Appendix Tables

Appendix Table A1.

Transition start ↓	End of transition								
	H	A	C	CA	D	DA	DC	DCA	Dead
H	27,954	1,867	2,227	434	755	60	96	30	680
A	1,308	2,062	152	371	42	79	10*	25	504
C	0	0	14,501	2,346	0	0	522	108	1,431
CA	0	0	1,346	3,710	0	0	59	193	1,968
D	0	0	0	0	4,182	471	471	123	169
DA	0	0	0	0	315	595	60	152	181
DC	0	0	0	0	0	0	3,540	976	581
DCA	0	0	0	0	0	0	615	1,968	907
Dead	0	0	0	0	0	0	0	0	ALL

Note: States include being healthy (H), being diabetic (D), having at least one chronic condition (C), having at least one ADL disability (A), being diabetic with at least one condition (DC), being diabetic with at least one ADL disability (DA), having at least one condition and one ADL disability (CA), being diabetic with a at least one condition and at least one ADL disability (DCA), and death. * Observations in this cell were assigned to DCA due to convergence issues.

Appendix Table A2. Posterior Means and 84% Credible Intervals for Various State Expectancies by Gender and Race, Healthy Population

Gender-Race ↓	Healthy Population							
	TLE	XLE	CLE	DLE	CDLE	XCLE	XDLE	XCDLE
F-W	32.1[31.6,32.7]	1.6[1.4,1.8]	5.8[5.5,6.2]	1.7[1.5,1.8]	2.7[2.5,2.9]	0.5[0.4,0.5]	2.0[1.7,2.2]	1.5[1.4,1.7]
F-B	30.2[29.5,30.9]	2.0[1.7,2.3]	3.9[3.5,4.3]	2.2[2.0,2.5]	2.7[2.4,3.0]	0.6[0.5,0.8]	1.7[1.5,2.0]	2.1[1.8,2.3]
F-H	33.1[31.8,34.3]	2.4[1.9,3.0]	4.5[3.7,5.3]	2.0[1.7,2.4]	2.1[1.8,2.6]	1.1[0.8,1.4]	1.9[1.5,2.3]	2.3[1.9,2.7]
M-W	28.3[27.8,28.9]	1.8[1.5,2.0]	6.2[5.8,6.5]	0.9[0.8,1.0]	1.7[1.5,1.8]	0.3[0.3,0.4]	2.6[2.3,2.9]	1.1[0.9,1.2]
M-B	25.9[25.2,26.6]	2.2[1.9,2.6]	4.0[3.6,4.4]	1.2[1.1,1.4]	1.6[1.4,1.8]	0.4[0.4,0.5]	2.2[1.9,2.5]	1.5[1.3,1.6]
M-H	29.4[28.2,30.7]	2.9[2.2,3.6]	4.9[4.1,5.8]	1.2[1.0,1.4]	1.4[1.1,1.7]	0.8[0.6,1.1]	2.4[1.9,2.9]	1.6[1.3,1.9]
		%XLE	%CLE	%DLE	%CDLE	%XCLE	%XDLE	%XCDLE
F-W		5.0[4.4,5.6]	18.1[17.1,19.2]	5.2[4.8,5.5]	8.3[7.8,8.9]	1.4[1.3,1.7]	6.1[5.5,6.9]	4.8[4.3,5.2]
F-B		6.6[5.6,7.7]	12.8[11.7,14.0]	7.4[6.8,8.2]	8.9[8.0,9.8]	2.1[1.8,2.5]	5.7[5.1,6.5]	6.9[6.1,7.7]
F-H		7.3[5.7,9.0]	13.7[11.4,16.1]	6.2[5.1,7.3]	6.5[5.4,7.7]	3.4[2.5,4.4]	5.7[4.5,7.0]	6.8[5.6,8.2]
M-W		6.2[5.4,7.1]	21.8[20.6,23.1]	3.2[3.0,3.5]	5.8[5.5,6.2]	1.1[0.9,1.3]	9.0[8.1,10.0]	3.7[3.4,4.2]
M-B		8.7[7.2,10.1]	15.3[13.8,16.9]	4.8[4.3,5.4]	6.1[5.5,6.8]	1.7[1.4,2.0]	8.5[7.4,9.6]	5.6[4.9,6.4]
M-H		9.8[7.7,12.2]	16.8[13.9,19.6]	4.0[3.3,4.8]	4.7[3.9,5.7]	2.9[2.1,3.7]	8.0[6.5,9.8]	5.5[4.5,6.6]

