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Research Material

The bootstrap approach to the multistate life table method using Stata: Does accounting for complex survey designs matter?

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The bootstrap approach to the multistate life table method using Stata: Does accounting for complex survey designs matter?¹

Nader Mehri²

Abstract

OBJECTIVE

I aim to develop a Stata program that estimates multistate life table quantities and their confidence intervals while controlling for covariates of interest, as well as adjusting for complex survey designs. Using the Health and Retirement Study (HRS) (2000–2016), I use the new program to estimate US females' total, healthy, and unhealthy life expectancies and their intervals by race/ethnicity at age 52 (the youngest age in the sample), while adjusting for education.

METHODS

Using the nonparametric bootstrap technique (with replacement), the present study offers and validates an age-inhomogeneous first-order Markov chain multistate life table program. The current proposed Stata program is the maximum likelihood version of Lynch and Brown's Bayesian approach to the multistate life table method, which has been developed in R.³ I use the estimates from the Bayesian approach to validate the estimates from the unweighted bootstrap approach. I also account for the HRS complex survey design using the HRS baseline survey design indicators (clustering, strata, and sample weights). I utilize the estimates from the unweighted and weighted bootstrap models to evaluate the extent to which ignoring the HRS complex survey design alters the estimates.

RESULTS

The health expectancy estimates obtained from the unweighted bootstrap approach are consistent with estimates from the Bayesian approach, which ignores complex survey designs. This indicates that the bootstrap approach developed in the current paper is valid. Also, the results show that ignoring the HRS complex survey design does not meaningfully alter the estimates.

¹ Appendix A presents a concise version of the Stata code. The detailed version of the code is available on the *Demographic Research* website. The current version of the manuscript offers a Stata model syntax (not a package extension) that can be used to estimate state expectancies of interests and their variabilities.

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³ Appendix B presents R codes for Lynch and Brown's Bayesian approach to the multistate life table method.

CONTRIBUTION

The paper contributes to the multistate life table methods literature by providing a flexible, valid, and user-friendly program to estimate multistate life table quantities and their variabilities in Stata.

1. Background

The multistate (increment-decrement) life table methods have been widely used to investigate transitions across individuals' life spans, including transitions in health and mortality, marital status, and labor force participation (Muniz 2020). Specifically, in the case of health and mortality transitions, one of the major products of the multistate life table methods includes healthy and unhealthy life expectancies (HLE and ULE). These expectancies simultaneously reflect the mortality and morbidity status of individuals by measuring the number of years that a hypothetical cohort could expect to live in good or poor health, respectively. Although the multistate life table technique is a complex method, its output can be easily understood by policymakers, practitioners, and the public (Zang and Lynch 2018).

Allowing for the inclusion of covariates and quantifying the uncertainty around the multistate life table quantities are key components for testing hypotheses of interest (Lynch and Brown 2005). A multistate life table method that is lacking these important features can produce only point estimates of the expectancies of interest and are therefore unable to test hypotheses or make inferences about the population despite using sample data (Lynch 2007). This limitation is especially relevant for Stata users because, despite the strengths and popularity of Stata among social and demographic researchers, the literature on the multistate life table method is lacking a Stata program that estimates the multistate life table quantities and their variabilities by covariates of interest while accounting for complex survey designs. Using the nonparametric bootstrap technique⁴ (with replacement), the present study fills this important gap by offering and validating an age-inhomogeneous first-order Markov chain multistate life table program⁵ that produces the distribution of multistate life table quantities while controlling for covariates of interest, as well as adjusting for complex survey designs. The variabilities for the multistate life table quantities (e.g., confidence intervals, standard errors) that are key components for testing hypotheses can be obtained by summarizing this distribution.

⁴ Bootstrap resamples the original data across, for example, 1,000 replications using a simple random sampling technique. This method is commonly referred to as nonparametric bootstrap (StataCorp 2021).

⁵ Transition probabilities are conditioned on age and status (e.g., healthy/unhealthy) in an age-inhomogeneous first-order Markov chain multistate life table model.

It is noteworthy that the current proposed Stata program is the maximum likelihood version of Lynch and Brown's Bayesian approach to the multistate life table method, which has been developed in R (Lynch and Brown 2005, 2010). The Bayesian multistate life table method has been used to investigate critical health-related issues among older adults, including hearing impairment life expectancy, cognitively intact and happy life expectancy, and regional disparities in the impact of diabetes on life expectancy (Bardo and Lynch 2021; Zang, Lynch, and West 2021; West and Lynch 2021). It is of note that the bootstrapping approach offered in the present paper improves the Bayesian approach by allowing users to account for complex survey designs using the baseline or terminal survey design indicators.

2. Accounting for complex survey designs in the context of multistate life table methods

Under simple random sample techniques, sampling units are selected randomly and independently with an equal selection probability (Aneshensel 2013). However, most social and health surveys are not simple random samples of the population but instead consist of respondents from complex survey designs. These designs often stratify the population based on one or more characteristics, including geography, race, age, and so on. In addition, the designs can be multistage, meaning that initial strata are created, then respondents are sampled from smaller units within those strata, also known as clusters (Aneshensel 2013). Contingent on the size of strata and clusters, the stratification and clustering usually lead to unequal selection probability of the survey respondents. Also, complex survey designs may involve oversampling subgroups (e.g., racial/ethnic minority groups), which in turn increases the selection probabilities for the oversampled respondents. Oversampling usually is needed to increase the sample size and therefore the accuracy of parameter estimates among oversampled respondents (Aneshensel 2013).

Ignoring complex survey designs can affect the standard errors of parameter estimates. Specifically, ignoring the stratification tends to overestimate the variance for the parameter estimates, whereas ignoring the clustering underestimates the variance. Ignoring both stratification and clustering tends to deflate the variance for the parameter estimates because clustering usually has a substantially stronger impact on the variance compared to stratification (Aneshensel 2013). As such, ignoring the stratification and clustering increases the chance of rejecting the null hypothesis while it is true (Type I error).

It is of note that several studies have challenged the necessity of weighting and adjusting for sampling designs. These studies argue that, although weighting is appropriate in the context of univariate analyses of characteristics of population, in the

context of regression analyses, weighting is more controversial and complicated than it is generally thought (Lynch and Brown 2008; Solon, Haider, and Wooldridge 2015; Winship and Radbill 1994). Winship and Radbill (1994) show that unweighted estimates from OLS regression models are unbiased, consistent, and more precise if sampling weights are solely a function of independent variables. Lynch and Brown (2008) argue that ignoring sampling designs may not alter the significant coefficients to nonsignificance given that surveys with complex survey design usually have a large sample size. Additionally, weight construction can be a subjective process. Typically, the ultimate goal for the weight construction process is fitting survey estimates with the population counterparts, including census values. As such, weight construction procedures involve obtaining post-stratification weights by repeatedly comparing weighted estimates to their population counterparts until the survey estimates fit the population counterparts. The procedure often involves arbitrary choices of characteristics such that different researchers may generate different weights depending on the chosen characteristics (Gelman 2007; Lynch and Brown 2008).⁶

The issue of accounting for complex survey designs is especially challenging in the context of longitudinal analyses given that the initially sampled cohort changes over time due to attrition and mortality. Therefore, sampling weights that are calibrated to the baseline population become incorrect as the cohort ages, which in turn may result in serious biases (HRS staff 2019).⁷ It should be noted that multistate life table methods that include mortality (and survivorship) as an outcome incorporate attrition due to death in the state space. Thus, using the baseline survey design indicators to estimate health expectancies controls only for attrition due to death. As such, using the baseline weights comes at the cost of the assumption that the pattern of age profiles of transition probabilities for individuals is fixed regardless of their age at baseline.

