Appendix: Life expectancy by county, race, and ethnicity in the USA, 2000–2019: a systematic analysis of health disparities

Contents

1 GATHER Checklist

Item #	Checklist item	Description of Compliance
Objectives and funding		
1	Define the indicator(s), populations (including age, sex, and geographic entities), and time period(s) for which estimates were made.	Abstract, Introduction, and Methods sections
2	List the funding sources for the work.	Abstract, Methods, and Acknowledgements sections
Data Inputs		
For all data inputs from multiple sources that are synthesized as part of the study:		
3	Describe how the data were identified and how the data were accessed.	Methods section
4	Specify the inclusion and exclusion criteria. Identify all ad-hoc exclusions.	Methods section
5	Provide information on all included data sources and their main characteristics. For each data source used, report reference information or contact name/institution, population represented, data collection method, year(s) of data collection, sex and age range, diagnostic criteria or measurement method, and sample size, as relevant.	Methods section, Appendix sections 2.1–2.2, 2.5, and 3.2–3.3
6	Identify and describe any categories of input data that have potentially important biases (e.g., based on characteristics listed in item 5).	Methods section
For data inputs that contribute to the analysis but were not synthesized as part of the study:		
7	Describe and give sources for any other data inputs.	N/A
For all data inputs:		
8	Provide all data inputs in a file format from which data can be efficiently extracted (e.g., a spreadsheet rather than a PDF), including all relevant meta-data listed in item 5. For any data inputs that cannot be shared because of ethical or legal reasons, such as third-party ownership, provide a contact name or the name of the institution that retains the right to the data.	GHDx link (upon publication)
Data analysis		
9	Provide a conceptual overview of the data analysis method. A diagram may be helpful.	Methods section, Appendix section 4.1
10	Provide a detailed description of all steps of the analysis, including mathematical formulae. This description should cover, as relevant, data cleaning, data pre-processing, data adjustments and weighting of data sources, and mathematical or statistical model(s).	Methods section, Appendix section 2
11	Describe how candidate models were evaluated and how the final model(s) were selected.	Appendix section 2
12	Provide the results of an evaluation of model performance, if done, as well as the results of any relevant sensitivity analysis.	Appendix section 2
13	Describe methods for calculating uncertainty of the estimates. State which sources of uncertainty were, and were not, accounted for in the uncertainty analysis.	Methods section, Appendix section 2
14	State how analytic or statistical source code used to generate estimates can be accessed.	GitHub link (upon publication)
Results and Discussion		
15	Provide published estimates in a file format from which data can be efficiently extracted.	GHDx link (upon publication)
16	Report a quantitative measure of the uncertainty of the estimates (e.g. uncertainty intervals).	Results section, GHDx link (upon publication)
17	Interpret results in light of existing evidence. If updating a previous set of estimates, describe the reasons for changes in estimates.	Introduction and Discussion sections
18	Discuss limitations of the estimates. Include a discussion of any modelling assumptions or data limitations that affect interpretation of the estimates.	Discussion section

Checklist template obtained from: http://gather-statement.org/

2 Supplemental Methods

2.1 Deaths and population data processing

We used de-identified death records from the National Vital Statistics System (NVSS) and population estimates from the National Center for Health Statistics (NCHS) for the years 2000–2019 for this analysis (section 3.2). Deaths and population were tabulated by county, age group (0, 1–4, 5–9, …, 80–84, 85+ years of age), sex, race/ethnicity, and year. In cases where age was missing (0.0177% of deaths), we calculated the proportion of deaths within each age group by state, year, sex, and race/ethnicity among those entries with age information and then reapportioned deaths without age information by using these proportions. This approach effectively assumes that age is missing at random. We are unable to verify this assumption; however, we believe it's unlikely that violations of this assumption would substantively impact the results of our analysis, given the rarity of missing age in the deaths data. In cases where death records were missing information on race or where race was coded as "other" (0·63%), NVSS imputed a value; in cases where multiple race information was collected and decedents were identified as two or more races (0·29%), NVSS included an imputed or "bridged" race value that corresponds to the predicted "primary" race for each decedent.[1] We used the imputed and bridged values for the present analysis. NVSS does not impute missing Latino ethnicity (0·29%); for the purposes of this analysis, deaths among individuals with unknown Latino ethnicity were redistributed in proportion to the size of the Latino and non-Latino populations in the same county, race, age, sex, and time period. To ensure stable ratios for this redistribution, we pooled data over time as needed to achieve a minimum population of 50. This threshold of 50 is somewhat arbitrary, but was selected in an attempt to balance the need for stable ratios with the desire to have ratios that reflect the distribution of the population within as specific a time-range as possible.

2.2 Covariate imputation and smoothing

The small area estimation models used in the present study to estimate mortality rates leverage observed relationships between the level of mortality and sociodemographic and socioeconomic factors (covariates) to improve estimates where populations are small and the observed number of deaths is an imprecise indicator of the underlying mortality rate. Among the five covariates used in this analysis, educational attainment (bachelor's degree or higher), poverty rate, and proportion foreign-born were stratified by both county and race/ethnicity, while median household income and population density were stratified only by county and represent estimates for the total population in that county (section

3.2). The race/ethnicity-stratified covariates contained missing values and displayed instability and low precision for some strata with small populations. As covariate estimates are required for all space-time-race/ethnicity combinations in order to derive mortality predictions, small area imputation models were developed for race/ethnicity-specific covariates to derive smoothed covariate estimates in all years, counties, and racial/ethnic groups prior to including these covariates in the mortality models. Covariates that were not stratified by race/ethnicity in addition to county were incorporated in the mortality models in their original (non-imputed) forms due to their larger effective sample sizes and complete spatial and temporal coverage.

The race/ethnicity-stratified covariates were modelled as binomial variables without stratification by age or sex. Covariate data were derived primarily from the American Community Survey (ACS) and decennial population census. Racial classifications in the tabulated ACS and census data include separate groups for Asians and for Native Hawaiians and Other Pacific Islanders (NHOPI); covariate data for these groups were combined into an Asian or Pacific Islander (API) group for consistency with the mortality models. Covariate data were also combined for merged counties to derive a stable location set matching that used in the mortality models (section 3.1). ACS provides estimates of uncertainty as Margins of Error (MOE) at a confidence level of 90%, rather than providing variance estimates. Per guidance from the Census Bureau,[2] variance was calculated for each subgroup as:

$$\mathrm{Var}(X_i) = \left(\frac{\mathrm{MOE}(X_i)}{1.645}\right)^2$$

where X_i is the mean estimate for subgroup i. Again per Census guidance, variances for merged geographic and demographic entities were then calculated as the sum of the variances over component subgroups, assuming independence:

$$\mathrm{Var}(X_1 + X_2) = \mathrm{Var}(X_1) + \mathrm{Var}(X_2)$$

where X_1 and X_2 are mean estimates for two subgroups that are to be merged.

As the ACS and decennial census data were derived from population samples but are reported as values scaled to total population sizes, their effective sample sizes were estimated in order to appropriately scale sampling variance in the imputation models, using a three-pronged strategy. The long-form decennial census questionnaires in 1990 and 2000, from which the education, poverty, and foreign-born data were derived for those years, were collected from a 20% and 17% population sample, respectively.[3] Effective sample sizes were therefore assumed to be 20% or 17% of the total population for each county-year-race/ethnicity stratum in 1990 and 2000, respectively.

Effective sample sizes for ACS data, for which variances were calculated as above, were estimated using the relationship between effective sample size, $\hat{n}_{eff}$, estimates of the population proportion, $\hat{p}$, and its variance, $\mathrm{Var}(\hat{p})$:[4]

$$\hat{n}_{eff} = \frac{\hat{p}(1-\hat{p})}{\mathrm{Var}(\hat{p})}$$

As observations with observed proportions of 0·0 or 1·0 yield effective sample sizes of 0·0, the reported population fractions ($\hat{p}$) for these county-year-race/ethnicity strata were transformed via an empirical logit transformation[5] and then inverse-transformed using the standard inverse logit function before calculating the corresponding effective sample sizes:

$$\hat{p}_{emp} = \mathrm{logit}^{-1}\left(\log\left(\frac{\hat{p}+\frac{\varepsilon}{2}}{1-\hat{p}+\frac{\varepsilon}{2}}\right)\right)$$

where logit^{-1} is the standard inverse logit function and ε is defined as the smallest non-zero proportion in the data set. Effective sample sizes were calculated using these transformed proportions and the original reported $\mathrm{Var}(\hat{p})$. Counts of individuals with the modelled outcome (attainment of a bachelor's degree or higher, living below the poverty line, or foreign-born) were then calculated for each row by multiplying their original reported proportions and estimated effective sample sizes.

Bayesian imputation models were fit in R-INLA[6] v.20.09.25 in R v3.5.1[7] using binomial likelihood models, and explicitly borrow strength over space, time, and race/ethnicity in an approach analogous to the small area mortality models:

$$Y_{j,t,r} \sim \mathrm{Binomial}(p_{j,t,r}, \hat{n}_{eff,j,t,r})$$
$$\mathrm{logit}(p_{j,t,r}) = \beta_0 + \gamma_{1,j} + \gamma_{2,j,t,r} + \gamma_{3,j,t} + \gamma_{4,r}$$

where $Y_{j,t,r}$ is the estimated count of individuals in county *j*, year *t*, and race/ethnicity group *r* with the modelled outcome, among an effective sample size of $\hat{n}_{eff,j,t,r}$ with proportion $p_{i,t,r}$. Model terms consist of:

- β_0, a global intercept with a Normal(0, 10) prior;
- $\gamma_{1,j}$, a county-level random effect with a Besag-York-Mollie-type prior (BYM2) combining a conditional autoregressive distribution for spatial autocorrelation, based on county adjacency, with independent-and-identically-distributed (IID) Gaussian distribution;
- $\gamma_{2,j,t,r}$, a county-, race/ethnicity-, and year-level random effect with a first-order autoregressive (AR1) temporal prior, grouped by county and race/ethnicity;
- $\gamma_{3,j,t}$, a county- and year-level random effect with an AR1 temporal prior grouped by county;
- and $\gamma_{4,r}$, a race/ethnicity-level random effect with an IID Gaussian prior.

Default INLA hyper-priors were used. The BYM2 parameterization includes a parameter, φ, which indicates the contribution of the structured spatial effect to the marginal variance; $\mathrm{logit}(\varphi)$ had a penalized complexity (PC) prior[8] corresponding to $\Pr(\varphi < 0.5) = 0.5$, and the log precision of the BYM2 model had a PC prior corresponding to $\Pr(\sigma > 1.0) = 0.1$. The AR1 models had Gamma(shape = 1·0, inverse-scale = $5*10^{-5}$) priors on the precision and Normal(mean = 0·0, precision = 0·15) priors on the logit of the 1-year lagged correlation (ρ). The race/ethnicity IID term had a Gamma(shape = 1·0, inverse-scale = $5*10^{-5}$) prior on the precision. These default priors were used as we considered them suitably vague, in the absence of *a priori* information with which to establish more informative priors. The INLA model employed a Gaussian approximation strategy, an empirical Bayes integration strategy, and a step-length for hyper-parameter gradient calculations of $1*10^{--3}$. Due to numerical instability in the model for foreign-born proportion, a series of model fits were performed with iteratively decreasing values added to the diagonal of the joint precision matrix (100, 10, and 1, respectively) to derive starting parameter values for the final model run. Mean posterior predictions from the small area covariate models were used as covariate estimates in the small area mortality models.

2.3 Small area model specification

County-race/ethnicity model

The following model was estimated separately for males and females:

$$D_{j,t,a,r} \sim \text{Poisson}\left(m_{j,t,a,r} \cdot P_{j,t,a,r}\right)$$

$$\log\left(m_{j,t,a,r}\right) = \beta_0 + \boldsymbol{\beta_1} \cdot \boldsymbol{X_{1,j,t}} + \left(\boldsymbol{\beta_2} + \boldsymbol{\gamma_{1,r}}\right) \cdot \boldsymbol{X_{2,j,t,r}}$$

$$+ \gamma_{2,j} + \gamma_{3,t,a,r} + \sum_{t'=1}^{k_t} \sum_{a'=1}^{k_a} \left(\gamma_{4,j,t',a',r} \cdot S_{t'}(t) \cdot S_{a'}(a)\right)$$

Priors:

$\boldsymbol{\gamma_1} \sim \text{IID}(\boldsymbol{\sigma_1})$

$\boldsymbol{\gamma_2} \sim \text{LCAR}(\rho_2, \sigma_2)$

$\boldsymbol{\gamma_3} \sim \text{LCAR: LCAR: IID}(\rho_{3,t}, \rho_{3,a}, \sigma_3)$

$\boldsymbol{\gamma_4} \sim \text{LCAR: LCAR: LCAR: MVN}(\rho_{4,a'}, \rho_{4,t'}, \rho_{4,j}, \boldsymbol{\sigma_4}, \theta)$

Hyper-priors:

$\sigma^{-2} \sim PC(\sigma_0 = 5, \alpha = 0.05) \rightarrow \Pr(\sigma > 5) = 0.05$

$\text{logit}(\rho) \sim \text{Normal}(0, 1.5)$

where

- j, t, a, and r are indices for the county, calendar year (2000–2019, renumbered sequentially from 0 to 19), age group (0, 1–4, 5–9, …, 80–84, and 85+ years old, recoded sequentially from 0 to 18), and race/ethnicity (White, Black, AIAN, API, and Latino, recoded in that order from 0 to 4), respectively;
- $D_{j,t,a,r}$ and $P_{j,t,a,r}$ are the observed number of deaths and the population count, respectively, in county j, year t, age group a, and race/ethnicity r;
- $m_{j,t,a,r}$ is the underlying mortality rate in county j, year t, age group a, and race/ethnicity r;
- $\boldsymbol{X_{1,j,t}}$ is a vector of covariates for county j and year t, and $\boldsymbol{\beta_1}$ is the associated vector of regression coefficients;
- $\boldsymbol{X_{2,j,t,r}}$ is a vector of covariates for county j, year t, and race/ethnicity r, and $\boldsymbol{\beta_2} + \boldsymbol{\gamma_{1,r}}$ is the associated vector of regression coefficients, made up of a fixed component ($\boldsymbol{\beta_2}$) shared by all racial/ethnic groups, and a random component ($\boldsymbol{\gamma_{1,r}}$) that varies by race/ethnicity;

- $\gamma_{2,j}$ is a county-level random intercept;
- $\gamma_{3,a,t,r}$ is an age group-, year-, and race/ethnicity-level random intercept;
- $\gamma_{4,j,t',a',r}$ is a county-, race/ethnicity-, year spline basis-, and age spline basis-level random intercept;
- k_t is the number of time knots (four knots, evenly spaced from 2000–2019) and t' is the corresponding index;
- k_a is the number of age knots (five knots, at age groups 0, 25–29, 45–49, 65–69, and 85+ years old) and a' is the corresponding index;
- $S_{t'}(t)$ is the value of spline basis t' for a linear spline on year, evaluated at year t;
- and $S_{a'}(a)$ is the value of spline basis a' for a linear spline on age, evaluated at age a.

Prior distributions were assigned for each random component:

- Each element of $\boldsymbol{\gamma_1}$—corresponding to each covariate in $\boldsymbol{X_1}$—was assumed to follow an independent and identically distributed (IID) mean-0 Normal distribution. $\boldsymbol{\gamma_1}$ is associated with three hyper-parameters ($\boldsymbol{\sigma_1^2}$), corresponding to the variance of this random effect for each covariate.
- $\boldsymbol{\gamma_2}$ was assumed to follow a conditional autoregressive distribution of the form described by Leroux, Lei, and Breslow (LCAR),[9] which corresponds to the following full conditional distribution for each individual element of $\boldsymbol{\gamma_2}$:

$$\gamma_j | \gamma_{k\sim j}, \sigma^2, \rho \sim \text{Normal}\left(\frac{\rho \cdot \sum_{k\sim j} \gamma_k}{n_j \cdot \rho + 1 - \rho}, \frac{\sigma^2}{n_j \cdot \rho + 1 - \rho}\right)$$

  where $k \sim j$ indicates the set of counties that are adjacent to county j and n_j is the number of counties in $k \sim j$. In this distribution, the σ^2 parameter controls the amount of spatial variation, while the ρ parameter, which varies between 0 and 1, determines the degree of spatial smoothness.
- $\boldsymbol{\gamma_3}$ was assumed to follow a mean-0, multivariate Normal distribution with a separable covariance structure defined via the Kronecker product of the covariance matrix of three distributions:[10,11] a conditional autoregressive distribution as in γ_2 but defined for age groups rather than counties; a second conditional autoregressive distribution as in γ_2 but defined for time period rather than counties; and a multivariate Normal distribution with a diagonal covariance matrix. This random

effect is associated with three hyper-parameters: $\rho_{3,a}$ and $\rho_{3,t}$, which control the correlation across age groups and time, respectively; and σ_3^2 which controls variation.

- $\boldsymbol{\gamma_4}$ was also assumed to follow a mean-0, multivariate Normal distribution, in this case with a separable covariance structure defined via the Kronecker product of the covariance matrix of four distributions: three conditional autoregressive distributions as described above, for county, age spline basis, and year spline basis; and a multivariate Normal distribution for race/ethnicity. For this random effect, there are three sets of hyper-parameters: $\rho_{4,a'}$, $\rho_{4,t'}$, and $\rho_{4,j}$, which control the smoothness over the age spline, year spline, and county, respectively; $\boldsymbol{\sigma_4^2}$ (length = 5) which controls the variation for each race/ethnicity group; and $\boldsymbol{\theta}$ (length = 10), the elements of a lower-triangular matrix $\boldsymbol{L}$ which defines the correlation matrix over race/ethnicity: $\boldsymbol{\Sigma} = \mathbf{D}^{-\frac{1}{2}}\mathbf{LL'}\mathbf{D}^{-\frac{1}{2}}$, where $\boldsymbol{D} = \operatorname{diag}(\boldsymbol{LL'})$.

Finally, hyper-priors were defined for the standard deviation (σ) and, where applicable, autocorrelation (ρ) hyper-parameters:

- Penalized complexity (PC) priors[8] were specified for the inverse variance ($1/\sigma^2$) of each random effect. PC priors shrink toward a base model, which in this case is where the marginal variance is 0. They are specified by setting the tail probability on each hyper-parameter. We followed the recommendation by Fuglstad et al.,[8] selecting priors that satisfy $Pr(\sigma > \sigma_0) = 0.05$ where σ_0 is between 2.5 and 40 times the expected true marginal standard deviation. Specifically, we set $\sigma_0 = 5;\ Pr(\sigma > \sigma_0) = 0.05$.
- Normal(0, 1.5) priors were specified for the logit-transform of the correlation parameters (ρ).

Posterior means and standard errors for these hyper-parameters are provided in section 3.5.