Note: Genders include female (F) and male (M), and races include non-Hispanic White (W), non-Hispanic Black (B), and Hispanic (H). Life expectancies include total life expectancy (TLE), life expectancy with only diabetes (XLE), life expectancy with only other chronic conditions (CLE), life expectancy with only ADLs (DLE), life expectancy with both ADLs and other chronic conditions (CDLE), life expectancy with diabetes and other chronic conditions (XCLE), life expectancy with diabetes and ADLs (XDLE), life expectancy with all three health issues (XCDLE). Proportions of various life expectancies are calculated by life expectancy in a state divided by total life expectancy. Estimates only apply to the US-born population.

Appendix Table A3. Posterior Means and 84% Credible Intervals for Various State Expectancies by Gender and Race, Diabetic Population

Gender-Race ↓	Diabetic Population				
	TLE	XLE	XCLE	XDLE	XCDLE
F-W	23.7[22.5,24.7]	10.3[9.2,11.4]	6.0[5.4,6.5]	2.4[2.0,2.9]	5.0[4.6,5.4]
F-B	22.5[20.9,24.2]	10.5[9.2,11.9]	4.1[3.6,4.7]	2.9[2.3,3.5]	5.1[4.4,5.7]
F-H	24.2[22.1,26.4]	10.3[8.3,12.3]	4.5[3.7,5.5]	3.6[2.6,4.7]	5.8[4.7,7.0]
M-W	21.5[20.2,23.0]	10.4[9.2,11.7]	6.7[6.1,7.4]	1.5[1.1,1.8]	2.9[2.6,3.2]
M-B	20.2[18.2,22.1]	10.9[9.4,12.5]	4.5[3.9,5.2]	1.8[1.3,2.3]	3.0[2.5,3.4]
M-H	22.3[19.9,24.8]	11.5[9.3,13.7]	4.8[3.9,5.8]	2.5[1.7,3.3]	3.6[2.9,4.4]
		%XLE	%XCLE	%XDLE	%XCDLE
F-W		43.3[39.7,47.0]	25.2[22.8,27.7]	10.3[8.6,12.3]	21.1[19.1,23.2]
F-B		46.7[42.2,50.8]	18.2[16.0,20.6]	12.7[10.4,15.2]	22.5[19.7,25.3]
F-H		42.3[35.9,48.6]	18.7[15.0,22.9]	14.9[11.1,19.2]	24.1[19.7,29.3]
M-W		48.4[44.4,52.3]	31.3[28.0,34.7]	6.8[5.4,8.4]	13.5[12.1,15.1]
M-B		54.1[49.5,58.1]	22.4[19.4,25.5]	8.8[7.0,10.7]	14.7[12.7,17.1]
M-H		51.1[44.6,57.1]	21.5[17.5,26.2]	11.1[8.1,14.6]	16.3[12.9,20.2]

Note: Genders include female (F) and male (M), and races include non-Hispanic White (W), non-Hispanic Black (B), and Hispanic (H). Life expectancies include total life expectancy (TLE), life expectancy with only diabetes (XLE), life expectancy with only other chronic conditions (CLE), life expectancy with only ADLs (DLE), life expectancy with both ADLs and other chronic conditions (CDLE), life expectancy with diabetes and other chronic conditions (XCLE), life expectancy with diabetes and ADLs (XDLE), life expectancy with all three health issues (XCDLE). Proportions of various life expectancies are calculated by life expectancy in a state divided by total life expectancy. Estimates only apply to the US-born population.