Ignoring complex survey designs in the context of the multistate life table methods has been controversial as well. For example, one study found that ignoring the stratification and clustering underestimates the variance for the total, active, and disabled life expectancies by 2% to 75%, although the size of the underestimation differed across state expectancy measures, gender, and race/ethnicity (Cai et al. 2010). In contrast, Lynch and Brown (2008, 2010) find that ignoring complex survey designs had a trivial impact on the interval estimates for the proportion of remaining life to be spent healthy (PLE).

⁶ There can be ‘objective’ weights. With an enumerated population, it is possible to have ‘exact’ sampling weights, which are by definition nonsubjective. There simply has to be a well-defined population and unequal sampling from that population in order for there to be the possibility of objective (i.e., not ‘subjective’) weights. As an example, the National Health and Aging Trends Study (NHATS), a major and well-known national survey, draws its sample from an enumerated list: all people aged 65 and over, enrolled in the Medicare program, on a given date.

⁷ Alternatively, one may use the terminal-year weight indicators, which are appropriate for the retrospective analyses. However, using the terminal-year weights may result in serious biases as well given that the terminal-weights ignores correcting for differential left censoring (HRS staff 2019).

They find that the distribution of PLE was broader and slightly shifted when the sample design was incorporated, as compared to the alternative approach that ignored the sample design (Lynch and Brown 2008).

Using the baseline survey design indicators (clustering, strata, sample weights) from the Health and Retirement Study (HRS), the present study reexamines the impact of accounting for the HRS complex survey design on estimates for total, healthy, and unhealthy life expectancies among non-Hispanic Whites, non-Hispanic Blacks, and Hispanics.

3. Steps in the bootstrapping approach to the multistate life table method using Stata

The steps for the bootstrapping multistate life table approach offered in the present paper share some properties with the Bayesian multistate life table method. The Bayesian approach involves using the Gibbs sampling technique to sample parameters from a discrete-time bivariate probit model.⁸ The bivariate normal integration is used to convert the sampled parameters to age-state-specific transition probabilities, which are then used to construct the distribution of the multistate life table quantities of interest. The corresponding variabilities for the multistate life table quantities can be obtained by summarizing the distribution (Lynch and Brown 2005, 2008b, 2010).

In a similar fashion, the approach offered in the present paper uses a nonparametric bootstrap technique to generate a sequence of discrete-time (weighted) multinomial logistic regression parameters, and (at each step) to generate a new set of age-state-specific transition probabilities.⁹ Specifically, as shown in Table 1, the steps for the bootstrap approach involve (1) obtaining the bootstrapped (weighted) multinomial regression coefficients, (2) computing the age-state-specific transition probabilities from each bootstrap sample, (3) obtaining the radix values, and (4) constructing the distribution of the multistate life table quantities using the standard demographic life table computations. The corresponding variabilities for the multistate life table quantities (i.e., standard error, confidence intervals) can be obtained by summarizing the distribution yielded in Step 4.

⁸ It should be noted that the extended version of the Bayesian multistate life table method uses discrete-time multinomial logit model (Zang and Lynch 2018). However, only the older version of the Bayesian approach is available for public use and comes with a user guideline. As such, throughout the current paper, I refer to the older version of the Bayesian approach, which uses a discrete-time bivariate probit model.

⁹ The bootstrap approach offered in the present paper is flexible by allowing users to choose their statistical model to obtain transition probabilities.

Table 1: The process of constructing multistate life table quantities and corresponding variabilities using the bootstrap approach in Stata

Step	Process	Input	Output	Tools	Stata command
1	Estimate a bootstrapped (weighted) discrete-time multinomial regression model	Raw data	A set of bootstrapped (weighted) logit coefficients	The (weighted) multinomial logistic regression model, the bootstrap technique, the bootstrap weights	<i>(svy)mllog</i> , <i>bootstrap</i> , <i>bsweights</i>
2	Compute age-state-specific transition probabilities from the bootstrapped parameters	Output at Step 1	Age-state-specific transition probabilities for each set of bootstrapped parameters	1.a, 1.b, and 1.c formulas	<i>margins</i>
3	Obtain the radix values	Raw data	Radix values at the starting age	The discrete-time (weighted) logistic regression, 1.a, 1.b, and 1.c formulas	<i>(svy)logit</i> , <i>margins</i>
4	Compute multistate life table quantities for each set of the bootstrapped parameters	Output at Steps 2 and 3	The distribution of the multistate life table quantities (e.g., HLE, ULE)	The standard demographic life table computations (Schoen 1988a)	<i>mslt</i>

Step 1: Obtaining the bootstrapped (weighted) multinomial logistic regression coefficients

Step 1 involves fitting a discrete-time (weighted) multinomial logistic regression model using a combination of age and starting state (i.e., healthy, unhealthy) as well as age-invariant covariates (i.e., sex, race) at time t to predict ending state at time $t + n$ (n is survey wave interval). The step also uses the nonparametric bootstrap technique (with replacement) to obtain simple random samples from the original sample and then estimate the parameters from the selected samples. For this step, *Cluster* and *idcluster* options are used to force Stata to randomly select the bootstrap samples from individuals, not the person-waves (Sanchez 2021).

Step 2: Computing the age-state-specific transition probabilities

Step 2 involves utilizing the Stata’s predictive *margins* post command to convert the bootstrapped parameters to the transition probabilities for being healthy, unhealthy, or dead. The age-state-specific transition probabilities for a given covariate profile (e.g., non-Hispanic White females with 12 years of education) are obtained by conditioning the transition probabilities on age and starting states (i.e., healthy, unhealthy) as well as the covariates involved in the discrete-time multinomial regression model at Step 1.

For example, assume that a combination of predictors ($X = x_1, x_2, \dots, x_k$), including age and starting state as well as the covariates of interest (e.g., race/ethnicity,

sex, education), is used to fit a bootstrapped discrete-time multinomial logistic regression model to predict ending state (y) with three categories: healthy (h), unhealthy (u), and dead (d). The multinomial regression model estimates a set of logit coefficients for being healthy, unhealthy, or dead for each bootstrap sample ($\beta^{(h)}$, $\beta^{(u)}$, and $\beta^{(d)}$). If the healthy state is omitted as a reference category, the transition probabilities for being healthy, unhealthy, or dead for each bootstrap sample are obtained by (1) multiplying the matrix for the logit coefficients for being unhealthy or dead to the X matrix¹⁰, (2) exponentiating the resulting matrix to obtain the relative probability of being unhealthy or dead over the healthy state ($e^{X\beta^{(u)}}$, $e^{X\beta^{(d)}}$), and (3) converting the relative probabilities to the transition probabilities for being healthy, unhealthy, or dead using formulas 1.a, 1.b, and 1.c, respectively (StataCorp 2021):

$$\Pr(y = \text{healthy}) = \frac{1}{1 + e^{X\beta^{(u)}} + e^{X\beta^{(d)}}} \quad (1.a)$$

$$\Pr(y = \text{unhealthy}) = \frac{e^{X\beta^{(u)}}}{1 + e^{X\beta^{(u)}} + e^{X\beta^{(d)}}} \quad (1.b)$$

$$\Pr(y = \text{dead}) = \frac{e^{X\beta^{(d)}}}{1 + e^{X\beta^{(u)}} + e^{X\beta^{(d)}}} \quad (1.c).$$

Step 3: Obtaining the radix values

Consistent with the Bayesian approach, Step 3 estimates the life table's radix values by modeling the starting state. This step utilizes a discrete-time (weighted) logistic regression model to predict the starting state (being healthy or unhealthy) using the same predictors involved in the discrete-time multinomial regression model at Step 1. The radix values represent the estimated proportion of healthy or unhealthy individuals at the starting age. An alternative would be to use an external source, such as the US Census, find the relevant distribution, and treat those values as nonstochastic. Also, for a status-based multistate life table, this step can be ignored.¹¹ The radix values as well as the bootstrapped transition probabilities are used in Step 4 to generate the distribution of multistate life table quantities and their variabilities.

