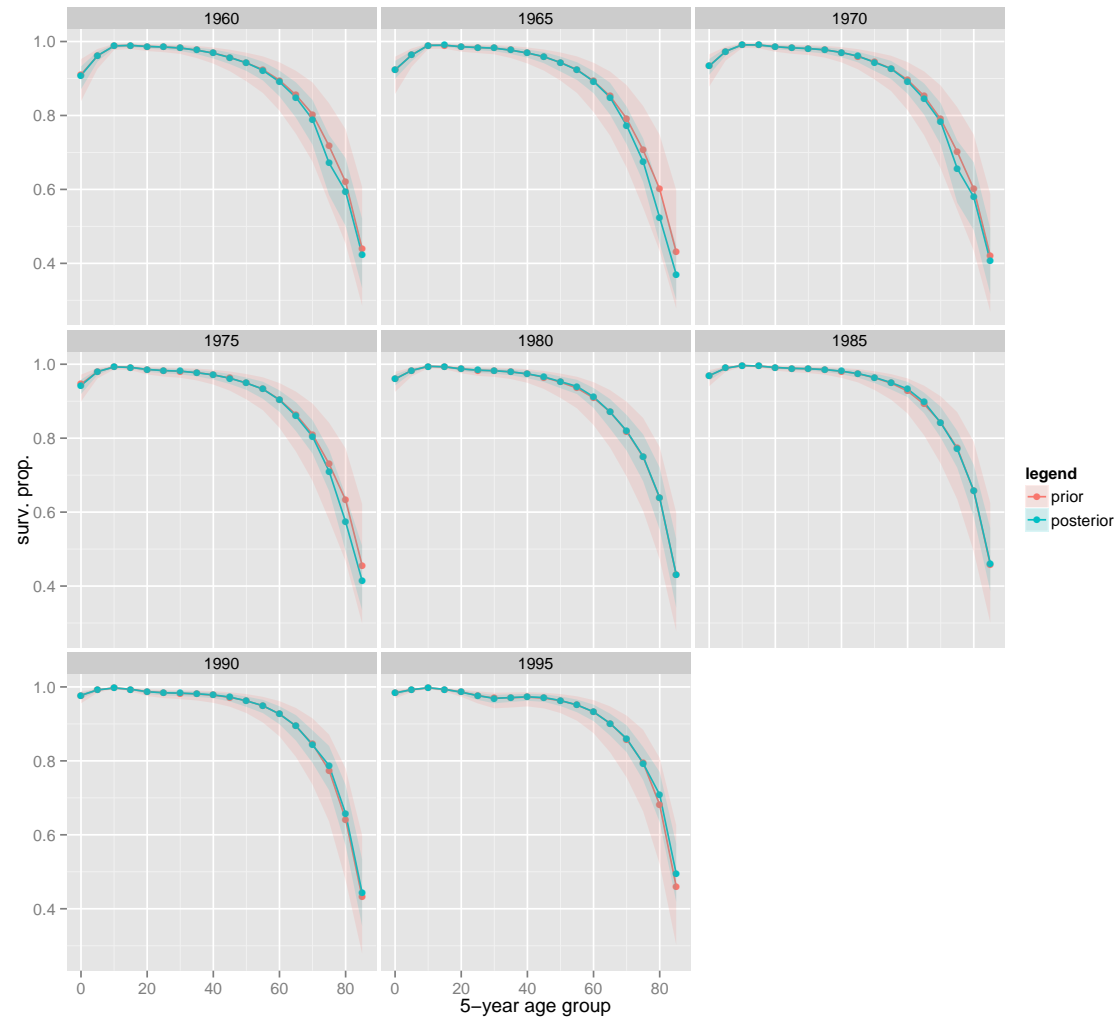


Figure 4.44. Prior and posterior medians and 95 percent credible intervals for age-specific male survival proportion for the reconstructed population of Thailand, 1960–2000.

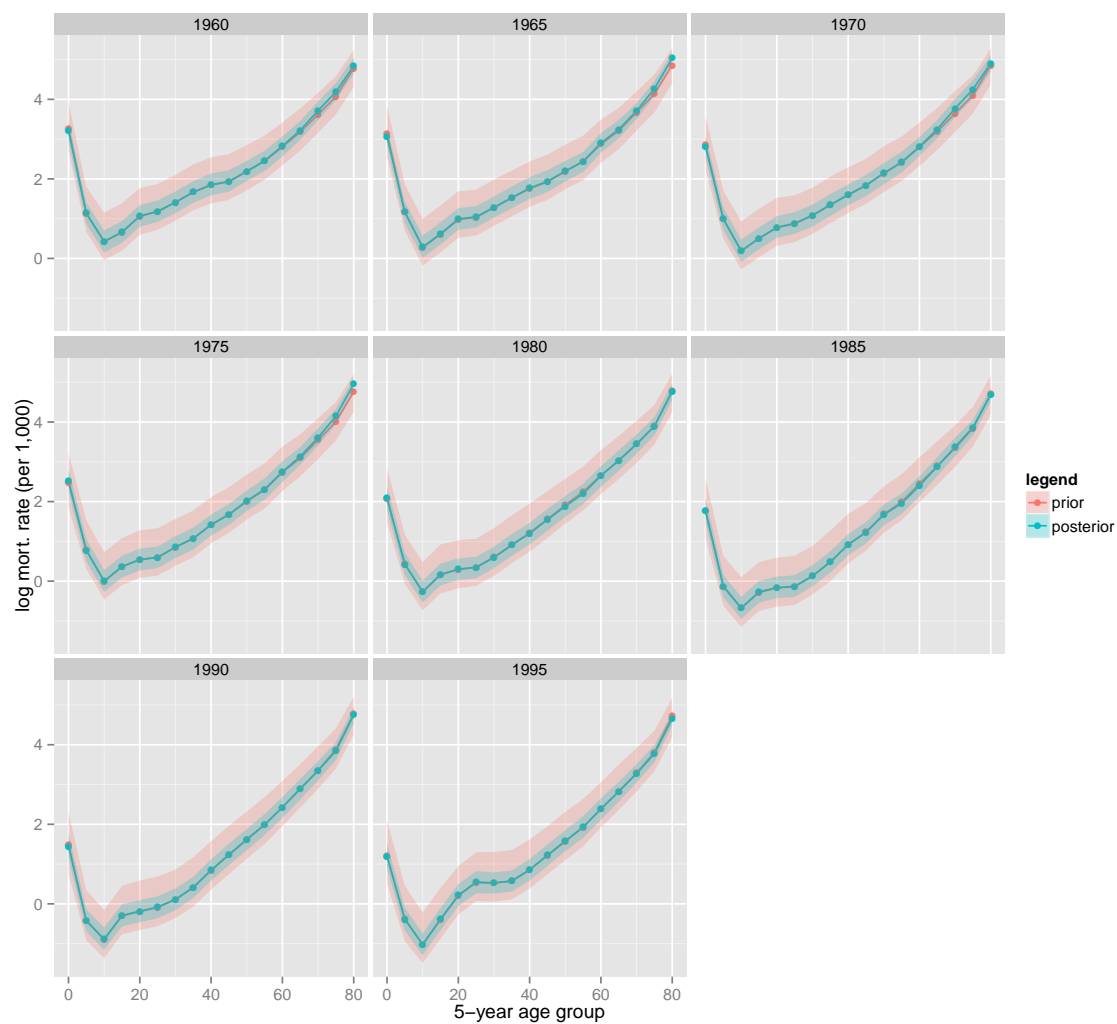


Figure 4.45. Prior and posterior medians and 95 percent credible intervals for age-specific female log mortality rate for the reconstructed population of Thailand, 1960–2000.

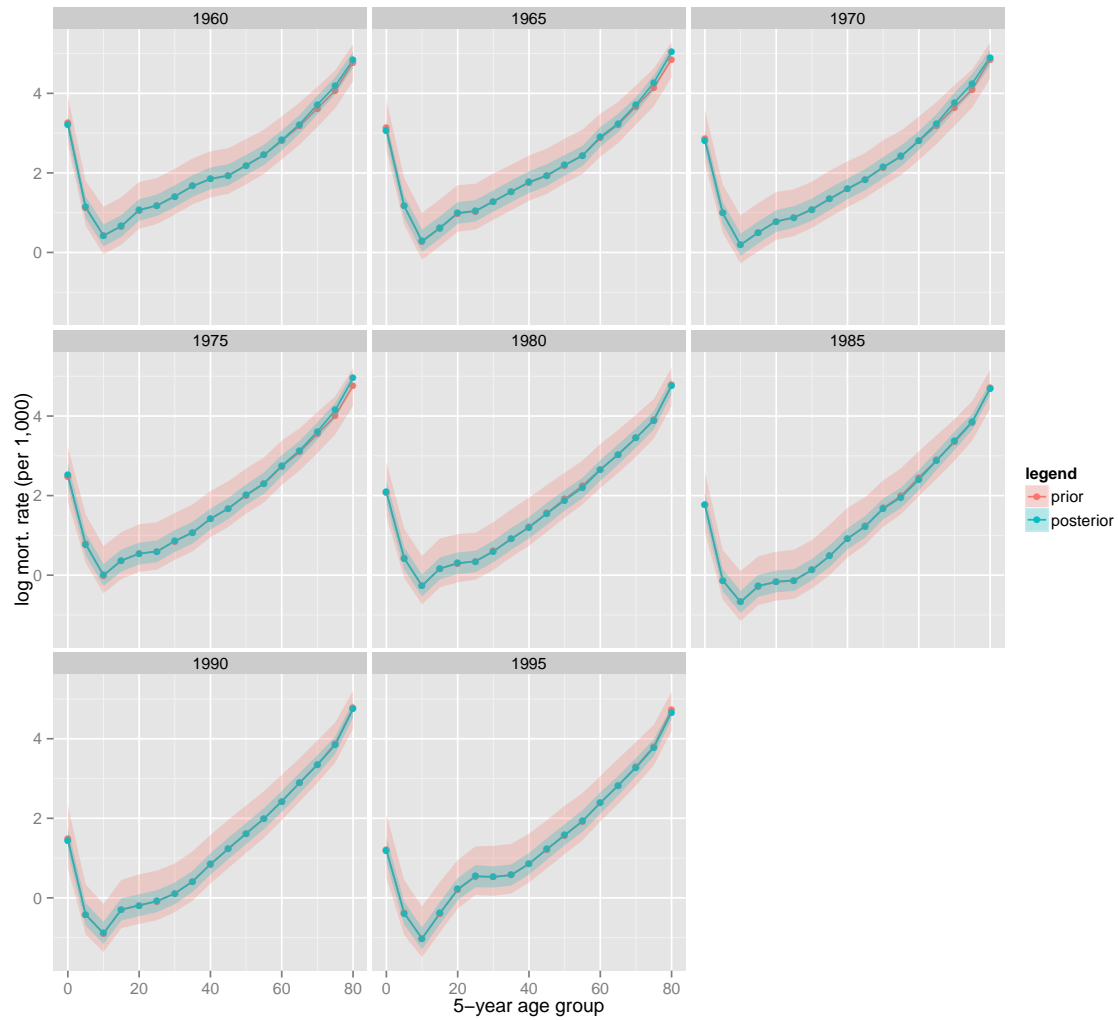


Figure 4.46. Prior and posterior medians and 95 percent credible intervals for age-specific male log mortality rate for the reconstructed population of Thailand, 1960–2000.



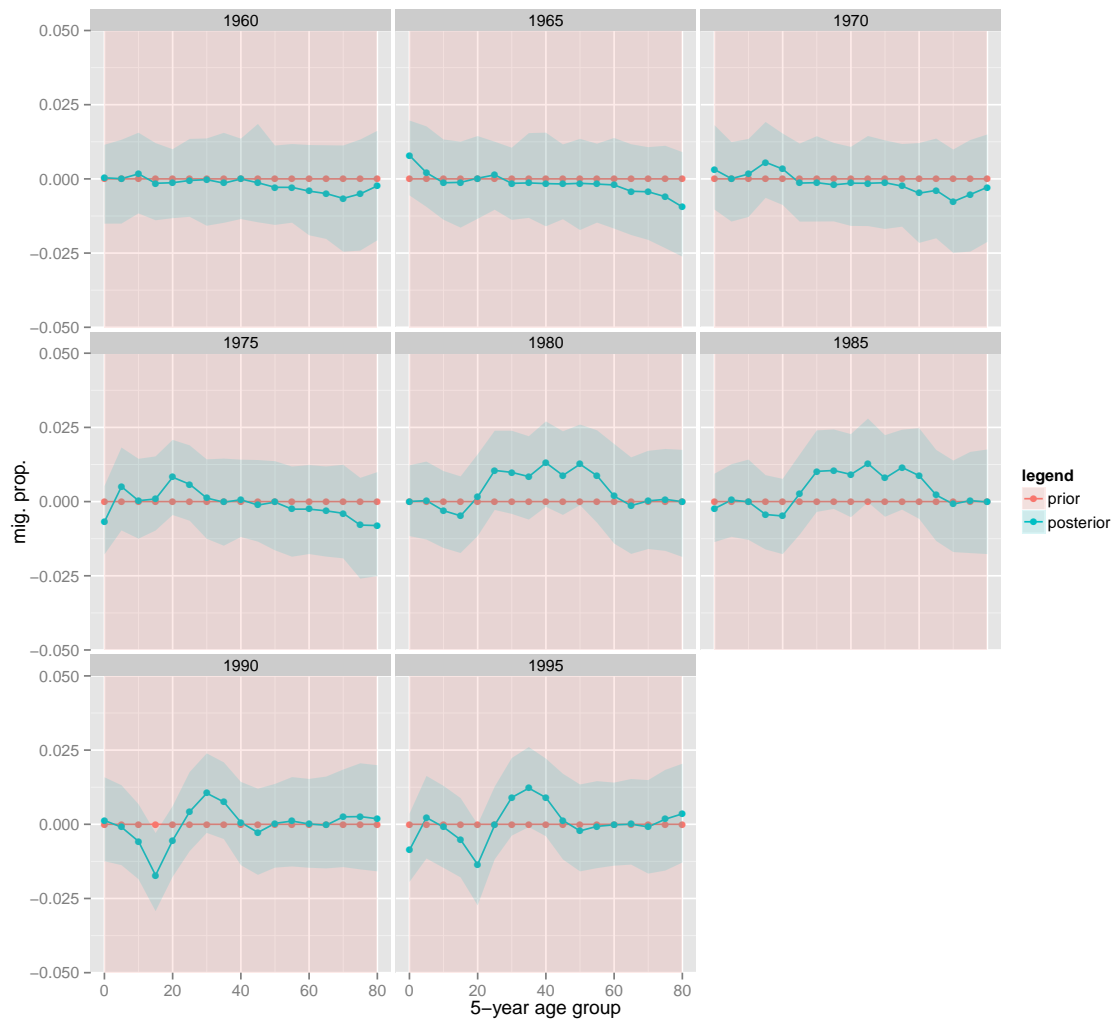


Figure 4.47. Prior and posterior medians and 95 percent credible intervals for age-specific female migration proportion for the reconstructed population of Thailand, 1960–2000.

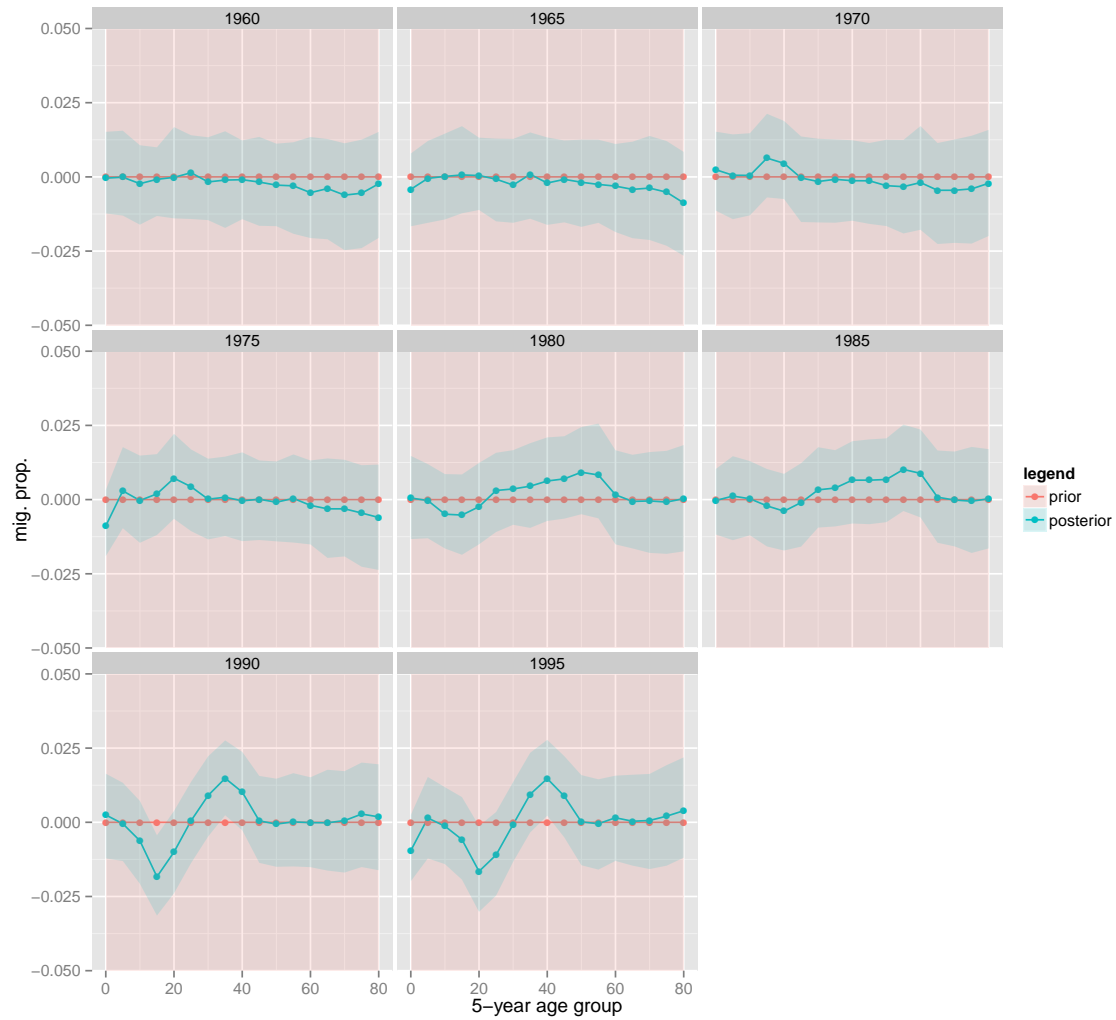


Figure 4.48. Prior and posterior medians and 95 percent credible intervals for age-specific male migration proportion for the reconstructed population of Thailand, 1960–2000.