Descriptively, this model specifies the log of the underlying mortality rate ($m_{j,t,a,r}$) as a function of covariates and additional variation by county, year, age, and race/ethnicity. The covariates we included in this model—educational attainment, poverty rate, proportion foreign-born, median household income, and population density—were selected based on data availability and previously observed relationships with mortality. The fixed effects ($\boldsymbol{\beta_1}, \boldsymbol{\beta_2}$) on both the county- and county-race/ethnicity-specific covariates ($\boldsymbol{X_{1,j,t}}, \boldsymbol{X_{2,j,t,r}}$) capture the relationships between each covariate and mortality. For the race/ethnicity-specific covariates, we additionally include random effects, $\boldsymbol{\gamma_1}$, to allow for the relationship between these variables and mortality to vary by race/ethnicity. The covariates do not explain all variation in mortality across time, age, geography, and race/ethnicity, so further random effects are included in the model to capture additional variation. The random effect $\boldsymbol{\gamma_2}$ allows for spatial (ie, between-county) variation in the level of mortality, shared across age, year, and race/ethnicity. The random effect $\boldsymbol{\gamma_3}$ allows for variation in mortality by age, time, and race/ethnicity group, shared across all counties. Finally, the random effect $\boldsymbol{\gamma_4}$ was included to allow for county-specific deviations in the mortality patterns by age, time, and race/ethnicity, compared to the general pattern captured by $\boldsymbol{\gamma_3}$. This random effect incorporates a linear spline in the age and time dimensions to reduce computational complexity: the equivalent model for all age groups and years was found to be computationally infeasible. Although the splines in this random effect are linear, we are not assuming that the time or age trends for $\log(m_{j,t,a,r})$ are linear, as both the contributions from the covariates as well as $\boldsymbol{\gamma_3}$ allow for non-linear variation. The purpose of these splines is rather to allow for additional variation along these dimensions for each county-race/ethnicity combination. The number of age and year knots were chosen to maximize flexibility while maintaining a reasonable runtime—this is the largest number of knots that we were able to include in a model that could be fitted in under two weeks. The placement of the age knots was determined by including the oldest and youngest ages and then spacing the inner age knots to align with common inflection points in the age pattern (excluding age 1 since we already included age 0). In testing several alternatives, we found that including the first and last ages proved to be most important for properly fitting the data, whereas the placement of the inner age knots typically did not have a large effect on the estimates. The year knots were simply distributed evenly over the study period. In testing, reasonable alternative placements of the year knots typically did not have a large effect on the resulting estimates.

In addition to the more formal model validation we describe below, we assessed model fit by inspecting plots comparing the estimated time and age trends in mortality to the observed data at the national, state, and (in selected counties) county level. Additionally, we used graphical posterior predictive checks[12] to assess if the observed data are over-dispersed and/or zero-inflated relative to our model; we found no evidence that this is the case. Finally, we examined plots of the binned residuals compared to each covariate in order to assess the assumption that the relationship between log mortality and each covariate is linear; we found no evidence of bias in our estimates as a result of non-linearity in these relationships.

We used the Template Model Builder (TMB) package[13] to fit these models using an empirical Bayes approach. TMB calculates analytic approximations to the posterior distribution based on Laplace approximations. We use TMB for fitting these models rather than INLA—another common alternative to classic Markov chain Monte Carlo (MCMC) methods and the tool that we used for the covariate imputation and smoothing models (section 2.2)—as TMB is substantially more flexible with respect to the model specification.[14] Of particular importance for this analysis: random effects in INLA are restricted to two-way interactions, whereas TMB allows us to incorporate higher-order interactions ($\boldsymbol{\gamma_3}$ and $\boldsymbol{\gamma_4}$) in our modelling approach.

County-level model

A similar model was estimated for all racial/ethnic groups combined. This was included in order to perform model calibration of the race/ethnicity-specific estimates in order to prevent the race/ethnicity misclassification adjustment from altering the overall (all racial/ethnic groups combined) mortality rate in any given county. This model is as follows, with all terms defined as described above:

$$D_{j,t,a} \sim \text{Poisson}\left(m_{j,t,a} \cdot P_{j,t,a}\right)$$

$$\begin{aligned}\log\left(m_{j,t,a}\right) &= \beta_0 + \boldsymbol{\beta_1} \cdot \boldsymbol{X_{1,j,t}} \\ &\quad + \gamma_{2,j} + \gamma_{3,t,a} + \sum_{t'=1}^{k_t} \sum_{a'=1}^{k_a} \left(\gamma_{4,j,t',a'} \cdot S_{t'}(t) \cdot S_{a'}(a)\right)\end{aligned}$$

Priors:

$$\boldsymbol{\gamma_2} \sim \text{LCAR}(\rho_2, \sigma_2)$$
$$\boldsymbol{\gamma_3} \sim \text{LCAR: LCAR}(\rho_{3,t}, \rho_{3,a}, \sigma_3)$$
$$\boldsymbol{\gamma_4} \sim \text{LCAR: LCAR: LCAR}(\rho_{4,a'}, \rho_{4,t'}, \rho_{4,j}, \sigma_4)$$

Hyper-priors:

$$\sigma^{-2} \sim PC(\sigma_0 = 5, \alpha = 0.05) \rightarrow \Pr(\sigma > 5) = 0.05$$
$$\text{logit}(\rho) \sim \text{Normal}(0, 1.5)$$

Hyper-prior sensitivity analysis

We considered a range of alternative specifications for the priors on standard deviation (σ) terms. This included three families of distributions—penalized complexity, Gamma, and half-Normal—and a range of parametrizations for each. For the penalized complexity priors, we tested all permutations of the following parameters: $\sigma_0 = 1, 5;\ \Pr(\sigma > \sigma_0) = 0.05, 0.02, 0.1, 0.4, 0.8$. The Gamma priors were specified for the inverse variance ($1/\sigma^2$) and were parameterized by shape and scale. Permutations of the following parameterizations were considered: $\text{shape} = 0.25, 0.5, 1, 2;\ \text{scale} = 1, 100, 1000$. The half-Normal priors were specified for the standard deviation (σ) and were parameterized by the mean (μ_d) and standard deviation (σ_d) of the corresponding Normal distribution. Permutations of the following parameterizations were tested: μ_d = 0; σ_d = 1, 2, 4. The figure in section 4.2 shows the difference in the estimates derived from models using these alternate prior specifications compared to our main model. These differences are generally very small across all parameterizations and prior specifications.

2.4 Small area model validation

Approach

The framework used to evaluate the performance of the models in this analysis is an extension of a previously proposed[15] and extensively used[16,17] framework designed specifically for county-level models in the USA. It was modified to allow for evaluation of performance with respect to generating estimates of life expectancy by county and race/ethnicity.

First, a “validation set” of county-race/ethnicity pairs was identified. The validation set is a collection of county-race/ethnicity pairs for which directly calculated mortality rates are a good representation of the underlying mortality rate, ie, where the population and corresponding number of deaths is sufficiently large to generate stable direct estimates. In order to increase the number of county-racial/ethnic groups that were retained in the validation set, deaths and population data were pooled across time using a moving window of three years for the purposes of defining the validation set. A series of criteria were used to remove county-racial/ethnic groups from the set of all county-racial/ethnic groups, with the remainder forming the validation set. First, any county-racial/ethnic groups with zero pooled deaths in any age, sex, or year (window) were removed. Second, among the remaining county-racial/ethnic groups, those where the median (across all years, sexes, and age groups) coefficient of variation was greater than 20% for the age-specific mortality rates or greater than 5% for the age-standardized and crude mortality rates were removed. In order to calculate the coefficient of variation, 1000 draws of death counts were simulated for each age group, sex, and year, assuming a Poisson distribution with rate and size equal to the observed mortality rate and population size, respectively; age-specific, crude (all-ages), and age-standardized mortality rates were then calculated for each draw; and finally the coefficient of variation was calculated as the standard deviation of the draws divided by their mean. The validation set has 138 county-race/ethnicity pairs, composed of 96 counties and 4 racial/ethnic groups (section 3.6). The AIAN group was not represented in the validation set. Once the validation set was identified, life tables were generated from the pooled mortality rates using the methods described in section 2.6. These pooled mortality rates and the corresponding estimates of life expectancy at birth were used as a "gold standard" against which to compare model predictions.

Next, "validation datasets" were constructed. A total of 40 validation sets were used: 5 iterations each of simulated datasets with reference population sizes of 10, 100, 1000, 3000, 5000, 10 000, 25 000, and 100 000. Additionally, a sixth iteration was prepared for each of these population sizes because, rarely, models for some iterations failed to converge; this sixth iteration was only used if a model failed to converge. The sizes 1000–100 000 were chosen because they correspond roughly to the 1st, 5th, 10th, 25th, 50th, and 80th percentiles for the total population (all racial/ethnic groups combined) across all counties and years. Sizes 10 and 100 were added because similar population sizes are common for specific racial/ethnic groups at the county level. To make these validation data sets, a population of the specified size was sampled for each county-race/ethnicity in the validation set, with the probability of sampling an individual of a given age and sex proportional to the observed population structure for that county-race/ethnicity. Then, for each age and sex within each county-race/ethnicity, deaths were simulated from a Poisson distribution with mean equal to the observed mortality rate times the sampled population for that age group and sex. The data for all county-race/ethnicity pairs that were not in the validation set were included without modification.

Finally, small area models were fit and predictions generated as described above to each of the 40 validation datasets. To evaluate the performance, the predictions based on each validation data set were compiled and compared against the gold standard mortality rates and life expectancies. First, errors were calculated as $e^{gs}_{j,t,a,r} - e^{pred}_{j,t,a,r}$ where $e^{gs}_{j,t,a,r}$ is the gold standard life expectancy at birth, and $e^{pred}_{j,t,a,r}$ is the predicted life expectancy at birth. The mean error and the mean absolute error—measures of bias and precision, respectively—were calculated across all county-racial/ethnic groups in the validation set and all iterations at each population level. Coverage (ie, the percentage of county-race/ethnicity-years where the gold standard estimate was between the lower and upper uncertainty intervals for the modelled estimate) was also recorded.

This validation procedure was used to assess and compare model performance of three models:

1. The racial/ethnic-group-specific model described in the previous section:

$$D_{j,t,a,r} \sim \text{Poisson}\left(m_{j,t,a,r} \cdot P_{j,t,a,r}\right)$$

$$\log\left(m_{j,t,a,r}\right) = \beta_0 + \boldsymbol{\beta_1} \cdot \boldsymbol{X_{1,j,t}} + \left(\boldsymbol{\beta_2} + \boldsymbol{\gamma_{1,r}}\right) \cdot \boldsymbol{X_{2,j,t,r}}$$

$$+ \gamma_{2,j} + \gamma_{3,t,a,r} + \sum_{t'=1}^{k_t} \sum_{a'=1}^{k_a} \left(\gamma_{4,j,t',a',r} \cdot S_{t'}(t) \cdot S_{a'}(a)\right)$$

2. The same model as in 1, but without covariates:

$$D_{j,t,a,r} \sim \text{Poisson}\left(m_{j,t,a,r} \cdot P_{j,t,a,r}\right)$$

$$\log\left(m_{j,t,a,r}\right) = \beta_0 + \gamma_{2,j} + \gamma_{3,t,a,r} + \sum_{t'=1}^{k_t} \sum_{a'=1}^{k_a} \left(\gamma_{4,j,t',a',r} \cdot S_{t'}(t) \cdot S_{a'}(a)\right)$$

3. The model for all racial/ethnic groups combined described in the previous section:

$$D_{j,t,a} \sim \text{Poisson}\left(m_{j,t,a} \cdot P_{j,t,a}\right)$$

$$\log\left(m_{j,t,a}\right) = \beta_0 + \boldsymbol{\beta_1} \cdot \boldsymbol{X_{1,j,t}} + \gamma_{2,j} + \gamma_{3,t,a} + \sum_{t'=1}^{k_t} \sum_{a'=1}^{k_a} \left(\gamma_{4,j,t',a'} \cdot S_{t'}(t) \cdot S_{a'}(a)\right)$$

The variant of the model without covariates (model 2) was included to assess whether including covariates improved performance of the model. The variant of the model with all racial/ethnic groups combined (model 3) was included to assess the performance of the model at the county level for all racial/ethnic groups combined. A separate validation set, gold standard, and validation data sets were prepared in order to assess performance of this final model variant. To make the all-racial/ethnic-group validation set, the same conditions that defined the racial/ethnic-group-specific validation set were applied to the same data aggregated to the all-racial/ethnic-group level. The gold standard and validation data sets were prepared as described above at the all-racial/ethnic-group level.

Results

The mean error, mean absolute error, and coverage for each model are provided in sections 3.7 (table) and 4.3 (figure). The mean error is a measure of bias, ie, it indicates if the estimates from the models were systematically higher or lower than the gold standard values. As expected, mean error tended to improve (was closer to 0) as the simulated population size increased for all models and all racial/ethnic groups. In model 1, there was little evidence of bias for most racial/ethnic groups. Mean errors were minimal at larger population sizes and relatively small at smaller population sizes for most racial/ethnic groups. There was some evidence of bias for the API and Black groups for counties with population <1000; the largest mean errors were for the API group, where the model underestimated by 0·86 years at size 10, and for the Black group, where the model overestimated by 0·39 years at size 10. However, the API group only had four counties in the validation set, so it is difficult to draw general conclusions about bias for this racial/ethnic group. Model 1 performed better than model 2 in terms of mean error: the mean errors for model 2 were larger than those for model 1 for most racial/ethnic groups at most population sizes, indicating that there was more bias in model 2 than in model 1. Mean errors for model 3 were larger in magnitude than those calculated across every racial/ethnic group at all sizes for model 1 and model 2. Nonetheless, the mean errors for models 2 and 3 were still relatively small, especially at larger population sizes.

The mean absolute error is a measure of overall error, ie, how much the model estimates differ from true estimates irrespective of direction. As expected, mean absolute errors tended to improve as size increased for all models and all racial/ethnic groups. In model 1, mean absolute error was relatively small, even at the smallest population sizes, indicating model 1 performed well for all racial/ethnic groups. Compared to model 1, model 2 performed worse overall in most racial/ethnic groups. While model 2 performed worse than model 1 in general, both models performed well at large population sizes; model 2 had similar mean absolute errors at largest population sizes in every racial/ethnic group. The mean absolute errors for model 3 were smaller than the mean absolute errors calculated across every racial/ethnic group at every size in model 2, and at sizes 5000 and larger in model 1, indicating that model 3 performed better at estimating all racial/ethnic groups together than models 1 and 2 did at estimating individual racial/ethnic groups overall.

Coverage is a measure of the calibration of the uncertainty intervals. Ideally, coverage should be close to 95% because that means that the 95% uncertainty intervals were an appropriate reflection of an estimate's uncertainty. Coverage tended to be closer to 95% in model 1 than in model 2: model 1 had more coverage values within +/- 1 percentage point of 95% compared to model 2. Coverage in model 2 varied more across racial/ethnic groups than in model 1; model 1 had more consistent values in a narrower range than model 2. Coverage tended to be highest at the smallest population sizes, and then decreased as population size increased for most models and racial/ethnic group. This is likely due to the wider uncertainty intervals at smaller population sizes, making it more likely for the gold standard to be inside the uncertainty interval. In model 2, coverage for the Black racial/ethnic group increased as population size increased until size 100 000.

2.5 Derivation of misclassification ratios by county, age, sex, and race/ethnicity

Extraction

Overall misclassification ratios, as well as misclassification ratios by age and sex, census region, and co-ethnic density were extracted from Arias et al.[18] for five racial/ethnic groups: White, Black, AIAN, API, and Latino. Specifically, data were extracted from the following locations:

- Overall misclassification ratios: Table 2, "Total" column for both sexes.
- Age-sex misclassification ratios: Table 2, age-specific columns for each sex separately.
- Census region misclassification ratios: Table 3, results by "Region"
- Co-ethnic density misclassification ratios: Table 3, results by "Coethnic concentration"; AIAN ratios extracted from the results shown for all AIAN because these were not available specifically for non-Latino AIAN.

The co-ethnic density misclassification ratios were assigned to a county using the same method outlined in Arias et al.:[18] for the AIAN population, counties in Contract Health Service Delivery Areas (CHSDAs) were considered to have high co-ethnic density; for the Latino population, counties with high co-ethnic density were those within the first 50th percentile of ranked deaths by county between 1999 and 2011. This method assumes that the relative increase or decrease in misclassification for counties with low or high co-ethnic density compared to the total misclassification ratio for AIAN (including both Latino and non-Latino AIAN) is representative of that for non-Latino AIAN. We are not aware of any studies on this topic, but we make this assumption in order to include adjustment by co-ethnic density given the evidence that this form of misclassification is especially important with respect to the AIAN population.[19–21]

Combination

1000 draws of each misclassification ratio were generated assuming these ratios are log-Normally distributed. We selected a log-Normal distribution as it is restricted to positive numbers, which is appropriate for this ratio; however, we acknowledge that this selection is somewhat arbitrary and is at best an approximation of the true ratio distribution. The draws of misclassification were then combined (without ordering) using the following approach:

$$ratio_{final} = ratio_{overall} \cdot \frac{ratio_{age,sex}}{ratio_{overall}} \cdot \frac{ratio_{region}}{ratio_{overall}} \cdot \frac{ratio_{co-ethnic\ density}}{ratio_{overall}}$$

For the White, Black, and API populations, $ratio_{co-ethnic\ density}$ is equal to $ratio_{overall}$, so the last term is equal to 1 (ie, no adjustment by co-ethnic density). For the AIAN population, the $ratio_{overall}$ in the denominator of the final term was the overall misclassification ratio for both Latino and non-Latino AIAN populations combined, to match the numerator, which was available only for Latino and non-Latino AIAN populations combined; in all other terms, the values for the non-Latino AIAN population alone were used.

This approach assumes that the degree of misclassification is independent across each dimension. Thus, the degree of misclassification reported for a particular facet (eg, by age/sex) is the same across all other facets (eg, region and co-ethnic density). For example, the age/sex pattern of misclassification for a given race/ethnicity group will be the same regardless of region.

Mortality rate adjustment

The 1000 draws of misclassification ratios were merged onto the 1000 posterior draws of the mortality rate by age, sex, county (which reflected both region and co-ethnic density), and race/ethnicity. The merge by age was conducted by aligning the age groups in the model (0, 1–4, 5–9, …, 80–84, and 85+ years old) with the age bin to which each of the modelled ages belongs (ie, age groups 0, 1–4, 5–9, 10–14, 15–19, and 20–24 were merged onto the age bin 0–24). These draws were not ordered, thus assuming independence between the mortality rate and the misclassification ratio. Mortality rate draws were adjusted by multiplying by the corresponding misclassification ratio draw.

Impact of misclassification adjustment and calibration

Both misclassification adjustment and model calibration play important roles in creating more accurate life expectancy estimates. First, misclassification adjustment accounts for under- or over-reporting of certain races/ethnicities on death certificates. However, because this adjustment is done independently for each racial/ethnic group, it can change the overall level of life expectancy estimated for a given county. Our calibration procedure thus serves two purposes: to constrain the adjusted estimates such that the overall level of mortality implied by the race/ethnicity-specific estimates is the same as when estimating at the county level; and to ensure consistency in the estimates at the county, state, and national level within this analysis and between this analysis and the Global Burden of Disease Study. Because these two processes are linked, we show here the cumulative impact of both adjustment for misclassification and calibration.

The figure in section 4.4 demonstrates the impact of these calculations on life expectancy at the national level. The estimate of total life expectancy is impacted only by calibration, which results in a slight shift downward. The estimates for each racial/ethnic group are impacted by both adjustment for misclassification and the calibration procedure. The combined effect is small for the White and Black populations, as expected given the small size of the misclassification adjustments for these two groups. There are moderate decreases in life expectancy for the API and Latino populations, as well as increases in the uncertainty of those estimates, reflecting the somewhat larger misclassification adjustments as well as increased uncertainty from these adjustments. These processes have the largest effect on life expectancy among the AIAN population: there are fairly large decreases in life expectancy once adjusted and calibrated in addition to a large increase in uncertainty.