¹⁰ For a given covariate profile, the X matrix will consist of specific values for age, starting state, and the covariates of interest (the constant is multiplied by 1). Age must be incremented across the age range to obtain age-state-specific transition probabilities. Also, age-invariant covariates involved in the regression model can be controlled by setting their values to the sample mean.

¹¹ Under the status-based approach, a cohort enters the life table in a given state at starting age (e.g., either healthy or unhealthy) whereas under the population-based approach, a cohort enters the life table with the distribution over starting states at starting age (e.g., healthy, and unhealthy) (Saito, Robin, and Crimmins 2014).

Step 4: Constructing the distribution of the multistate life table quantities

Step 4 utilizes the standard demographic life table computations (Schoen 1988; Palloni 2001) to obtain the multistate life table quantities of interest for each bootstrap sample for a given covariate profile (e.g., non-Hispanic White females with 12 years of education). Specifically, Step 4 uses Stata's recently developed multistate life table (*mslt*) command (Muniz 2020) to obtain the distribution of multistate life table quantities of interest. The variabilities for the multistate life table quantities of interest are obtained by summarizing the distribution. Specifically, Step 4 involves (1) converting the transition probabilities to transition rates under linear or exponential assumptions depending on the functionality of the risk of event within age groups, (2) obtaining the number of survivors at ages above the starting age by applying the transitions rates to the radix values, (3) obtaining the person-years lived above age x (T_x) in transient states, and (4) obtaining state expectancies of interest by dividing (3) by (2). Equations for these steps are available in Muniz (2020).

4. An example

For the sake of explication, I use the HRS (2000–2016) to estimate US females' health expectancies and their variabilities (95% intervals) by race/ethnicity at age 52¹² while controlling for education. I estimate the health expectancies using three sets of estimations: (1) the Bayesian bivariate probit model, which ignores the HRS complex survey design; (2) the unweighted bootstrap multinomial logistic model, which ignores the HRS complex survey design; and (3) the weighted bootstrap multinomial logistic model, which accounts for the HRS complex survey design. I use the estimates from the Bayesian approach to validate the estimates from the unweighted bootstrap approach as described in the subsequent section. Also, I utilize the estimates from the unweighted and weighted bootstrap models to evaluate the extent to which ignoring the HRS complex survey design alters the estimates.

4.1 Validating the bootstrapping approach to the multistate life table method using Stata

To validate the bootstrap approach offered in the present paper, I estimate the health expectancies and corresponding 95% intervals using the Bayesian bivariate probit

¹² Age 52 is the youngest age in the sample for this example.

approach.¹³ Given that the Bayesian approach ignores complex survey designs, the estimates from the Bayesian and the unweighted bootstrap approaches are expected to be relatively consistent, which will confirm that the approach offered in the current paper is valid. It is of note that negligible differences in the estimates are expected due to using dissimilar statistical models (multinomial logistic vs. bivariate probit) as well as the dissimilar sampling techniques employed in the bootstrap approach and the Bayesian approach, which uses the Gibbs sampling technique.

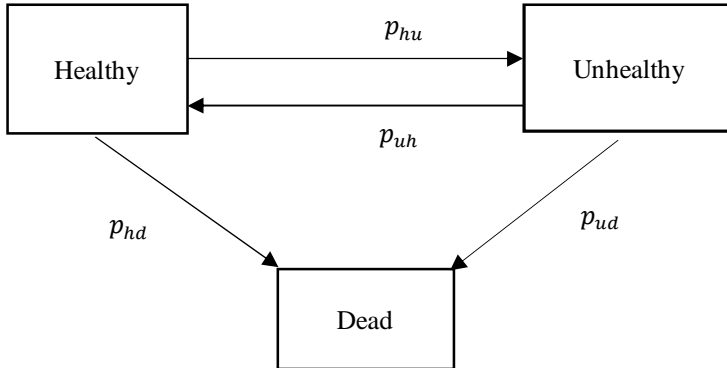
To be consistent with the Bayesian approach, however, I estimate the population-based health expectancies using 1,000 bootstrap samples while assuming linearity to solve the multistate life table equations. It is noteworthy that the Bayesian approach involves estimating a discrete-time bivariate probit model to predict health and mortality outcomes, therefore the health status will be missing for those who are dead. To address this issue, Lynch and Brown's Bayesian approach simulates a health score at each iteration of the Gibbs sampler for those who die by integrating the entire distribution of possible health status among them. In contrast, given that the Stata program offered in the current paper utilizes the multinomial logistic model, this simulation phase is eliminated. Using the multinomial logistic model, health and mortality status can be categorized as healthy, unhealthy, or dead; therefore, there is no need for simulating the health status of those who are deceased. It is of note that the extended version of the Bayesian multistate life table method uses discrete-time multinomial logit model rather than the bivariate probit model (Zang and Lynch 2018). However, at the time of writing this paper, only the older version of the Bayesian approach was available for public use and comes with a user guideline.

4.2 Analytic strategy

The multistate life table program offered in the current paper can handle unlimited transient states but at most one absorbing state. However, for the sake of explication, I use a three-state space multistate system with four possible transitions: healthy to unhealthy, unhealthy to healthy, healthy to dead, and unhealthy to dead (Figure 1). The absorbing state, death, is assumed irreversible.

¹³ Stata does not have an official command for handling the same probit model employed in the Bayesian approach.

Figure 1: A three-state space multistate system involving four possible transitions



Notes: p = the transition probability, h = healthy, u = unhealthy, d = dead.

5. Data

The study sample of the present paper comprises the 2000 HRS respondents (the baseline) that are followed for 16 years to 2016. The HRS is a nationally representative panel survey of US adults aged 51 and over and their spouses/partners (Health and Retirement Study 2016). The HRS is sponsored by the National Institute on Aging (grant number NIA U01AG009740) and has been conducted biannually since 1992 by the University of Michigan. Given that the sampling weights for the nursing home residents were included in the HRS since 2000, I use waves 2000 through 2016 (the RAND version) to appropriately account for the HRS complex survey design (the RAND HRS Longitudinal File 2018 (V1) 2021).

5.1 Accounting for the HRS complex survey design

The HRS uses a multistage area probability sampling design involving four stages: (1) using the probability proportionate to size method, two primary sampling units (PSUs) consisting of US metropolitan statistical areas (MSAs) and non-MSA counties are selected from 56 strata; (2) second stage sampling of area segments (SSUs) are sampled from PSUs; (3) all housing units (HUs) that are located within SSUs boundaries are listed

and systematically selected for the sampled SSUs; and (4) an age-eligible person within a sampled HU is randomly selected. The spouse/partner (at any age) of the sampled age-eligible person is also selected (HRS 2008; Aneshensel 2013). Also, the HRS oversamples non-Hispanic Blacks, Hispanics, and residents of Florida such that the sampling probability of Blacks and Hispanics is nearly two times greater than that of Whites (Sonnega et al. 2014; Aneshensel 2013).