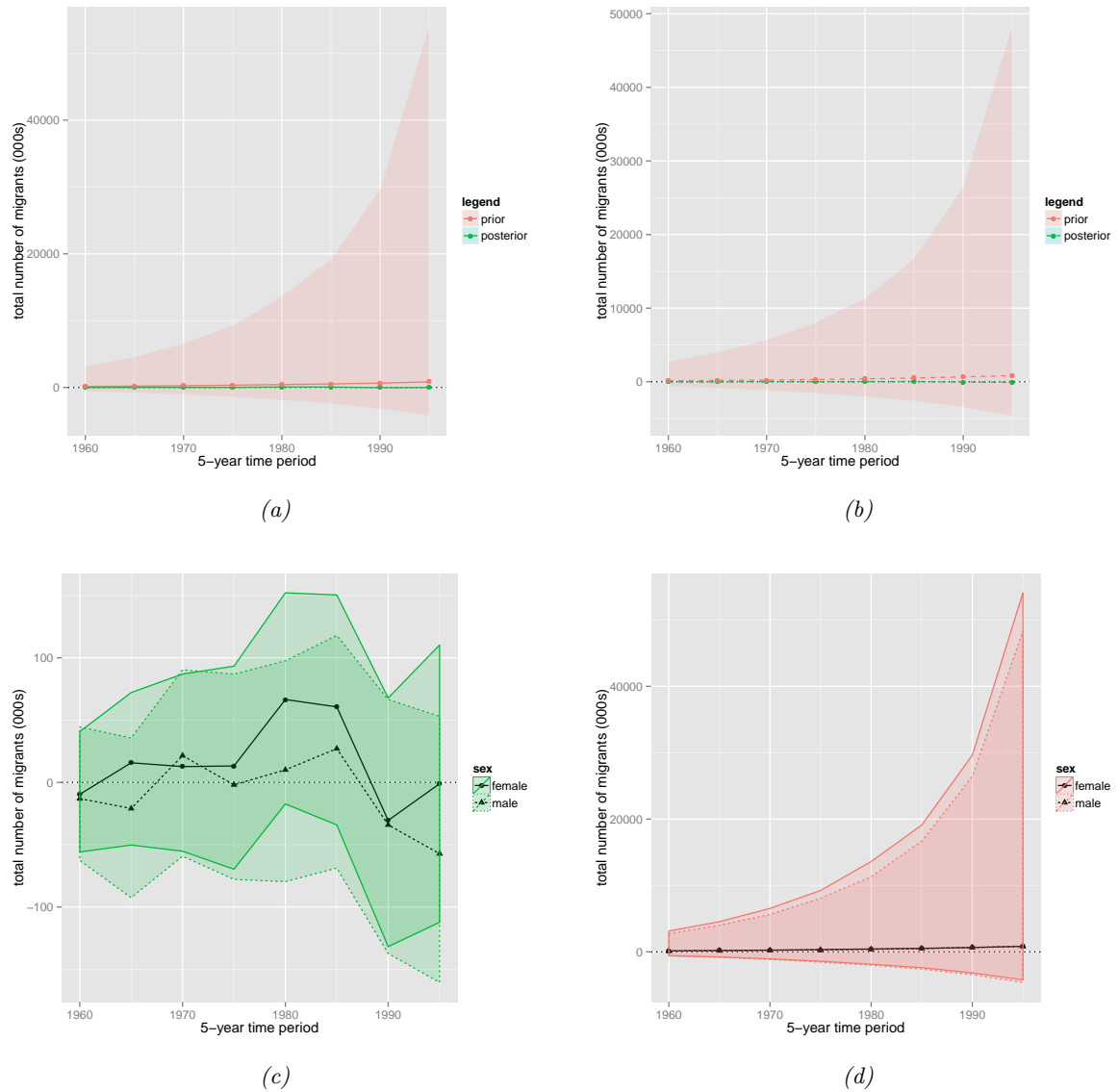


Figure 4.49. Prior and posterior medians and 95 percent credible intervals for the average annual net number of migrants for the reconstructed population of Thailand, 1960–2000: (a) females; (b) males; (c) female and male posterior quantiles only; (d) female and male prior quantiles only.

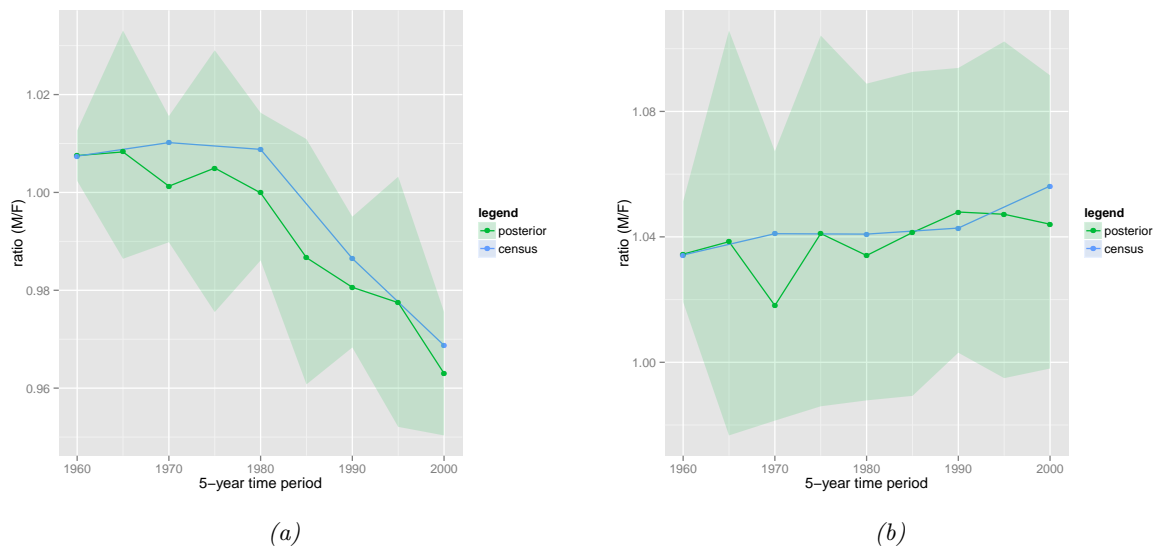


Figure 4.50. Prior and posterior medians and 95 percent credible intervals for the reconstructed population of Thailand, 1960–2000: (a) sex ratio in the total population (SRTP); (b) population aged 0–4.

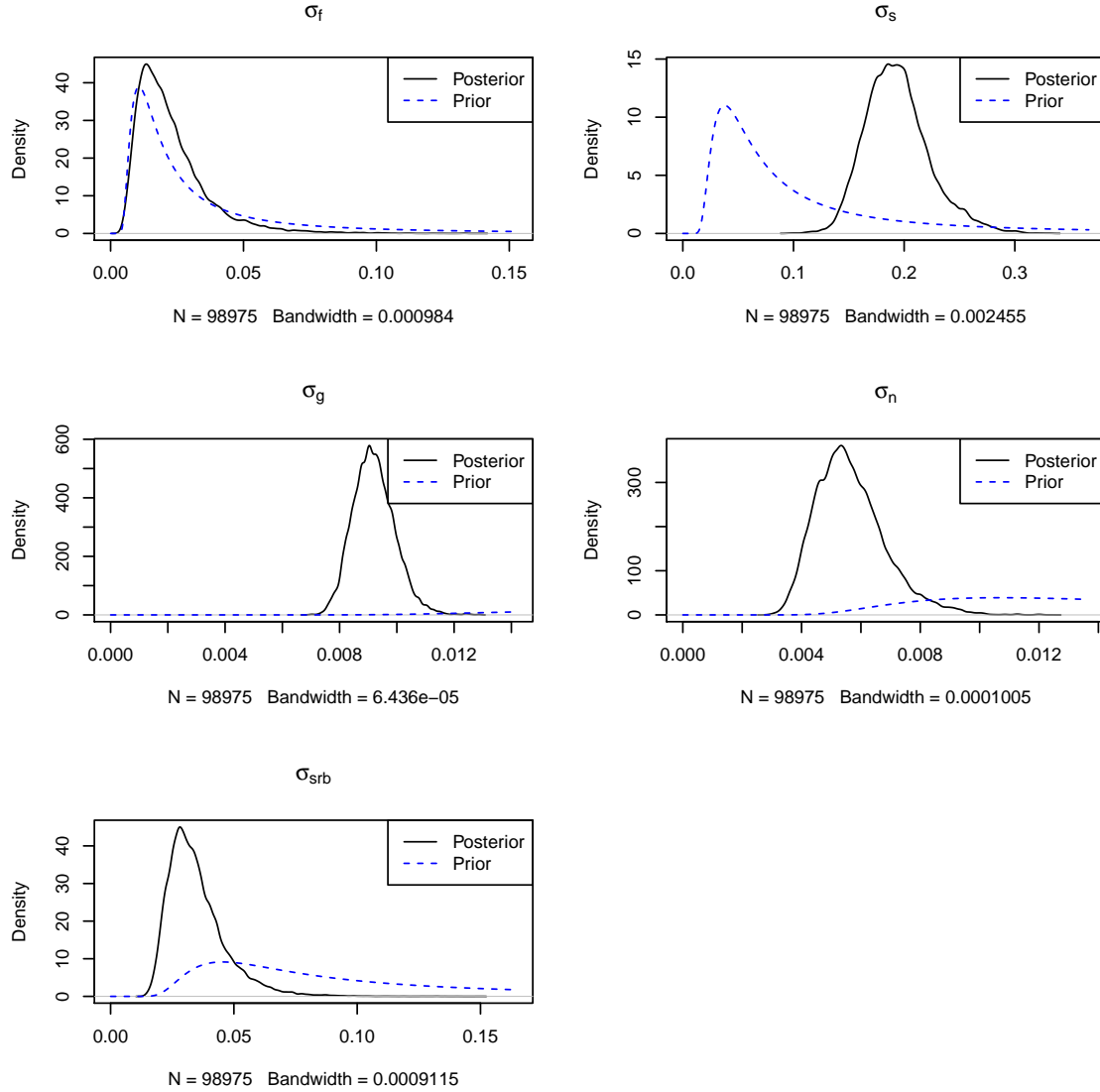


Figure 4.51. Prior and posterior densities of model standard deviation parameters,  $\sigma_v$ ,  $v = \{n, f, s, g\}$  for the reconstructed population of Thailand, 1960–2000. Posterior densities are kernel density estimates.

### 4.C.3 India 1971–2001

#### *Population Counts*

Total population counts are in Tables 4.10 and 4.11.

*Table 4.10.* Initial estimates, posterior medians and 95 percent credible intervals for population count for the reconstructed female population of India, 1971–2001, in millions.

Year	Posterior Percentile			Init. Est.
	2.5th	50th	97.5th	
1971	269	271	274	271
1976	297	305	313	
1981	339	344	348	343
1986	375	385	396	
1991	423	430	436	428
1996	461	474	488	
2001	510	519	528	515

#### *Age-specific Fertility Rates*

Results for age-specific fertility rates are in Figure 4.52.

#### *Age-specific Survival Proportions*

Results for age-specific survival proportions are in Figures 4.53 and 4.54.

#### *Age-specific Mortality Rates*

Results for age-specific mortality rates on the log scale are in Figures 4.55 and 4.56.

#### *Age-specific Migration Proportions*

Posterior estimates for the age-specific migration proportions are in Figures 4.57 and 4.58.

*Table 4.11.* Initial estimates, posterior medians and 95 percent credible intervals for population count for the reconstructed male population of India, 1971–2001, in millions.

Year	Posterior Percentile			Init. Est.
	2.5th	50th	97.5th	
1971	293	295	298	295
1976	322	331	340	
1981	368	372	377	373
1986	404	416	427	
1991	455	461	468	463
1996	492	507	521	
2001	543	552	561	555

#### *Total Net Number of Migrants*

Results for the average annual net number of migrants are in Figure 4.59. Uncertainty is large and the mean half-width is 824,473.

#### *Prior and Posterior Density Estimates for Variance Parameters*

Prior and posterior kernel density estimates for the standard deviation parameters  $\sigma_v$ ,  $v = \{n, f, s, g\}$  are shown in Figure 4.60.

#### **Appendix 4.D MCMC Chain Lengths**

The number of burn-in iterations and the number used for inference in each case study are given in Table 4.12.

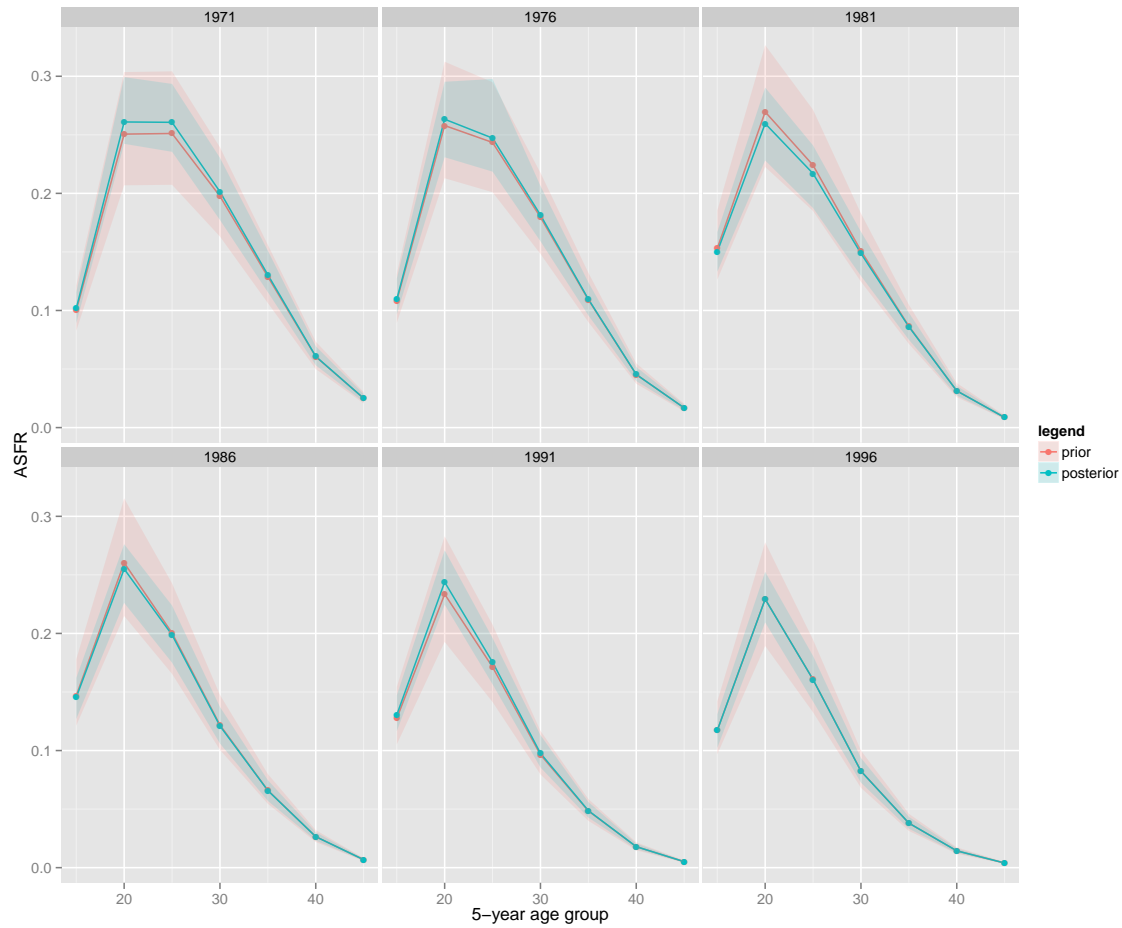


Figure 4.52. Prior and posterior medians and 95 percent credible intervals for age-specific fertility rates (ASFRs) for the reconstructed population of India, 1971–2001.

Table 4.12. MCMC chain lengths used for each case study.

Country	Burn-in	Used
Laos	10000	795276
Thailand	6025	98975
India	6319	98681



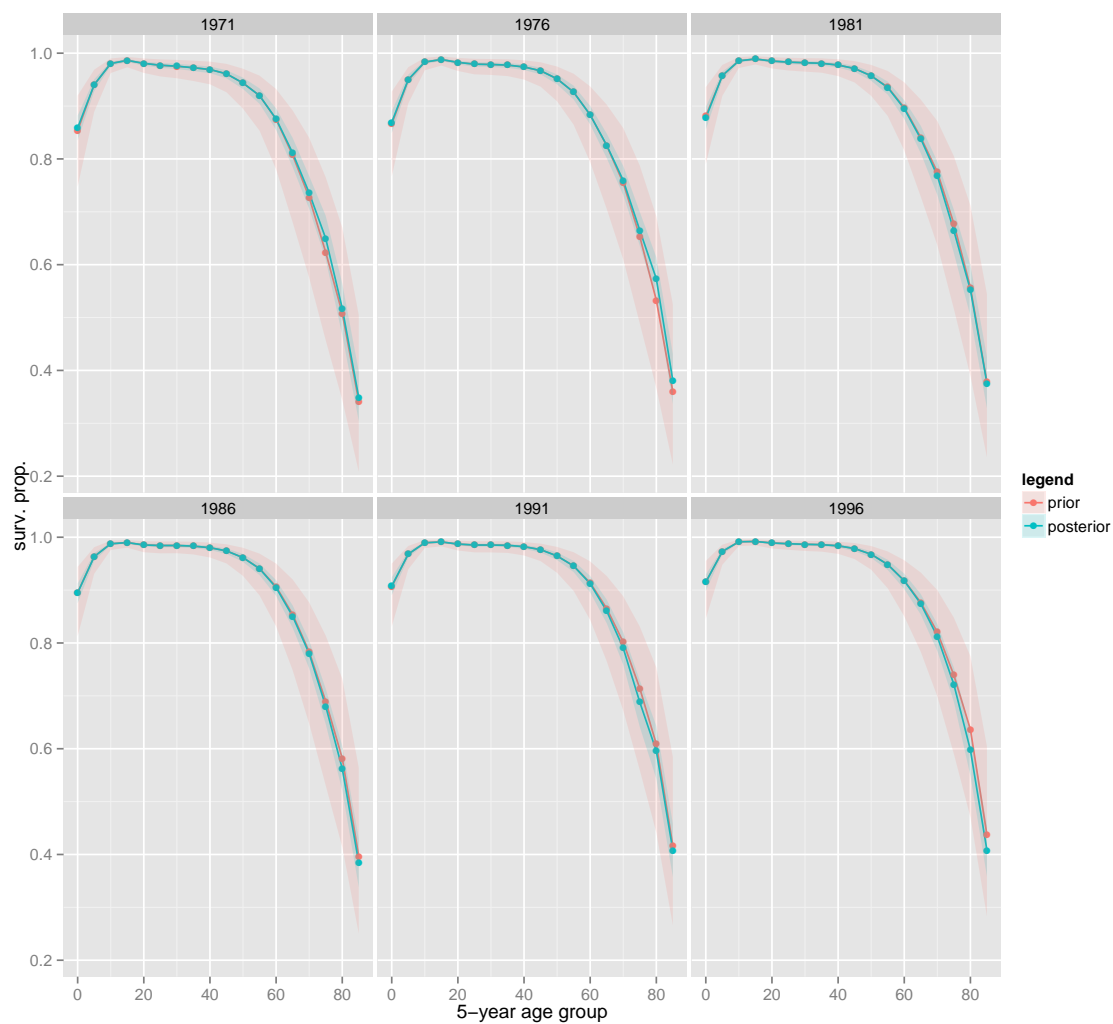


Figure 4.53. Prior and posterior medians and 95 percent credible intervals for age-specific female survival proportion for the reconstructed population of India, 1971–2001.