Appendix Table A4. Posterior Means and 84% Credible Intervals for Various State Expectancies by Gender and Education Level, Healthy Population

Gender-Education ↓	Healthy Population							
	TLE	XLE	CLE	DLE	CDLE	XCLE	XDLE	XCDLE
F-BH	30.2[29.6,30.8]	1.6[1.3,1.8]	4.7[4.4,5.1]	1.9[1.7,2.1]	2.7[2.4,2.9]	0.6[0.5,0.7]	1.8[1.6,2.0]	1.8[1.6,2.0]
F-HS	33.7[33.1,34.3]	1.8[1.6,2.1]	6.2[5.9,6.5]	1.7[1.6,1.8]	2.6[2.4,2.8]	0.4[0.4,0.5]	2.1[1.8,2.4]	1.5[1.4,1.7]
F-CH	36.4[35.6,37.2]	2.1[1.8,2.5]	6.7[6.2,7.2]	1.5[1.4,1.7]	2.7[2.4,3.0]	0.4[0.3,0.5]	2.3[1.9,2.7]	1.3[1.1,1.5]
M-BH	26.2[25.6,26.8]	1.8[1.5,2.1]	5.0[4.6,5.3]	1.1[0.9,1.2]	1.6[1.5,1.8]	0.4[0.3,0.5]	2.3[2.0,2.6]	1.2[1.1,1.4]
M-HS	29.9[29.3,30.5]	2.0[1.7,2.3]	6.6[6.2,7.0]	0.9[0.9,1.0]	1.6[1.5,1.7]	0.3[0.2,0.3]	2.7[2.4,3.1]	1.1[1.0,1.2]
M-CH	33.0[32.1,33.9]	2.2[1.9,2.6]	7.3[6.8,7.8]	0.8[0.8,0.9]	1.7[1.5,1.8]	0.2[0.2,0.3]	3.2[2.7,3.8]	0.9[0.8,1.1]
		%XLE	%CLE	%DLE	%CDLE	%XCLE	%XDLE	%XCDLE
F-BH		5.2[4.4,6.0]	15.7[14.6,16.9]	6.3[5.8,6.8]	8.8[8.1,9.5]	2.0[1.7,2.4]	6.0[5.3,6.7]	6.1[5.4,6.7]
F-HS		5.5[4.8,6.2]	18.4[17.5,19.3]	5.0[4.7,5.3]	7.7[7.2,8.3]	1.3[1.1,1.5]	6.2[5.5,7.0]	4.6[4.1,5.1]
F-CH		5.8[4.8,6.8]	18.4[17.2,19.7]	4.1[3.7,4.5]	7.5[6.8,8.2]	1.1[0.8,1.4]	6.3[5.2,7.5]	3.4[2.9,4.0]
M-BH		6.8[5.7,7.9]	19.0[17.6,20.5]	4.0[3.6,4.4]	6.2[5.7,6.8]	1.6[1.3,1.9]	8.7[7.7,9.8]	4.8[4.2,5.3]
M-HS		6.7[5.8,7.6]	22.0[20.8,23.3]	3.1[2.9,3.4]	5.4[5.0,5.8]	0.9[0.8,1.1]	9.1[8.2,10.2]	3.6[3.2,4.0]
M-CH		6.7[5.7,7.8]	22.2[20.7,23.7]	2.5[2.3,2.8]	5.1[4.6,5.6]	0.7[0.6,0.9]	9.7[8.2,11.4]	2.8[2.4,3.3]

Note: Genders include female (F) and Male (M), and education levels include below high school (BH), high school diploma and some college (HS), and college degree or higher (CH). Life expectancies include total life expectancy (TLE), life expectancy with only diabetes (XLE), life expectancy with only other chronic conditions (CLE), life expectancy with only ADLs (DLE), life expectancy with both ADLs and other chronic conditions (CDLE), life expectancy with diabetes and other chronic conditions (XCLE), life expectancy with diabetes and ADLs (XDLE), life expectancy with all three health issues (XCDLE). Proportions of various life expectancies are calculated by life expectancy in a state divided by total life expectancy. Estimates only apply to the US-born population.