As shown in the Stata syntax in Figure 2, I use the HRS sample design indicators (weights, clusters, and strata) from the baseline, or 2000 HRS wave, to account for the complex survey design. Also, to properly adjust for the HRS complex survey design within the bootstrapping framework, I use the balanced bootstrap approach, by which the survey's sampling weights are reconstructed by tracking the number of times a respondent falls into the bootstrapped sample (Kolenikov 2010). The Stata *bsweights* package implements the balanced bootstrap approach by generating rescaled 1,000 replicate weights across each replication (Kolenikov 2010).

Figure 2: The Stata syntax for accounting for the HRS complex survey design across 1,000 bootstrap replications

```
svyset raehsamp_base [pweight=rwtcrnh_base], strata (raestrat_base)
bsweights bw, reps(1000) n(0) seed(9999)
svyset [pweight=rwtcrnh_base], bsrweight(bw*)
```

5.2 Measures

The independent variables for this example consist of age, starting state (self-rated health), race/ethnicity, and education. The dependent variable is the ending state categorized as healthy, unhealthy, and dead. Age intervals must match up with the survey wave spacing in the multistate life table framework. The survey wave spacing is two years in the HRS, hence age intervals must be two years beginning at the youngest age in the sample (i.e., 52 to 53). Consistent with Lynch and Brown (2008), I set the youngest age group to be 0 and increment it across the age range (i.e., 52 to 53 = 0, 54 to 55 = 1, ..., over 100 = 24). Also, the open-ended age group is set to be 100 or more. Self-rated health is a dichotomous measure created from the self-rated health question, where respondents who said their health was excellent, very good, or good are identified as 'healthy' and respondents who said their health was fair or poor are 'unhealthy.' Race/ethnicity was categorized as non-Hispanic White, non-Hispanic Black, and Hispanic. Education was measured using years of schooling ranging from 0 to 17 or more.

5.3 Analytic sample

I create a person-wave data format such that each HRS 2000 respondent represents a single time interval between subsequent HRS waves between 2000 and 2016. Given that the HRS wave spacing is two years, the respondents contributed up to eight person-wave observations for this example. The HRS 2000 respondents included 10,444 non-Hispanic White, non-Hispanic Black, and Hispanic females who were given a nonzero sampling weights.¹⁴ These respondents contributed a total of 60,251 person-wave observations from 2000 to 2016, of which 2,479 (4.1%) observations were excluded because they were missing in a certain HRS wave. After excluding person-wave observations with missing values among age, self-rated health, race/ethnicity, and education (0.2%), the analytic sample included 57,648 person-wave observations.

As shown in Table 2, 63.1%, 28.7%, and 8.2% of person-wave observations were reported as healthy, unhealthy, and dead, respectively, at the end of intervals. Likewise, 69% and 31% reported that they were healthy and unhealthy at the beginning of the intervals, respectively. On average, the analytic sample was 72.5 years of age and had approximately 12 years of schooling. Also, 77.1% of the analytic sample was non-Hispanic White, 14.8% was non-Hispanic Black, and 8.1% was Hispanic.

Table 2: Characteristics of the analytic sample (2000–2016)

Variables	Mean (sd) or %
<i>Ending state</i>	
Healthy	63.1%
Unhealthy	28.7%
Dead	8.2%
<i>Starting state</i>	
Healthy	69%
Unhealthy	31%
Age	72.5 (9.7)
School years	12.1 (3.1)
<i>Race/ethnicity</i>	
Non-Hispanic White	77.1%
Non-Hispanic Black	14.8%
Hispanic	8.1%
Total (person-wave observations)	57,648

¹⁴ Given that the HRS sample eligibility is determined by birth cohort, the ineligible HRS cohort respondents are given zero weights. Also, individuals that enter the study as young spouses do not receive a weight until their birth cohort is sampled.

5.4 The Stata syntax to estimate state expectancies

Step 1: Obtaining the bootstrapped (weighted) multinomial logistic regression coefficients

As shown in the Stata syntax in Figure 3, I use age, self-rated health (starting state), race/ethnicity, education, and several interactions (age \times starting state, age \times race, and education \times race) in a discrete-time (weighted) multinomial logistic model to predict the ending state, categorized as healthy, unhealthy, and dead. The *baseoutcome(0)* option omits the ending state of being healthy as a reference category. The HRS complex survey design can be ignored by simply removing the *svy* prefix.

Step 2: Computing the age-state-specific transition probabilities

The *margins* post command and the *bootstrap* command generate the age-state-specific transition probabilities for being healthy, unhealthy, or dead across 1,000 bootstrap replications for the three race/ethnicity categories with around 12 years of schooling. Any main effect variables included in the regression model must be given a value in the *margins* post command. For example, as shown in the Stata syntax in Figure 3, the specified values for age, starting state, and race/ethnicity require Stata to generate age-state-specific transition probabilities for the three race/ethnicity categories. The *atmeans* option sets the sample mean for any covariates that are not given a value in the *margins* post command (i.e., education). For interactions, Stata automatically calculates the appropriate values using the specified values for the main effects variables. As such, there is no need to specify values for the interactions involved in the regression model.

Specifically, the *margins* post command shown in the Stata syntax in Figure 3 indicates that age is incremented by one unit across the age range from the youngest age group (52 to 53 = 0) to the open-ended age group (100 or more = 24). The starting state is given two values of 0 or 1 for being healthy or unhealthy, respectively. The specified values for the race/ethnicity variable require Stata to generate age-state-specific transition probabilities for non-Hispanic Whites, non-Hispanic Blacks, and Hispanics coded as 0, 1, and 2, respectively. For this example, given that education is not given a value, the *atmeans* option sets its value to the sample mean, which is approximately 12 years of schooling.

The *bootstrap* command uses the nonparametric bootstrap technique (with replacement) to obtain 1,000 simple random samples from the original sample and then generates the age-state-specific transition probabilities from the selected samples as described above. *Cluster* and *idcluster* options force Stata to randomly select the

bootstrap samples from the individuals, not the person-waves (Sanchez 2021).¹⁵ The *nose* option accelerates the computation process by allowing Stata to skip computing the standard errors for the transition probabilities, which are redundant for the purpose of multistate life table constructions. Given the specified values for the covariates, Stata generates 450 age-state-specific transition probabilities¹⁶ across 1,000 iterations and then saves the obtained 1,000 age-state-specific transition probabilities in the specified Stata data file in the *saving* option.

Figure 3: The Stata syntax for generating age-state-specific transition probabilities across 1,000 iterations

```
capture program drop savemargins
program savemargins, rclass

    svy: mlogit SRH_E_new c.age_100 i.SRH_B c.age_100#i.SRH_B i.race c.
    age_100#i.race c.education c.education#i.race, baseoutcome(0)

    margins , predict (outcome (0)) predict (outcome (1)) predict (outcome (2))
    at ( age_100=(0 (1) 24) SRH_B=(0 1) race=(0 (1) 2) ) atmeans post nose

end
bootstrap _b, saving(boot_mlog_F_repW_atmeans, replace ) reps(1000) cluster(
hhidpn) idcluster(newwid) : savemargins nose
```

Step 3: Obtaining the radix values

Figure 4 presents Stata syntax to obtain the radix values by fitting a discrete-time (weighted) logistic regression model to predict the starting state (being healthy or unhealthy) using the same predictors involved in the discrete-time multinomial regression model at Step 1. The *margins* post command generates the estimated proportion of being healthy or unhealthy at the youngest age group (i.e., 52 to 53 = 0) for non-Hispanic Whites, non-Hispanic Blacks, and Hispanics. The *atmeans* option controls for education by setting its value to the sample mean (~12 years of schooling). The HRS complex survey design can be ignored simply by removing the *svy* prefix.