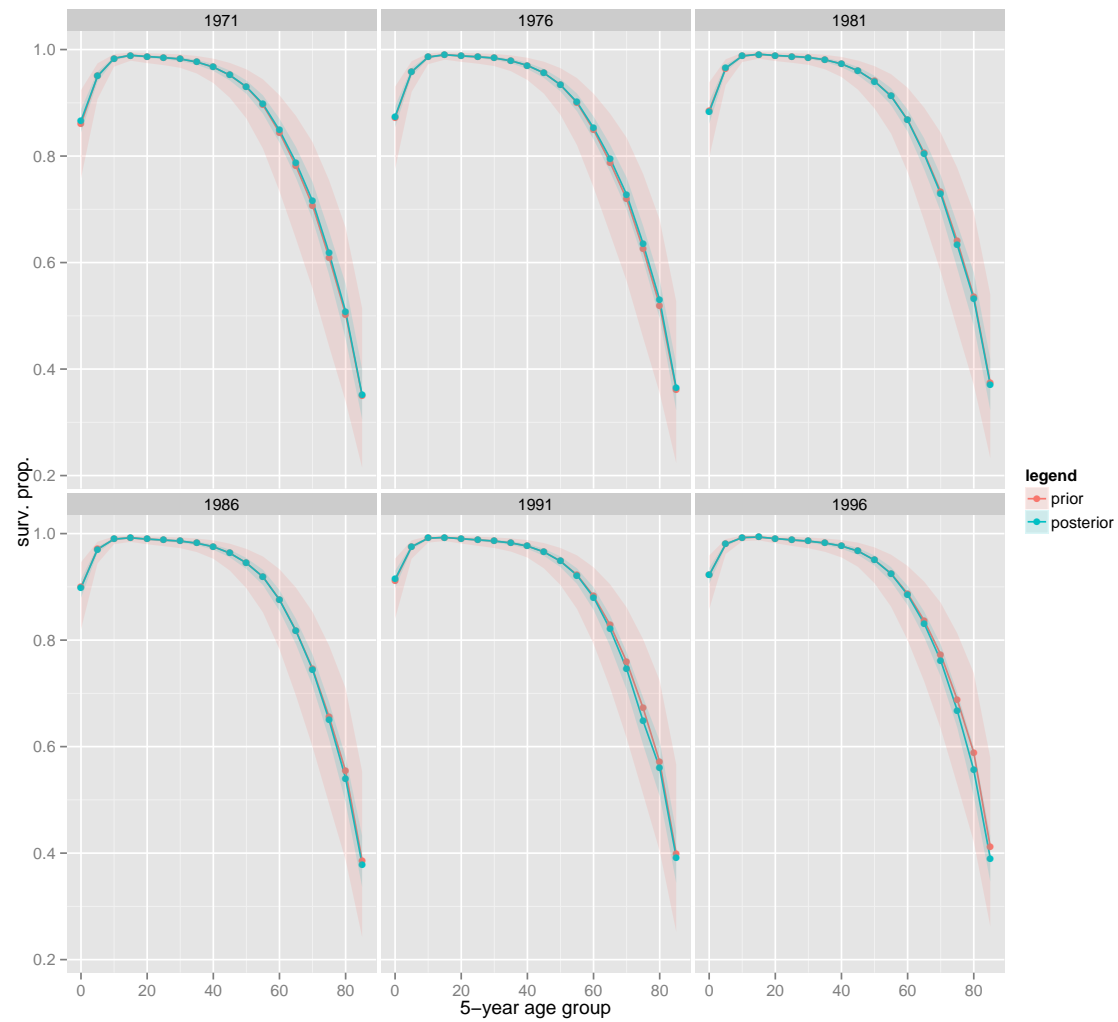


Figure 4.54. Prior and posterior medians and 95 percent credible intervals for age-specific male survival proportion for the reconstructed population of India, 1971–2001.

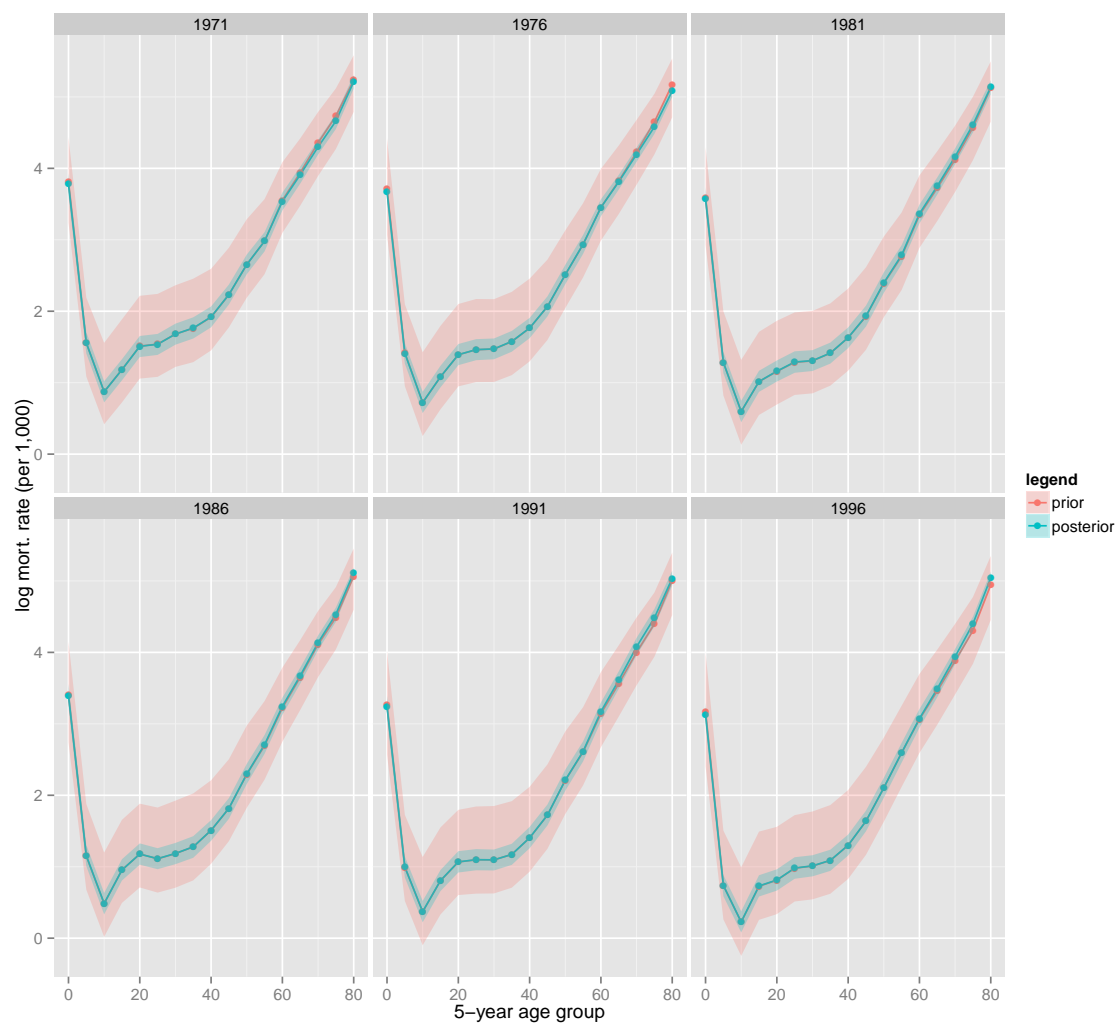


Figure 4.55. Prior and posterior medians and 95 percent credible intervals for age-specific female log mortality rate for the reconstructed population of India, 1971–2001.

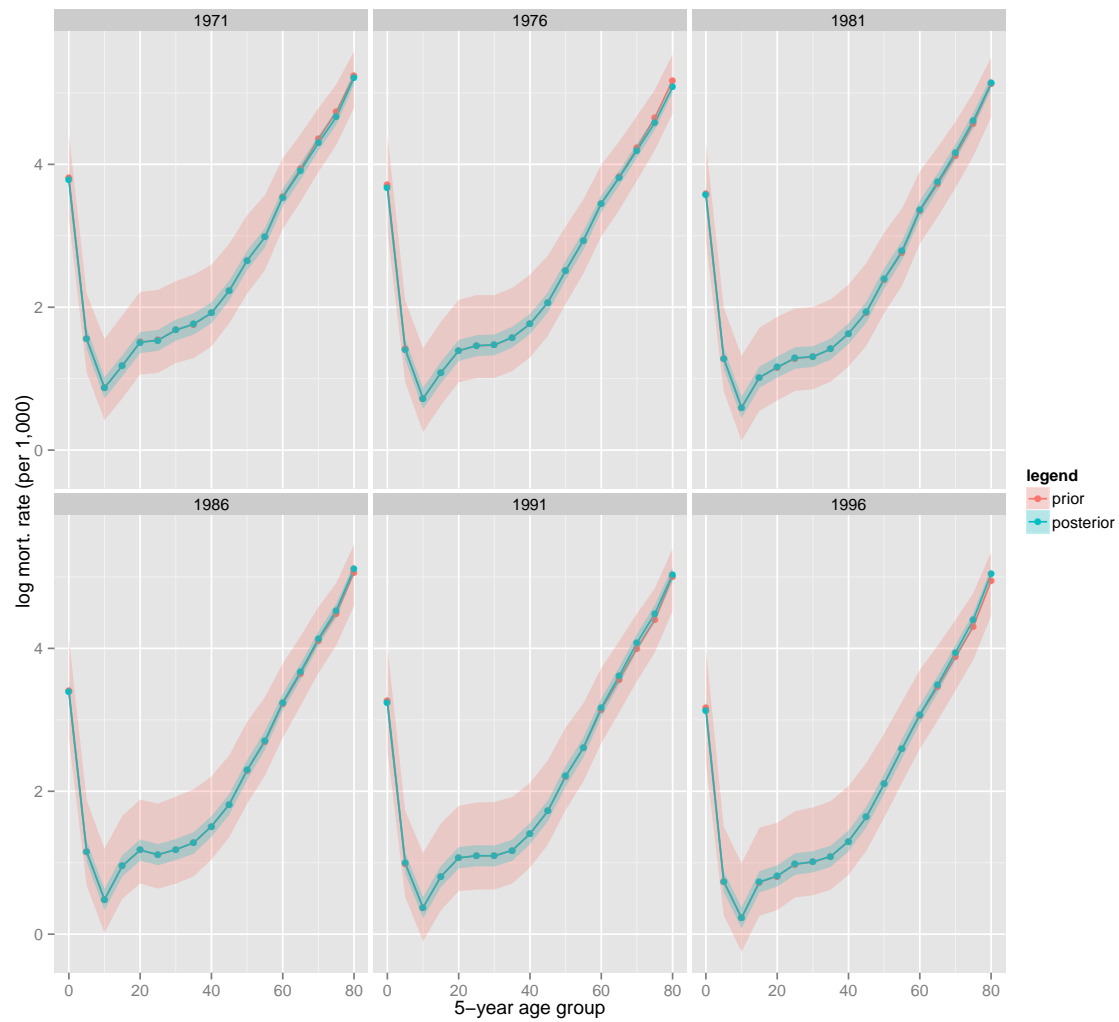


Figure 4.56. Prior and posterior medians and 95 percent credible intervals for age-specific male log mortality rate for the reconstructed population of India, 1971–2001.

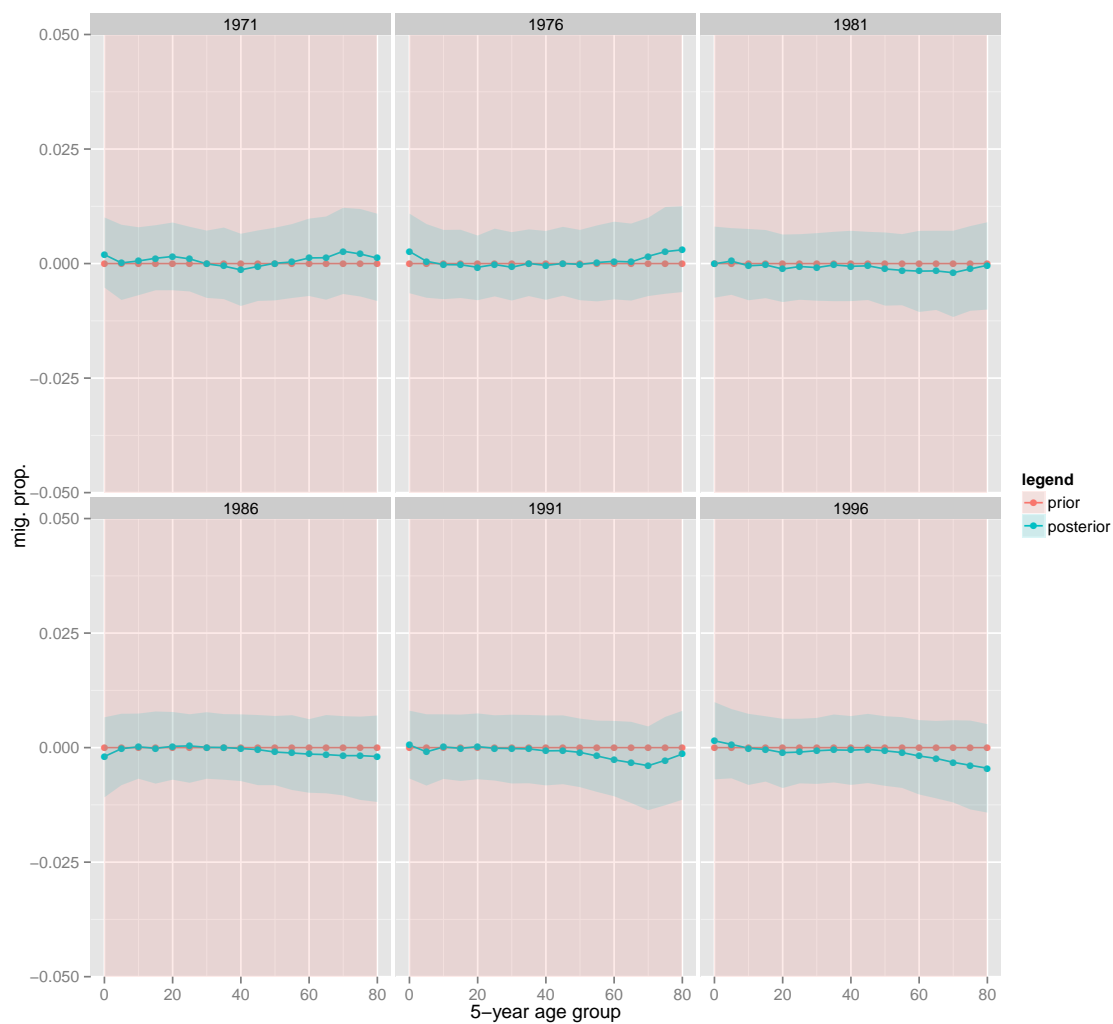


Figure 4.57. Prior and posterior medians and 95 percent credible intervals for age-specific female migration proportion for the reconstructed population of India, 1971–2001.