The maps in section 4.5 show the corresponding impact at the county level. Again, for the total life expectancy values, these changes are caused by calibration alone, and we can observe many of these same calibration effects in the maps for life expectancy among the White and Black populations especially. The more substantial changes in life expectancy noted at the national level for the Latino, API, and AIAN population are again noted here, with changes at the county level generally in the same direction (ie, decreases in life expectancy). Perhaps counterintuitively, there are instances where for a particular county and race/ethnicity, the change in life expectancy after misclassification adjustment and calibration is not in the same direction as at the national level. This is caused by the interaction between adjustment and calibration. For example, in Bethel Census Area, Alaska, misclassification adjustment alone caused a decrease in life expectancy, but calibration caused the life expectancy to increase because the GBD estimates for Alaska are higher than our model's unadjusted estimates for Alaska. Another example is Bennett County, South Dakota, where life expectancy for the AIAN population is higher once adjusted and calibrated. In this case, this is not due to the GBD results being higher for South Dakota. Instead, this is due to misclassification adjustment. This county—along with many of the other unmasked counties in South Dakota—is a Contract Health Service Delivery Area (CHSDA), and therefore has a lower misclassification adjustment. This adjustment is 1.17, while the denominator is 1.4 (the total AIAN misclassification ratio for both Latino and non-Latino AIAN). Thus, the ratios of ratios is less than 1. This is combined with the region misclassification ratio, which is 1.12 and has a denominator of 1.33 (the total non-Latino AIAN misclassification ratio). Thus, the contribution from the region misclassification ratio is also less than 1. This means that the combined misclassification ratios are less than 1 for most ages and sexes in this county, thus leading to a higher life expectancy. In contrast, Brown County, South Dakota exhibits decreases in life expectancy due to raking and calibration. This is because Brown County is not a CHSDA, and thus its associated adjustment is larger than 1.

2.6 Life table calculations

Standard demographic methods[22] were used to construct abridged period life tables for each county, year, sex, and race/ethnicity from the age-specific mortality rates estimated by the small area model. A key component of this process involves estimating ${}_na_x$, the average years lived within the age interval x to $x+n$ by individuals who died within that age interval. For age groups 0 and 1–4, we use the formulas described by Preston et al.[22] (Table 3.3, p 48) adapted from the Coale and Demeny “West” model life tables.[23] For age groups 5–9, ..., 80–84, we start with an initial value for ${}_na_x$ of 2.5, ie, assuming deaths occurred, on average, midway through the interval. Then, for age groups 10–14, ..., 75–79, we improve upon these initial values using the iterative graduation procedure proposed by Keyfitz[24] as described by Preston et al. (pp 44–45);[22] this procedure requires inputs from adjacent age intervals of the same length, so we are unable to use this same approach to adjust the ${}_na_x$ values for age groups 5–9 or 80–84 which instead remain set at 2.5. Another key component involves estimating e_{85} or life expectancy in the terminal age group. The “classic” approach is to calculate e_{85} as $1/m_{85}$, a formula that assumes the population is stationary—ie, is neither growing nor shrinking, and has a constant age structure. Previous research has shown that this approach can result in substantially biased estimates of life expectancy at age 85 and, by extension, biased estimates of life expectancy at birth; in most settings, this bias is positive, reflecting growing populations at older ages which are consequently younger on average than implied by the stationary model.[25] We instead use the method proposed by Horiuchi and Coale, which incorporates the population growth rate for the terminal age group to allow for non-stationarity: $e_{85} = (1/m_{85}) \cdot \exp(-0.095 \cdot m_{85}^{-1.4} \cdot r)$.[25,26] Population growth rates calculated at the county level are highly unstable, so we instead use national-level, race/ethnicity-specific growth rates for each county, averaged over the preceding ten-year period. For the purposes of calculating life expectancy for all racial/ethnic groups combined at the county level, we calculate a population-weighted average of the national-level growth rates, using the observed county-level populations by racial/ethnic group.

These life table calculations are carried out for each of the 1000 posterior draws of the age-specific mortality rates for each location, year, sex, and race/ethnicity so that lower and upper uncertainty bounds can be estimated for life expectancy at birth using the 2.5th and 97.5th percentiles of these draws. For internal consistency, we calculate point estimates of the mortality rate and ${}_{n}a_{x}$ as the mean of these draws, and then recalculate the remainder of the life table using the same methods described above to generate final point estimates of life expectancy.

2.7 References

1 Kochanek KD, Murphy SL, Xu J, Arias E. Deaths: final data for 2017. *Natl Vital Stat Rep* 2019; **68**. https://www.cdc.gov/nchs/data/nvsr/nvsr68/nvsr68_09-508.pdf (accessed Dec 23, 2019).

2 US Census Bureau. Instructions for applying statistical testing to American Community Survey data. 2019. https://www2.census.gov/programs-surveys/acs/tech_docs/statistical_testing/2019_Instructions_for_Stat_Testing_ACS.pdf (accessed Dec 17, 2020).

3 US Census Bureau. Overview - History - U.S. Census Bureau. https://www.census.gov/history/www/through_the_decades/overview/ (accessed Dec 17, 2020).

4 Franco C, Little RJA, Louis TA, Slud EV. Comparative study of confidence intervals for proportions in complex sample surveys. *J Surv Stat Methodol* 2019; **7**: 334–64.

5 Warton DI, Hui FKC. The arcsine is asinine: the analysis of proportions in ecology. *Ecology* 2011; **92**: 3–10.

6 Rue H, Martino S, Chopin N. Approximate Bayesian inference for latent Gaussian models by using integrated nested Laplace approximations. *J R Stat Soc Ser B Stat Methodol* 2009; **71**: 319–92.

7 R Core Team. R: A language and environment for statistical computing. Vienna, Austria: R Foundation for Statistical Computing, 2019 https://www.R-project.org/.

8 Fuglstad G-A, Simpson D, Lindgren F, Rue H. Constructing priors that penalize the complexity of Gaussian random fields. *J Am Stat Assoc* 2019; **114**: 445–52.

9 Leroux BG, Lei X, Breslow N. Estimation of disease rates in small areas: a new mixed model for spatial dependence. In: Statistical Models in Epidemiology, the Environment, and Clinical Trials. New York: Springer-Verlag, 2000: 179–91.

10 Clayton D. Generalized linear mixed models. In: Gilks W, Richardson S, Spiegelhalter D, eds. Markov Chain Monte Carlo in Practice, 1st edn. Great Britain: Chapman & Hall, 1996: 275–302.

11 Knorr-Held L. Bayesian modelling of inseparable space-time variation in disease risk. *Stat Med* 2000; **19**: 2555–67.

12 Gelman A, Carlin JB, Stern HS, Dunson DB, Vehtari A, Rubin DB. Bayesian data analysis, Third edition. Boca Raton: CRC Press, 2014.

13 Kristensen K, Nielsen A, Berg CW, Skaug H, Bell B. TMB: automatic differentiation and Laplace approximation. *J Stat Softw* 2016; **70**: 1–21.

14 Osgood-Zimmerman A, Wakefield J. A statistical introduction to Template Model Builder: a flexible tool for spatial modeling. *ArXiv210309929 Stat* 2021; published online March 17. http://arxiv.org/abs/2103.09929 (accessed March 30, 2022).

15 Srebotnjak T, Mokdad AH, Murray CJ. A novel framework for validating and applying standardized small area measurement strategies. *Popul Health Metr* 2010; **8**: 26.

16 Dwyer-Lindgren L, Mokdad AH, Srebotnjak T, Flaxman AD, Hansen GM, Murray CJ. Cigarette smoking prevalence in US counties: 1996-2012. *Popul Health Metr* 2014; **12**: 5.

17 Dwyer-Lindgren L, Bertozzi-Villa A, Stubbs RW, *et al.* US county-level trends in mortality rates for major causes of death, 1980-2014. *JAMA* 2016; **316**: 2385–401.

18 Arias E, Heron M, Hakes J. The validity of race and Hispanic-origin reporting on death certificates in the United States: an update. *Vital Health Stat* 2016; **2**. https://www.cdc.gov/nchs/data/series/sr_02/sr02_172.pdf.

19 Dankovchik J, Hoopes MJ, Warren-Mears V, Knaster E. Disparities in life expectancy of Pacific Northwest American Indians and Alaska Natives: analysis of linkage-corrected life tables. *Public Health Rep* 2015; **130**: 71–80.

20 Joshi S, Weiser T, Warren-Mears V. Drug, opioid-Involved, and heroin-involved overdose deaths among American Indians and Alaska Natives — Washington, 1999–2015. *Morb Mortal Wkly Rep* 2018; **67**: 1384–7.

21 Arias E, Schauman WS, Eschbach K, Sorlie PD, Backlund E. The validity of race and Hispanic origin reporting on death certificates in the United States. *Vital Health Stat 2* 2008; **2**.

22 Preston SH, Heuveline P, Guillot M. Demography: measuring and modeling population processes. Malden, MA: Blackwell Publishers, 2001.

23 Coale AJ, Demeny PG. Regional model life tables and stable populations, 2nd ed. New York: Academic Press, 1983.

24 Keyfitz N. A life table that agrees with the data. *J Am Stat Assoc* 1966; **61**: 305–12.

25 Ediev DM. Expectation of life at old age: revisiting Horiuchi-Coale and reconciling with Mitra. *Genus* 2018; **74**: 3.

26 Horiuchi S, Coale AJ. A simple equation for estimating the expectation of life at old ages. *Popul Stud* 1982; **36**: 317–26.

3 Supplemental Methods Tables

3.1 Counties combined to create historically stable units of analysis

State	Group	Counties (FIPS)
Alaska	1	Chugach Census Area (2063), Copper River Census Area (2066), Valdez-Cordova Census Area (2261)*
	2	Kusilvak Census Area (2158), Wade Hampton Census Area (2270)*
	3	Kobuk Census Area (2140)*, Northwest Arctic Borough (2188)
	4	Aleutian Islands Census Area (2010)*, Aleutians East Borough (2013), Aleutians West Census Area (2016)
	5	Dillingham Census Area (2070), Lake and Peninsula Borough (2164)
	6	Denali Borough (2068), Yukon-Koyukuk Census Area (2290)
	7	Hoonah-Angoon Census Area (2105), Skagway Municipality (2230), Skagway-Yakutat-Angoon Census Area (2231)*, Skagway-Hoonah-Angoon Census Area (2232)*, Yakutat City and Borough (2282)
	8	Ketchikan Gateway Borough (2130), Petersburg Borough (2195), Prince of Wales-Hyder Census Area (2198), Prince of Wales-Outer Ketchikan Census Area (2201)*, Wrangell City and Borough (2275), Wrangell-Petersburg Census Area (2280)*
Arizona	1	La Paz County (4012), Yuma County (4027)
Colorado	1	Adams County (8001), Arapahoe County (8005), Boulder County (8013), Broomfield County (8014), Denver County (8031), Jefferson County (8059), Weld County (8123)
Florida	1	Dade County (12025)*, Miami-Dade County (12086)
Hawaii	1	Kalawao County (15005), Maui County (15009)
Maryland	1	Montgomery County (24031), Prince George's County (24033)
Montana	1	Park County (30067), Yellowstone National Park (30113)*
New Mexico	1	Cibola County (35006), Valencia County (35061)
South Dakota	1	Oglala Lakota County (46102), Shannon County (46113)*
	2	Jackson County (46071), Washabaugh County (46131)*
Virginia	1	Fairfax County (51059), Fairfax City (51600)
	2	Rockingham County (51165), Harrisonburg City (51660)
	3	James City County (51095), Williamsburg City (51830)
	4	Prince William County (51153), Manassas City (51683), Manassas Park City (51685)
	5	Rockbridge County (51163), Buena Vista City (51530)
	6	Spotsylvania County (51177), Fredericksburg City (51630)
	7	Augusta County (51015), Staunton City (51790), Waynesboro City (51820)
	8	Pittsylvania County (51143), Danville City (51590)
	9	Greensville County (51081), Emporia City (51595)
	10	Albemarle County (51003), Charlottesville City (51540)
	11	Bedford County (51019), Bedford City (51515)*
	12	Halifax County (51083), South Boston City (51780)*
	13	Southampton County (51175), Franklin City (51620)
	14	Alleghany County (51005), Clifton Forge City (51560)*
	15	York County (51199), Newport News City (51700)

*County no longer exists due to boundary or name change.

3.2 Deaths and population data sources

Data Type	Data Source / Citations
Deaths	National Center for Health Statistics. National Vital Statistics System: Mortality Multiple Cause – All Counties Files, 2000–2019. Hyattsville, MD: National Center for Health Statistics, 2021. https://www.cdc.gov/nchs/nvss/nvss-restricted-data.htm
Population	National Center for Health Statistics, Centers for Disease Control and Prevention, US Census Bureau. United States Bridged-Race Intercensal Population Estimates 2000–2009. Hyattsville, United States: National Center for Health Statistics, Centers for Disease Control and Prevention, 2012. https://www.cdc.gov/nchs/nvss/bridged_race.htm. Accessed October 30, 2012. National Center for Health Statistics, Centers for Disease Control and Prevention, US Census Bureau. United States Vintage 2019 Bridged-Race Postcensal Population Estimates 2010–2019. Hyattsville, United States: National Center for Health Statistics, Centers for Disease Control and Prevention, 2020. https://www.cdc.gov/nchs/nvss/bridged_race.htm. Accessed July 28, 2020.

3.3 Covariate data sources

Covariate	Data Sources	Data Processing	Citations
Household median income	2000–2019 Small Area Income and Poverty Estimates [1]; 2000–2019 Bureau of Labor Statistics, Consumer Price Index [2]	Data were adjusted for inflation using the consumer price index.	[1] US Census Bureau. Small Area Income and Poverty Estimates. https://www.census.gov/programs-surveys/saipe/data/datasets.html. Accessed April 9, 2021. [2] US Bureau of Labor Statistics. Consumer Price Index: All Urban Consumers History, All Items 1913–2019. https://www.bls.gov/data/. Accessed July 28, 2020.
Population density	2000–2019 NCHS bridged race files [3–4]; 2013 cartographic boundary file, state-county for United States [5]	The area of each county was calculated using an Albers Equal Area Conic projection. The total population of each county was divided by the total area of the county and was then log-transformed.	[3] National Center for Health Statistics, Centers for Disease Control and Prevention, US Census Bureau. United States Bridged-Race Intercensal Population Estimates 2000–2009. Hyattsville, United States: National Center for Health Statistics, Centers for Disease Control and Prevention, 2012. https://www.cdc.gov/nchs/nvss/bridged_race.htm. Accessed October 30, 2012. [4] National Center for Health Statistics, Centers for Disease Control and Prevention, US Census Bureau. United States Vintage 2019 Bridged-Race Postcensal Population Estimates 2010–2019. Hyattsville, United States: National Center for Health Statistics, Centers for Disease Control and Prevention, 2020. https://www.cdc.gov/nchs/nvss/bridged_race.htm. Accessed July 28, 2020. [5] US Census Bureau. TIGER/Line Shapefile, 2013 Cartographic Boundary File, State-County for United States, 1:20,000,000. https://catalog.data.gov/dataset/2013-cartographic-boundary-file-state-county-for-united-states-1-20000000. Accessed February 2, 2015.

Covariate	Data Sources	Data Processing	Citations
Percent of the population age 25 and older who have completed a bachelor's degree by race and ethnicity	1990 census [6]; 2000 census [7]; 2010–2019 ACS [8]	ACS estimates for Black, American Indian or Alaskan Native (AIAN), and Asian or Pacific Islander (API) were not available stratified by Latino ethnicity and were used as proxies for non-Latino Black, non-Latino AIAN, and non-Latino API estimates, respectively. Imputation via a small area estimation model was used to generate and smooth missing values.	[6] Minnesota Population Center. 1990 Census Summary Tape File 4, Table NPB44. IPUMS National Historical Geographic Information System: Version 15.0. Minneapolis, MN: IPUMS 2020. https://www.nhgis.org/. Accessed August 25, 2020. [7] Minnesota Population Center. 2000 Census Summary File 4, Table NPCT064C. IPUMS National Historical Geographic Information System: Version 15.0. Minneapolis, MN: IPUMS 2020. https://www.nhgis.org/. Accessed August 25, 2020. [8] US Census Bureau. American Community Survey, 2010–2019 American Community Survey 5-Year Estimates, Tables C15002A–C15002I; using Census data portal; https://data.census.gov/cedsci/. Accessed April 9, 2021.
Percent of the population below the poverty line by race and ethnicity	1990 census [9]; 2000 census [10]; 2010–2019 ACS [11]	ACS estimates for Black, American Indian or Alaskan Native (AIAN), and Asian or Pacific Islander (API) were not available stratified by Latino ethnicity and were used as proxies for non-Latino Black, non-Latino AIAN, and non-Latino API estimates, respectively. Imputation via a small area estimation model was used to generate and smooth missing values.	[9] Minnesota Population Center. 1990 Census Summary Tape File 4, Table NPB100. IPUMS National Historical Geographic Information System: Version 15.0. Minneapolis, MN: IPUMS 2020. https://www.nhgis.org/. Accessed August 30, 2020. [10] Minnesota Population Center. 2000 Census Summary File 4, Table NPCT142A. IPUMS National Historical Geographic Information System: Version 15.0. Minneapolis, MN: IPUMS 2020. https://www.nhgis.org/. Accessed August 30, 2020. [11] US Census Bureau. American Community Survey, 2010–2019 American Community Survey 5-Year Estimates, Tables B17001A–B17001I; using Census data portal; https://data.census.gov/cedsci/. Accessed April 9, 2021.

Covariate	Data Sources	Data Processing	Citations
Percent of the population that is foreign-born by race and ethnicity	1990 census [12]; 2000 census [13]; 2010–2019 ACS [14]	ACS estimates for Black, American Indian or Alaskan Native (AIAN), and Asian or Pacific Islander (API) were not available stratified by Latino ethnicity and were used as proxies for non-Latino Black, non-Latino AIAN, and non-Latino API estimates, respectively. Imputation via a small area estimation model was used to generate and smooth missing values.	[12] Minnesota Population Center. 1990 Census Summary Tape File 4, Table NPB28. IPUMS National Historical Geographic Information System: Version 15.0. Minneapolis, MN: IPUMS 2020. https://www.nhgis.org/. Accessed October 8, 2020. [13] Minnesota Population Center. 2000 Census Summary File 4, Table NPCT043A. IPUMS National Historical Geographic Information System: Version 15.0. Minneapolis, MN: IPUMS 2020. https://www.nhgis.org/. Accessed October 8, 2020. [14] US Census Bureau. American Community Survey, 2010–2019 American Community Survey 5-Year Estimates, Tables B05003A–B05003I; using Census data portal; https://data.census.gov/cedsci/. Accessed April 9, 2021.