¹⁵ Given that the survey wave spacing is two years in the HRS, the *Cluster* and *idcluster* options are defined as follows:

```
. generate long newwid = hhidpn
. tsset newwid year, delta(2)
```

¹⁶ Stata will generate 450 age-state-specific transition probabilities given 3 categories for ending state, 25 age groups, 2 categories for the starting state, and 3 race/ethnicity categories: $3 \times 25 \times 2 \times 3 = 450$.

Figure 4: The Stata syntax for obtaining the weighted radix values for the three race/ethnicity categories

```
svyset raehsamp_base [pweight=rwtcrnh_base], strata (raestrat_base)
svy:logit SRH_B c.age_100 i.race c.age_100#i.race c.education c.education#i.race
margins race, at ( age_100=0 ) atmeans
```

As shown in the Stata output in Figure 5, 16.7% of non-Hispanic Whites at age 52 to 53 are estimated to be unhealthy after adjusting for education. The corresponding estimates are 34.7% and 37% among non-Hispanic Blacks and Hispanics, respectively. The radix values for being healthy are simply obtained by subtracting 1 from the proportions reported in Figure 5. The radix values as well as the age-state-specific transition probabilities are used in Step 4 to generate the distribution of healthy and unhealthy life expectancies.

Figure 5: The weighted radix values for being unhealthy by race/ethnicity

	Delta-method				
	Margin	Std. Err.	t	P> t	[95% Conf. Interval]
race					
0.non-Hispanic White	.166926	.0090026	18.54	0.000	.148861 .184991
1.non-Hispanic Black	.3468686	.0360615	9.62	0.000	.2745059 .4192314
2.Hispanic	.3702465	.0428109	8.65	0.000	.2843401 .4561529

Step 4: Constructing the distribution of the healthy and unhealthy life expectancies by race/ethnicity

The Stata syntax shown in Figure 6 uses the 1,000 age-state-specific transition probabilities yielded in Step 2 as well as the radix values from Step 3 to generate and save 1,000 healthy and unhealthy life expectancies across the age range among non-Hispanic Whites. The total life expectancy can be obtained by summing the healthy and unhealthy life expectancies. The $m12$, $m13$, $m21$, and $m23$ are transition probabilities, respectively, for healthy to unhealthy, healthy to dead, unhealthy to healthy, and unhealthy to dead. The radix values for being unhealthy and healthy must be specified within parentheses for $l0$. The $R1$ and $R2$ indicate the radix values for being healthy and unhealthy, respectively. Given that the *mslt* command can handle a multistate life table system without an absorbing state, the *death* option in the *mslt* command must be specified to indicate that our multistate life table of interest involves an absorbing state. The *proportion* option indicates that transition probabilities are used as input instead of rates. The *constant* option assumes a linear solution instead of an exponential solution to

solve the multistate life table equations. The rest of the codes shown below combine the 1,000 health expectancies and save them in the specified Stata data file. To obtain the distribution for state expectancies among non-Hispanic Blacks or Hispanics, the below Stata code must be rerun using the corresponding transition probabilities as well as radix values.

Figure 6: The Stata syntax for constructing the distribution of health expectancies for non-Hispanic Whites

```
keep profile age m*
order profile age m12 m13 m21 m23
quietly levelsof profile, clean local(plist)
set graphics off
foreach p of local plist {
    clear matrix
    preserve
    quietly keep if (profile == "`p'")
    drop profile
    keep age m12 m13 m21 m23
    local R2=.166926 // The radix values for being healthy (non-Hispanic Whites)
    local R1=1-`R2'
    quietly mslt, l0(`R1' `R2' 0) death proportion constant
    matrix rename ei_x `p'_ei_x
    xsvmat `p'_ei_x, norestore
    rename (`p'_ei_x1 `p'_ei_x2) (ei_x1 ei_x2)
    gen profile="`p'"
    quietly append using MSLT_results_repW_mlog_boot.dta.dta
    quietly save MSLT_results_repW_mlog_boot.dta, replace
    restore
}
```

The point estimates for the total, healthy, and unhealthy life expectancies as well as their variabilities can be obtained by summarizing the 1,000 state expectancies yielded in this step. Specifically, the point estimate and the standard error of the state expectancies can be calculated by obtaining the mean and the standard deviation of the 1,000 state expectancies yielded in Step 4. The corresponding 95% confidence intervals can be obtained by taking the 25th and the 975th values of the 1,000 state expectancies as the lower and upper bounds. Additionally, the point estimates and their standard errors can be used for hypothesis testing¹⁷ using standard statistical tests, such as independent t-test or ANOVA.

¹⁷ E.g., whether the state expectancies among the three race/ethnicity categories are statistically different from each other.

5.5 Total, healthy, and unhealthy life expectancies and their variabilities by different estimation approaches

Table 3 and Figure 7 show that the estimates for total, healthy, and unhealthy life expectancies from the Bayesian and the unweighted bootstrap approaches are comparable despite using dissimilar statistical models and sampling techniques. The unweighted bootstrap 95% intervals considerably overlap with the Bayesian 95% intervals, indicating that the unweighted bootstrap approach performs well and is valid.¹⁸ For example, the estimates from the Bayesian approach show that after controlling for education, non-Hispanic White females at age 52 could expect to live 30 (95% CI: 29.6–30.4) additional years, of which 22.6 (95% CI: 22.1–22.9) and 7.4 years (95% CI: 7.2–7.7) were expected to be healthy and unhealthy years, respectively. The corresponding estimates from the unweighted bootstrap approach are similar to the Bayesian approach: 29.7 (95% CI: 29.3–30), 22.3 (95% CI: 21.9–22.7), and 7.3 (95% CI: 7.1–7.6) years, respectively, for total, healthy, and unhealthy life expectancies. Likewise, the estimates from the Bayesian and the unweighted bootstrap approaches are consistent for non-Hispanic Blacks as well as Hispanics. In sum, Table 3 and Figure 7 show that the estimated differences between the Bayesian and unweighted bootstrap approaches for the total, healthy, and unhealthy life expectancies are trivial among non-Hispanic Whites, non-Hispanic Blacks, and Hispanics. This confirms that the bootstrap approach to the multistate life table method offered in the current paper is valid.

Table 4 and Figure 7 show that ignoring the HRS complex survey design has a trivial impact on the estimates. Generally, the 95% intervals from the multinomial logistic model that account for the HRS complex survey design considerably overlap with the 95% intervals that ignores the HRS complex survey design. As such, it is not possible to conclude that the population (true) values are different with and without weights.

¹⁸ It should be noted that we cannot directly compare the estimates from the maximum likelihood approach to the estimates from the Bayesian work as their interpretation is fundamentally different (see Lynch 2007). I compare these estimates for the purpose of validating the Stata syntax only.