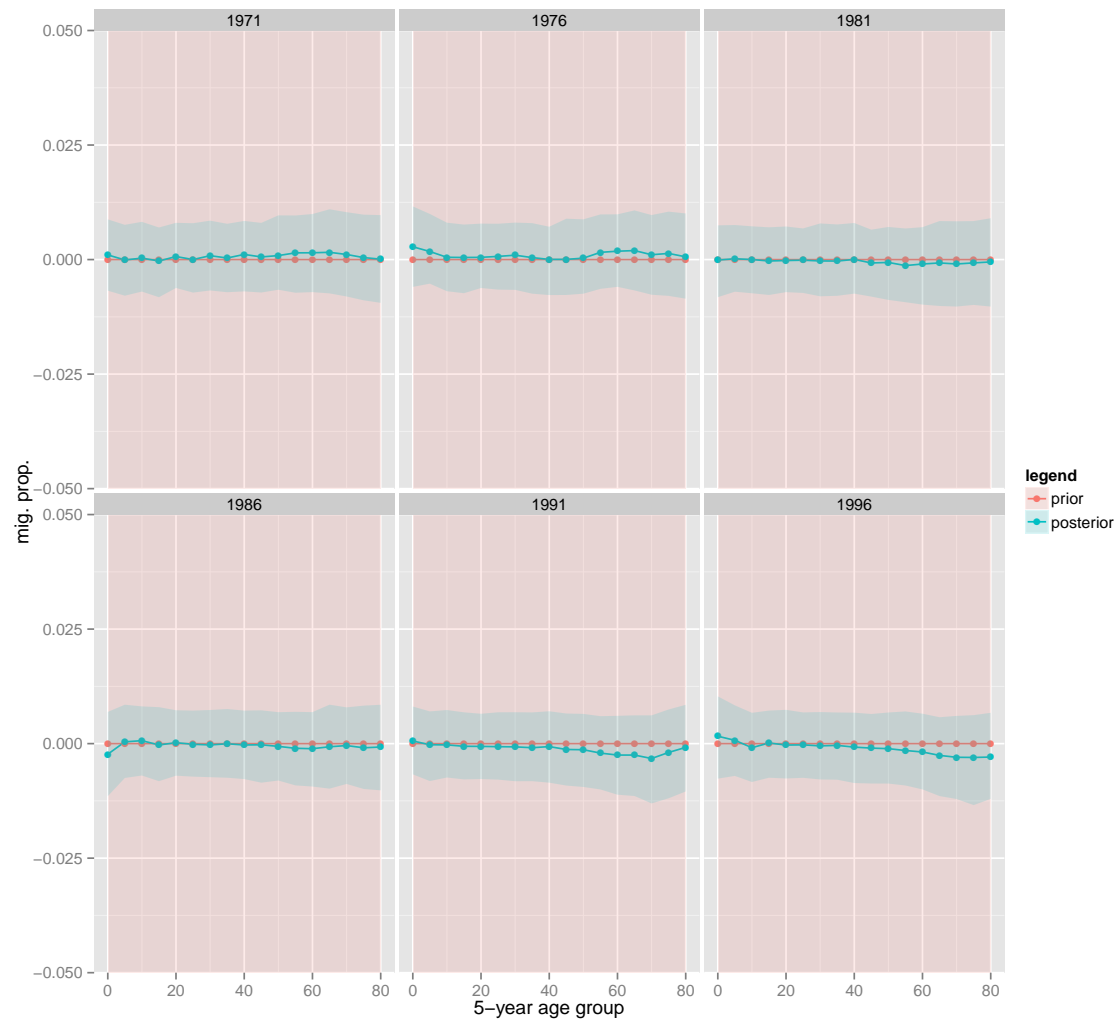
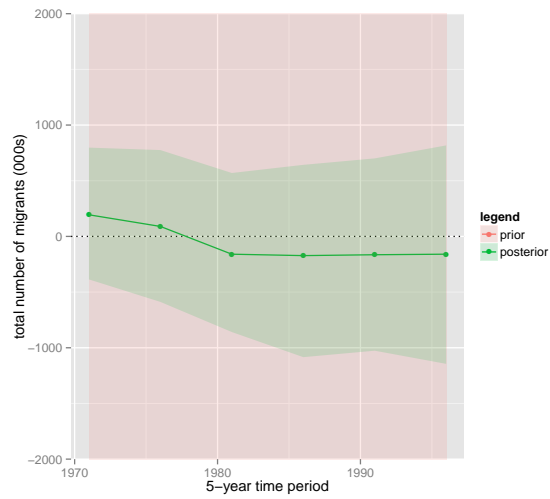
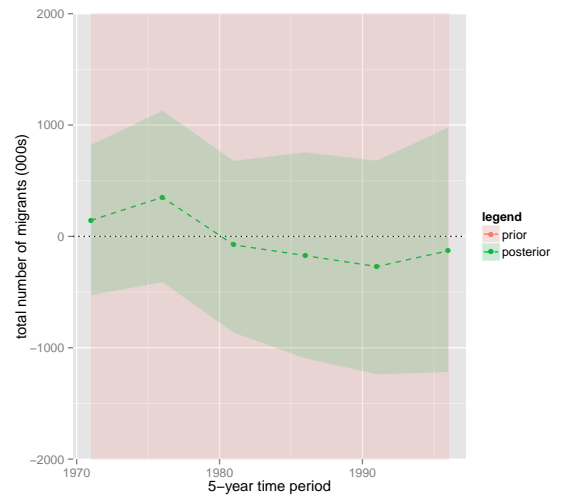


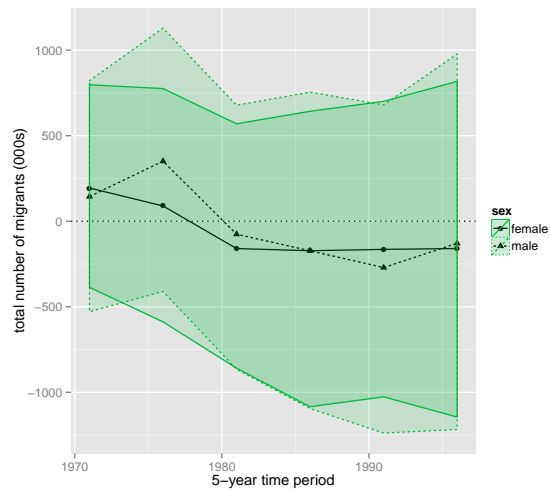
Figure 4.58. Prior and posterior medians and 95 percent credible intervals for age-specific male migration proportion for the reconstructed population of India, 1971–2001.



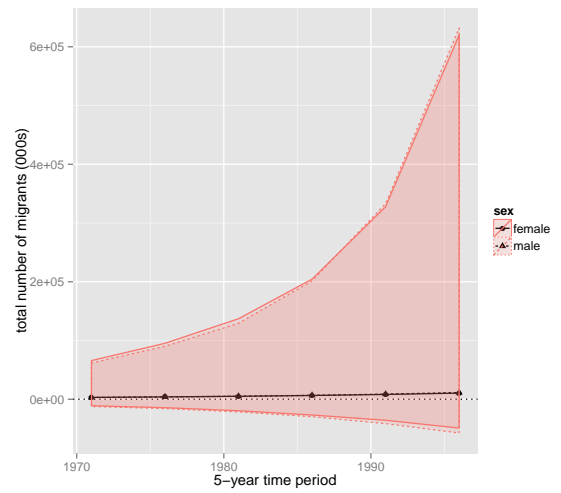
(a)



(b)



(c)



(d)

Figure 4.59. Prior and posterior medians and 95 percent credible intervals for the average annual net number of migrants for the reconstructed population of India, 1971-2004: (a) females; (b) males; (c) female and male posterior quantiles only; (d) female and male prior quantiles only.

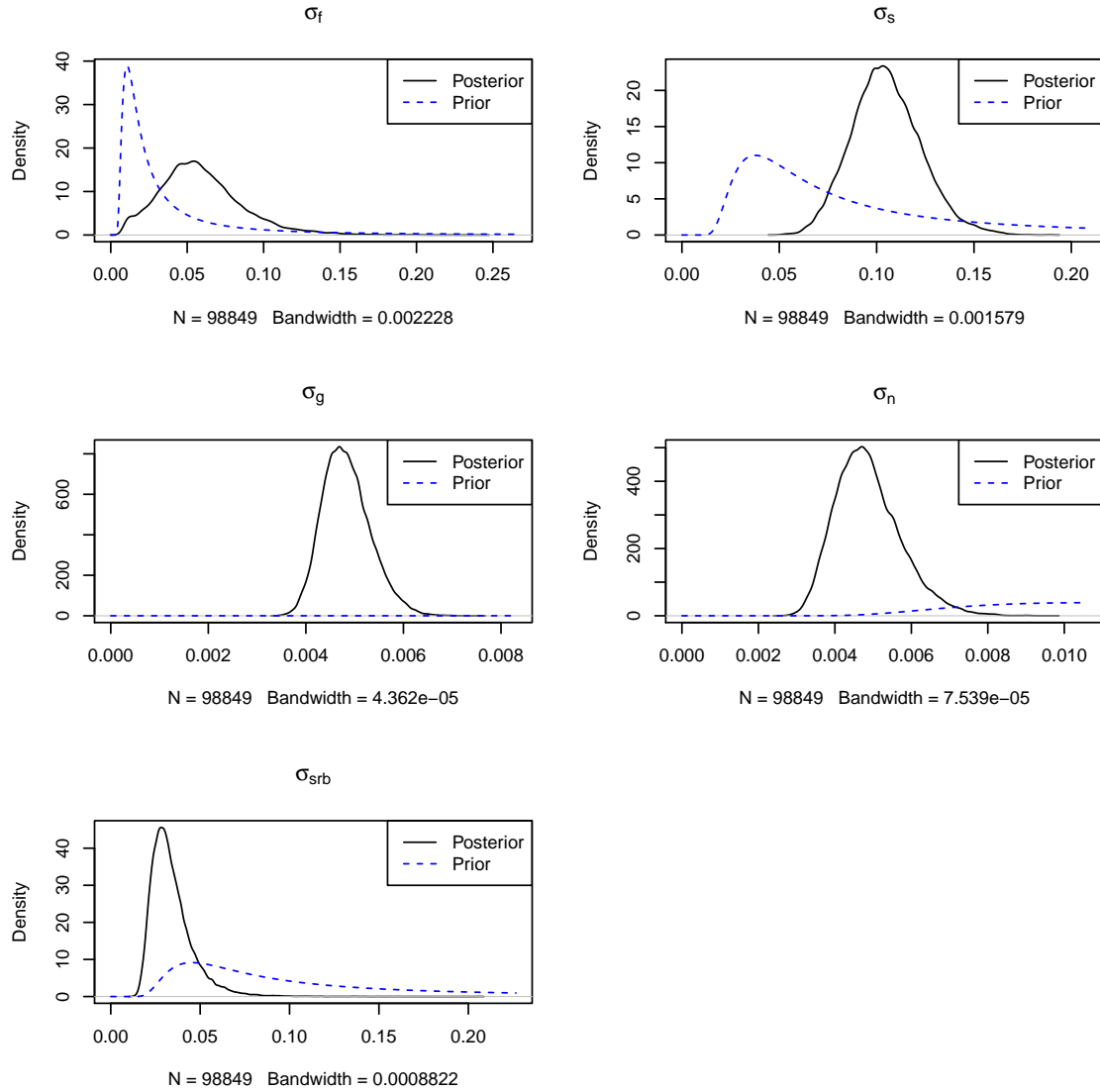


Figure 4.60. Prior and posterior densities of model standard deviation parameters,  $\sigma_v$ ,  $v = \{n, f, s, g\}$  for the reconstructed population of India, 1971–2004. Posterior densities are kernel density estimates.



## Chapter 5

## CONCLUSION

Key contributions and some ideas for further work are given in this chapter. Further details can be found in the Discussion sections of the main chapters (Sections 2.6, 3.5 and 4.4).

### 5.1 *Contributions to Research*

A new method has been proposed for reconstructing human populations of the recent past by age and sex, which produces quantitative, probabilistic estimates of uncertainty. It is called “Bayesian reconstruction”. It is designed to work with the type of data commonly collected in modern demographic surveys and censuses and should be especially useful for reconstructing the populations of developing countries for which the data are often fragmentary and subject to measurement error. The required inputs are bias-reduced initial estimates of age-, sex-specific fertility rates, survival and migration proportions and population counts from censuses (or similar), all by five-year time period. Expert opinion about measurement error is also required and this can be informed by data if it is available. Temporal relationships are modeled using the cohort component method of population projection (CCMPP).

A major improvement that Bayesian reconstruction brings over existing methods is that measurement error is accounted for in a fully probabilistic manner through a hierarchical statistical model. Moreover, expert opinion about measurement error is incorporated transparently and probabilistically. This is done through informative priors which can be informed by data where available. Previous methods of reconstruction did not account for measurement error, or imposed fixed age-patterns on some parameters. Age-patterns of vital events are not fixed in Bayesian reconstruction.

All available data are synthesized automatically and coherently, including data from

censuses and direct and indirect estimates of fertility and mortality rates (vital rates) from surveys and vital registration. Projection consistency is ensured through the CCMPP. This means that, in each sample trajectory in the joint posterior, the age-specific population counts for year  $t$  are those one gets by projecting the counts in year  $t - 5$  using the corresponding trajectories of vital rates and migration. Under the current United Nations Population Division (UNPD) procedure, this is achieved through an iterative, manual process which is not easy to replicate. Given the same inputs, Bayesian reconstruction will always produce the same outputs (to within Monte Carlo error); iterative, manual adjustments are not necessary.

Other contributions to methodology include an improved treatment of migration and the use of Bayesian reconstruction to choose between model life tables. Specifically, migration is treated in the same way as fertility and mortality. In many existing methods, migration is ignored or is estimated as a “residual” in a separate stage. It was also shown that Bayesian reconstruction can be used to help choose between competing model life tables for countries lacking good data on age-specific mortality.

Bayesian reconstruction was applied to real data, resulting in probabilistic reconstructions for six countries: Burkina Faso, Sri Lanka, New Zealand (female populations only), Laos, Thailand, and India (full populations). The two sex reconstructions also gave probabilistic estimates of sex ratios. These examples show how new probabilistic methods can be developed for demography and that they have the potential to provide previously unavailable quantitative information about uncertainty. Developing ways to augment standard demographic statistics with probabilistic estimates of uncertainty is currently an active area of research and I hope this work is a useful contribution.

The work in this dissertation forms the basis of contributions to the literature in the form of the article by [Wheldon et al. \(forthcoming\)](#) and the *R* package *popReconstruct* (Appendix B).

## 5.2 Future Work

Currently, Bayesian reconstruction is for national populations only. This is the level at which the United Nations (UN) operates and the level at which most data are available. The

method could be adapted to produce sub-national estimates. This might be particularly useful for large, demographically diverse countries like India, where vital rates and sex ratios differ greatly among states. Such an extension would be straightforward if it could be assumed that migration among the sub-national regions was negligible over the period of reconstruction, and if separate initial estimates were available for each region. In that case, the sub-national regions could be treated like separate countries. If the migration assumption cannot be made, a model for migration among regions would be needed. If sub-national data are not available, a model relating sub-national initial estimates to national ones would be needed.

Only net international migration is estimated in the current formulation since the CCMPP requires net migration as an input. Separating migration into immigration and emigration would be a worthwhile enhancement. Unfortunately, the requisite data are either unavailable, very fragmentary or unreliable. In cases where good information about both in- and out-migration is collected in population registers or border control agencies it might be reasonable to model the two flows separately on a country-by-country basis. However, even in western Europe, where statistical agencies are very well funded, it has been difficult to reconcile the migration estimates of different countries (e.g., [Raymer et al., 2011](#)).

In the single sex model (Section [2.3.3](#)), there is a single variance parameter for each age group and time period, per vital rate parameter. In the two sex version (Section [4.2.3](#)) these variances are also constant across sex. Future work might explore ways of explicitly modeling correlations such as those between adjacent age groups and time periods, and between the sexes. This is discussed further in [Appendix A](#).

Statistically, the current model is over-parameterized. For instance, all age-specific fertility rates together with under-five mortality and under-five migration in year  $t$  are identified through census counts for a single five year age group in year  $t + 5$ . A Bayesian approach, which imposes some additional structure through the prior, allowed progress to be made but attempting to reduce this under-identification might be worthwhile. One way this might be done is to incorporate more of the original, raw data into the model rather than rely solely on the data-derived initial estimates. Initial estimates were used because raw data often suffer from well-known, non-negligible biases due to recall error, age-heaping and other

“non-sampling” sources. The initial estimate approach allowed standard demographic techniques, such as the  $P/F$  ratio method and the use of model life tables, to be employed separately to reduce these biases. This allows Bayesian reconstruction to be used for almost any country with census data since the bias reduction techniques needed vary widely across data-sources, countries and time. If raw data on fertility and mortality are to be used in Bayesian reconstruction, biases will have to be adequately accounted for in a standard way. [Alkema et al. \(2012\)](#) developed a method for estimating both bias and measurement error in data on total fertility rate (TFR) in several west African countries. One promising approach, at least for fertility, might be to try and build a model like [Alkema et al.’s \(2012\)](#) into Bayesian reconstruction so that raw data can be used. A suitable alternative prior for age-specific fertility will have to be developed.

In its current form, the software used to implement Bayesian reconstruction, *popReconstruct* for *R*, is slow. For example, the reconstruction of the female population of Sri Lanka took two to three days on a fast computer. If this method is to be used routinely by demographers, enhancements to improve speed would probably be welcomed. An obvious modification would be to re-write portions of the source code in a compiled language such as *C* or *FORTRAN*.

## Appendix A

### MODELING CORRELATION IN AGE, TIME AND SEX

#### A.1 Introduction

The models in Sections 2.3.3 and 4.2.3 have a single variance for each Level 3 parameter  $x_{a,t}$ ,  $x = \log n, \log f, \text{logit } s, g$ , which is constant across age groups, time periods and sex. As a result, the *a priori* correlations among age, time and sex are zero, conditional on the initial estimates  $\log n^*, \log f^*, \text{logit } s^*, \log n^*$ . Moreover, so are the same correlations for the measurement errors  $x_{a,t} - x_{a,t}^*$ . However, this might not be so in practice and such correlations could be modeled explicitly. To investigate whether or not this might be worthwhile, I study the following difference quantities:

$$\epsilon_{a,t,l,x} \equiv x_{a,t,l}^* - \tilde{x}_{a,t,l}$$

$$x \in \{\log n, \log f, \text{logit } s, g\}, a = 0, 5, \dots, 85+, t = t_0, \dots, T, l = F, M.$$

where  $\tilde{x}_{a,t,l}$  is the posterior median of  $x_{a,t,l}$ . The  $x_{a,t,l}^*$  are the “initial estimates” which, *a priori*, are medians of the distributions in Level 3. The difference quantities give an indication of the measurement error in the initial estimates. They are calculated separately for each country (a corresponding index has been omitted for clarity). Systematic patterns in the  $\epsilon_{a,t,l,x}$  over age, time or sex would suggest that there is some structure to the measurement errors that could be explicitly modeled.

## A.2 Analysis

### A.2.1 Correlation in Age and Time

The association between measurement errors in adjacent age groups and time periods was investigated by computing the lag-one autocorrelations:

$$r_x^{[a]} \equiv \frac{\sum_{a=5:5}^{85} \sum_{t=t_0:5}^T \sum_{l=F,M} (\epsilon_{a,t,l,x} \cdot \epsilon_{a-5,t,l,x})}{\sqrt{\sum_{a=5:5}^{85} \sum_{t=t_0:5}^T \sum_{l=F,M} \epsilon_{a,t,l,x}^2} \sqrt{\sum_{a=5:5}^{85} \sum_{t=t_0:5}^T \sum_{l=F,M} \epsilon_{a-5,t,l,x}^2}}$$

$$r_x^{[t]} \equiv \frac{\sum_{t=t_0+5:5}^T \sum_{a=0:5}^{85} \sum_{l=F,M} (\epsilon_{a,t,l,x} \cdot \epsilon_{a,t-5,l,x})}{\sqrt{\sum_{t=t_0+5:5}^T \sum_{a=0:5}^{85} \sum_{l=F,M} \epsilon_{a,t,l,x}^2} \sqrt{\sum_{t=t_0+5:5}^T \sum_{a=0:5}^{85} \sum_{l=F,M} \epsilon_{a,t-5,l,x}^2}}$$

where the notation “:5” in the lower limits of the sums means that the values are incremented by 5. The standardization due to the denominators means that the  $r_x$ s will be in the interval  $[-1, 1]$  and comparison of their magnitudes across parameters will make sense. The  $\epsilon_{a,t,l,x}$  are not centered prior to computing the cross-products because I am interested in deviations relative to the initial estimates, which have already been subtracted, not relative to the sample means of the  $\epsilon$ s. The sign of the  $r_x$ s indicates the nature of the association between deviations in adjacent age groups (same time period) and adjacent time periods (same age group). For example,  $r_x^{[a]}$  in the interval  $(0, 1]$  would suggest that positive (negative) deviations at age  $a$  are most frequently followed by positive (negative) deviations at age  $a + 5$ , within time period. Conversely,  $r_x^{[a]}$  in  $[-1, 0)$  would suggest that positive (negative) deviations are followed by negative (positive) deviations. Values of  $r_x^{[a]}$  close to zero indicate no systematic pattern in adjacent deviations. Positive (negative) deviations come about when the initial estimates are lower (higher) than the posterior medians. The larger the magnitudes of the deviations, the larger the  $r_x$ s, all else being equal.