3.4 Population and uncertainty mask

Race/ Ethnicity	Population Mask			Uncertainty Mask			Combined Mask		
	Counties masked	County-years masked	Person-years masked*	Counties masked	County-years masked	Person-years masked*	Counties masked	County-years masked	Person-years masked*
White	59 (1·9%)	1180 (1·9%)	0·8 (0·0%)	6 (0·2%)	47 (0·1%)	0·1 (0·0%)	62 (2·0%)	1205 (1·9%)	0·8 (0·0%)
Black	1622 (52·2%)	32440 (52·2%)	7·5 (1·0%)	503 (16·2%)	4677 (7·5%)	0·5 (0·1%)	1634 (52·5%)	32501 (52·3%)	7·6 (1·0%)
AIAN	2636 (84·8%)	52720 (84·8%)	9·1 (17·8%)	2644 (85·0%)	47323 (76·1%)	8·8 (17·2%)	2752 (88·5%)	54175 (87·1%)	11·9 (23·3%)
API	2443 (78·6%)	48860 (78·6%)	8·5 (2·6%)	1 (0·0%)	4 (0·0%)	0·0 (0·0%)	2443 (78·6%)	48860 (78·6%)	8·5 (2·6%)
Latino	1632 (52·5%)	32640 (52·5%)	11·4 (1·2%)	70 (2·3%)	367 (0·6%)	0·1 (0·0%)	1636 (52·6%)	32655 (52·5%)	11·4 (1·2%)
Total	31 (1·0%)	620 (1·0%)	0·4 (0·0%)	0 (0·0%)	0 (0·0%)	0·0 (0·0%)	31 (1·0%)	620 (1·0%)	0·4 (0·0%)

*Person-years masked are given in millions.

Population and uncertainty mask, by census region

Race/ Ethnicity	Census Region	Population Mask			Uncertainty Mask			Combined Mask			Percent Persion-Years in Region
		Counties masked	County-years masked	Person-years masked*	Counties masked	County-years masked	Person-years masked*	Counties masked	County-years masked	Person-years masked*	
Latino	South	686 (48·8%)	13720 (48·8%)	5·4 (1·5%)	9 (0·6%)	47 (0·2%)	0·0 (0·0%)	687 (48·8%)	13721 (48·8%)	5·4 (1·5%)	35·9%
	West	152 (35·3%)	3040 (35·3%)	0·9 (0·2%)	21 (4·9%)	160 (1·9%)	0·0 (0·0%)	155 (36·0%)	3054 (35·4%)	0·9 (0·2%)	40·7%
	Northeast	67 (30·9%)	1340 (30·9%)	0·7 (0·5%)	4 (1·8%)	15 (0·3%)	0·0 (0·0%)	67 (30·9%)	1340 (30·9%)	0·7 (0·5%)	14·1%
	Midwest	727 (68·9%)	14540 (68·9%)	4·4 (4·9%)	36 (3·4%)	145 (0·7%)	0·0 (0·0%)	727 (68·9%)	14540 (68·9%)	4·4 (4·9%)	9·2%
Black	South	451 (32·1%)	9020 (32·1%)	2·8 (0·6%)	27 (1·9%)	167 (0·6%)	0·0 (0·0%)	451 (32·1%)	9020 (32·1%)	2·8 (0·6%)	56·1%
	West	319 (74·0%)	6380 (74·0%)	1·2 (1·6%)	143 (33·2%)	1308 (15·2%)	0·1 (0·2%)	320 (74·2%)	6390 (74·1%)	1·2 (1·7%)	9·2%
	Northeast	69 (31·8%)	1380 (31·8%)	0·6 (0·4%)	21 (9·7%)	208 (4·8%)	0·0 (0·0%)	70 (32·3%)	1383 (31·9%)	0·6 (0·4%)	16·4%
	Midwest	783 (74·2%)	15660 (74·2%)	3·0 (2·1%)	314 (29·8%)	2976 (14·1%)	0·3 (0·2%)	792 (75·1%)	15707 (74·4%)	3·1 (2·1%)	18·4%
White	South	19 (1·4%)	380 (1·4%)	0·2 (0·0%)	0 (0·0%)	0 (0·0%)	0·0 (0·0%)	19 (1·4%)	380 (1·4%)	0·2 (0·0%)	34·8%
	West	18 (4·2%)	360 (4·2%)	0·3 (0·0%)	5 (1·2%)	33 (0·4%)	0·1 (0·0%)	20 (4·6%)	379 (4·4%)	0·3 (0·0%)	19·5%
	Northeast	0 (0·0%)	0 (0·0%)	0·0 (0·0%)	0 (0·0%)	0 (0·0%)	0·0 (0·0%)	0 (0·0%)	0 (0·0%)	0·0 (0·0%)	19·3%
	Midwest	22 (2·1%)	440 (2·1%)	0·3 (0·0%)	0 (0·0%)	0 (0·0%)	0·0 (0·0%)	22 (2·1%)	440 (2·1%)	0·3 (0·0%)	26·4%
AIAN	South	1246	24920	3·9	1281	23046	3·5	1297	25341	4·5	32·0%

Race/ Ethnicity	Census Region	Population Mask			Uncertainty Mask			Combined Mask			Percent Persion-Years in Region
		Counties masked	County-years masked	Person-years masked*	Counties masked	County-years masked	Person-years masked*	Counties masked	County-years masked	Person-years masked*	
		(88·6%)	(88·6%)	(23·5%)	(91·0%)	(81·9%)	(21·2%)	(92·2%)	(90·1%)	(27·2%)	
	West	269 (62·4%)	5380 (62·4%)	1·3 (5·6%)	231 (53·6%)	3943 (45·7%)	0·5 (2·2%)	272 (63·1%)	5386 (62·5%)	1·3 (5·6%)	44·3%
	Northeast	172 (79·3%)	3440 (79·3%)	0·9 (30·6%)	217 (100·0%)	4284 (98·7%)	2·9 (93·9%)	217 (100·0%)	4297 (99·0%)	2·9 (94·2%)	6·0%
	Midwest	949 (90·0%)	18980 (90·0%)	3·0 (33·5%)	915 (86·7%)	16050 (76·1%)	1·9 (21·5%)	966 (91·6%)	19151 (90·8%)	3·3 (36·4%)	17·7%
API	South	1137 (80·8%)	22740 (80·8%)	4·0 (5·7%)	0 (0·0%)	0 (0·0%)	0·0 (0·0%)	1137 (80·8%)	22740 (80·8%)	4·0 (5·7%)	21·6%
	West	309 (71·7%)	6180 (71·7%)	1·2 (0·8%)	1 (0·2%)	5 (0·1%)	0·0 (0·0%)	309 (71·7%)	6180 (71·7%)	1·2 (0·8%)	46·5%
	Northeast	110 (50·7%)	2200 (50·7%)	0·8 (1·3%)	0 (0·0%)	0 (0·0%)	0·0 (0·0%)	110 (50·7%)	2200 (50·7%)	0·8 (1·3%)	20·0%
	Midwest	887 (84·1%)	17740 (84·1%)	2·5 (6·5%)	0 (0·0%)	0 (0·0%)	0·0 (0·0%)	887 (84·1%)	17740 (84·1%)	2·5 (6·5%)	11·9%
Total	South	8 (0·6%)	160 (0·6%)	0·1 (0·0%)	0 (0·0%)	0 (0·0%)	0·0 (0·0%)	8 (0·6%)	160 (0·6%)	0·1 (0·0%)	37·0%
	West	9 (2·1%)	180 (2·1%)	0·1 (0·0%)	0 (0·0%)	0 (0·0%)	0·0 (0·0%)	9 (2·1%)	180 (2·1%)	0·1 (0·0%)	23·2%
	Northeast	0 (0·0%)	0 (0·0%)	0·0 (0·0%)	0 (0·0%)	0 (0·0%)	0·0 (0·0%)	0 (0·0%)	0 (0·0%)	0·0 (0·0%)	18·0%
	Midwest	14 (1·3%)	280 (1·3%)	0·2 (0·0%)	0 (0·0%)	0 (0·0%)	0·0 (0·0%)	14 (1·3%)	280 (1·3%)	0·2 (0·0%)	21·8%

*Person-years masked are given in millions.

Population and uncertainty mask, by 2013 NCHS urban-rural classification

Race/ Ethnicity	Urban/ Rural Code	Population Mask			Uncertainty Mask			Combined Mask			Percent Person-Years in Code
		Counties masked	County-years masked	Person-years masked*	Counties masked	County-years masked	Person-years masked*	Counties masked	County-years masked	Person-years masked*	
Latino	Large central metro	0 (0·0%)	0 (0·0%)	0·0 (0·0%)	0 (0·0%)	0 (0·0%)	0·0 (0·0%)	0 (0·0%)	0 (0·0%)	0·0 (0·0%)	49·5%
	Large fringe metro	103 (26·0%)	1447 (22·8%)	0·7 (0·4%)	0 (0·0%)	0 (0·0%)	0·0 (0·0%)	103 (26·0%)	1447 (22·8%)	0·7 (0·4%)	17·2%
	Medium metro	121 (24·8%)	1549 (22·7%)	0·7 (0·4%)	1 (0·2%)	3 (0·0%)	0·0 (0·0%)	121 (24·8%)	1549 (22·7%)	0·7 (0·4%)	19·8%
	Small metro	149 (33·9%)	1841 (30·6%)	0·8 (1·4%)	1 (0·2%)	1 (0·0%)	0·0 (0·0%)	149 (33·9%)	1841 (30·6%)	0·8 (1·4%)	5·9%
	Micropolitan	307 (37·5%)	4499 (36·9%)	2·3 (4·8%)	8 (1·0%)	21 (0·2%)	0·0 (0·0%)	309 (37·7%)	4501 (36·9%)	2·3 (4·8%)	4·9%
	Noncore	1399 (76·6%)	23304 (78·9%)	6·8 (25·7%)	62 (3·4%)	342 (1·2%)	0·0 (0·2%)	1401 (76·7%)	23317 (79·0%)	6·9 (25·8%)	2·7%
Black	Large central metro	0 (0·0%)	0 (0·0%)	0·0 (0·0%)	0 (0·0%)	0 (0·0%)	0·0 (0·0%)	0 (0·0%)	0 (0·0%)	0·0 (0·0%)	42·1%
	Large fringe metro	83 (21·0%)	1217 (19·2%)	0·5 (0·3%)	1 (0·3%)	1 (0·0%)	0·0 (0·0%)	83 (21·0%)	1217 (19·2%)	0·5 (0·3%)	20·8%
	Medium metro	115 (23·6%)	1458 (21·3%)	0·5 (0·4%)	9 (1·8%)	33 (0·5%)	0·0 (0·0%)	115 (23·6%)	1458 (21·3%)	0·5 (0·4%)	19·0%
	Small metro	125 (28·4%)	1531 (25·4%)	0·5 (0·9%)	26 (5·9%)	119 (2·0%)	0·0 (0·1%)	129 (29·3%)	1551 (25·8%)	0·5 (1·0%)	6·9%

Race/ Ethnicity	Urban/ Rural Code	Population Mask			Uncertainty Mask			Combined Mask			Percent Person-Years in Code
		Counties masked	County-years masked	Person-years masked*	Counties masked	County-years masked	Person-years masked*	Counties masked	County-years masked	Person-years masked*	
	Micropolitan	384 (46·9%)	5723 (47·0%)	2·4 (4·9%)	98 (12·0%)	571 (4·7%)	0·2 (0·3%)	390 (47·6%)	5754 (47·2%)	2·4 (5·1%)	6·1%
	Noncore	1340 (73·3%)	22511 (76·2%)	3·6 (9·1%)	428 (23·4%)	3935 (13·3%)	0·3 (0·8%)	1342 (73·5%)	22520 (76·3%)	3·6 (9·1%)	5·1%
White	Large central metro	0 (0·0%)	0 (0·0%)	0·0 (0·0%)	0 (0·0%)	0 (0·0%)	0·0 (0·0%)	0 (0·0%)	0 (0·0%)	0·0 (0·0%)	22·1%
	Large fringe metro	0 (0·0%)	0 (0·0%)	0·0 (0·0%)	0 (0·0%)	0 (0·0%)	0·0 (0·0%)	0 (0·0%)	0 (0·0%)	0·0 (0·0%)	24·8%
	Medium metro	1 (0·2%)	7 (0·1%)	0·0 (0·0%)	0 (0·0%)	0 (0·0%)	0·0 (0·0%)	1 (0·2%)	7 (0·1%)	0·0 (0·0%)	22·1%
	Small metro	2 (0·5%)	14 (0·2%)	0·0 (0·0%)	0 (0·0%)	0 (0·0%)	0·0 (0·0%)	2 (0·5%)	14 (0·2%)	0·0 (0·0%)	10·4%
	Micropolitan	9 (1·1%)	91 (0·7%)	0·1 (0·0%)	0 (0·0%)	0 (0·0%)	0·0 (0·0%)	9 (1·1%)	91 (0·7%)	0·1 (0·0%)	11·2%
	Noncore	59 (3·2%)	1068 (3·6%)	0·7 (0·2%)	5 (0·3%)	33 (0·1%)	0·1 (0·0%)	61 (3·3%)	1087 (3·7%)	0·8 (0·2%)	9·4%
AIAN	Large central metro	8 (10·1%)	86 (6·6%)	0·1 (0·7%)	39 (49·4%)	455 (35·1%)	1·2 (14·2%)	39 (49·4%)	469 (36·2%)	1·2 (14·4%)	16·5%
	Large fringe metro	309 (78·0%)	4887 (77·2%)	1·5 (28·7%)	320 (80·8%)	4284 (67·6%)	1·6 (31·0%)	347 (87·6%)	5338 (84·3%)	2·2 (41·4%)	10·4%
	Medium metro	359 (73·6%)	4875 (71·3%)	1·5 (14·9%)	375 (76·8%)	4464 (65·3%)	1·7 (16·7%)	402 (82·4%)	5277 (77·2%)	2·1 (21·1%)	19·5%
	Small metro	356 (80·9%)	4800 (79·7%)	1·3 (22·0%)	347 (78·9%)	3966 (65·8%)	1·0 (16·6%)	370 (84·1%)	4913 (81·6%)	1·5 (24·6%)	11·6%
	Micropolitan	717 (87·5%)	10721 (88·0%)	2·1 (21·4%)	687 (83·9%)	9090 (74·6%)	1·6 (15·8%)	722 (88·2%)	10783 (88·5%)	2·3 (22·7%)	19·5%
	Noncore	1694 (92·7%)	27351 (92·6%)	2·6 (22·5%)	1639 (89·7%)	25064 (84·9%)	1·7 (14·9%)	1700 (93·0%)	27395 (92·8%)	2·7 (23·2%)	22·4%
API	Large central metro	0 (0·0%)	0 (0·0%)	0·0 (0·0%)	0 (0·0%)	0 (0·0%)	0·0 (0·0%)	0 (0·0%)	0 (0·0%)	0·0 (0·0%)	51·8%
	Large fringe metro	184 (46·5%)	2673 (42·2%)	0·9 (1·1%)	0 (0·0%)	0 (0·0%)	0·0 (0·0%)	184 (46·5%)	2673 (42·2%)	0·9 (1·1%)	24·7%
	Medium metro	239 (49·0%)	3094 (45·3%)	0·9 (1·7%)	0 (0·0%)	0 (0·0%)	0·0 (0·0%)	239 (49·0%)	3094 (45·3%)	0·9 (1·7%)	15·9%
	Small metro	241 (54·8%)	3100 (51·5%)	1·0 (8·1%)	0 (0·0%)	0 (0·0%)	0·0 (0·0%)	241 (54·8%)	3100 (51·5%)	1·0 (8·1%)	3·8%
	Micropolitan	693 (84·6%)	10643 (87·4%)	3·5 (37·0%)	0 (0·0%)	0 (0·0%)	0·0 (0·0%)	693 (84·6%)	10643 (87·4%)	3·5 (37·0%)	2·9%
	Noncore	1805 (98·8%)	29350 (99·4%)	2·2 (83·2%)	1 (0·1%)	5 (0·0%)	0·0 (0·0%)	1805 (98·8%)	29350 (99·4%)	2·2 (83·2%)	0·8%
Total	Large central metro	0 (0·0%)	0 (0·0%)	0·0 (0·0%)	0 (0·0%)	0 (0·0%)	0·0 (0·0%)	0 (0·0%)	0 (0·0%)	0·0 (0·0%)	30·6%
	Large fringe metro	0 (0·0%)	0 (0·0%)	0·0 (0·0%)	0 (0·0%)	0 (0·0%)	0·0 (0·0%)	0 (0·0%)	0 (0·0%)	0·0 (0·0%)	23·0%
	Medium metro	0 (0·0%)	0 (0·0%)	0·0 (0·0%)	0 (0·0%)	0 (0·0%)	0·0 (0·0%)	0 (0·0%)	0 (0·0%)	0·0 (0·0%)	21·0%
	Small metro	1 (0·2%)	7 (0·1%)	0·0 (0·0%)	0 (0·0%)	0 (0·0%)	0·0 (0·0%)	1 (0·2%)	7 (0·1%)	0·0 (0·0%)	8·9%
	Micropolitan	6 (0·7%)	70 (0·6%)	0·0 (0·0%)	0 (0·0%)	0 (0·0%)	0·0 (0·0%)	6 (0·7%)	70 (0·6%)	0·0 (0·0%)	9·2%
	Noncore	31 (1·7%)	543 (1·8%)	0·4 (0·1%)	0 (0·0%)	0 (0·0%)	0·0 (0·0%)	31 (1·7%)	543 (1·8%)	0·4 (0·1%)	7·4%

*Person-years masked are given in millions.

Modelled life expectancy estimates were masked (not displayed) under two conditions: first, estimates for any county-race/ethnicity with an average annual population of less than 1000 were masked in all years; second, estimates for any location-year-sex-race/ethnicity where the width of the uncertainty interval was greater than ten years were also masked. The number of unique counties masked, the number of county-years, and the person-years in millions represented by these county-years are listed in this table for the population mask (first criteria), uncertainty mask (second criteria), and the combined mask (both criteria combined).

3.5 Hyper-parameter posterior means and standard errors

Model	Sex	Effect		Mean (SE) *
By race/ethnicity and county	Females	γ_1	Standard deviation, Proportion with Bachelor's Degree	0·026 (SE = 0·012)
			Standard deviation, Proportion in poverty	0·028 (SE = 0·012)
			Standard deviation, Proportion foreign born	0·133 (SE = 0·056)
		γ_2	Standard deviation	0·009 (SE = 0·007)
			Correlation parameter, County	0·555 (SE = 0·351)
		γ_3	Standard deviation	0·017 (SE = 0·001)
			Correlation parameter, Year	>0.999 (SE < 0.001)
			Correlation parameter, Age	0·945 (SE = 0·010)
		γ_4	Standard deviation, Race/Ethnicity = White	0·147 (SE = 0·002)
			Standard deviation, Race/Ethnicity = Black	0·156 (SE = 0·003)
			Standard deviation, Race/Ethnicity = AIAN	0·423 (SE = 0·009)
			Standard deviation, Race/Ethnicity = API	0·164 (SE = 0·005)
			Standard deviation, Race/Ethnicity = Latino	0·196 (SE = 0·004)
			Correlation parameter, County	0·983 (SE = 0·002)
			Correlation parameter, Year spline	0·935 (SE = 0·002)
			Correlation parameter, Age spline	0·481 (SE = 0·011)
	Males	γ_1	Standard deviation, Proportion with Bachelor's Degree	0·065 (SE = 0·027)
			Standard deviation, Proportion in poverty	0·026 (SE = 0·011)
			Standard deviation, Proportion foreign born	0·171 (SE = 0·071)
		γ_2	Standard deviation	0·008 (SE = 0·006)
			Correlation parameter, County	0·562 (SE = 0·348)
		γ_3	Standard deviation	0·02 (SE = 0·001)
			Correlation parameter, Year	>0.999 (SE < 0.001)
			Correlation parameter, Age	0·943 (SE = 0·009)
		γ_4	Standard deviation, Race/Ethnicity = White	0·13 (SE = 0·002)
			Standard deviation, Race/Ethnicity = Black	0·225 (SE = 0·003)
			Standard deviation, Race/Ethnicity = AIAN	0·367 (SE = 0·008)
			Standard deviation, Race/Ethnicity = API	0·163 (SE = 0·004)
			Standard deviation, Race/Ethnicity = Latino	0·203 (SE = 0·004)
			Correlation parameter, County	0·977 (SE = 0·002)
			Correlation parameter, Year spline	0·959 (SE = 0·001)
			Correlation parameter, Age spline	0·539 (SE = 0·01)
By county	Females	γ_2	Standard deviation	0·06 (SE = 0·012)
			Correlation parameter, County	0·092 (SE = 0·101)
		γ_3	Standard deviation	0·016 (SE = 0·001)
			Correlation parameter, Year	>0.999 (SE < 0.001)
			Correlation parameter, Age	0·930 (SE = 0·019)
		γ_4	Standard deviation	0·151 (SE = 0·002)
			Correlation parameter, County	0·973 (SE = 0·004)

Model	Sex	Effect		Mean (SE) *
			Correlation parameter, Year spline	0·939 (SE = 0·002)
			Correlation parameter, Age spline	0·334 (SE = 0·016)
	Males	$\boldsymbol{\gamma_2}$	Standard deviation	0·077 (SE = 0·008)
			Correlation parameter, County	0·060 (SE = 0·043)
		$\boldsymbol{\gamma_3}$	Standard deviation	0·017 (SE = 0·001)
			Correlation parameter, Year	>0.999 (SE < 0.001)
			Correlation parameter, Age	0·939 (SE = 0·016)
		$\boldsymbol{\gamma_4}$	Standard deviation	0·145 (SE = 0·002)
			Correlation parameter, County	0·964 (SE = 0·005)
			Correlation parameter, Year spline	0·954 (SE = 0·001)
			Correlation parameter, Age spline	0·273 (SE = 0·015)

*Estimates are reported by TMB on the log standard deviation and logit correlation parameter scale. For convenience, we have transformed these using a delta transformation for the standard error.