Appendix Table A5. Posterior Means and 84% Credible Intervals for Various State Expectancies by Gender and Education Level, Diabetic Population

Gender-Education ↓	Diabetic Population				
	TLE	XLE	XCLE	XDLE	XCDLE
F-BH	22.2[21.0,23.3]	9.1[8.1,10.3]	4.9[4.3,5.5]	2.9[2.3,3.5]	5.3[4.7,5.9]
F-HS	25.1[23.8,26.4]	11.7[10.5,12.9]	6.3[5.7,6.9]	2.2[1.8,2.7]	4.9[4.4,5.4]
F-CH	27.7[25.7,29.7]	13.9[12.3,15.5]	7.4[6.3,8.5]	2.0[1.5,2.6]	4.4[3.9,5.0]
M-BH	20.0[18.6,21.5]	9.6[8.5,11.0]	5.5[4.8,6.1]	1.8[1.4,2.3]	3.1[2.7,3.6]
M-HS	22.8[21.4,24.4]	11.6[10.4,13.1]	7.0[6.3,7.8]	1.3[1.0,1.6]	2.8[2.5,3.1]
M-CH	25.8[23.6,28.0]	13.3[11.6,15.1]	8.7[7.5,10.1]	1.1[0.8,1.5]	2.6[2.3,3.1]
		%XLE	%XCLE	%XDLE	%XCDLE
F-BH		41.2[37.1,45.2]	22.1[19.6,24.6]	12.9[10.6,15.4]	23.9[21.3,26.6]
F-HS		46.5[42.9,50.0]	25.1[22.8,27.5]	8.9[7.4,10.7]	19.5[17.6,21.7]
F-CH		50.0[45.7,54.3]	26.7[23.3,30.2]	7.3[5.6,9.2]	16.0[14.0,18.3]
M-BH		48.1[43.9,52.3]	27.3[24.1,30.7]	9.1[7.0,11.2]	15.6[13.6,17.6]
M-HS		51.0[47.3,54.4]	30.8[28.0,33.9]	5.8[4.7,7.1]	12.5[11.1,14.1]
M-CH		51.6[47.1,56.2]	33.8[29.7,38.1]	4.4[3.2,5.7]	10.3[8.8,11.9]

Note: Genders include female (F) and Male (M), and education levels include below high school (BH), high school diploma and some college (HS), and college degree or higher (CH). Life expectancies include total life expectancy (TLE), life expectancy with only diabetes (XLE), life expectancy with only other chronic conditions (CLE), life expectancy with only ADLs (DLE), life expectancy with both ADLs and other chronic conditions (CDLE), life expectancy with diabetes and other chronic conditions (XCLE), life expectancy with diabetes and ADLs (XDLE), life expectancy with all three health issues (XCDLE). Proportions of various life expectancies are calculated by life expectancy in a state divided by total life expectancy. Estimates only apply to the US-born population.

Appendix Table A6. Gaps in Total Life Expectancies between Healthy and Diabetic Populations, with 84% Credible Intervals

Gender-Race	Median and 84% CI	Gender-Education	Median and 84% CI
F-W	8.5[7.4, 9.6]	F-BH	8.0[6.9, 9.2]
F-B	7.7[6.1, 9.3]	F-HS	8.6[7.4, 9.8]
F-H	8.9[7.0, 10.7]	F-CH	8.7[7.0, 10.5]
M-W	6.8[5.5, 8.2]	M-BH	6.2[4.9, 7.6]
M-B	5.7[3.9, 7.5]	M-HS	7.1[5.5, 8.4]
M-H	7.0[5.1, 9.1]	M-CH	7.2[5.3, 9.1]

Note: See notes above.