Figure A.1 shows  $r_x^{[a]}$  and  $r_x^{[t]}$  for each of the reconstructed countries. Most are positive, suggesting that positive (negative) measurement errors are frequently followed by positive (negative) measurement errors both over age groups and time periods. The average magnitude of the  $r_x^{[a]}$ s is larger than that of the  $r_x^{[t]}$ s (0.61 vs. 0.32, baseline count excluded). Among the  $r_x^{[a]}$ s, those for fertility and migration have the highest average value and the lowest variance across countries. Among the  $r_x^{[t]}$ , the migration values are the highest, on average, and most the concentrated.

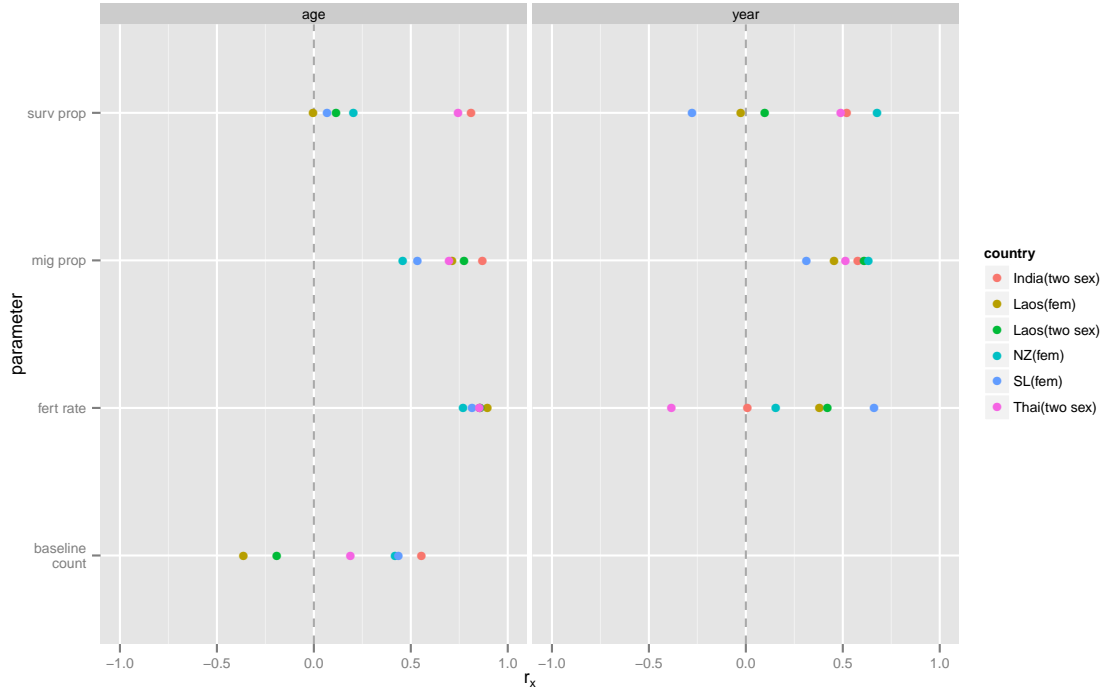


Figure A.1. Lag-one autocorrelations,  $r_x$ , across age and time for each of the reconstructed countries.

### A.2.2 Correlation Between Sex

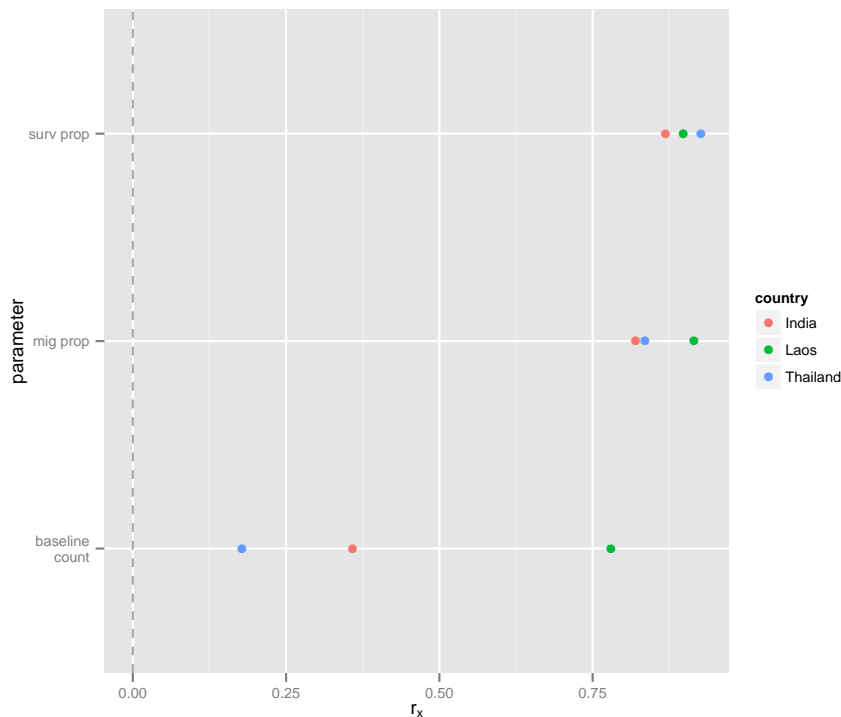
The association between female and male measurement errors was investigated using the statistic

$$r_x^{[l]} \equiv \frac{\sum_{a=0:5}^{85} \sum_{t=t_0:5}^T (\epsilon_{a,t,F,x} \cdot \epsilon_{a,t,M,x})}{\sqrt{\sum_{a=0:5}^{85} \sum_{t=t_0:5}^T \epsilon_{a,t,F,x}^2} \sqrt{\sum_{a=0:5}^{85} \sum_{t=t_0:5}^T \epsilon_{a,t,M,x}^2}}.$$

This is an analogue of  $r_x^{[a]}$  and  $r_x^{[t]}$ . The  $r_x^{[l]}$ s for all three of the two-sex reconstructions were positive (Figure A.2). Those for migration and survival were particularly large for all countries.

## A.3 Discussion

The lag-one correlations for age and time were mostly positive and large. The correlations between log fertility rates, and between migration proportions, in adjacent age groups within



*Figure A.2.* Correlations between female and male measurement errors for each of the two sex reconstructions.

time period were particularly large for all countries. Correlations between migration proportions in adjacent time periods within age groups were also positive and quite large in all countries. Correlations between male and female survival proportions and male and female migration proportions were also large and positive for all of the two sex reconstructions.

It seems reasonable to assume that similar patterns of association in measurement error might hold in most countries. This association could be explicitly modeled by adding parameters to the current model. I give an example of how this might be done below. For clarity, I use the single sex model and discuss migration only. The example should be seen as a first step toward building a more sophisticated covariance model motivated by the statistics studied above. Other possibilities should be considered if the covariance structure is of high interest.



### A.3.1 A Banded Covariance Matrix Model for Migration Proportions

The model for the migration proportions can be written

$$\log \mathbf{g}_{\cdot, \cdot} | \sigma_g^2 \sim \text{MVN}_{KJ}(\mathbf{g}_{\cdot, \cdot}^*, \Sigma_g^{[D]})$$

where  $K$  is the number of age groups,  $J$  is the number of time periods and  $\Sigma_g^{[D]}$  is a  $KJ \times KJ$  variance-covariance matrix with all diagonal entries equal to  $\sigma_g^2$  and all other elements equal to zero. The vectors  $\mathbf{g}_{\cdot, \cdot}$  and  $\mathbf{g}_{\cdot, \cdot}^*$  are  $KJ$  vectors formed by stacking the  $g_{a,t}$  and  $g_{a,t}^*$  with age varying fastest; for example,

$$\mathbf{g}_{\cdot, \cdot} \equiv \begin{bmatrix} g_{0,t_0} & g_{5,t_0} & \cdots & g_{0,t_0+5} & g_{5,t_0+5} & \cdots & g_{75,T} & g_{80,T} \end{bmatrix}'.$$

Covariances between adjacent age-groups and time periods can be achieved by replacing  $\Sigma_g^{[D]}$  with  $\Sigma_g^{[B]}$  which has the following block structure:

$$\Sigma_g^{[B]} \equiv \begin{bmatrix} \Sigma_{f(1,1)} & \cdots & \Sigma_{f(1,J)} \\ \vdots & \ddots & \vdots \\ \Sigma_{f(J,1)} & \cdots & \Sigma_{f(J,J)} \end{bmatrix},$$

Each  $\Sigma_{f(i,j)}$ ,  $i, j = 1, \dots, J$ , is the  $K \times K$  variance-covariance matrix for age specific migration proportions in the time periods  $i$  and  $j$ ; it has diagonal elements  $\sigma_g^2$ . If the correlation between adjacent age groups is denoted  $\rho_g$ , constant across age, then putting  $\rho_g \sigma_g^2$  on the sub- and super-diagonals of  $\Sigma_{f(i,i)}$ ,  $i = 1, \dots, J$ , allows this to be modeled explicitly. The diagonal entries of the sub- and super-diagonal blocks of  $\Sigma_g^{[B]}$ ,  $\Sigma_{f(i,i+1)}$ ,  $i = 1, \dots, J-1$  and  $\Sigma_{f(j,j-1)}$ ,  $j = 2, \dots, J$ , contain the covariances between migration proportions in adjacent time periods, same age group. If these correlations are denoted  $\tau_g$ , they can be modeled by specifying  $\Sigma_{f(i,i+1)} = \Sigma_{f(j,j-1)}$  as matrices with  $\tau_g \sigma_g^2$  on their main diagonals and zeros elsewhere. Thus, we have

$$\Sigma_{f(i,i)} \equiv \begin{bmatrix} \sigma_g^2 & \rho_g \sigma_g^2 & 0 & \cdots & 0 \\ \rho_g \sigma_g^2 & \sigma_g^2 & \rho_g \sigma_g^2 & \cdots & 0 \\ 0 & \rho_g \sigma_g^2 & \sigma_g^2 & \cdots & 0 \\ \vdots & \vdots & \vdots & \ddots & \vdots \\ 0 & 0 & 0 & 0 & \sigma_g^2 \end{bmatrix}, \quad i = 1, \dots, J$$

and

$$\Sigma_{f,(i,i+1)} = \Sigma_{f,(j,j-1)} \equiv \begin{bmatrix} \tau_g \sigma_g^2 & 0 & 0 & \cdots & 0 \\ 0 & \tau_g \sigma_g^2 & 0 & \cdots & 0 \\ 0 & 0 & \tau_g \sigma_g^2 & \cdots & 0 \\ \vdots & \vdots & \vdots & \ddots & \vdots \\ 0 & 0 & 0 & 0 & \tau_g \sigma_g^2 \end{bmatrix}, \quad i = 1, \dots, J-1, j = 2, \dots, J$$

The correlations  $\rho_g$  and  $\tau_g$  are parameters to be estimated. To do this in the Bayesian framework, they require priors. A sensible choice is independent  $\text{Unif}[-1, 1]$  distributions for each.

Correlations between measurement errors of fertility and survival could be modeled by modifying the covariance matrices in the same way using parameter-specific correlations (e.g.,  $\rho_f$ ,  $\rho_s$ , etc.).

I have discussed this simple banded model because it follows naturally from the lag-one correlations studied above. However, it only has parameters for a specific set of correlations, namely those between adjacent age groups within time period, and adjacent time periods within age group. For example, measurement errors in age group  $a$ , time period  $t$  and age group  $a + 5$ , time period  $t + 5$ , are assumed independent; the corresponding entries in  $\Sigma_g^{[B]}$  are zero. Classes of models that include covariance matrices which do not make such assumptions could be investigated as an alternative. The separable factor analysis models proposed by Foskick and Hoff (2012) are an example of such a class.

### A.3.2 Conclusion

I have used simple cross-correlation statistics to summarize the correlations between measurement errors in adjacent age-groups (within time period), adjacent time periods (within age groups) and between the sexes. Strong, positive correlations were indicated, especially for fertility and migration. This suggests that explicitly modeling these associations through additional terms in the model might be worthwhile. I showed how this might be done by way of a simple banded covariance matrix for migration in the single sex case. Further work in this area should involve considering a variety of covariance structures.

## Appendix B

### *popReconstruct* (VERSION 1.0): AN R PACKAGE

#### B.1 Introduction

*popReconstruct* is a method for reconstructing populations of the recent past. It simultaneously estimates age-specific population counts, fertility rates, mortality rates and net international migration flows from fragmentary data, and incorporates measurement error. Population dynamics over the period of reconstruction are modeled by embedding formal demographic accounting relationships in a Bayesian hierarchical model. Informative priors are required for vital rates, migration rates, population counts at baseline, and their respective measurement error variances. Inference is based on the joint posterior probability distribution which yields fully probabilistic interval estimates. A sample from this distribution is drawn using a Markov chain Monte Carlo algorithm.

The main function for doing the reconstruction is `popRecon.sampler()`. See the help file for a complete list of its arguments.

This vignette demonstrates the main features of the *popReconstruct* package by reconstructing the female population of Burkina Faso from 1960–2005, as described in Chapter 2. It is also available as part of the package which can be downloaded from a Comprehensive R Archive Network (CRAN) repository. Go to <http://www.r-project.org/> for a link to CRAN.

#### B.2 Notation

We use the symbols  $n$ ,  $s$ ,  $g$  and  $f$  to denote population counts, survival (a measure of mortality), net international migration (immigrants minus emigrants) and fertility, respectively. All of these parameters will be indexed by five-year increments of age, denoted by  $a$ , and time, denoted by  $t$ . For example,  $f_{a,t}$  is the average annual age-specific fertility rate for women in the age range  $[a, a + 5)$  over the period  $[t, t + 5)$ . Reconstruction will be done over

the time interval [1960, 2005). The age scale runs from 0 to 85 for survival and 0 to 80 for all other parameters.

### B.3 Doing the Reconstruction

#### B.3.1 Initial Estimates and Census Counts

Bias-reduced initial estimates of age-specific fertility rates, survival and migration proportions, population counts in the baseline year and census counts in subsequent years are required. Ideally, initial estimates will be based on data which have been pre-processed to reduce systematic biases. For example, population counts based on censuses should be adjusted to reduce bias due to undercount of certain age groups and age heaping. Similarly, fertility rate data based on surveys should be adjusted to reduce bias due to omission and misplacement of births. See Chapter 2 for further details.

Initial estimates and census counts for this vignette can be loaded by issuing the command `data(burkina_faso_females)`. This loads the object `burkina_faso_females`, a list with the following components: `fertility.rates`, `survival.proportions`, `migration.proportions`, `baseline.pop.counts`, and `census.pop.counts`. Each of these is a matrix with one row per age-group and one column per time period.

The row and column names of the initial estimate matrices are important. They must indicate the start points of the age-groups and time-periods to which the corresponding matrix elements refer. The width of the age-groups and time-periods must be the same and `popRecon.sampler()` uses the row and column names to check this.

**Fertility Rates** These should be average annual age-specific fertility rates,  $f_{a,t}$ , over five-year age and time intervals. The rates in this matrix should not be pre-multiplied by the width of the age range; total fertility rate is  $5 \sum_a f_{a,t}$ . Rows corresponding to ages for which fertility is assumed to be zero should contain all zeros. For Burkina Faso females, we have

```
> burkina_faso_females$fertility.rates
      1960      1965      1970      1975      1980      1985
0  0.00000000 0.00000000 0.00000000 0.00000000 0.00000000 0.00000000
5  0.00000000 0.00000000 0.00000000 0.00000000 0.00000000 0.00000000
10 0.00000000 0.00000000 0.00000000 0.00000000 0.00000000 0.00000000
```

```

15 0.23106147 0.23804582 0.21518491 0.20215256 0.1862599 0.17116025
20 0.36513859 0.37617574 0.36118334 0.35102655 0.3355970 0.32161538
25 0.30798362 0.31729312 0.32172783 0.32253858 0.3190999 0.31455564
30 0.25784739 0.26564141 0.27617698 0.28052655 0.2810202 0.27886583
35 0.17804816 0.18343007 0.20440064 0.21453214 0.2221399 0.22421363
40 0.09118707 0.09394340 0.11090145 0.11878804 0.1253564 0.12492814
45 0.01953255 0.02012296 0.02936577 0.03366143 0.0377618 0.03836757
50 0.00000000 0.00000000 0.00000000 0.00000000 0.0000000 0.00000000
55 0.00000000 0.00000000 0.00000000 0.00000000 0.0000000 0.00000000
60 0.00000000 0.00000000 0.00000000 0.00000000 0.0000000 0.00000000
65 0.00000000 0.00000000 0.00000000 0.00000000 0.0000000 0.00000000
70 0.00000000 0.00000000 0.00000000 0.00000000 0.0000000 0.00000000
75 0.00000000 0.00000000 0.00000000 0.00000000 0.0000000 0.00000000
80 0.00000000 0.00000000 0.00000000 0.00000000 0.0000000 0.00000000
      1990      1995      2000
0 0.00000000 0.00000000 0.00000000
5 0.00000000 0.00000000 0.00000000
10 0.00000000 0.00000000 0.00000000
15 0.15774539 0.15017654 0.14602395
20 0.30946628 0.29813440 0.28785888
25 0.30698795 0.29369783 0.28117157
30 0.27138711 0.25797783 0.24662582
35 0.21880702 0.20568412 0.19252220
40 0.11853181 0.10822704 0.09985643
45 0.03745104 0.03471384 0.03291629
50 0.00000000 0.00000000 0.00000000
55 0.00000000 0.00000000 0.00000000
60 0.00000000 0.00000000 0.00000000
65 0.00000000 0.00000000 0.00000000
70 0.00000000 0.00000000 0.00000000
75 0.00000000 0.00000000 0.00000000
80 0.00000000 0.00000000 0.00000000
>

```

**Survival Proportions** The survival proportions,  $s_{a,t}$ , give the proportion of those aged  $a - 5$  to  $a$  at time  $t$  who survive to be aged  $a$  to  $a + 5$  at time  $t + 5$ . Also,  $s_{80,t}$  is the proportion aged  $[75, 80)$  at exact time  $t$  who survive to time  $t + 5$ , by which time they are in the age group  $[85, \infty)$ . We allow for subsequent survival in this age group by letting  $s_{85,t}$  be the proportion aged  $[85, \infty)$  at time  $t$  who survive five more years. The matrix of survival proportions for Burkina Faso females has the same form as the matrix of fertility rates.

**Migration Proportions** Net international migration,  $g_{a,t}$ , is measured as a proportion of the respective age-, time-specific population size. Therefore, the net number of migrants

aged  $[a, a + 5)$  to the population during the time period  $[t, t + 5)$  is  $g_{a,t}n_{a,t}$ . The matrix of survival proportions for Burkina Faso females has the same form as the matrix of fertility rates.