3.6 County-racial/ethnic groups in the validation set

State	Merged County	Racial/Ethnic Group*
Alabama	Jefferson	All racial/ethnic groups, Black
	Madison	All racial/ethnic groups
	Mobile	All racial/ethnic groups, Black
Alaska	Anchorage Municipality	All racial/ethnic groups
Arizona	Maricopa	All racial/ethnic groups, Latino, Black, White
	Pima	All racial/ethnic groups, Latino
	Pinal	All racial/ethnic groups
Arkansas	Pulaski	All racial/ethnic groups
California	Alameda	All racial/ethnic groups, Latino
	Contra Costa	All racial/ethnic groups, White
	Fresno	All racial/ethnic groups, Latino
	Kern	All racial/ethnic groups, Latino, White
	Los Angeles	All racial/ethnic groups, Latino, API, Black, White
	Merced	All racial/ethnic groups
	Monterey	All racial/ethnic groups, Latino
	Orange	All racial/ethnic groups, Latino, White
	Riverside	All racial/ethnic groups, Latino, White
	Sacramento	All racial/ethnic groups
	San Bernardino	All racial/ethnic groups, Latino, Black
	San Diego	All racial/ethnic groups, Latino, White
	San Francisco	All racial/ethnic groups
	San Joaquin	All racial/ethnic groups, Latino
	San Mateo	All racial/ethnic groups
	Santa Clara	All racial/ethnic groups, Latino, API
	Solano	All racial/ethnic groups
	Sonoma	All racial/ethnic groups
	Stanislaus	All racial/ethnic groups
	Tulare	All racial/ethnic groups, Latino
	Ventura	All racial/ethnic groups
Colorado	Adams/Arapahoe/Boulder/Broomfield/Denver/Jefferson/Weld	All racial/ethnic groups, Latino, White
	El Paso	All racial/ethnic groups
Connecticut	Fairfield	All racial/ethnic groups, White
	Hartford	All racial/ethnic groups
	New Haven	All racial/ethnic groups, White
District of Columbia	District of Columbia	All racial/ethnic groups, Black
Florida	Brevard	All racial/ethnic groups

State	Merged County	Racial/Ethnic Group*
	Broward	All racial/ethnic groups, Black, White
	Miami-Dade	All racial/ethnic groups, Latino, Black
	Duval	All racial/ethnic groups, Black, White
	Hillsborough	All racial/ethnic groups, Latino, Black, White
	Lee	All racial/ethnic groups
	Orange	All racial/ethnic groups
	Palm Beach	All racial/ethnic groups, Latino, White
	Pasco	All racial/ethnic groups
	Pinellas	All racial/ethnic groups
	Polk	All racial/ethnic groups
	Seminole	All racial/ethnic groups
Georgia	Bibb	All racial/ethnic groups
	Cobb	All racial/ethnic groups, White
	DeKalb	All racial/ethnic groups, Black
	Fulton	All racial/ethnic groups, Black, White
	Gwinnett	All racial/ethnic groups
Hawaii	Honolulu	All racial/ethnic groups, API
Illinois	Cook	All racial/ethnic groups, Latino, Black, White
	DuPage	All racial/ethnic groups
	Kane	All racial/ethnic groups
	Lake	All racial/ethnic groups
	Will	All racial/ethnic groups, White
Indiana	Allen	All racial/ethnic groups
	Elkhart	All racial/ethnic groups
	Lake	All racial/ethnic groups, Black
	Marion	All racial/ethnic groups, Black, White
Iowa	Polk	All racial/ethnic groups
Kansas	Sedgwick	All racial/ethnic groups, White
Kentucky	Jefferson	All racial/ethnic groups, White
Louisiana	Caddo	All racial/ethnic groups
	East Baton Rouge	All racial/ethnic groups, Black
	Jefferson	All racial/ethnic groups
	Orleans	All racial/ethnic groups, Black
Maryland	Anne Arundel	All racial/ethnic groups
	Baltimore	All racial/ethnic groups
	Baltimore City	All racial/ethnic groups, Black
	Montgomery/Prince George's	All racial/ethnic groups, Black
Massachusetts	Bristol	All racial/ethnic groups
	Essex	All racial/ethnic groups

State	Merged County	Racial/Ethnic Group*
	Hampden	All racial/ethnic groups
	Middlesex	All racial/ethnic groups, White
	Suffolk	All racial/ethnic groups
	Worcester	All racial/ethnic groups
Michigan	Genesee	All racial/ethnic groups
	Kent	All racial/ethnic groups
	Macomb	All racial/ethnic groups, White
	Oakland	All racial/ethnic groups
	Wayne	All racial/ethnic groups, Black, White
Minnesota	Hennepin	All racial/ethnic groups, White
	Ramsey	All racial/ethnic groups
Mississippi	Hinds	All racial/ethnic groups, Black
Missouri	Jackson	All racial/ethnic groups, White
	Saint Louis	All racial/ethnic groups, Black, White
Nebraska	Douglas	All racial/ethnic groups
Nevada	Clark	All racial/ethnic groups, Latino, White
	Washoe	All racial/ethnic groups
New Jersey	Bergen	All racial/ethnic groups, White
	Burlington	All racial/ethnic groups
	Camden	All racial/ethnic groups
	Essex	All racial/ethnic groups, Black
	Hudson	All racial/ethnic groups
	Mercer	All racial/ethnic groups
	Middlesex	All racial/ethnic groups
	Monmouth	All racial/ethnic groups, White
	Ocean	All racial/ethnic groups, White
	Passaic	All racial/ethnic groups
	Union	All racial/ethnic groups
New Mexico	Bernalillo	All racial/ethnic groups, Latino
	Dona Ana	All racial/ethnic groups
	San Juan	All racial/ethnic groups
New York	Bronx	All racial/ethnic groups, Latino, Black
	Erie	All racial/ethnic groups, White
	Kings	All racial/ethnic groups, Latino, Black, White
	Monroe	All racial/ethnic groups, White
	Nassau	All racial/ethnic groups, White
	New York	All racial/ethnic groups, Latino
	Onondaga	All racial/ethnic groups
	Queens	All racial/ethnic groups, Latino, API, Black

State	Merged County	Racial/Ethnic Group*
	Suffolk	All racial/ethnic groups, White
	Westchester	All racial/ethnic groups, White
North Carolina	Durham	All racial/ethnic groups
	Forsyth	All racial/ethnic groups
	Mecklenburg	All racial/ethnic groups, White
	Wake	All racial/ethnic groups, White
Ohio	Cuyahoga	All racial/ethnic groups, Black, White
	Franklin	All racial/ethnic groups, Black
	Hamilton	All racial/ethnic groups, Black, White
	Lucas	All racial/ethnic groups
	Montgomery	All racial/ethnic groups, White
Oklahoma	Oklahoma	All racial/ethnic groups, White
	Tulsa	All racial/ethnic groups, White
Oregon	Multnomah	All racial/ethnic groups
Pennsylvania	Allegheny	All racial/ethnic groups, Black, White
	Chester	All racial/ethnic groups, White
	Delaware	All racial/ethnic groups, White
	Lancaster	All racial/ethnic groups, White
	Montgomery	All racial/ethnic groups, White
	Philadelphia	All racial/ethnic groups, Latino, Black, White
Rhode Island	Providence	All racial/ethnic groups, White
South Carolina	Greenville	All racial/ethnic groups, White
	Spartanburg	All racial/ethnic groups
Tennessee	Davidson	All racial/ethnic groups, Black
	Knox	All racial/ethnic groups
	Montgomery	All racial/ethnic groups
	Shelby	All racial/ethnic groups, Black
Texas	Bell	All racial/ethnic groups
	Bexar	All racial/ethnic groups, Latino, White
	Cameron	All racial/ethnic groups, Latino
	Collin	All racial/ethnic groups, White
	Dallas	All racial/ethnic groups, Latino, Black, White
	Denton	All racial/ethnic groups, White
	El Paso	All racial/ethnic groups, Latino
	Fort Bend	All racial/ethnic groups
	Galveston	All racial/ethnic groups
	Harris	All racial/ethnic groups, Latino, Black, White
	Hidalgo	All racial/ethnic groups, Latino
	Jefferson	All racial/ethnic groups

State	Merged County	Racial/Ethnic Group*
	McLennan	All racial/ethnic groups
	Montgomery	All racial/ethnic groups
	Tarrant	All racial/ethnic groups, Latino, White
	Travis	All racial/ethnic groups, White
	Webb	All racial/ethnic groups, Latino
Utah	Salt Lake	All racial/ethnic groups, White
	Utah	All racial/ethnic groups, White
Virginia	Chesapeake City	All racial/ethnic groups
	Fairfax/Fairfax City	All racial/ethnic groups
	Norfolk City	All racial/ethnic groups
	York/Newport News City	All racial/ethnic groups
Washington	Clark	All racial/ethnic groups
	King	All racial/ethnic groups, White
	Pierce	All racial/ethnic groups, White
	Spokane	All racial/ethnic groups
	Yakima	All racial/ethnic groups
Wisconsin	Milwaukee	All racial/ethnic groups, Black, White
	Rock	All racial/ethnic groups

*All racial/ethnic groups was validated separately from individual racial/ethnic groups.

3.7 Validation results for life expectancy at birth for all models and racial/ethnic groups

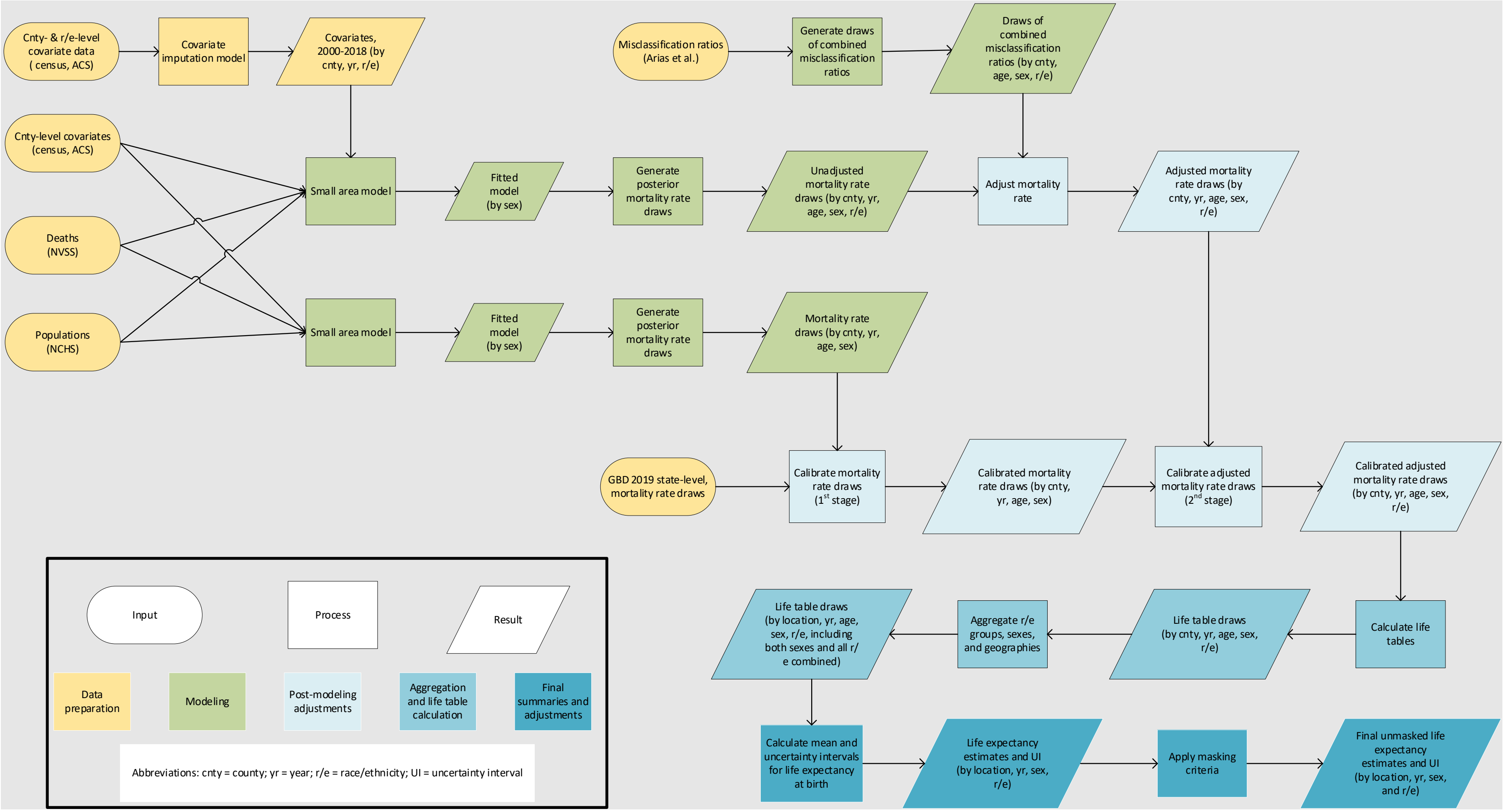
		Model 1			Model 2			Model 3		
Racial/Ethnic Group	**Size**	Mean Error	Mean Absolute Error	Coverage	Mean Error	Mean Absolute Error	Coverage	Mean Error	Mean Absolute Error	Coverage
Across all Racial/Ethnic Groups	10	0·06	0·91	96·57	-0·02	1·41	92·50			
	100	0·05	0·89	96·47	-0·03	1·35	92·33			
	1000	0·08	0·78	95·20	0·02	1·02	91·42			
	3000	-0·02	0·65	94·33	-0·06	0·78	91·77			
	5000	0·02	0·59	93·35	-0·02	0·67	91·57			
	10 000	-0·01	0·48	93·22	-0·04	0·53	92·16			
	25 000	-0·01	0·38	91·83	-0·02	0·39	91·83			
	100 000	0·00	0·27	86·73	0·00	0·27	87·14			
All Racial/Ethnic Groups combined	10							0·41	1·01	94·85
	100							0·38	0·98	94·86
	1000							0·26	0·85	92·91
	3000							0·15	0·66	92·86
	5000							0·13	0·58	91·98
	10 000							0·04	0·48	91·40
	25 000							0·03	0·36	90·68
	100 000							0·01	0·24	86·43
Latino	10	-0·24	1·08	98·89	0·06	1·11	97·46			
	100	-0·26	1·06	98·75	0·01	1·12	98·46			
	1000	-0·07	0·88	97·49	0·13	1·00	96·82			
	3000	-0·17	0·75	97·84	-0·06	0·84	97·53			
	5000	-0·09	0·69	96·78	0·01	0·75	95·85			
	10 000	0·00	0·57	96·30	0·05	0·59	96·25			
	25 000	-0·02	0·45	94·72	0·01	0·46	94·58			
	100 000	0·01	0·34	89·31	0·02	0·34	88·72			

Racial/Ethnic Group	Size	Model 1			Model 2			Model 3		
		Mean Error	Mean Absolute Error	Coverage	Mean Error	Mean Absolute Error	Coverage	Mean Error	Mean Absolute Error	Coverage
NH API	10	-0·87	0·87	100·00	-0·68	0·92	100·00			
	100	-0·83	0·85	100·00	-0·58	0·95	100·00			
	1000	-0·53	0·64	98·68	-0·26	0·76	97·79			
	3000	-0·33	0·47	98·09	-0·14	0·58	97·94			
	5000	-0·28	0·53	96·76	-0·04	0·60	95·59			
	10 000	-0·16	0·44	96·32	-0·06	0·44	97·06			
	25 000	-0·06	0·35	95·88	0·00	0·35	96·18			
	100 000	-0·01	0·26	90·29	0·00	0·25	92·65			
NH Black	10	0·39	1·22	92·84	1·52	2·24	84·58			
	100	0·37	1·19	93·04	1·36	2·09	84·58			
	1000	0·35	1·00	91·98	0·88	1·42	84·82			
	3000	0·18	0·80	91·94	0·48	0·97	87·89			
	5000	0·17	0·69	91·65	0·36	0·80	88·81			
	10 000	0·05	0·58	91·73	0·15	0·62	90·83			
	25 000	0·02	0·44	90·41	0·06	0·45	91·14			
	100 000	0·00	0·30	85·83	0·01	0·30	86·68			
NH White	10	0·09	0·64	97·22	-0·89	1·13	93·86			
	100	0·09	0·64	96·97	-0·80	1·08	92·96			
	1000	0·04	0·61	95·59	-0·50	0·83	91·88			
	3000	-0·03	0·51	93·57	-0·36	0·65	90·51			
	5000	0·00	0·48	92·28	-0·24	0·55	90·60			
	10 000	-0·05	0·39	92·22	-0·20	0·45	90·42			
	25 000	-0·02	0·31	90·84	-0·09	0·33	90·48			
	100 000	-0·01	0·22	85·63	-0·02	0·22	86·20			

*"Across all racial/ethnic groups" indicates that errors and coverage were calculated across all racial/ethnic groups for models 1 and 2, while "All racial/ethnic groups combined" refers to model 3, where the data were aggregated across racial/ethnic groups before fitting models.