Appendix Table A7. Gaps in Health Outcomes between Whites and Blacks, with 84% Credible Intervals

Health Outcomes	Healthy Population		Diabetic Population	
	Female	Male	Female	Male
TLE	1.9[1.3, 2.6]	2.4[1.7, 3.1]	1.1[-0.3, 2.6]	1.3[-0.2, 2.9]
%XLE	-3.5[-6.7, 0.2]	-5.8[-9.5, -1.9]	-1.6[-2.6, -0.7]	-2.5[-3.8, -1.2]
%XDLE	-2.4[-4.3, -0.5]	-2.0[-3.4, -0.6]	-0.7[-1.0, -0.4]	-0.6[-0.9, -0.3]

Note: See notes above.

Appendix Table A8. Gaps in Health Outcomes between Persons with and without a College Degree, with 84% Credible Intervals

Health Outcomes	Healthy Population		Diabetic Population	
	Female	Male	Female	Male
TLE	2.7[2.0, 3.4]	3.1[2.3, 3.9]	2.7[0.7, 4.5]	3.1[1.1, 4.8]
%XLE	0.3[-0.6, 1.2]	0.0[-1.0, 1.0]	3.5[-0.4, 7.6]	0.7[-3.3, 4.7]
%XDLE	-0.2[-0.4, 0.1]	-0.2[-0.4, 0.0]	-1.7[-3.4, 0.2]	-1.5[-2.6, -0.3]

Note: See notes above.

Appendix: Bayesian Multistate Life Table Methods for Complex, High-Dimensional State Spaces

Our method is an extension of the method developed in Lynch and Brown (2005). In their approach, parameters are sampled from a two-dimensional discrete-time multinomial probit model using a Gibbs sampler. As with bootstrapping, a life table is produced for each post-burn-in parameter sample, and (credible) interval estimates of any life table quantity of interest can be computed from the life tables using a typical Bayesian approach of sorting estimates and selecting the values at the desired quantiles. A pair of C and R programs were developed by the authors to facilitate implementation. Aside from the ability of this approach to incorporate prior information if desired, the method does not resample data and therefore does not risk obtaining samples that are missing transitions. Further, the method does not require asymptotic assumptions regarding the shape of the posterior distribution for life table quantities.

The key limitation of their method, however, is that, as developed, the method can handle only two living states. Additionally, as developed, the method treats the state as the start of a time interval as a covariate, with the state at the end of the interval as the multinomial outcome. Although this approach can yield identical results to those obtained by treating the transition itself as the outcome, it prohibits the ability to incorporate "partially absorbing states" (i.e., structural zeros in the transition matrices) into the model. For instance, in our case, individuals may transition to becoming diabetic, but once diagnosed, they cannot return to any non-diabetic state. Thus, under the original Lynch-Brown method, for any state that does not also involve diabetes (e.g., nondiabetic with serious chronic health conditions), a covariate representing "diabetic" may only take one value (1; diabetic), making estimation of transitions impossible, because of lack of variability in the covariate for some outcome states.

We extend the Lynch-Brown approach to handle much higher dimensional state spaces with partially absorbing states, resolving the two key limitations of the previous method. Our

MLST method involves two steps: 1) sampling from the posterior distribution for a Bayesian discrete time multinomial logit model for transitions, with covariates including age as predictors using panel data; and 2) generating life tables using typical multistate demographic calculations applied to the posterior samples.

The multinomial logit model is a model for qualitatively distinct, mutually exclusive outcomes, with covariates predicting the probability of each outcome. Let $p(Y_i = j)$ represent the probability that individual i experiences outcome j from a total of $j = 1,\ldots, J$ possible outcomes. Then,

$$P(Y_i = j) = \frac{\exp\,(\beta_j X_i)}{\sum_{s=1}^{J} \exp\,(\beta_s X_i)},$$

where X_i is a $k \times 1$ vector of covariates for individual i, and β_j is a vector of the coefficients for the effects of the covariates on outcome j, with one outcome omitted as a reference outcome. These probabilities can be inserted into a typical multinomial mass function to obtain a likelihood function:

$$L(\beta|Y) \propto \prod_{i=1}^{n} (\prod_{j=1}^{J} p(Y_i = j)^{I(Y_{i=j})})$$

where $I(Y_i = j)$ is the indicator function indicating whether respondent i experienced outcome j. We assume that all covariates predict each outcome and that there are no outcome-specific covariates.