Table 3: Total, healthy, and unhealthy life expectancies and their 95% intervals for females at age 52, US 2000–2016 (Bayesian vs. the unweighted bootstrap approaches)

Race/ethnicity	Quantity	Bayesian (95% CI)	Bootstrap (95% CI)
		Unweighted bivariate probit model	Unweighted multinomial logistic model
Non-Hispanic White	TLE	30.0(29.6–30.4)	29.7(29.3–30.0)
	HLE	22.6(22.1–22.9)	22.3(21.9–22.7)
	ULE	7.4(7.2–7.7)	7.3(7.1–7.6)
Non-Hispanic Black	TLE	27.9(26.9–28.8)	27.6(26.6–28.5)
	HLE	17.3(16.5–18.2)	17.0(16.1–18.0)
	ULE	10.5(9.9–11.1)	10.6(9.9–11.2)
Hispanic	TLE	31.2(29.6–32.7)	31.0(29.5–32.7)
	HLE	18.1(16.5–19.6)	17.7(16.0–19.3)
	ULE	13.1(12.0–14.4)	13.3(11.9–14.7)

Notes: TLE = total life expectancy, HLE = healthy life expectancy, ULE=unhealthy life expectancy. School years was controlled by setting its value to the sample mean (~12 years of schooling). The unweighted model ignores the HRS complex survey design.

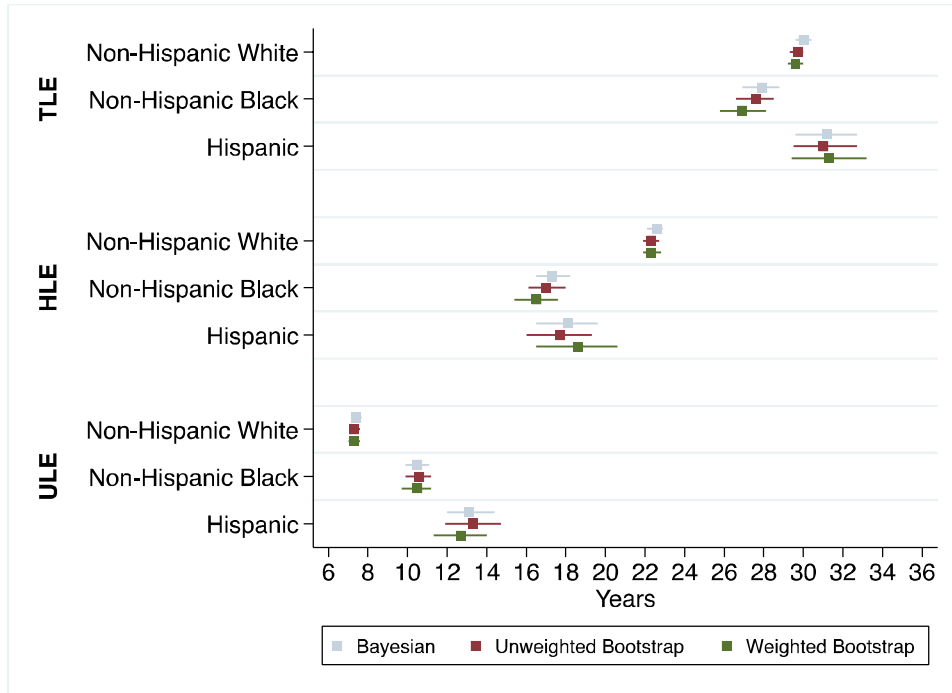
Generally, the 95% interval estimates are wider when the HRS complex survey design is taken into account. This is especially true for the estimates among non-Hispanic Blacks and Hispanics, who had a substantially lower sample size when compared to non-Hispanic Whites. This indicates that sample size plays a crucial role in minimizing the impact of ignoring the complex survey design on the width of the intervals for the total, healthy, and unhealthy life expectancies. Altogether, the results indicate that ignoring the HRS complex survey design does not meaningfully alter the estimates.

Table 4: Total, healthy, and unhealthy life expectancies and their 95% intervals for females at age 52, US 2000–2016 (unweighted vs. weighted bootstrap approaches)

Race/ethnicity	Quantity	Unweighted multinomial logistic model	Weighted multinomial logistic model
Non-Hispanic White	TLE	29.7(29.3–30.0)	29.6(29.2–30.0)
	HLE	22.3(21.9–22.7)	22.3(21.9–22.8)
	ULE	7.3(7.1–7.6)	7.3(7.0–7.6)
Non-Hispanic Black	TLE	27.6(26.6–28.5)	26.9(25.8–28.1)
	HLE	17.0(16.1–18.0)	16.5(15.4–17.6)
	ULE	10.6(9.9–11.2)	10.5(9.7–11.2)
Hispanic	TLE	31.0(29.5–32.7)	31.3(29.4–33.2)
	HLE	17.7(16.0–19.3)	18.6(16.5–20.6)
	ULE	13.3(11.9–14.7)	12.7(11.3–14.0)

Notes: TLE = total life expectancy, HLE = healthy life expectancy, ULE=unhealthy life expectancy. School years was controlled by setting its value to the sample mean (~12 years of schooling). The unweighted model ignores the HRS complex survey design whereas the weighted model accounts for the HRS complex survey design using the HRS baseline (the 2000 wave) survey design indicators.

Figure 7: Total, healthy, and unhealthy life expectancies and their 95% intervals by different estimation approaches, females at age 52, US 2000–2016



Notes: TLE = total life expectancy, HLE = healthy life expectancy, ULE = unhealthy life expectancy. School years was controlled by setting its value to the sample mean (~12 years of schooling). The Bayesian and the unweighted bootstrap approaches ignore the HRS complex survey design whereas the weighted bootstrap approach accounts for the HRS complex survey design using the HRS baseline (the 2000 wave) survey design indicators.

6. Discussion

Using the bootstrap technique, the present paper contributes to the multistate life table methods literature by offering and validating a Stata program that estimates the multistate life table quantities and their variabilities by covariates of interest while accounting for complex survey designs. Using the HRS (2000–2016), I estimated US females' total, healthy, and unhealthy life expectancies and their variabilities (95% intervals) by race/ethnicity at age 52 while controlling for education. The results show that the health expectancies and their intervals from the unweighted bootstrap approach are considerably

consistent with Lynch and Brown's Bayesian approach, which ignores complex survey designs. This indicates that the bootstrap approach offered in the current paper is valid.

Also, the results show that ignoring the HRS complex survey design does not meaningfully alter the estimates.¹⁹ Nonetheless, this does not always guarantee the robustness of the estimates against ignoring complex survey designs in all studies given that each survey has a unique sampling design. Consistent with Solon, Haider, and Wooldridge (2015), it is important to report both the weighted and unweighted state expectancies of interest and explain their implications for interpreting the results.

Additionally, the implementation and modification of the bootstrap approach offered in the current paper is more flexible than Lynch and Brown's Bayesian approach and will be accessible to Stata users. For example, users may prefer to use probit models instead of the originally suggested multinomial logistic regression model to obtain their transition probabilities of interest. This is achievable by slightly modifying the Stata program offered in the current paper. Likewise, users can obtain the distribution of status-based or population-based state expectancies by simply changing the corresponding option in the Stata's *mslt* command. Also, users can specify linear or exponential options to solve the life table equations depending on the functionality of the risk of event within age groups. For the Bayesian approach, however, this amount of flexibility is not available such that the changes noted above may require substantial modifications of the corresponding R programs.

In addition, the inclusion of the age-squared term and the interactions between the starting state and other covariates are not allowed in Lynch and Brown's Bayesian approach to the multistate life table method. Using the current Stata program, the age-squared term (i.e., the interaction between age with itself) and any interaction terms can be simply added to the regression model. Nonetheless, these limitations are unlikely to meaningfully alter the estimates from the Bayesian multistate life table method.