**Population Counts at Baseline** The total number of people in each age group at the baseline year,  $n_{a,t_0}$  is entered as a single column matrix. In our case,

```
> burkina.faso.females$baseline.pop.counts
      1960
0 386000
5 292000
10 260000
15 244000
20 207000
25 175000
30 153000
35 135000
40 117000
45 98000
50 78000
55 60000
60 43000
65 29000
70 17000
75 8000
80 2000
>
```

**Census Counts** Bias reduced census counts are also required for at least one of the years between the baseline year and the end year. These must be at regular five-yearly intervals to coincide with the five-yearly intervals of the initial estimates. Censuses were conducted in Burkina Faso in 1975, 1985, 1995 and 2005. The census count matrix follows the same form as the fertility, survival and migration matrices.

### *B.3.2 MCMC Control Parameters*

The reconstruction is done by the function `popRecon.sampler()`. Among other arguments, this function requires the size of the MCMC sample to be specified via `n.iter` and the additional number of burn-in iterations via `burn.in`. The parameters are updated using

Metropolis steps with Gaussian random walk proposals. Each age- time-specific parameter has its own proposal variance which can be modified to achieve an acceptable proportion of acceptances. The variances must be supplied via the `prop.vars` argument. This must be a list with components `fert.rate`, `surv.prop`, `mig.prop` and `baseline.pop.count`. Each component is a matrix with the same shape as the corresponding matrix of initial estimates (Section B.3.1), except for the `fert.rate` component. The matrix of proposal variances for fertility rates has the rows corresponding to ages of zero fertility removed. Alternatively, the elements can be a vector such that the  $i$ th element corresponds to the same age and time as the  $i$ th element of the corresponding component of `burkina.faso.females`, after removing rows of non-zero fertility for the fertility rate matrix. This is the same ordering achieved by applying `as.vector()` to the proposal variance matrices.

Metropolis proposal variances for this example are in the object `burkina.faso.prop.vars`, loaded by `data(burkina-faso-females)`.

### B.3.3 Calling `popRecon.sampler()`

This runs the sampler for 50000 iterations with a burn in of 500 iterations, storing every 50th:

```
> ## set the seed random for the random number generator
> set.seed(1)
> ###
> ### The reconstruction:
> ###
> ##
> ## !!! WARNING: This takes over 24 hours !!!
> ##
> ## commented out --->|
> ## BKFem.Recon.MCMC <-
> ##     popRecon.sampler(## Size of the MCMC sample and burn in
> ##                     n.iter = 4E4,
> ##                     burn.in = 500,
> ##                     thin.by = 50,
> ##
> ##                     ## initial estimates and census counts
> ##                     mean.f = burkina.faso.females$fertility.rates,
> ##                     mean.s = burkina.faso.females$survival.proportions,
> ##                     mean.g = burkina.faso.females$migration.proportions,
> ##                     mean.b = burkina.faso.females$baseline.pop.counts,
> ##                     pop.data = burkina.faso.females$census.pop.counts,
```

```

>
> ##                      ## Metropolis proposal variances
> ##                      prop.vars = burkina.faso.prop.vars,
> ##                      verb=TRUE
> ##                      )
> ## save(BKFem.Recon.MCMC, file = "Burkina_Faso_Recon_RESULTS.RData")
> ## |<--- end comment
> load(file = file.path(Fal.root, "PPGp", "RPrograms", "BRecon"
, "popReconstruct", "vignettes", "Burkina_Faso_Recon_RESULTS.RData"))
>

```

## B.4 Results

In this section, we illustrate how the joint posterior generated by `popRecon.sampler()` might be summarized. `popRecon.sampler()` returns a list containing (among other things) the MCMC chains for each of the age-specific input parameters, namely fertility rates, survival proportions, migration proportions and the population counts at baseline. These are of class `mcmc` from the *coda* package.

### B.4.1 Age-Specific Parameters

The marginal posterior distributions for all age-specific input parameters can be summarized by plotting upper and lower quantiles of 95 percent Bayesian confidence intervals (credible intervals) and the posterior median. These are shown in Figures B.1–B.4. These plots are based on the `fert.rate.mcmc`, `surv.prop.mcmc`, `mig.prop.mcmc` and `baseline.count.mcmc` objects, which are components of the list returned by `popRecon.sampler()`. For example, the posterior quantiles plotted in the first panel of Figure B.1 are

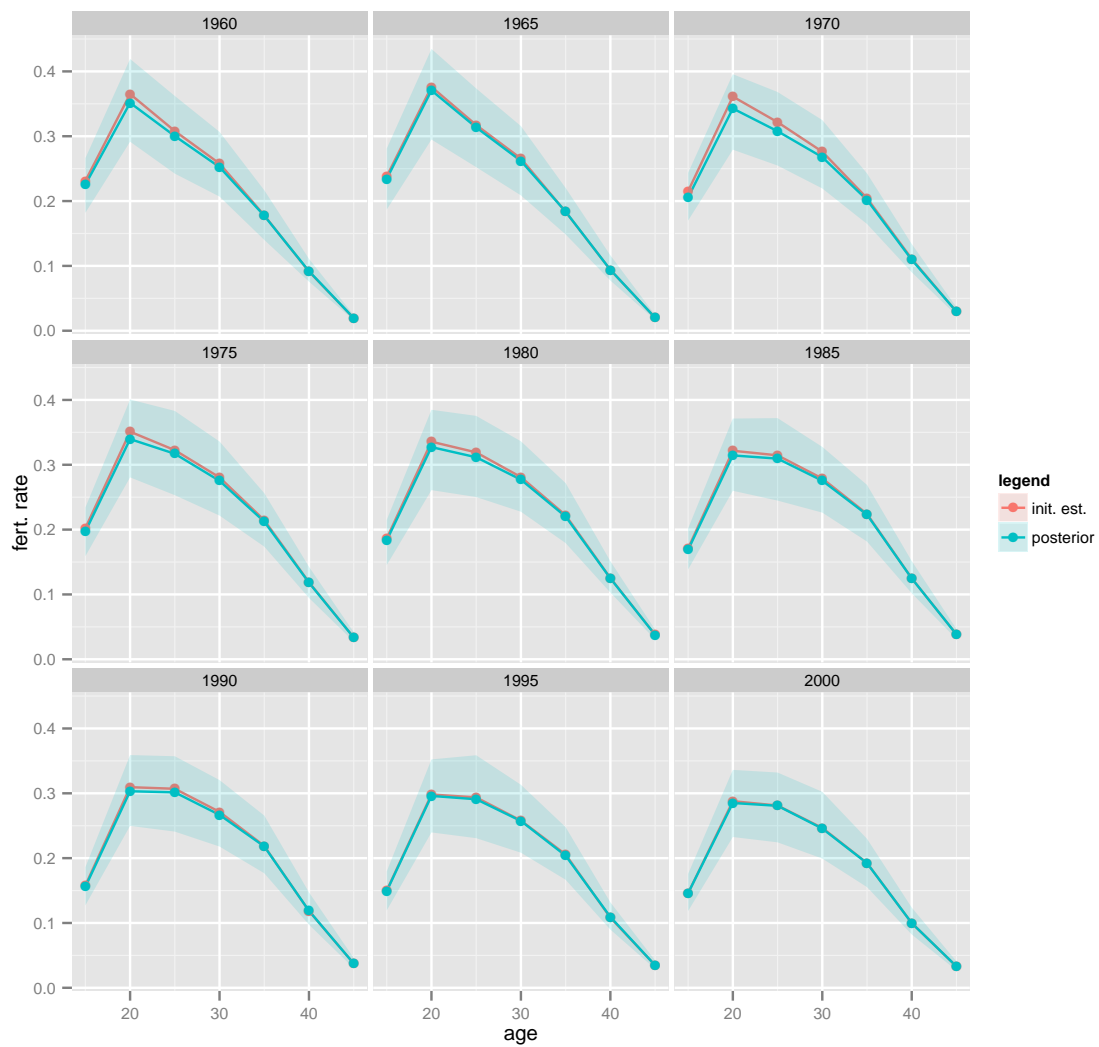
```

> apply(BKFem.Recon.MCMC[["fert.rate.mcmc"]], 2, "quantile", c(0.025, 0.5, 0.975))[,1:7]
      1960.15  1960.20  1960.25  1960.30  1960.35  1960.40
2.5%  0.1817824 0.2915397 0.2423299 0.2068800 0.1400807 0.07565362
50%   0.2254250 0.3515437 0.3003057 0.2524275 0.1773157 0.09187010
97.5% 0.2661050 0.4192471 0.3621569 0.3067635 0.2167117 0.11092761
      1960.45
2.5%  0.01612173
50%   0.01951576
97.5% 0.02412479
>

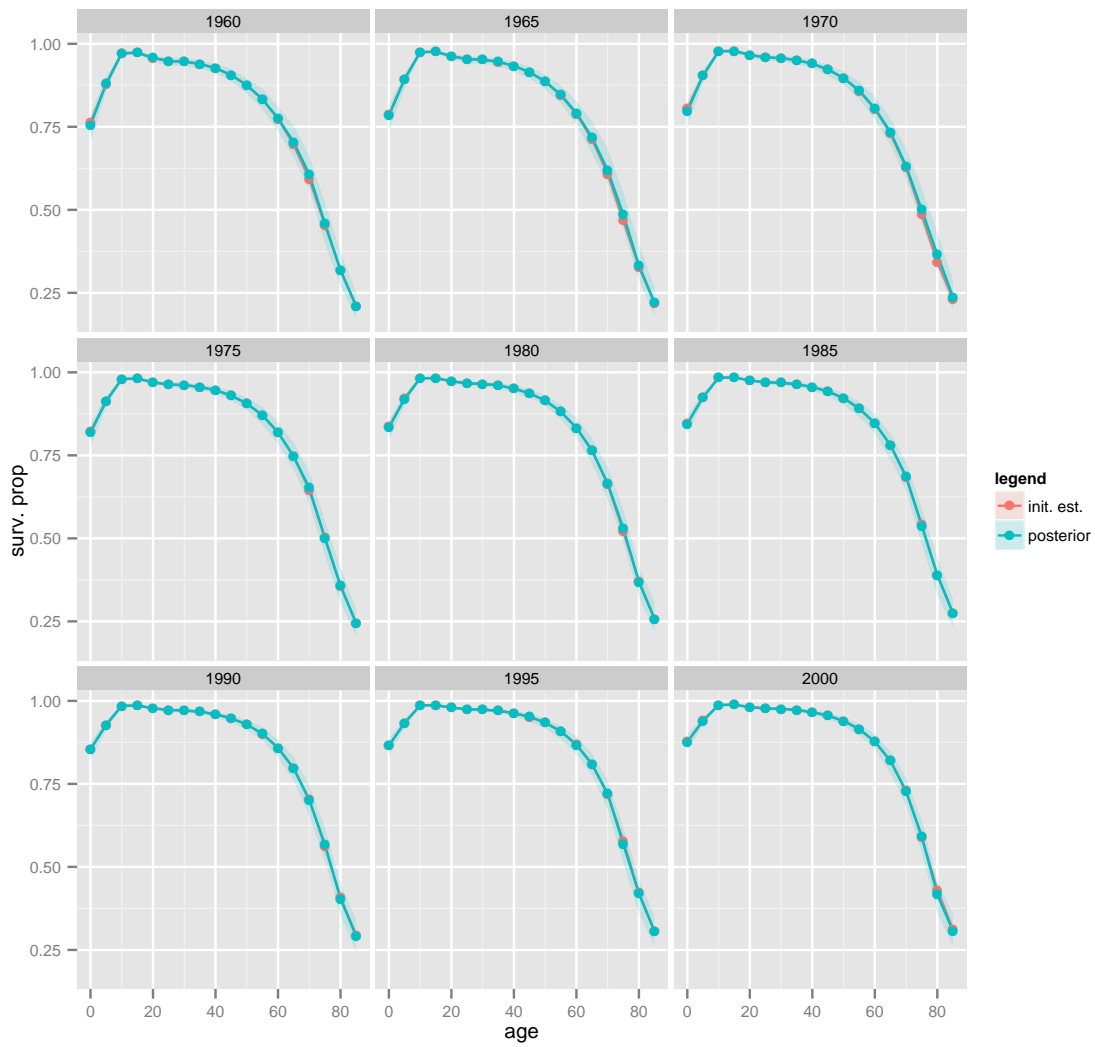
```

R code to produce these plots is in Appendix B.A.

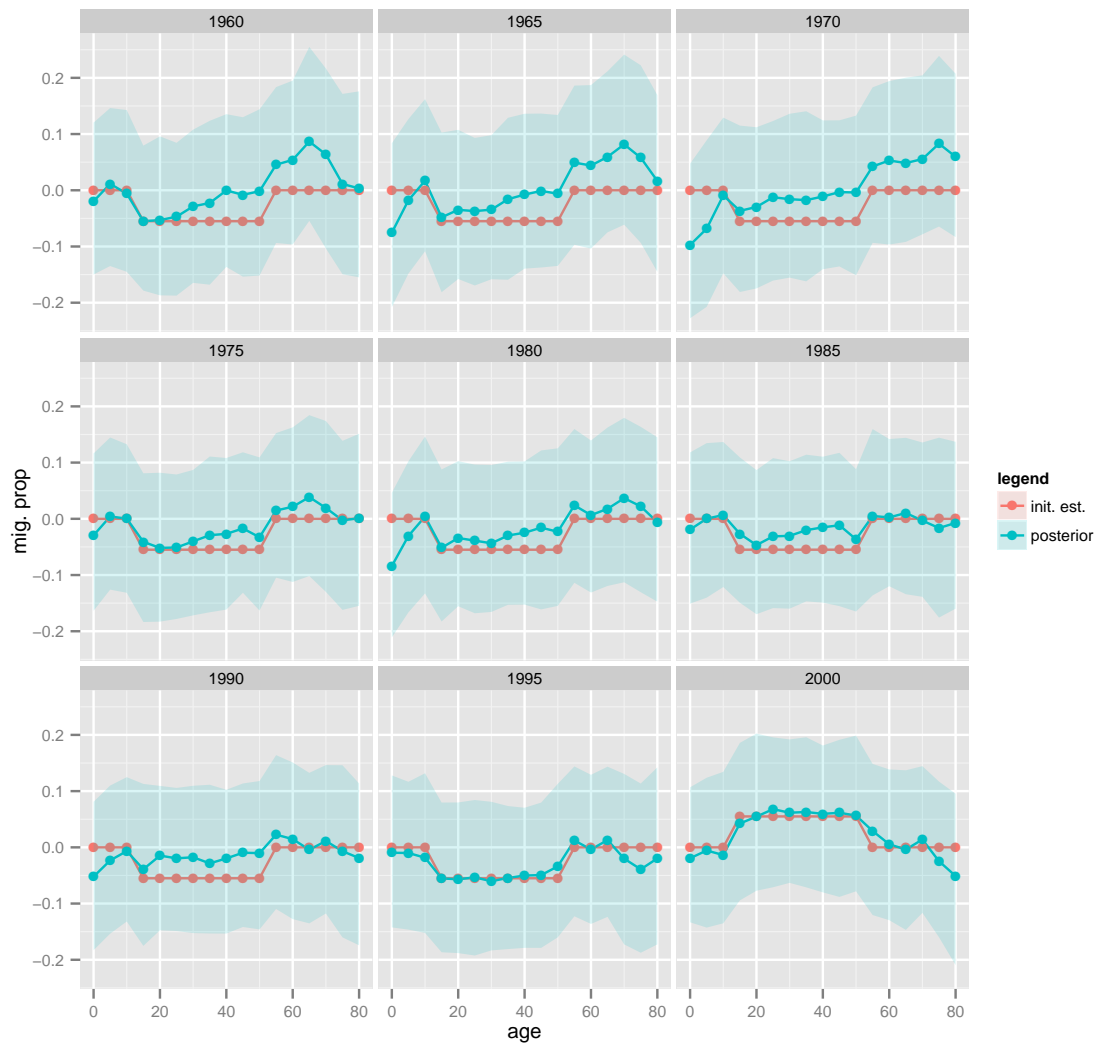




*Figure B.1.* Ninety-five percent Bayesian confidence intervals and posterior medians for age-specific fertility rates for the female population of Burkina Faso, 1960–2005. Also shown are the initial estimates.



*Figure B.2.* Ninety-five percent Bayesian confidence intervals and posterior medians for age-specific survival proportions for the female population of Burkina Faso, 1960–2005. Also shown are the initial estimates.



*Figure B.3.* Ninety-five percent Bayesian confidence intervals and posterior medians for age-specific migration proportions for the female population of Burkina Faso, 1960–2005. Also shown are the initial estimates.

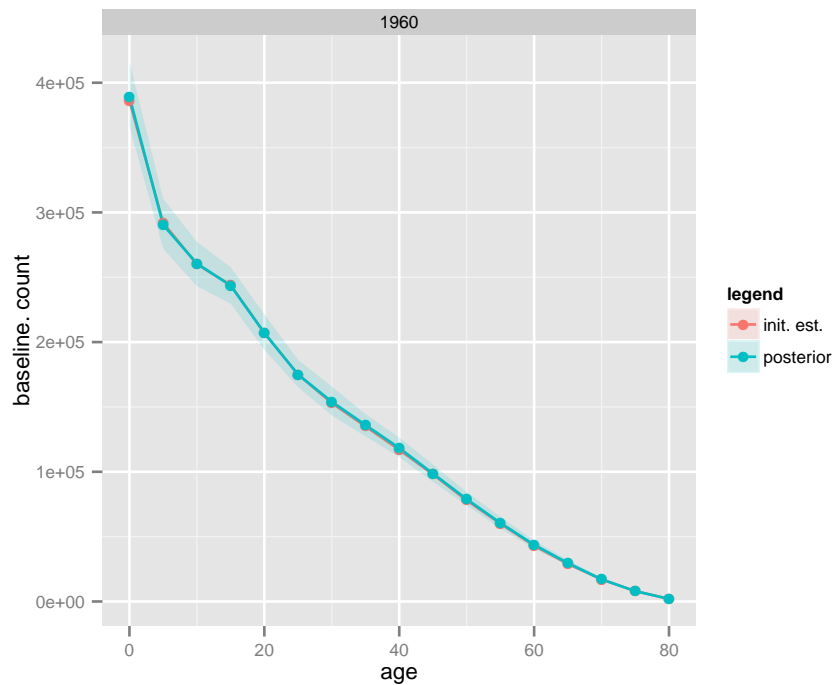


Figure B.4. Ninety-five percent Bayesian confidence intervals and posterior medians for age-specific baseline counts for the female population of Burkina Faso in 1960. Also shown are the initial estimates.