In our case, n represents the number of person-interval records in the data, where an interval can be defined as the time interval between successive survey waves. The outcomes, Y, are transitions individuals experienced over an interval of length m years (or months, days, etc.), with the states at time t and $t + m$ defining the transition. Thus, the ending state at time $t + m$ for the interval that begins at time t is the starting state for the interval that begins at time $t + m$ and runs to $t + 2m$. In our specification, we assume that m does not vary across survey waves nor across individuals, although that assumption can be relaxed in various ways. Individuals who die between survey waves (or are censored in some other way, e.g., attrition) contribute no further person-interval records to the data. Given this data structure, the model can be described as a discrete time hazard model (see Allison (1984)).

Defining the transition experienced over an interval as the outcome—rather than defining the ending state as the outcome with a covariate for the starting state used to help define the transition—resolves one limitation of the Lynch and Brown (2005) method: transitions that are not possible (i.e., structural zeroes) are simply not included as an outcome in the multinomial regression model. A complication of this approach, however, is that it increases the dimensionality of the outcome, posing another problem. While the number of outcomes in the model is theoretically unlimited, from a practical standpoint, parameters of the multinomial logit model become increasingly difficult to estimate when the dimensionality becomes large, in both maximum likelihood and Bayesian settings.

In the Bayesian setting, the multinomial probit model is often used instead of the logit, because it lends itself to Gibbs sampling, and Gibbs samplers are fairly easy to implement with data augmentation strategies (McCulloch and Rossi, 1994; Albert and Chib, 1993; Imai and Van Dyk, 2005). In contrast, estimation of logit model parameters in the Bayesian setting requires

more general Metropolis-Hastings or other samplers, because there has been no analagous data augmentation strategy that yields exact conditional posterior distributions for β that are of known forms. In lower dimensions, the Gibbs sampler for the probit model and MH algorithms for the logit model both work well, and for medium-dimensional outcomes, the multinomial probit model using data augmentation works far better than MH routines for the logit model. However, beyond dimensions of 20 or so, both the Gibbs sampler for the probit model and MH routines for the logit model become computationally difficult or even infeasible.

Fortunately, the recent development of a Gibbs sampling routine for the logit model has resolved much of the difficulty. Polson et al. (2013) developed a Gibbs sampler for the multinomial logit model using a data augmentation strategy with Polya-Gamma latent variables. Details of the approach can be found in both the authors' original paper and in their technical supplement. The Polya-Gamma strategy can be thought of as an analogue to the probit data augmentation strategy developed by Albert and Chib (1993) in that they both introduce latent variables that enable exact posterior inference through Gibbs sampling. The main difference from an analytic perspective is that, while the posterior distribution for regression parameters (β) in the probit model is a location mixture of normals in which the locations are influenced by truncated normal latent variables, the Polya-Gamma strategy results in a scale mixture posterior. A second difference is that while the latent variables used in the probit model were motivated by their direct interpretation as the “utility” of each category in the context of a discrete choice model, the Polya-Gamma latent variables have no apparent intuitive interpretation.

Compared to other Bayesian strategies for estimating multinomial logit models, this data-augmentation strategy is more efficient and easier to use when the dimensionality of the outcome is large (Polson et al., 2013). As with any full Gibbs sampler, the method does not require tuning

parameters like MH algorithms do. In our own trials, this strategy is orders of magnitude much faster computationally to converge and mix and generates more reliable estimates when the dimensionality is high compared to an independence sampler or an adaptive random walk Metropolis-Hastings algorithm. Specifically, in other substantive research we have found that an independence sampler using a multivariate normal proposal with a mean vector equal to the ML estimates and a covariance matrix equal to the ML covariance matrix of estimates works well when the outcome dimensionality is less than 20 (self-identifying reference omitted), but we rely on the Polya-Gamma strategy for models with higher-dimensional outcomes, such as in our example here.