Basically, any limitations for Stata's *mslt* command (Muniz 2020) are applicable to the bootstrap approach offered in the current paper as well. For example, a notable limitation could be allowing unlimited transient states but only one absorbing state, as in Lynch and Brown's Bayesian approach. In addition, the bootstrapping approach offered in the current paper is slower than Lynch and Brown's Bayesian approach, which uses R. For example, depending on the sample size and the complexity of the multinomial logistic regression model, obtaining the transition probabilities from 1,000 bootstrap samples may take several hours, whereas the similar process takes less than an hour using Lynch and Brown's R programs. Likewise, obtaining the state expectancies using their R programs is faster than the Stata program offered in the present paper. Nevertheless, I believe that the benefits of the newly developed program outweigh these limitations.

¹⁹ Using the baseline weights comes at the cost of the assumption that the pattern of age profiles of transition probabilities for individuals is fixed regardless of their age at baseline.

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Appendix A. The concise version of Stata code for the bootstrap approach to the multistate life table method²⁰

***Account for the HRS complex survey design using the baseline sample design indicators (HRS 2000 wave) across 1,000 bootstrap replications**

```
svyset raehsamp_base [pweight=rwtcrnh_base], strata (raestrat_base)
bsweights bw, reps(1000) n(0) seed(9999)
svyset [pweight=rwtcrnh_base], bsrweight(bw*)
```

***Define *Cluster* and *idcluster* options to force Stata to randomly select the bootstrap samples from the individuals and not the person-waves (Sanchez 2021)**

```
tsset, clear
generate long newid = hhidpn
tsset newid year, delta (2)
```

***Step 1 and 2: Obtaining the bootstrapped (weighted) multinomial logistic regression coefficients and computing the age-state-specific transition probabilities for a given covariate profile (e.g., non-Hispanic White with around 12 years of education)**

```
capture program drop savemargins
program savemargins, rclass
    svy: mlogit SRH_E_new c.age_100 i.SRH_B c.age_100#i.SRH_B i.race
        c.age_100#i.race c.education c.education#i.race, baseoutcome(0)
    margins, predict (outcome (0)) predict (outcome (1)) predict (outcome (2)) at
        (age_100=(0 (1) 24) SRH_B=(0 1) race=(0 (1) 2) ) atmeans post nose
end
```

***Generate a sequence of discrete-time multinomial logistic regression parameters, and (at each step) generate a new set of age-state-specific transition probabilities for a given covariate profile (e.g., non-Hispanic White females with around 12 years of education)**

```
bootstrap _b, saving (boot_mlog_F_repW_atmeans, replace) reps(1000) cluster(hhidpn)
    idcluster(newid): savemargins nose
```

²⁰ The detailed version of the code is needed to replicate the results of the current paper which is available on the Demographic Research website.

***Step 3: Obtaining the weighted radix values for the three race/ethnicity categories**

```
svyset raehsamp_base [pweight=rwtcrnh_base], strata (raestrat_base)
svy:logit SRH_B c.age_100 i.race c.age_100#i.race c.education c.education#i.race
margins race, at ( age_100=0 ) atmeans
*W=.166926 , B=.3468686 , H=.3702465
```

***Step 4: Constructing the distribution of the multistate life table quantities for a given covariate profile (e.g., non-Hispanic White with around 12 years of education)**

```
save MSLT_results_repW_mlog_boot.dta, emptyok replace
rename (HU HD UH UD ) (m12 m13 m21 m23)
keep profile age m*
order profile age m12 m13 m21 m23
quietly levelsof profile, clean local(plist)
set graphics off
foreach p of local plist {
    clear matrix
    preserve
    quietly keep if (profile == "`p'")
    drop profile
    keep age m12 m13 m21 m23
    local R2=.166926 // The radix values for being healthy (non-Hispanic Whites)
    local R1=1-`R2'
    quietly mslt, l0(`R1' `R2' 0) death proportion constant
    matrix rename ei_x `p'_ei_x
    xsvmat `p'_ei_x, norestore
    rename (`p'_ei_x1 `p'_ei_x2) (ei_x1 ei_x2)
    gen profile=`p'
    quietly append using MSLT_results_repW_mlog_boot.dta.dta
    quietly save MSLT_results_repW_mlog_boot.dta, replace
    restore
}
```

Appendix B. R codes for the Bayesian approach to the multistate life table method

Appendix B1. R codes for the Gibbs sampler for a bivariate dichotomous probit hazard model (GSMLThazard.R version .91)

#Copyright 2006 Scott M. Lynch (Princeton University) and J. Scott Brown (Miami University). If you use this software, cite our Lynch and Brown (2005) Sociological Methodology_ paper and see the instruction manual. We acknowledge support of NICHD grant 1R03HD050374-01 in constructing this program

#This is a Gibbs sampler for a bivariate dichotomous probit hazard model with k covariates. The second program, GMSLT_tables.R, produces life tables for a specified covariate profile using the output of this program

#Required data file is space-delimited ascii with variables in this order:

#1 a column of ones for the intercept

#2 age (in one- or five-year age groups numbered successively starting at 0)

#3 starting state (time 1) indicator (0/1) healthy or not

#4 an age*starting state interaction

#5 sequence of covariates (e.g., sex, race, income...)

#6 sequence of age*covariate interactions in same order as variables listed in step 5

#7 healthy/unhealthy indicator (0/1) at time 2

#8 dead/alive indicator (1/0) at time 2

e.g., 1 age start age*start male black income age*male age*black unhealthy2 dead2

#NOTES:

#If dead, health is indeterminate, so set ending health indicator at 0.

#Starting state by covariate interactions not allowed in this version.

#To run program, you only need to change the following:

#1. number of X variables (k), including intercept, age, starting state, etc.

#2. name of the input data file

#3. name of the Gibbs sampler output file

#4. width of proposal density for error correlation. This is technical but should be modified to obtain a stable acceptance rate of .25-.75 for the error correlation parameter. This is the last column reported in the output while Gibbs sampler is running and is usually a function of the sample size. Try $1/\sqrt{n}$ for starters again; see manual for more detail.

```
setwd (“~/Desktop/multistate life table/MLE”)
library(haven)
Bayes_input_F <- read_dta(“Bayes_input_F.dta”)
k=11
inf=(“~/Desktop/multistate life table/MLE/Bayes_input_F.dat”)
outf=(“~/Desktop/multistate life table/MLE/Bayes_input_F.par”)
w=1/sqrt(57648)

#DO NOT MODIFY ANYTHING BELOW HERE
starttime=Sys.time()
x=as.matrix(read.table(inf)[,1:k])
z=as.matrix(read.table(inf)[,(k+1):(k+2)])
zstar=matrix(0,nrow(z),2)
d=2
b=matrix(0,(d*k))
s=diag(d); cs=diag(d)
acctot=0
tz=matrix(0,4); ctz=matrix(0,4)
tz[1]=-Inf; tz[2]=0; tz[3]=tz[4]=Inf
write(c(0,t(b),t(s),0),file=outf,ncolumns=(d*k+d*d+2),append=T)

for(i in 2:10000){
#draw latent data
bb=matrix(b,k,2)
m=x%*%bb
#mvn gibbs sampler
mm=m[,2] + s[1,2]*(zstar[,1]-m[,1])
ss=1-s[1,2]^2
zstar[,2]=qnorm(runif(nrow(z)),
min=pnorm(tz[z[,2]+1],mm,sqrt(ss)),
max=pnorm(tz[z[,2]+2],mm,sqrt(ss))),mean=mm,sd=sqrt(ss))
mm=m[,1] + s[1,2]*(zstar[,2]-m[,2])
ss=1-s[1,2]^2
zstar[,1]=qnorm(runif(nrow(z)),
min=pnorm(tz[z[,1]-z[,2]+1],mm,sqrt(ss)),
max=pnorm(tz[z[,1]+z[,2]+2],mm,sqrt(ss))),mean=mm,sd=sqrt(ss))
#draw b from mvn
vb=solve(solve(s)%ax%(t(x)%*%ax))
mn=vb%*%(as.vector(t(x)%*%zstar%*%t(solve(s))))
```

```

b=mn+t(rnorm((d*k),0,1)%*%chol(vb))
#simulate s using MH sampling
e=matrix((as.vector(zstar)-(diag(d)%x%x%*%b)),nrow(z),d)
v=t(e)%*%e
like=-.5*(d+nrow(z)+1)*log(det(s))-5*sum(diag(v%*%solve(s)))
cs[1,2]=cs[2,1]=s[1,2]+rnorm(1,mean=0,sd=w)
if(abs(cs[1,2])<1){
  cslike=-.5*(d+nrow(z)+1)*log(det(cs))-5*sum(diag(v%*%solve(cs)))
  if((cslike-like)>log(runif(1,0,1)))
    {s[1,2]=s[2,1]=cs[1,2]; acctot=acctot+1}
}
if(i%%10==0){print(c(i,b[1],b[1+k],s[1,2],acctot/i),digits=5)}

      if(i%%5==0){write(c(i,t(b),t(s),acctot/i),file=outf,ncolumns=(d*k+d*d+2),ap
pend=T)}
}
print(Sys.time()-starttime)