#### B.4.2 Age-Summarized Parameters

Posterior estimates for standard age-summarized parameters can also be produced. Here we show total fertility rate (TFR), life expectancy at birth ( $e_0$ ) and total average annual net number of migrants.

##### Total Fertility Rate

Total fertility rate is defined as

$$\text{TFR}_t = 5 \sum_a f_{a,t}.$$

Ninety-five percent Bayesian confidence intervals and posterior medians are shown in Figure B.5. These were calculated from the age-specific fertility rate MCMC, `BKFem.Recon.MCMC$-fert.rate.mcmc`, chains using the code in Appendix B.B.1.

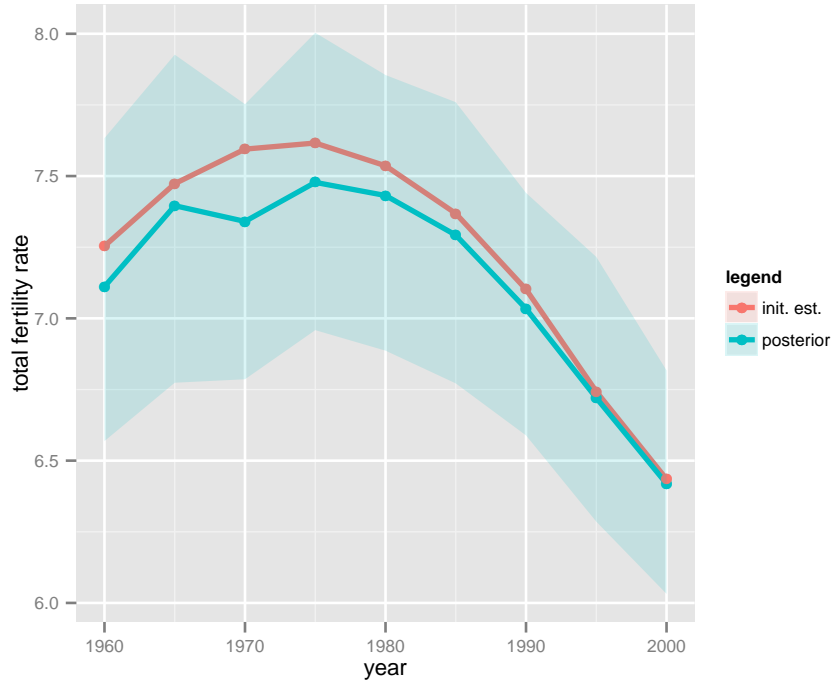


Figure B.5. Ninety-five percent Bayesian confidence intervals and posterior medians for TFR for the female population of Burkina Faso, 1960–2005. Also shown are the initial estimates.

### *Life Expectancy at Birth*

In a stationary population, the survival proportions can be converted to life expectancies at birth in each five-year period,  $e_{0,t}$ , by the transformation

$$e_{0,t} = 5 \sum_{a=0}^{80} \prod_{i=0}^a s_{i,t} + \left( \prod_{i=0}^{80} s_{i,t} \right) (s_{85+,t} / (1 - s_{85+,t})), \quad (\text{B.1})$$

Ninety-five percent Bayesian confidence intervals and posterior medians are shown in Figure B.7. These were calculated from the age-specific survival proportion MCMC chains, `BKFem.Recon.MCMC$surv.prop.mcmc`, using the function `life.expectancy.stationary()` and the code in Appendix B.B.2.

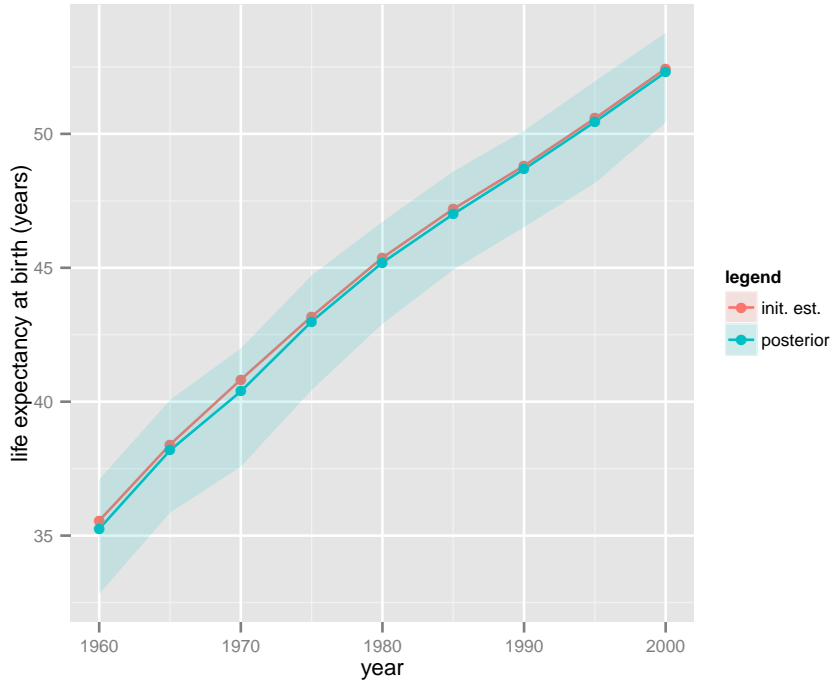


Figure B.6. Ninety-five percent Bayesian confidence intervals and posterior medians for  $e_0$  for the female population of Burkina Faso, 1960–2005. Also shown are the initial estimates.

#### Total Average Annual Net Migration

A posterior sample of total net number of migrants can be calculated using the posterior samples of the age-specific migration proportions and age-specific population counts at each five-year step within the interval of reconstruction. These can be calculated by deterministically projecting the posterior samples of age-specific fertility rates, survival proportions, migration proportions and baseline counts. The deterministic projection is done by the cohort component method of population projection (CCMPP) (e.g., [Preston et al., 2001](#), Ch. 6), i.e.,

$$\mathbf{n}_{t+5}^{[k]} = L^{[k]} \cdot (\mathbf{n}_t^{[k]} + (1/2) \cdot \tilde{\mathbf{g}}_t^{[k]}) + (1/2) \cdot \tilde{\mathbf{g}}_t^{[k]} \quad (\text{B.2})$$

where  $k$  indexes elements of the posterior sample and runs from 1 to the value of `n.iter` passed to `popRecon.sampler()` (see Section B.3),  $L$  is the Leslie matrix of the projection,  $I$  is the identity matrix, and  $\tilde{\mathbf{g}}_t^{[k]} \equiv \mathbf{g}_t^{[k]} \circ \mathbf{n}_t^{[k]}$ , where  $\circ$  is the element-wise product. The

average annual net number of migrants for iteration  $k$  over the interval  $[t, t+5)$ ,  $\tilde{\mathbf{g}}_t^{[k]}$ , is then the solution to (B.2):

$$\tilde{\mathbf{g}}_t^{[k]} = 2 \cdot (L^{[k]} + I)^{-1} \cdot (\mathbf{n}_{t+5}^{[k]} - L^{[k]} \cdot \mathbf{n}_t^{[k]})$$

The CCMPP is implemented in the function `popRecon.ccmp.female`.

Ninety-five percent Bayesian confidence intervals and posterior medians are shown in Figure B.7. These were calculated by the code in Appendix B.B.3 which uses the posterior changes of all the input parameters, namely the components `fert.rate.mcmc`, `surv.prop.mcmc` and `mig.prop.mcmc` in `BKFem.Recon.MCMC`.

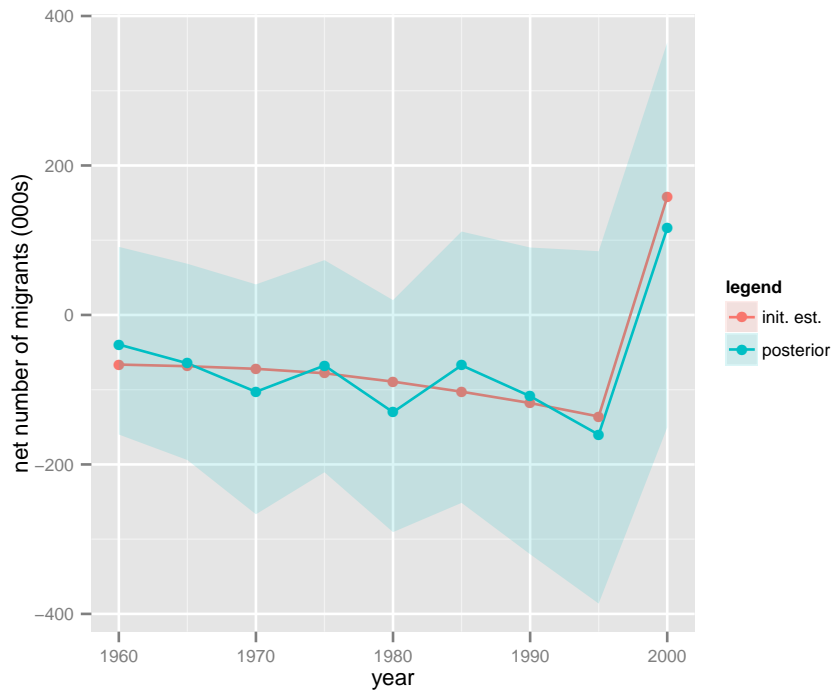


Figure B.7. Ninety-five percent Bayesian confidence intervals and posterior medians for total average annual net number of migrants for the female population of Burkina Faso, 1960–2005. Also shown are the initial estimates.

## Appendix B.A Code to Produce Plots of Age-Specific Parameters

### B.A.1 Fertility Rates

```

> #####
> ###
> ### Calculate posterior quantiles for age-specific fertility rate and
> ### plot
> ###
> #####
>
> require(ggplot2)
> require(gdata)
> ##
> ## Posterior quantiles
> ##
> vital.chain <- BKFem.Recon.MCMC$fert.rate.mcmc
> q.to.plot = c(0.025, 0.5, 0.975)
> q.vital <- apply(vital.chain, 2, function(z) quantile(z, probs = q.to.plot))
> dimnames(q.vital) <- list(as.character(q.to.plot), colnames(vital.chain))
> ##
> ## Age, year labels
> ##
> colspl <- strsplit(colnames(vital.chain), ".", fixed = TRUE)
> years <- unique(sapply(colspl, FUN = function(z) z[1]))
> fert.ages <- unique(sapply(colspl, FUN = function(z) z[2]))
> fert.ages.numeric <- as.numeric(gsub("[^0-9]", "", fert.ages))
> ##
> ## Reshape data frame
> ##
> qvit.melt <- melt(q.vital)
> qvit.melt.col <- cbind(qvit.melt
                        ,expand.grid(quant = q.to.plot, ages = fert.ages.numeric
                                      ,years = years)
                        )
> ##
> ## Initial estimates
> ##
> nzfr <- BKFem.Recon.MCMC$alg.params$non.zero.fert.rows
> vital.init.est <-
  BKFem.Recon.MCMC$fixed.params$mean.fert.rate[nzfr,]
> vital.init.est.melt.col <-
  cbind(value = melt(vital.init.est)$value
        ,expand.grid(ages = fert.ages.numeric
                      ,years = years, quant = 5) # use quant=5 for init.est
        )
> ##
> ## Prepare data sets
> ##

```



```

> alpha <- BKFem.Recon.MCMC$fixed.params$alpha.fert.rate
> beta <- BKFem.Recon.MCMC$fixed.params$beta.fert.rate
> qvit.melt.df <- t(q.vital)
> colnames(qvit.melt.df) <-
  paste("fert.rate.", prettyNum(as.numeric(colnames(qvit.melt.df)) * 100)
    , "pctl", sep = "")
> qvit.melt.df <-
  data.frame(qvit.melt.df
    ,age = sapply(strsplit(rownames(qvit.melt.df), split = "[^0-9]")
    , "[", 2)
    ,year = sapply(strsplit(rownames(qvit.melt.df), split = "[^0-9]")
    , "[", 1)
    ,legend = "posterior"
  )
> vital.init.est <-
  melt(BKFem.Recon.MCMC$fixed.params$mean.fert.rate[nzfr,])
> vital.init.est <-
  rename.vars(vital.init.est, from = c("X1", "X2", "value")
    ,to = c("age", "year", "fert.rate.50pctl"))
> vital.init.est.melt.df <-
  data.frame(vital.init.est, fert.rate.97.5pctl = NA
    ,fert.rate.2.5pctl = NA
    ,legend = "init. est."
  )
> plot.df <- rbind(vital.init.est.melt.df, qvit.melt.df)
> plot.df$age <- as.numeric(plot.df$age)
> plot.df$year <- as.numeric(plot.df$year)
> plot.df$legend <- relevel(factor(plot.df$legend), ref = "init. est.")
> ##
> ## Plot quantiles
> ##
> print(
  ggplot(data = plot.df, aes(x = age, y = fert.rate.50pctl, color = legend)) +
    facet_wrap(~ year) +
    geom_line() +
    geom_point() +
    geom_ribbon(aes(ymin = fert.rate.2.5pctl
      ,ymax = fert.rate.97.5pctl, fill = legend), alpha = 0.15
      ,color = NA
    ) +
    ylab("fert. rate")
  )
>

```

### B.A.2 Survival Proportions

```

> #####
> ###

```

```

> ### Calculate posterior quantiles for age-specific survival
> ### proportion and plot
> ###
> #####
>
> require(ggplot2)
> require(gdata)
> ##
> ## Posterior quantiles
> ##
> vital.chain <- BKFem.Recon.MCMC$urv.prop.mcmc
> q.to.plot = c(0.025, 0.5, 0.975)
> q.vital <- apply(vital.chain, 2, function(z) quantile(z, probs = q.to.plot))
> dimnames(q.vital) <- list(as.character(q.to.plot), colnames(vital.chain))
> ##
> ## Age, year labels
> ##
> colspl <- strsplit(colnames(vital.chain), ".", fixed = TRUE)
> years <- unique(sapply(colspl, FUN = function(z) z[1]))
> surv.ages <- unique(sapply(colspl, FUN = function(z) z[2]))
> surv.ages.numeric <- as.numeric(gsub("[^0-9]", "", surv.ages))
> ##
> ## Reshape data frame
> ##
> qvit.melt <- melt(q.vital)
> qvit.melt.col <- cbind(qvit.melt
                        ,expand.grid(quant = q.to.plot, ages = surv.ages.numeric
                                      ,years = years)
                        )
> ##
> ## Initial estimates
> ##
> vital.init.est <-
  BKFem.Recon.MCMC$fixed.params$mean.surv.prop
> vital.init.est.melt.col <-
  cbind(value = melt(vital.init.est)$value
        ,expand.grid(ages = surv.ages.numeric
                      ,years = years, quant = 5) # use quant=5 for init.est
        )
> ##
> ## Prepare data sets
> ##
> alpha <- BKFem.Recon.MCMC$fixed.params$alpha.surv.prop
> beta <- BKFem.Recon.MCMC$fixed.params$beta.surv.prop
> qvit.melt.df <- t(q.vital)
> colnames(qvit.melt.df) <-
  paste("surv.prop.", prettyNum(as.numeric(colnames(qvit.melt.df)) * 100)
        , "pctl", sep = "")
> qvit.melt.df <-
  data.frame(qvit.melt.df

```

```

    ,age = sapply(strsplit(rownames(qvit.melt.df), split = "[^0-9]")
    , "[", 2)
    ,year = sapply(strsplit(rownames(qvit.melt.df), split = "[^0-9]")
    , "[", 1)
    ,legend = "posterior"
  )
> vital.init.est <-
  melt(BKFem.Recon.MCMC$fixed.params$mean.surv.prop)
> vital.init.est <-
  rename.vars(vital.init.est, from = c("X1", "X2", "value")
  ,to = c("age", "year", "surv.prop.50pctl"))
> vital.init.est.melt.df <-
  data.frame(vital.init.est, surv.prop.97.5pctl = NA
  ,surv.prop.2.5pctl = NA
  ,legend = "init. est."
  )
> plot.df <- rbind(vital.init.est.melt.df, qvit.melt.df)
> plot.df$age <- as.numeric(plot.df$age)
> plot.df$year <- as.numeric(plot.df$year)
> plot.df$legend <- relevel(factor(plot.df$legend), ref = "init. est.")
> ##
> ## Plot quantiles
> ##
> print(
  ggplot(data = plot.df, aes(x = age, y = surv.prop.50pctl, color = legend)) +
  facet_wrap(~ year) +
  geom_line() +
  geom_point() +
  geom_ribbon(aes(ymin = surv.prop.2.5pctl
  ,ymax = surv.prop.97.5pctl, fill = legend), alpha = 0.15
  ,color = NA) +
  ylab("surv. prop")
  )
>

```

### B.A.3 Migration Proportions

```

> #####
> ###
> ### Calculate posterior quantiles for age-specific migration
> ### proportion and plot
> ###
> #####
>
> require(ggplot2)
> require(gdata)
> ##
> ## Posterior quantiles

```

```

> ##
> vital.chain <- BKFem.Recon.MCMC$mig.prop.mcmc
> q.to.plot = c(0.025, 0.5, 0.975)
> q.vital <- apply(vital.chain, 2, function(z) quantile(z, probs = q.to.plot))
> dimnames(q.vital) <- list(as.character(q.to.plot), colnames(vital.chain))
> ##
> ## Age, year labels
> ##
> colspl <- strsplit(colnames(vital.chain), ".", fixed = TRUE)
> years <- unique(sapply(colspl, FUN = function(z) z[1]))
> mig.ages <- unique(sapply(colspl, FUN = function(z) z[2]))
> mig.ages.numeric <- as.numeric(gsub("[^0-9]", "", mig.ages))
> ##
> ## Reshape data frame
> ##
> qvit.melt <- melt(q.vital)
> qvit.melt.col <- cbind(qvit.melt
                        ,expand.grid(quant = q.to.plot, ages = mig.ages.numeric
                                      ,years = years)
                        )
> ##
> ## Initial estimates
> ##
> vital.init.est <-
  BKFem.Recon.MCMC$fixed.params$mean.mig.prop
> vital.init.est.melt.col <-
  cbind(value = melt(vital.init.est)$value
        ,expand.grid(ages = mig.ages.numeric
                      ,years = years, quant = 5) # use quant=5 for init.est
        )
> ##
> ## Prepare data sets
> ##
> alpha <- BKFem.Recon.MCMC$fixed.params$alpha.mig.prop
> beta <- BKFem.Recon.MCMC$fixed.params$beta.mig.prop
> qvit.melt.df <- t(q.vital)
> colnames(qvit.melt.df) <-
  paste("mig.prop.", prettyNum(as.numeric(colnames(qvit.melt.df)) * 100)
        , "pctl", sep = "")
> qvit.melt.df <-
  data.frame(qvit.melt.df
            ,age = sapply(strsplit(rownames(qvit.melt.df), split = "[^0-9]")
                          , "[[", 2)
            ,year = sapply(strsplit(rownames(qvit.melt.df), split = "[^0-9]")
                           , "[[", 1)
            ,legend = "posterior"
            )
> vital.init.est <-
  melt(BKFem.Recon.MCMC$fixed.params$mean.mig.prop)
> vital.init.est <-