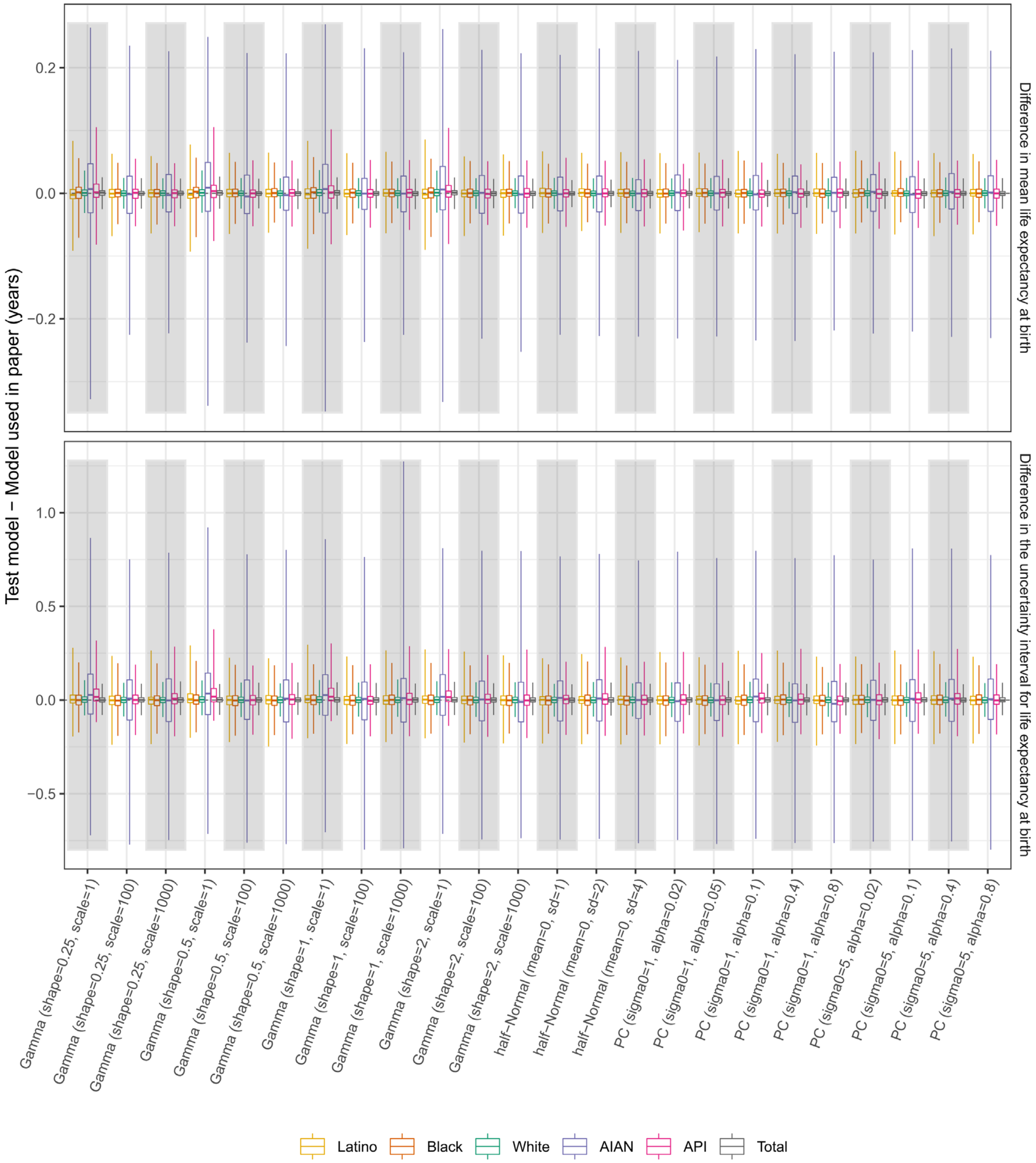
4 Supplemental Methods Figures

4.1 Analysis flow chart



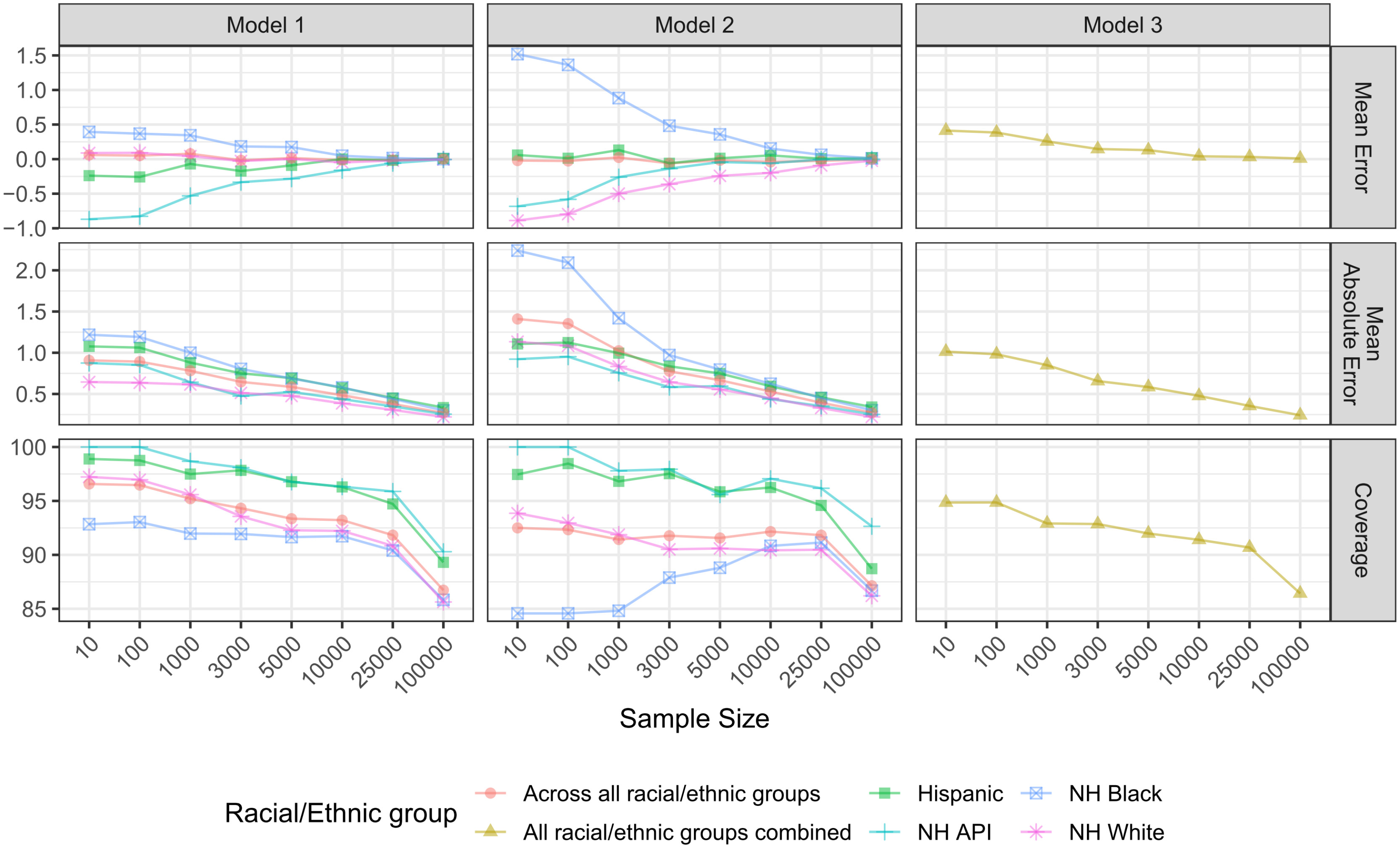
Abbreviations: cnty = county; yr = year; r/e = race/ethnicity; UI = uncertainty interval

4.2 Hyper-prior sensitivity analysis results



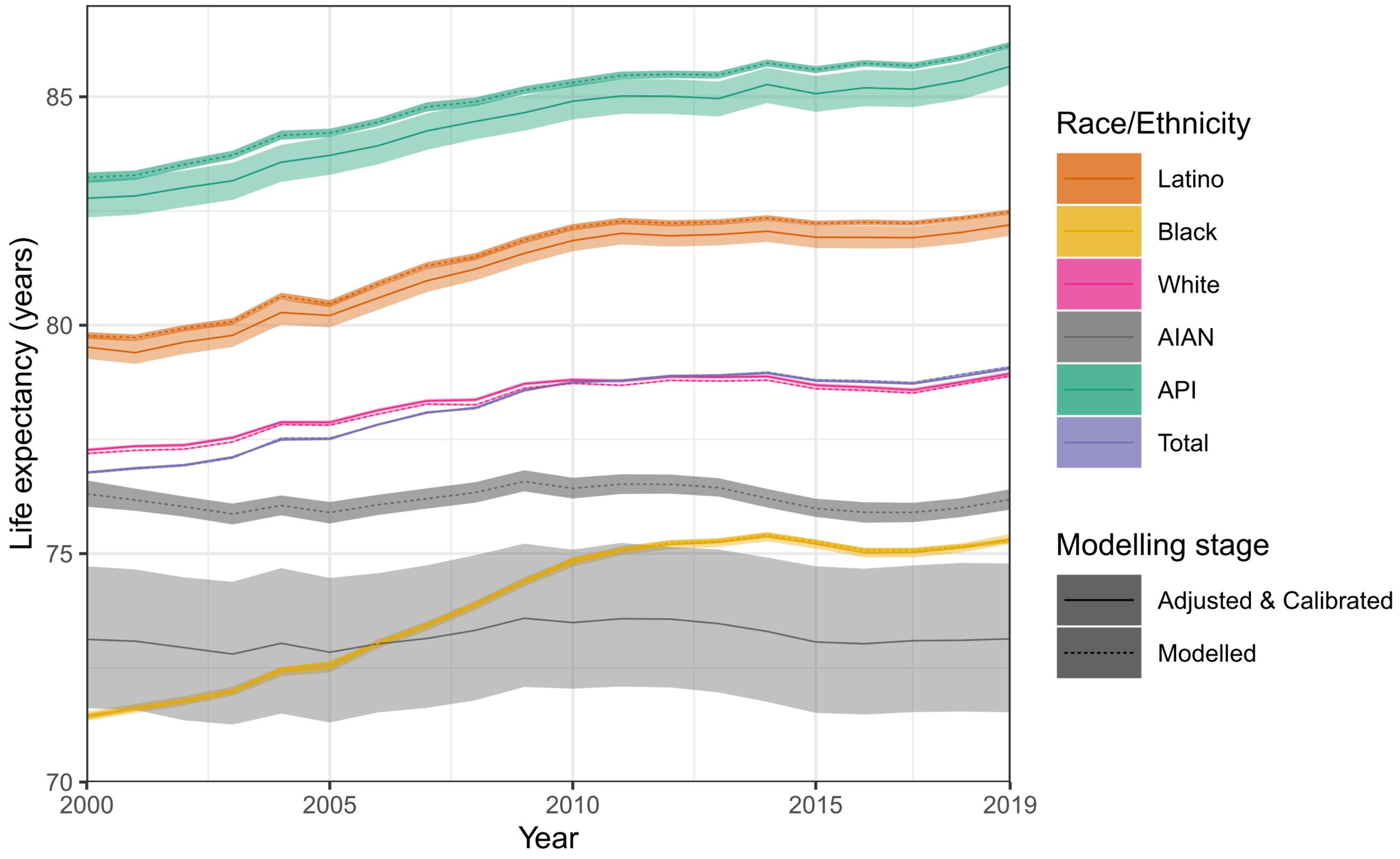
County-race/ethnicity-level, population-weighted summary of differences in life expectancy at birth for males and females combined in 2000, 2010, and 2019 compared to that of the model used in this paper (penalized complexity models, $\sigma_0 = 5, \alpha = 0.05$). Boxes show the IQR, while the whiskers extend to 1st and 99th percentiles, weighted by the average population across all years in each county-race/ethnicity. The data shown are for both masked and unmasked data. The comparison shown here for the "Total" group is from the county-level model, while the comparison for all other groups is from the county-race/ethnicity model.

4.3 Model validation results



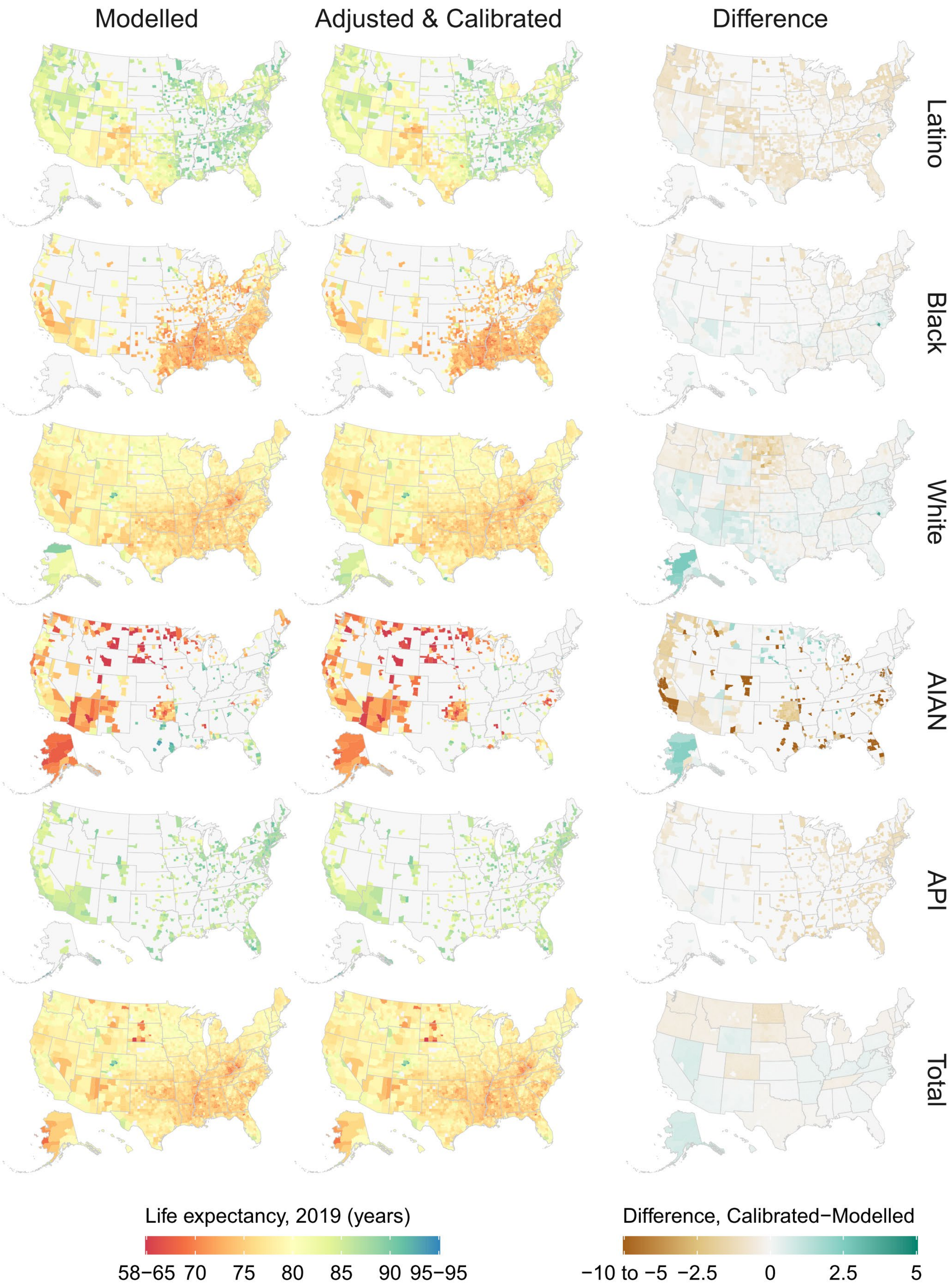
*"Across all racial/ethnic groups" means that errors and coverage were calculated across all racial/ethnic group for models 2 and 3, while "All racial/ethnic groups combined" refers to model 3, where the data were aggregated across racial/ethnic groups before fitting models.

4.4 Impact of misclassification adjustment on national life expectancy estimates



National life expectancy estimates before adjustment for misclassification ("Modelled") and after adjustment and calibration ("Adjusted & Calibrated"), ie, the final estimates.

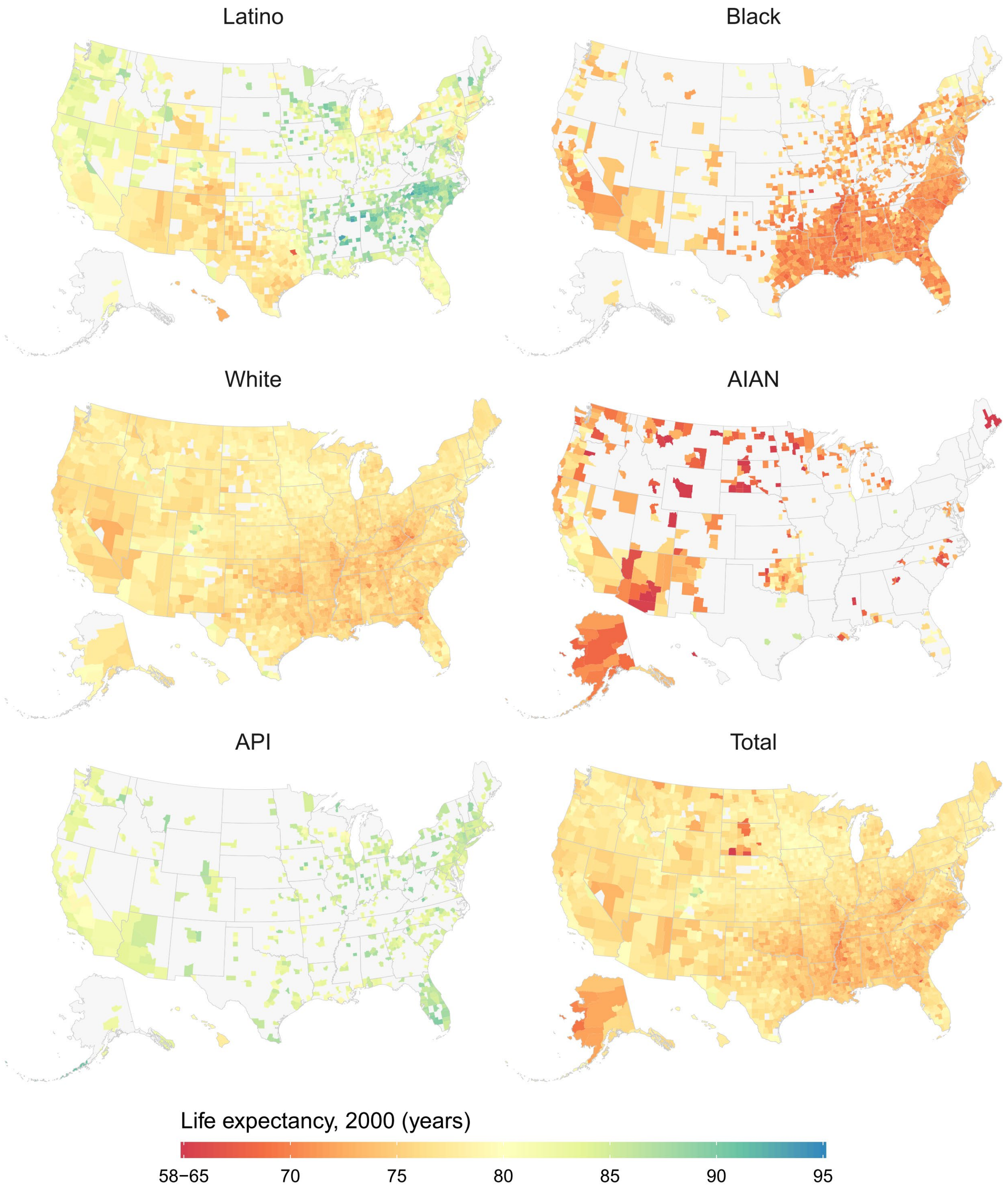
4.5 Impact of misclassification adjustment on county life expectancy estimates



County life expectancy estimates before adjustment for misclassification ("Modelled") and after adjustment and calibration ("Adjusted & Calibrated"), ie, the final estimates.