```

Appendix B2. R codes for producing life tables using Gibbs samples from a bivariate probit model program (GMSLTtables.R version .91)

#Copyright 2006 Scott M. Lynch (Princeton University) and J. Scott Brown (Miami University). If you use this software, cite our Lynch and Brown (2005). Sociological Methodology paper and see the instruction manual. We acknowledge support from NICHD grant 1R03HD050374-01 in constructing this program.

#This program produces life tables using Gibbs samples from a bivariate probit model program (GMSLThazard.R) applied to a user-specified covariate profile

#To run program, you need to change the following:

- #1. the number of early Gibbs samples to discard prior to convergence (burnin)
- #2. the number of life tables to generate (samples). burnin+samples cannot exceed the length of the parameter output file.
- #3. the youngest age in the sample in years (startage)
- #4. the width of the age groups in the data (typically either 1 or 5) (yearscale)
- #5. the number of covariates in the model, not counting the intercept, age, starting state, age*starting state, nor interactions between age and covariates (numx)
- #6. the number of interactions of covariates with age (numinter)
- #7. the values at which you wish the covariates to be set (covval)
- #8. the original data used by the hazard program (origdat)
- #9. the input data file name (output of Gibbs sampler) (inf)
- #10. the output file for the life tables (outf)

```
setwd (“~/Desktop/multistate life table/MLE”)
burnin=1000
samples=1000
startage=52
yearscales=2
numx=5
numinter=2
covval=matrix(NA,3,5)
#non-Hispanic Whites with around 12 years of schooling
covval[1,]=c(0,0, 12.07679,0,0)
#non-Hispanic Blacks with around 12 years of schooling
covval[2,]=c(1,0, 12.07679, 12.07679,0)
#Hispanics with around 12 years of schooling
covval[3,]=c(0,1, 12.07679,0, 12.07679)
require(mvtnorm)
for(loop in 1:3){
  origdat=(“~/Desktop/multistate life table/MLE/Bayes_input_F.dat”)
}
```



```
inf=(“~/Desktop/multistate life table/MLE/Bayes_input_F.par”)
outf=(“~/Desktop/multistate life table/MLE/Bayes_input_F.tab”)
transition=(“~/Desktop/multistate life table/MLE/Bayes_input_F_transition.tab”)
```

```
#DO NOT MODIFY ANYTHING BELOW HERE
```

```
starttime<-Sys.time()
num=(100-startage)/yearscales +1
inter=matrix(1,num+1)
starts=matrix(1,num+1,2)
if(numx>0){cv=t(matrix(covval[loop,],numx,num+1))}
pmat=matrix(0,3,3)
fb=matrix(NA,num+1,2)
b=matrix(NA,numx+numinter+4,2)
g=as.matrix(read.table(inf,header=F))
ages=matrix(seq(0,num),num+1)
if(numx>0 & numinter==0){x<-cbind(inter,ages,starts,cv)}
if(numx>0 & numinter>0){x<-cbind(inter,ages,starts,cv,ages[,1]*cv[,1:numinter])}
if(numx==0){x<-cbind(inter,ages,starts)}
#gets radix from regression on starting state
dat=read.table(origdat)
oy=as.matrix(dat[,3])
ox=as.matrix(dat[,c(2,5:(numx+numinter+4))])
vvv=as.matrix(coefficients(glm(oy~ox,family=binomial(link=probit))))
cvv=as.matrix(c(1,0,covval[loop,],rep(0,numinter)))
radix=c(1-pnorm(t(cvv)%*%vvv,0,1),pnorm(t(cvv)%*%vvv,0,1),0)
print(radix)
#start computations of life tables
for(m in (burnin+1):(burnin+samples)){
#read in parameter sample
b[(1:(numx+numinter+4)),1]=g[m,(2:(numx+numinter+5))]
b[(1:(numx+numinter+4)),2]=g[m,((numx+numinter+6):(2*(numx+
numinter+4)+1))]
rho=g[m,(2*(numx+numinter+4)+3)]
sig=matrix(c(1,rho,rho,1),2,2)
#compute predicted values for transitions: start h
x[,3]=0; x[,4]=0
hfb=x%*%b
#compute predicted values for transitions: start u
x[,3]=1; x[,4]=x[,2]
```

```

ufb=x%*%b
l=matrix(radix,num,3,byrow=T)
bl<-matrix(0,num,3)
tl<-matrix(0,num,3)
#get transition probabilities matrices across age from pred. vals.
for(a in 1:num){
  pmat[1,3]=pmvnorm(lower=c(-Inf,-
    Inf),upper=c(+Inf,hfb[a,2]),mean=c(0,0),corr=sig)
  pmat[2,3]=pmvnorm(lower=c(-Inf,-
    Inf),upper=c(+Inf,ufb[a,2]),mean=c(0,0),corr=sig)
  pmat[1,2]=pmvnorm(lower=c(-
    Inf,hfb[a,2]),upper=c(hfb[a,1],+Inf),mean=c(0,0),corr=sig)
  pmat[2,2]=pmvnorm(lower=c(-
    Inf,ufb[a,2]),upper=c(ufb[a,1],+Inf),mean=c(0,0),corr=sig)
  pmat[1,1]=1-(pmat[1,2]+pmat[1,3])
  pmat[2,1]=1-(pmat[2,2]+pmat[2,3])
  pmat[3,3]=1
  write(c(t(pmat)),file=transition,append=T,ncolumns=(9*num))
  if(a<num){
    l[a+1,]=l[a,]%*%pmat
    bl[a,]=.5*yearscales*(l[a,]+l[a+1,])
  }
  if(a==num){
    bl[a,1:2]=l[a,1:2]%*%solve(diag(2)-pmat[1:2,1:2])
  }
}
le=matrix(NA,num,3)
for(a in 1:(num-1)){
  tl[a,]=colSums(bl[a:num,])
  le[a,]=tl[a,]/sum(l[a,1:2])
}
tl[num,]=bl[num,]
le[num,]=tl[num,]/sum(l[num,1:2])
write(c(t(le)),file=outf,append=T,ncolumns=(3*num))
print(c(m,le[1,]))
}
print(Sys.time()-starttime)
}

```