For our purposes, $J - 1$ of the J possible transitions across an interval are treated as outcomes in the multinomial logit model, with all covariates $x_1 \ldots x_k$ (including an intercept and an age variable) included as predictors of each transition. After G post-burn n iterations of the Gibbs sampler involving Poly-gamma latent variables, we will have G samples of β, a $k \times (J - 1)$ matrix of coefficients. For life table construction, we first determine a covariate profile for which we wish to generate a life table, and we construct a $T \times k$ matrix Z, and T is the number of age groups included in the life table calculations ($a = 1 \ldots T$). Each row in Z consist of the fixed covariate values (and intercept) plus a value of age that is incremented across rows.

The product $Z\beta$ yields a $T \times (J - 1)$ matrix of predicted values from which probabilities for each transition can be computed row-wise via:

$$pr_j(a) = \frac{\exp\left((Z\beta)_{aj}\right)}{1 + \sum_{j=2}^{J} \exp\left((Z\beta)_{aj}\right)}.$$

The probability for the omitted transition can be computed by subtracting the sum of the computed probabilities from 1. The result is a matrix, $f(Z\beta)$, from which age-specific transition probability matrices, *P(a)*, $a = 1 \ldots T$ can be constructed. Specifically, each row of $f(Z\beta)$ is placed in a square matrix of dimension $d \times d$ based on the starting and ending states represented by the probabilities. Structural zeros are included, and a final row of zeros with a trailing 1 is also included, to reflect the fact that individuals cannot transition from the deceased state. It is important to note that *d* is the number of starting/ending states across a transition interval, while *J* is the total number of estimated possible transitions, so that $J < d^2$. The rows of these square matrices are then normalized so that each row sums to 1 by adding all elements in a given row and then dividing each element in the row by the sum. This produces a set of right-stochastic matrices, one for each age group.

With a complete set of age-specific transition probability matrices for a specific covariate profile, we can construct MSLTs in a straightforward fashion using mostly traditional calculations. Let *l* be an $N \times d$ matrix of counts of individuals in each of the *d* states at the start of each age interval, and let *l(a)* reference row *a* of the matrix. Then, *l(1)* is the radix population, *l(2)* is the number of persons in each state at age *k*, *l(3)* is the number of persons in each state at age *2k*, and so one, and *l(a = N)* is the number of persons alive at the start of the open-ended interval.

The radix population can either be derived from the row sums of the unnormalized probabilities in $f\left(Z\beta^{(g)}\right)$ at age 0 ($a = 1$) in order to produce "population-based" life tables, or it can be fixed at specific values to produce "status-based" life tables. For example, we could set the radix such that all persons in the population are in a specific state at age 0 (e.g., diabetic

without other chronic conditions defined previously or ADL disabilities) in order to estimate state expectancies for persons who enter the life table at age 0 in that state.

Given a radix, we can compute *l(a)* for all age groups except the last as:

$$l(a+1) = l(a)P(a).$$

Person years lived in each state in age group *a* can be computed using the linear assumption:

$$L(a) = .5k[l(a) + l(a+1)],$$

where, again, *k* is the width of the age interval.

As with any life table procedure, the final age interval requires a different computation than other intervals. In particular, we compute *L(T)* as:

$$L(N) = kl(N\big(I - P(N)\big)^{-1},$$

where the last row and column of *l(N)* and *P(N)* is omitted.

The more conventional calculation for years lived in the open-ended interval is $L(\Omega) = kl(a)\mu^{-1}$, where μ is the intensity or rate matrix of transitions in the oldest age group (Palloni, 2001). In a continuous time framework, this calculation provides the waiting time for absorption (death), assuming constant transition *rates* from age Ω forward. Our calculation simply assumes constant transition *probabilities*, rather than *rates*, from age Ω forward, so that waiting times are geometrically distributed. $(I - P(N))^{-1}$ is the sum of the infinite geometric series implied by the

transition probability matrix at age Ω. Given that we generate predicted transition probability matrices to age 110+ (the oldest age for which we often have some data in panels), there is almost no difference in estimates of state expectancies at age 0, nor at age Ω. We prefer this calculation to converting *P(N)* to a rate matrix and performing the usual computation as a matter of coherence with the discrete time modeling strategy.