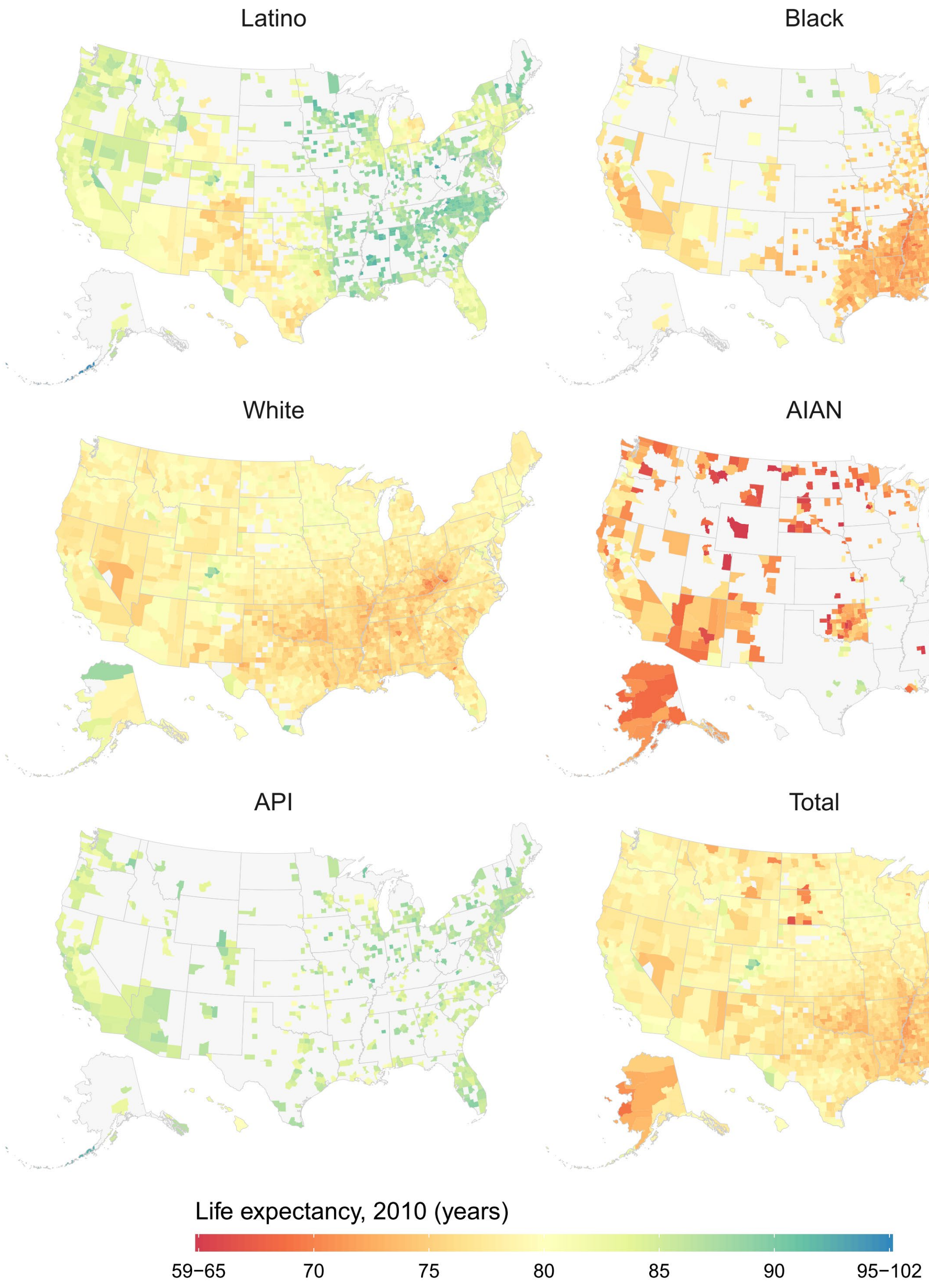
5 Supplemental Results Figures

5.1 County life expectancy by racial/ethnic group, 2000



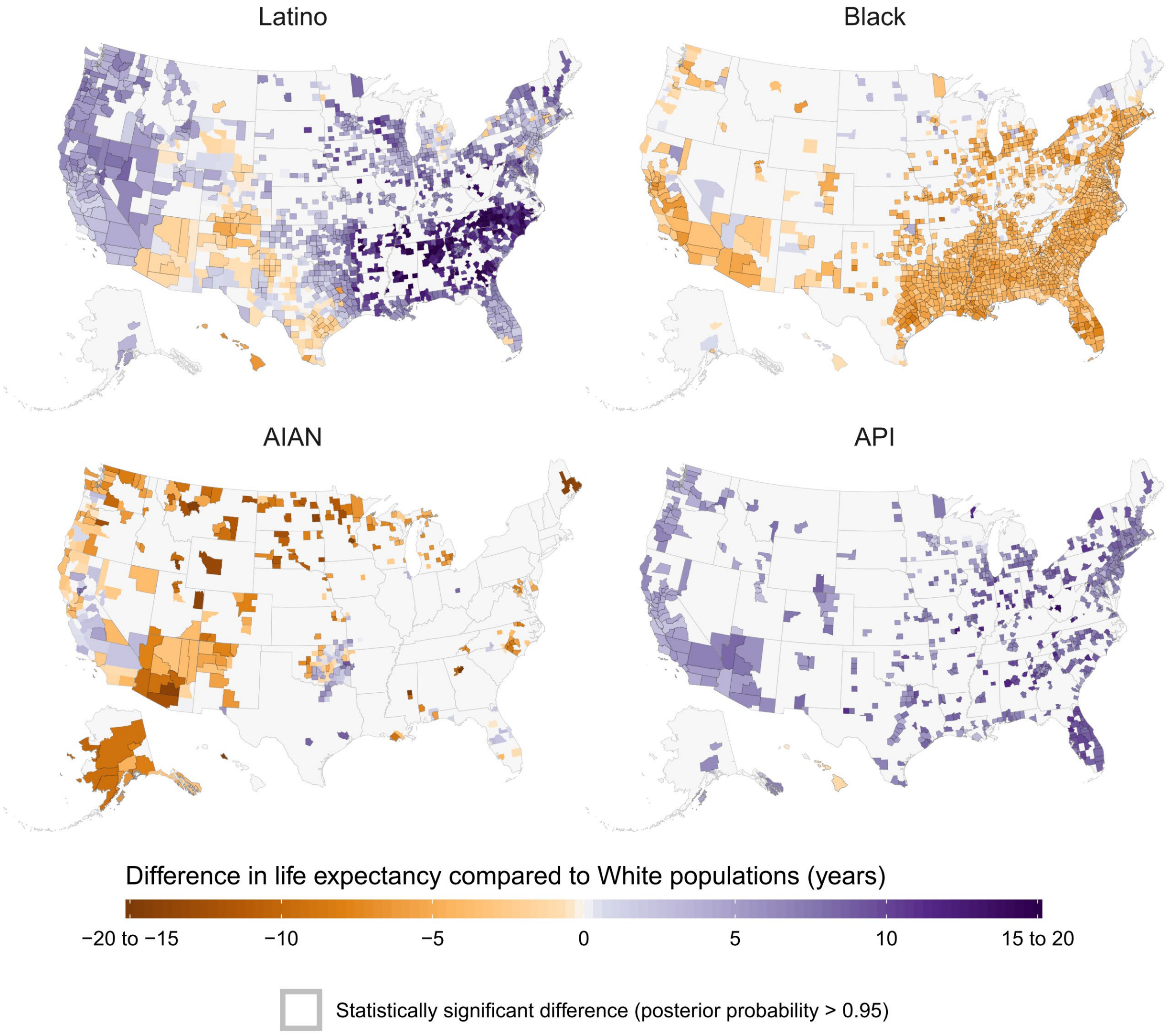
County life expectancy at birth by racial/ethnic group in 2000. The colour scale is truncated at 65 and 95 years, as indicated by the ranges in the legend. Estimates of life expectancy in county-racial/ethnic group combinations with an average annual population less than 1000 people and/or estimates with an uncertainty interval width greater than ten years are masked and depicted here in grey.

5.2 County life expectancy by racial/ethnic group, 2010



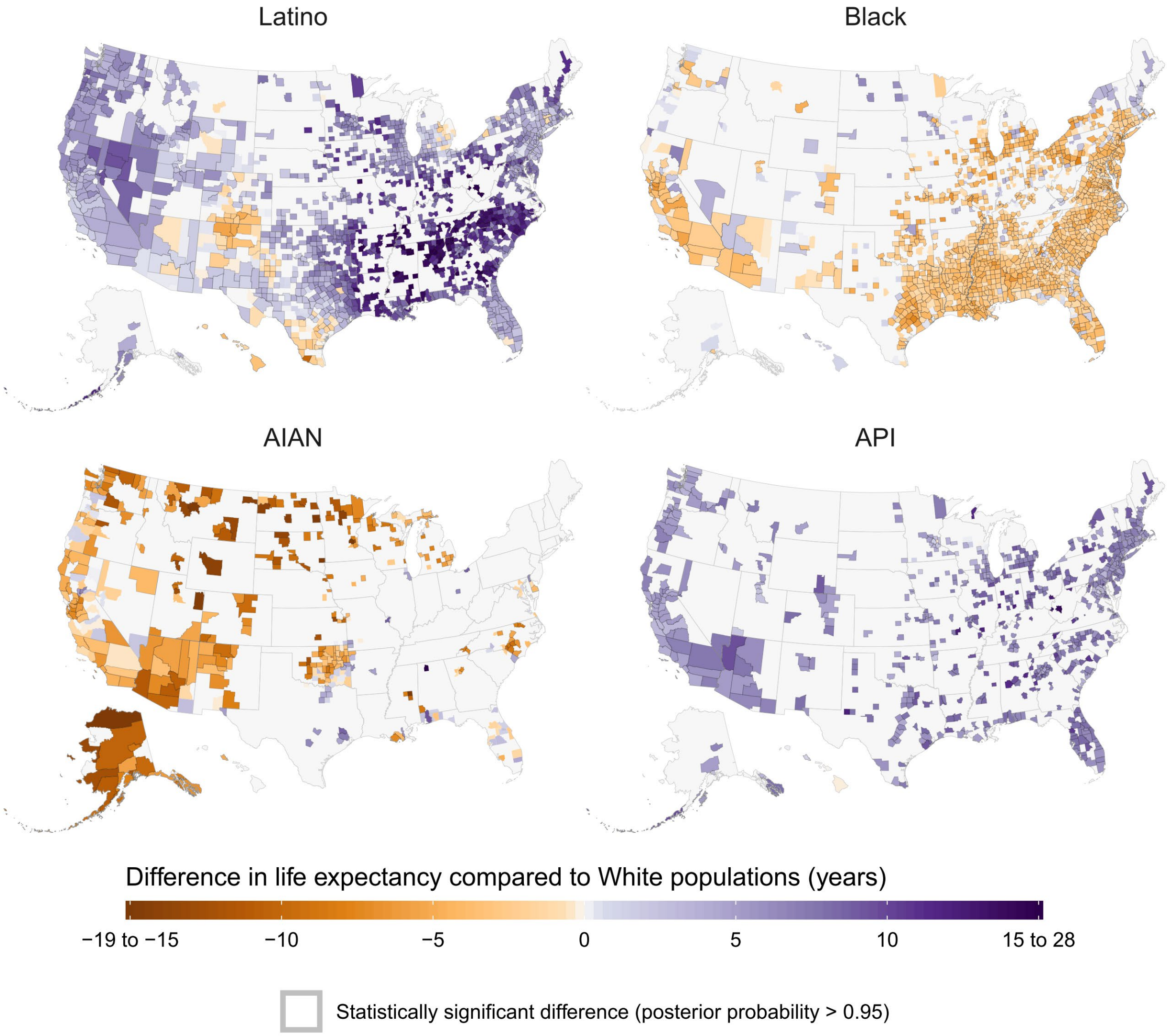
County life expectancy at birth by racial/ethnic group in 2010. The colour scale is truncated at 65 and 95 years, as indicated by the ranges in the legend. Estimates of life expectancy in county-racial/ethnic group combinations with an average annual population less than 1000 people and/or estimates with an uncertainty interval width greater than ten years are masked and depicted here in grey.

5.3 Differences in county life expectancy among racial/ethnic groups compared to the White population, 2000



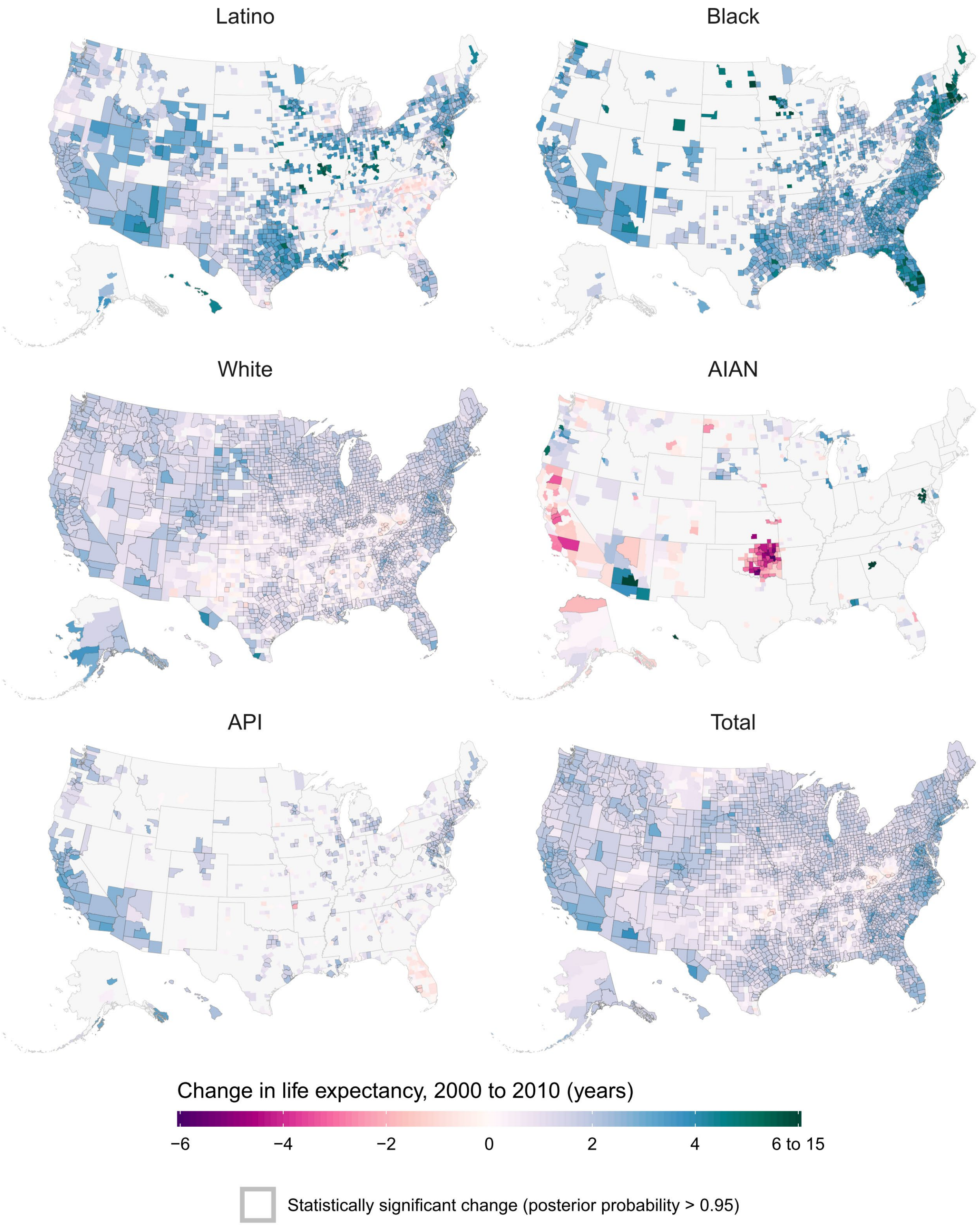
Absolute difference in county life expectancy at birth by racial/ethnic group in 2000, relative to life expectancy for the White population in the same county. The colour scale is truncated at –15 and 15 years, as indicated by the ranges in the legend. Grey boundaries around a county indicate an estimated difference in life expectancy that is statistically significant. Estimates of life expectancy in county-racial/ethnic group combinations with an average annual population less than 1000 people and/or estimates with an uncertainty interval width greater than ten years are masked and depicted here in grey.

5.4 Differences in county life expectancy among racial/ethnic groups compared to the White population, 2010



Absolute difference in county life expectancy at birth by racial/ethnic group in 2010, relative to life expectancy for the White population in the same county. The colour scale is truncated at –15 and 15 years, as indicated by the ranges in the legend. Grey boundaries around a county indicate an estimated difference in life expectancy that is statistically significant. Estimates of life expectancy in county-racial/ethnic group combinations with an average annual population less than 1000 people and/or estimates with an uncertainty interval width greater than ten years are masked and depicted here in grey.