```

```

      rename.vars(vital.init.est, from = c("X1", "X2", "value")
                  ,to = c("age", "year", "mig.prop.50pctl"))
> vital.init.est.melt.df <-
  data.frame(vital.init.est, mig.prop.97.5pctl = NA
             ,mig.prop.2.5pctl = NA
             ,legend = "init. est."
             )
> plot.df <- rbind(vital.init.est.melt.df, qvit.melt.df)
> plot.df$age <- as.numeric(plot.df$age)
> plot.df$year <- as.numeric(plot.df$year)
> plot.df$legend <- relevel(factor(plot.df$legend), ref = "init. est.")
> ##
> ## Plot quantiles
> ##
> print(
  ggplot(data = plot.df, aes(x = age, y = mig.prop.50pctl, color = legend)) +
    facet_wrap(~ year) +
    geom_line() +
    geom_point() +
    geom_ribbon(aes(ymin = mig.prop.2.5pctl
                  ,ymax = mig.prop.97.5pctl, fill = legend), alpha = 0.15
              ,color = NA) +
    ylab("mig. prop")
  )
>

```

#### B.A.4 Baseline Counts

```

> #####
> ###
> ### Calculate posterior quantiles for age-specific baseline count
> ### and plot
> ###
> #####
>
> require(ggplot2)
> require(gdata)
> ##
> ## Posterior quantiles
> ##
> vital.chain <- BKFem.Recon.MCMC$baseline.count.mcmc
> q.to.plot = c(0.025, 0.5, 0.975)
> q.vital <- apply(vital.chain, 2, function(z) quantile(z, probs = q.to.plot))
> dimnames(q.vital) <- list(as.character(q.to.plot), colnames(vital.chain))
> ##
> ## Age, year labels
> ##
> colspl <- strsplit(colnames(vital.chain), ".", fixed = TRUE)

```

```

> years <- unique(sapply(colspl, FUN = function(z) z[1]))
> baseline.ages <- unique(sapply(colspl, FUN = function(z) z[2]))
> baseline.ages.numeric <- as.numeric(gsub("[^0-9]", "", baseline.ages))
> ##
> ## Reshape data frame
> ##
> qvit.melt <- melt(q.vital)
> qvit.melt.col <- cbind(qvit.melt
                        ,expand.grid(quant = q.to.plot, ages = baseline.ages.numeric
                                      ,years = years)
                        )
> ##
> ## Initial estimates
> ##
> vital.init.est <-
  BKFem.Recon.MCMC$fixed.params$mean.baseline.count
> vital.init.est.melt.col <-
  cbind(value = melt(vital.init.est)$value
        ,expand.grid(ages = baseline.ages.numeric
                      ,years = years, quant = 5) # use quant=5 for init.est
        )
> ##
> ## Prepare data sets
> ##
> alpha <- BKFem.Recon.MCMC$fixed.params$alpha.population.count
> beta <- BKFem.Recon.MCMC$fixed.params$beta.population.count
> qvit.melt.df <- t(q.vital)
> colnames(qvit.melt.df) <-
  paste("baseline.count.", prettyNum(as.numeric(colnames(qvit.melt.df)) * 100)
        , "pctl", sep = "")
> qvit.melt.df <-
  data.frame(qvit.melt.df
            ,age = sapply(strsplit(rownames(qvit.melt.df), split = "[^0-9]")
                        , "[", 2)
            ,year = sapply(strsplit(rownames(qvit.melt.df), split = "[^0-9]")
                          , "[", 1)
            ,legend = "posterior"
            )
> vital.init.est <-
  melt(BKFem.Recon.MCMC$fixed.params$mean.baseline.count)
> vital.init.est <-
  rename.vars(vital.init.est, from = c("X1", "X2", "value")
            ,to = c("age", "year", "baseline.count.50pctl"))
> vital.init.est.melt.df <-
  data.frame(vital.init.est, baseline.count.97.5pctl = NA
            ,baseline.count.2.5pctl = NA
            ,legend = "init. est."
            )
> plot.df <- rbind(vital.init.est.melt.df, qvit.melt.df)
> plot.df$age <- as.numeric(plot.df$age)

```

```

> plot.df$year <- as.numeric(plot.df$year)
> plot.df$legend <- releval(factor(plot.df$legend), ref = "init. est.")
> ##
> ## Plot quantiles
> ##
> print(
  ggplot(data = plot.df, aes(x = age, y = baseline.count.50pctl, color = legend)) +
    facet_wrap(~ year) +
    geom_line() +
    geom_point() +
    geom_ribbon(aes(ymin = baseline.count.2.5pctl
                    ,ymax = baseline.count.97.5pctl, fill = legend), alpha = 0.15
                ,color = NA) +
    ylab("baseline. count")
  )
>

```

## ***Appendix B.B Code to Produce Plots of Age-Summarized Parameters***

### *B.B.1 Total Fertility Rate*

```

> #####
> ###
> ### Calculate posterior quantiles for TFR and plot
> ###
> #####
>
> require(ggplot2)
> q.to.plot = c(0.025, 0.5, 0.975)
> ###
> ### Posterior
> ###
> dn <- list(NULL,
  unique(sapply(strsplit(colnames(BKFem.Recon.MCMC$fert.rate.mcmc)
                        ,"\\"), FUN = function(z) z[[1]]))
  )
> BKFem.Recon.tfr <-
  matrix(0, nrow = nrow(BKFem.Recon.MCMC$fert.rate.mcmc)
        ,ncol = length(dn[[2]])
        ,dimnames = dn
        )
> fert.rate.mcmc.colYrs <-
  sapply(strsplit(colnames(BKFem.Recon.MCMC$fert.rate.mcmc)
                  ,"\\"), FUN = function(z) z[[1]])
> ##
> ## calculate tfr
> ##

```

```

> for(i in 1:ncol(BKFem.Recon.tfr)) {
  colYrs.index <- fert.rate.mcmc.colYrs == colnames(BKFem.Recon.tfr)[i]
  BKFem.Recon.tfr[,i] <-
    apply(BKFem.Recon.MCMC$fert.rate.mcmc[,colYrs.index]
      ,1
      ,FUN = function(z) 5 * sum(z)
      )
}
> ##
> ## tfr quantiles
> ##
> BKFem.Recon.tfrQuant <- apply(BKFem.Recon.tfr, 2, FUN = function(z)
  {
    quantile(z, probs = q.to.plot)
  })
> BKFem.Recon.tfrQuant.df <-
  as.data.frame(t(BKFem.Recon.tfrQuant))
> colnames(BKFem.Recon.tfrQuant.df) <-
  paste("tfr.", strsplit(colnames(BKFem.Recon.tfrQuant.df), split = "%")
    ,"pctl", sep = "")
> BKFem.Recon.tfrQuant.df$legend = "posterior"
> BKFem.Recon.tfrQuant.df$year = as.numeric(rownames(BKFem.Recon.tfrQuant.df))
> ###
> ### Initial estimates
> ###
> BKFem.Recon.tfr.init.est <-
  data.frame(year = colnames(BKFem.Recon.MCMC$fixed.params$mean.fert.rate)
    ,tfr.50pctl =
      melt(5 * colSums(BKFem.Recon.MCMC$fixed.params$mean.fert.rate))[,1]
    )
> BKFem.Recon.tfr.init.est$legend <- "init. est."
> BKFem.Recon.tfr.init.est$tfr.2.5pctl <-
  BKFem.Recon.tfr.init.est$tfr.97.5pctl <- NA
> ###
> ### Plot
> ###
> plot.df <-
  rbind(BKFem.Recon.tfrQuant.df, BKFem.Recon.tfr.init.est)
> plot.df$legend <- relevel(factor(plot.df$legend), ref = "init. est.")
> plot.df$year <- as.numeric(plot.df$year)
> print(ggplot(data = plot.df, aes(x = year, y = tfr.50pctl, color = legend)) +
  geom_line(size = 1) +
  geom_point() +
  geom_point() + geom_ribbon(aes(ymin = tfr.2.5pctl
    ,ymax = tfr.97.5pctl, fill = legend)
    ,alpha = 0.15, color = NA) +
  ylab("total fertility rate")
  )
>

```



### B.B.2 Life Expectancy at Birth

```

> #####
> ###
> ### Calculate posterior quantiles for life expectancy at birth and
> ### plot
> ###
> #####
>
> require(ggplot2)
> q.to.plot = c(0.025, 0.5, 0.975)
> surv.prop.years <-
  sapply(strsplit(colnames(BKFem.Recon.MCMC$surv.prop.mcmc), "\\."), "[[", 1)
> message("Calculating life expectancy at birth ...")
> BKFem.leb.stationary.df <-
  apply(BKFem.Recon.MCMC$surv.prop.mcmc[,], 1, function(z) {
    tapply(z, INDEX = surv.prop.years, FUN = "life.expectancy.stationary")
  })
> message("... done")
> BKFem.leb.stationary.Quantiles <-
  apply(BKFem.leb.stationary.df, 1, "quantile", probs = q.to.plot)
> BKFem.leb.stationary.Quantiles.df <-
  as.data.frame(t(BKFem.leb.stationary.Quantiles))
> colnames(BKFem.leb.stationary.Quantiles.df) <-
  paste("leb.",
        , strsplit(colnames(BKFem.leb.stationary.Quantiles.df)
                    , split = "%")
        ,"pctl", sep = "")
> BKFem.leb.stationary.Quantiles.df$legend <- "posterior"
> BKFem.leb.stationary.Quantiles.df$year <-
  as.numeric(rownames(BKFem.leb.stationary.Quantiles.df))
> ###
> ### Prior by converting posterior quantiles of survival and assuming
> ### stationary population relation holds
> ###
> lebp.yrs <- as.numeric(colnames(BKFem.Recon.MCMC$fixed.params$mean.surv.prop))
> BKFem.lebPrior.stationary.df <-
  data.frame(year = lebp.yrs
             ,leb.50pctl = apply(BKFem.Recon.MCMC$fixed.params$mean.surv.prop
                                ,2
                                ,FUN = "life.expectancy.stationary"
                                ))
> BKFem.lebPrior.stationary.df$leb.2.5pctl <-
  BKFem.lebPrior.stationary.df$leb.97.5pctl <- NA
> BKFem.lebPrior.stationary.df$legend <- "init. est."
> ###
> ### Plot
> ###
> plot.df <-
  rbind(BKFem.lebPrior.stationary.df, BKFem.leb.stationary.Quantiles.df)

```

```

> plot.df$legend <- relevel(factor(plot.df$legend), ref = "init. est.")
> print(ggplot(data = plot.df, aes(x = year, y = leb.50pctl, color = legend)) +
  geom_line() +
  geom_point() +
  geom_ribbon(aes(ymin = leb.2.5pctl
                  ,ymax = leb.97.5pctl, fill = legend)
            ,alpha = 0.15, color = NA) +
  ylab("life expectancy at birth (years)")
)
>

```

### *B.B.3 Total Average Annual Net Migration*

```

> #####
> ###
> ### Calculate posterior quantiles for average annual total net
> ### number of migrants
> ###
> #####
>
> require(ggplot2)
> q.to.plot = c(0.025, 0.5, 0.975)
> ## NB: Can't simply sum migration proportions because they are based
> ##      on different population totals. Need to get net number of migrants
> ##      and convert back into proportions. Use Leslie matrix formula from
> ##      article draft.
> ##
>
> ###
> ### Posterior distribution
> ###
>
> ##
> ## Prepare output matrix
> ##
> BKFem.Recon.netMig <-
  matrix(0, nrow = nrow(BKFem.Recon.MCMC$mig.prop.mcmc)
        ,ncol = ncol(BKFem.Recon.MCMC$fixed.params$mean.mig.prop)
        ,dimnames = list(NULL,
                          unique(sapply(strsplit(colnames(BKFem.Recon.MCMC$mig.prop.mcmc)
                                                ,"\\"), FUN = function(z) z[[1]]))
                          )
        )
>
> ##
> ## The 5-year sub-intervals to be used as an index into the columns of
> ## BKFem.Recon.netMig
> ##

```

```

> mig.prop.mcmc.colYrs <-
  sapply(strsplit(colnames(BKFem.Recon.MCMC$mig.prop.mcmc)
                  ,"\\"), FUN = function(z) z[[1]])
> mig.prop.mcmc.colYrsUniq <- unique(mig.prop.mcmc.colYrs)
> ##
> ## Years used in survival proportions
> ##
> surv.prop.mcmc.colYrs <-
  sapply(strsplit(colnames(BKFem.Recon.MCMC$surv.prop.mcmc)
                  ,"\\"), FUN = function(z) z[[1]])
> ##
> ## Concatenate baseline and lx to get a single matrix with population
> ## counts
> ##
>
> pop.mat <- cbind(BKFem.Recon.MCMC$baseline.count.mcmc
                  ,BKFem.Recon.MCMC$lx.mcmc)
> ##
> ## Index for population years
> ##
>
> pop.mat.colYrs <- sapply(strsplit(colnames(pop.mat)
                  ,"\\"), FUN = function(z) z[[1]])
> pop.mat.colYrsUniq <- unique(pop.mat.colYrs)
> message("Calculating net number of migrants ...")
> for(k in 1:nrow(BKFem.Recon.MCMC$mig.prop.mcmc)) {
  if(k %% 1000 == 0)
    message(paste("row ", k, " of "
                  ,nrow(BKFem.Recon.MCMC$mig.prop.mcmc), sep = "")
            )
  ##
  ## cycle through years
  for(i in 1:ncol(BKFem.Recon.netMig)) {
    ##
    ## 5-year sub-intervals for indexing columns
    mig.colYrs.index <-
      colnames(BKFem.Recon.netMig) == mig.prop.mcmc.colYrsUniq[i]
    surv.colYrs.index <-
      surv.prop.mcmc.colYrs == mig.prop.mcmc.colYrsUniq[i]
    fert.colYrs.index <-
      fert.rate.mcmc.colYrs == mig.prop.mcmc.colYrsUniq[i]
    pop.colYrs.index1 <-
      pop.mat.colYrs == mig.prop.mcmc.colYrsUniq[i]
    pop.colYrs.index2 <-
      pop.mat.colYrs == as.numeric(mig.prop.mcmc.colYrsUniq[i]) + 5
    ##
    ## get vital rates and make leslie matrix
    sk <- BKFem.Recon.MCMC$surv.prop.mcmc[k,surv.colYrs.index]
    fk <- rep(0, nrow(BKFem.Recon.MCMC$fixed.params$mean.fert.rate))
    fk[BKFem.Recon.MCMC$alg.params$non.zero.fert.rows] <-

```

```

      BKFem.Recon.MCMC$fert.rate.mcmc[k,fert.colYrs.index]
    popk1 <- pop.mat[k,pop.colYrs.index1]
    popk2 <- pop.mat[k,pop.colYrs.index2]
    Lk <- make.leslie.matrix(pop = popk1, surv = sk, fert = fk, srb = 1.05
                           ,age.int = 5)

    ##
    ## calculate net number of migrants
    netMigk <- net.number.migrants(n1 = popk1, n2 = popk2, L = Lk)
    ##
    ## store
    BKFem.Recon.netMig[k, mig.colYrs.index] <- sum(netMigk)
  }
}
> message("... done")
> ##
> ### Posterior quantiles
> ##
> BKFem.nmig.post.quant <-
  apply(BKFem.Recon.netMig, 2, FUN = function(z)
        {
          quantile(z, probs = q.to.plot)
        })
> BKFem.nmig.post.quant.df <-
  as.data.frame(t(BKFem.nmig.post.quant))
> colnames(BKFem.nmig.post.quant.df) <-
  paste("total.mig.count.", strsplit(colnames(BKFem.nmig.post.quant.df)
                                     , split = "%")
        ,"pctl", sep = "")
> BKFem.nmig.post.quant.df$legend <- "posterior"
> BKFem.nmig.post.quant.df$year <-
  as.numeric(rownames(BKFem.nmig.post.quant.df))
> ###
> ### Initial estimates
> ###
>
> ##
> ## Prepare output matrix
> ##
> BKFem.nmig.input <- rep(0, ncol(BKFem.Recon.MCMC$fixed.params$mean.mig.prop))
> names(BKFem.nmig.input) <-
  colnames(BKFem.Recon.MCMC$fixed.params$mean.mig.prop)
> ##
> ## Input population counts
> ##
> pop.input.mat <-
  popRecon.ccmp.female(pop=BKFem.Recon.MCMC$fixed.params$mean.baseline.count
                      ,surv=BKFem.Recon.MCMC$fixed.params$mean.surv.prop
                      ,fert=BKFem.Recon.MCMC$fixed.params$mean.fert.rate
                      ,mig=BKFem.Recon.MCMC$fixed.params$mean.mig.prop
                      )

```

```

> ##
> ## Calculate input net migration
> ##
> for(k in 1:(ncol(pop.input.mat)-1)) {
  Lk <- make.leslie.matrix(pop = pop.input.mat[,k]
    ,surv = BKFem.Recon.MCMC$fixed.params$mean.surv.prop[,k]
    ,fert = BKFem.Recon.MCMC$fixed.params$mean.fert.rate[,k]
    ,srb = 1.05
    ,age.int = 5)
  netMigk <- net.number.migrants(n1 = pop.input.mat[,k]
    ,n2 = pop.input.mat[,k+1]
    ,L = Lk)
  BKFem.nmig.input[k] <- sum(netMigk)
}
> BKFem.nmig.input.df <-
  data.frame(year = as.numeric(names(BKFem.nmig.input))
    ,total.mig.count.50pctl = BKFem.nmig.input
    )
> BKFem.nmig.input.df$total.mig.count.2.5pctl <- NA
> BKFem.nmig.input.df$total.mig.count.97.5pctl <- NA
> BKFem.nmig.input.df$legend <- "init. est."
> ###
> ### Plot
> ###
> plot.df <- rbind(BKFem.nmig.input.df, BKFem.nmig.post.quant.df)
> plot.df$year <- as.numeric(plot.df$year)
> plot.df$legend <- relevel(factor(plot.df$legend), ref = "init. est.")
> print(ggplot(data = plot.df, aes(x = year
  , y = total.mig.count.50pctl/1E3, color = legend)) +
  geom_line() +
  geom_point() + geom_ribbon(aes(ymin = total.mig.count.2.5pctl/1E3
    ,ymax = total.mig.count.97.5pctl/1E3, fill = legend)
    ,alpha = 0.15, color = NA) +
  ylab("net number of migrants (000s)")
  )
>

```

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