The vector *T(a)*, the person years to be lived in each state from age (group) *a* forward, can be computed as:

$$T(a) = \sum_{i=a}^{N} L(i)$$

Finally, state expectancies can be computed for each age group by dividing *T(a)* by $\sum l(a)$, where $\sum l(a)$ is the total number of persons alive at age *a*, regardless of state. This computation apportions the total years to be lived in each state from a given age forward across all persons surviving to the beginning of age group *a*.

We note that this method produces estimates that are a compromise between a period and cohort life table. Panel data generally follow an accelerated longitudinal design: multiple birth cohorts are followed over an extended time period, but no birth cohort is observed over the complete age range observed in the study. Here, if birth cohort is included as a covariate in the multinomial regression model (and we argue it should be), then it must be fixed at a value for life table estimation. Fixing cohort at a specific value means that the resulting life table is a cohort life table, but estimates will obviously be informed by patterns of other cohorts, implying that the results assume some degree of stationarity.

To be a little more specific, for each of the posterior samples obtained from the Gibbs sample, we compute sets of age-specific probabilities for each outcome transition as discussed earlier. These matrices are not transition probability matrices, but appear as:

$$f(Z\beta(a)) = \begin{array}{c|ccccccccc} & H & A & C & CA & D & DA & DC & DCA & Death \\ \hline H & pr_1 & pr_2 & pr_3 & pr_4 & pr_5 & pr_6 & pr_7 & pr_8 & pr_9 \\ A & pr_{10} & pr_{11} & pr_{12} & pr_{13} & pr_{14} & pr_{15} & 0 & pr_{16} & pr_{17} \\ C & 0 & 0 & pr_{18} & pr_{19} & 0 & 0 & pr_{20} & pr_{21} & pr_{22} \\ CA & 0 & 0 & pr_{23} & pr_{24} & 0 & 0 & pr_{25} & pr_{26} & pr_{27} \\ D & 0 & 0 & 0 & 0 & pr_{28} & pr_{29} & pr_{30} & pr_{31} & pr_{32} \\ DA & 0 & 0 & 0 & 0 & pr_{33} & pr_{34} & pr_{35} & pr_{36} & pr_{37} \\ DC & 0 & 0 & 0 & 0 & 0 & 0 & pr_{38} & pr_{39} & pr_{40} \\ DCA & 0 & 0 & 0 & 0 & 0 & 0 & pr_{41} & pr_{42} & pr_{43} \\ Death & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 1 \end{array},$$

where the collection of *pr* sum to 1 across all values ($\sum_{j=1}^{43} pr_j = 1$). Transition probability matrices are obtained by normalizing the cell probabilities by their row marginals. For example, we can obtain the transition probability, p_{11}, (the H-H transition) as:

$$p_{11} = \frac{pr_1}{\sum_{j=1}^{9} pr_j}.$$

Thus, the 43 age-specific outcome probabilities are converted to the non-zero elements of the 9 × 9 age-specific transition probability matrix necessary for life table calculations.

We have tested our method using simulated data that mimics the HRS study design, and the method performs extremely well. We have done simulations for both a single-decrement

model and for a two-state model. The simulation results show that our approach yields results that are very close to the population data from which the simulated data were generated, even though our modeling assumptions are not entirely aligned with the data generation process. For example, while the spacing between waves in the HRS is 2 years on average, it is not exactly two years for everyone. Therefore, in our simulations, we generated a sample in which the average spacing between survey waves for each person was 2 years, but we randomly generated survey times to be up to .8 years away from exactly 2 years ($u \sim U(1{:}2;\ 2{:}8)$). Further, our transition rates were generated using Gompertz (i.e., exponential across age) curves. Despite using a sigmoidal function (logit) and assuming exact two year spacing between survey occasions, we found a very close match between estimates obtained via our method and the "true" values in our contrived population.

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