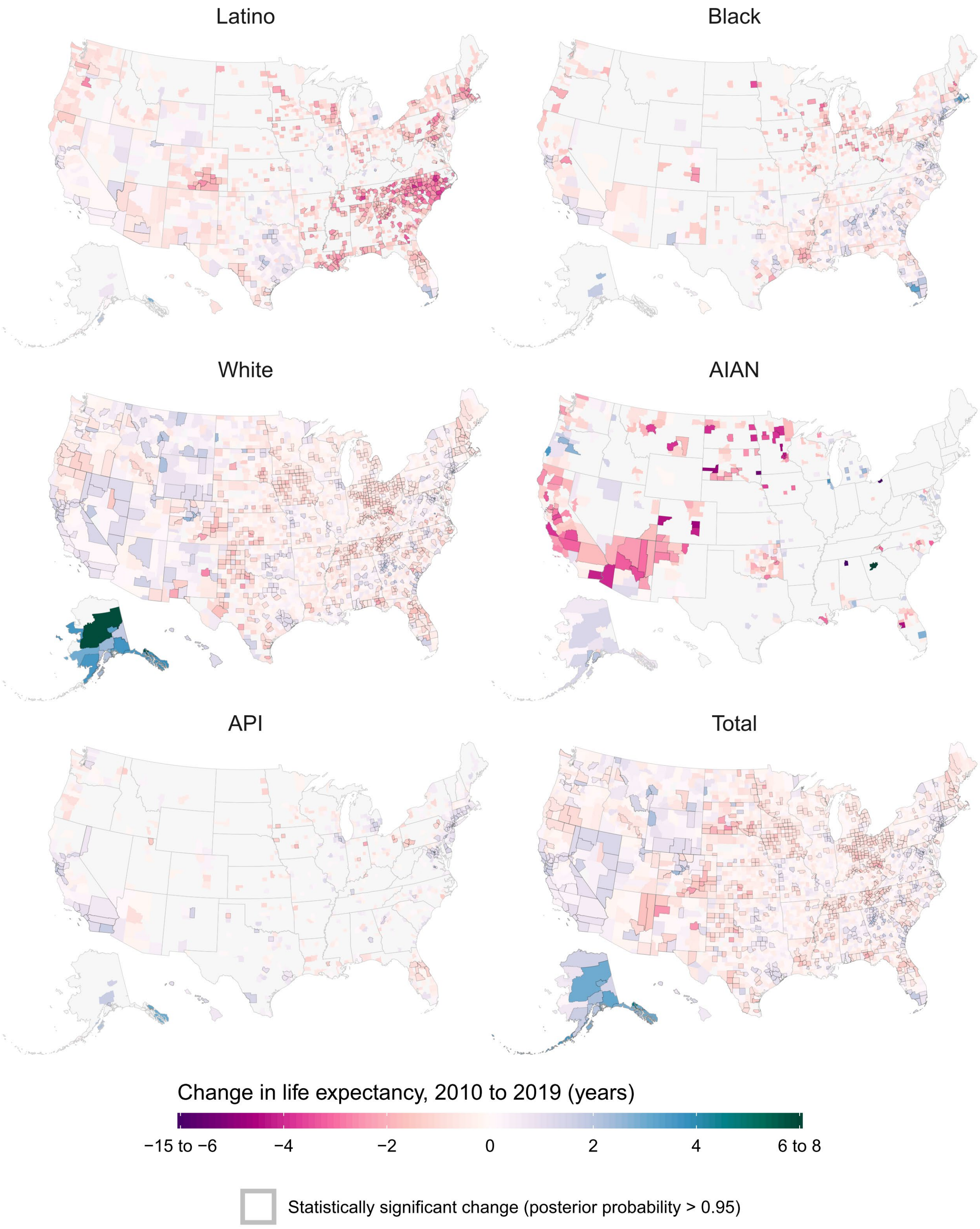
5.5 Change in county life expectancy by racial/ethnic group, 2000–2010



Absolute change in county life expectancy at birth from 2000 to 2010 by racial ethnic group. The colour scale is truncated at an absolute difference of –6 and 6 years, as indicated by the ranges in the legend.

Grey boundaries around a county indicate an estimated change in life expectancy that is statistically significant. Estimates of life expectancy in county-racial/ethnic group combinations with an average annual population less than 1000 people and/or estimates with an uncertainty interval width greater than ten years are masked and depicted here in grey.

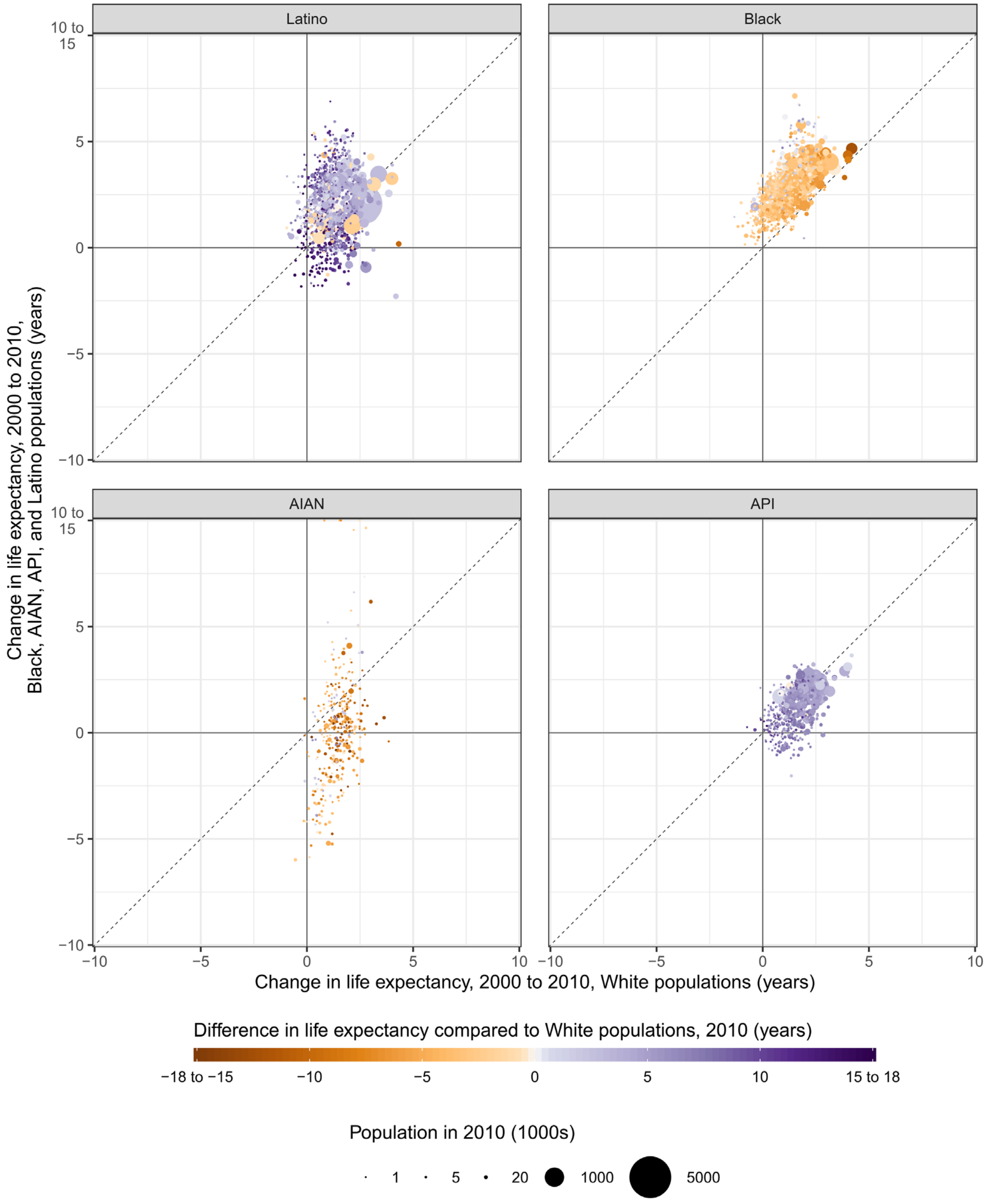
5.6 Change in county life expectancy by racial/ethnic group, 2010–2019



Absolute change in county life expectancy at birth from 2010 to 2019 by racial ethnic group. The colour scale is truncated at an absolute difference of –6 and 6 years, as indicated by the ranges in the legend.

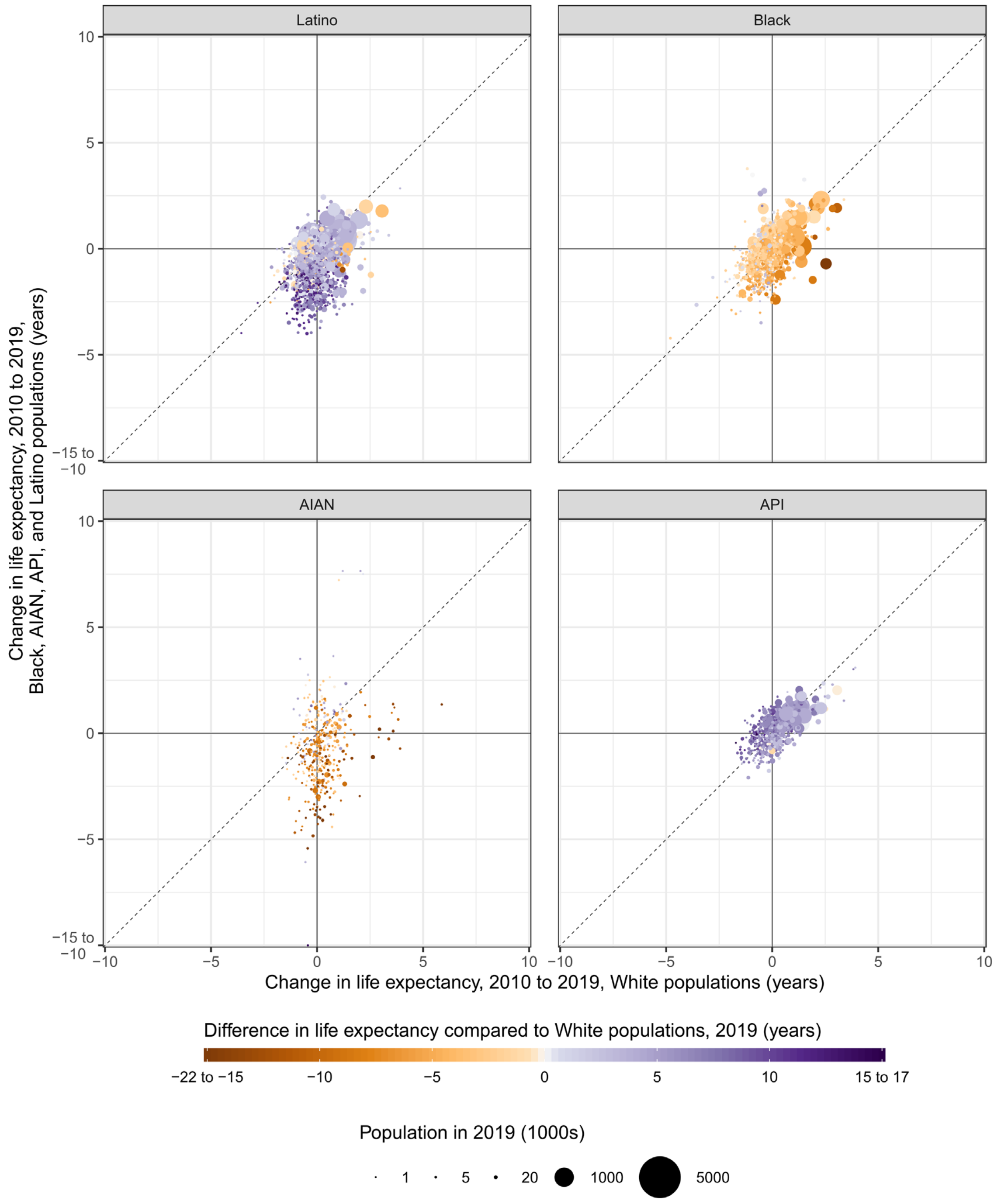
Grey boundaries around a county indicate an estimated change in life expectancy that is statistically significant. Estimates of life expectancy in county-racial/ethnic group combinations with an average annual population less than 1000 people and/or estimates with an uncertainty interval width greater than ten years are masked and depicted here in grey.

5.7 Change in county life expectancy by racial/ethnic group compared to the White population, 2000–2010



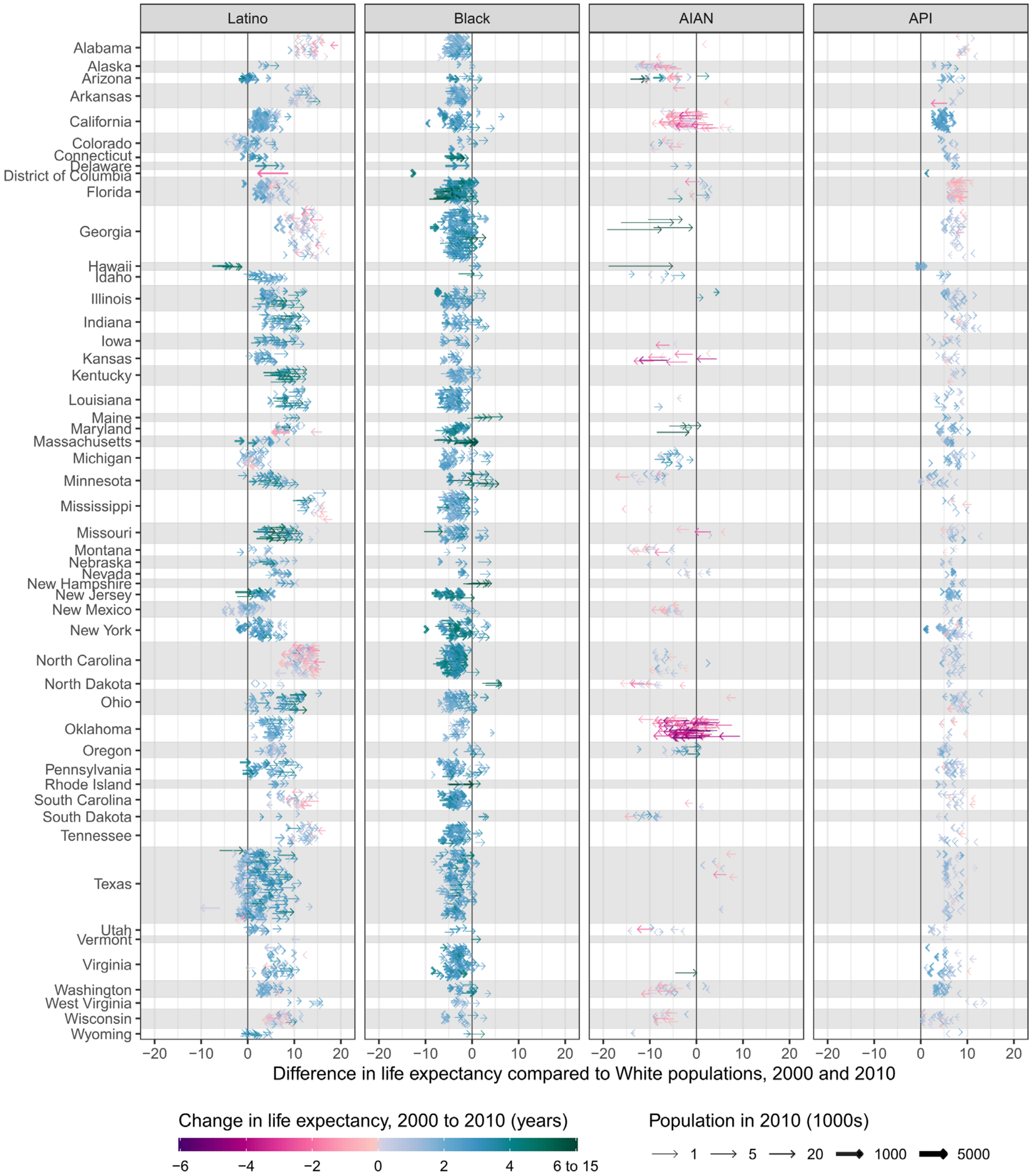
Absolute change in county life expectancy at birth from 2000 to 2010 for each racial ethnic group compared to this same change for the White population in the same county. Each point corresponds to a county, the colour of each point indicates the difference in life expectancy in this county in 2010 between the racial/ethnic group specified in the panel title and the White population, and the size of the point indicates the population in this county in 2010 for the racial/ethnic group specified. The axes are truncated at –10 and ten years, as indicated by the axis labels and the colour scale is truncated at –15 and 15 years, as indicated by the ranges in the legend. Estimates of life expectancy in county-racial/ethnic group combinations with an average annual population less than 1000 people and/or estimates with an uncertainty interval width greater than ten years are not displayed.

5.8 Change in county life expectancy by racial/ethnic group compared to the White population, 2010–2019



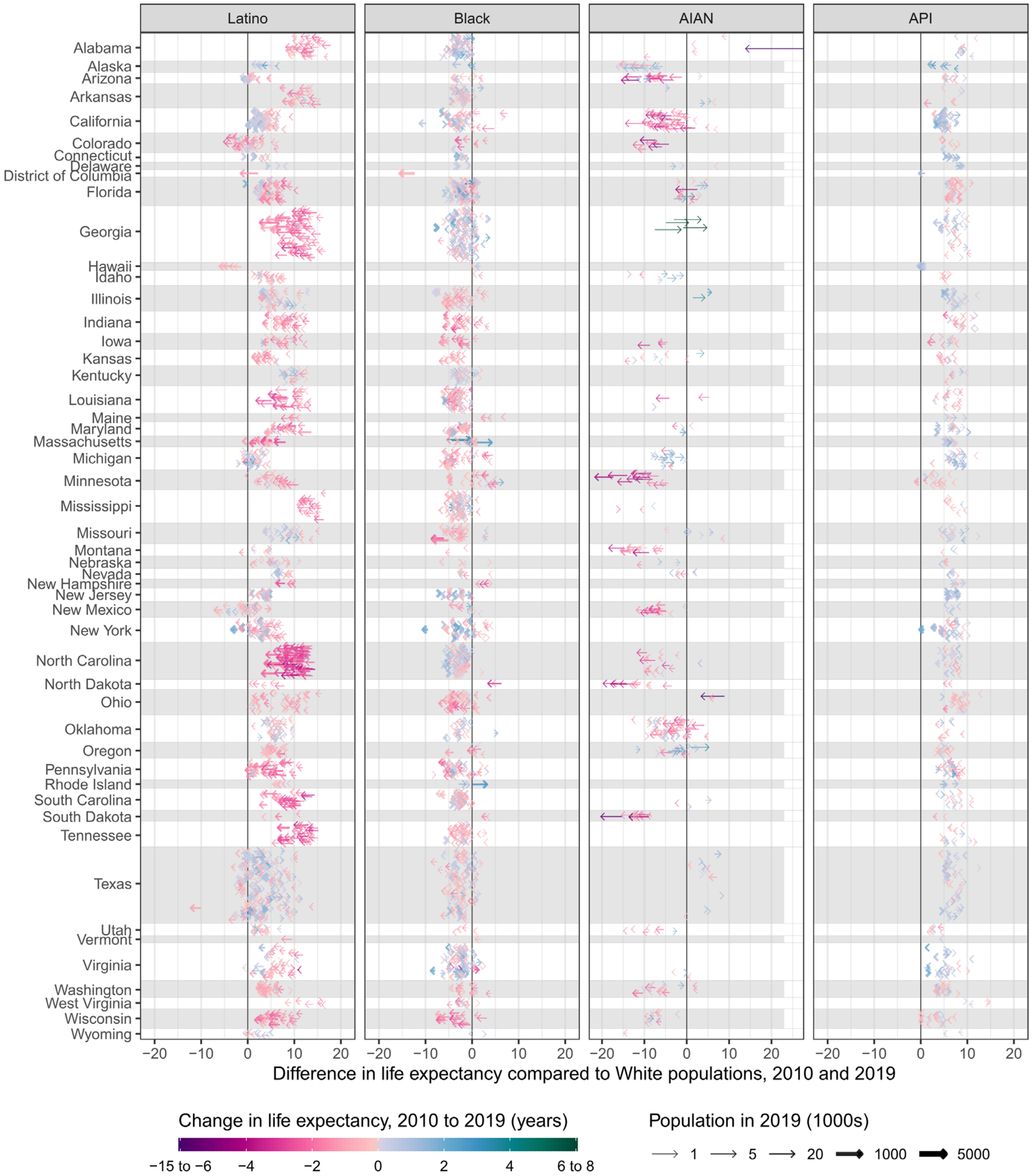
Absolute change in county life expectancy at birth from 2010 to 2019 for each racial ethnic group compared to this same change for the White population in the same county. Each point corresponds to a county, the colour of each point indicates the difference in life expectancy in this county in 2019 between the racial/ethnic group specified in the panel title and the White population, and the size of the point indicates the population in this county in 2019 for the racial/ethnic group specified. The axes are truncated at –10 and 10 years, as indicated by the axis labels and the colour scale is truncated at –15 and 15 years, as indicated by the ranges in the legend. Estimates of life expectancy in county-racial/ethnic group combinations with an average annual population less than 1000 people and/or estimates with an uncertainty interval width greater than ten years are not displayed.

5.9 Change in differences in county life expectancy among racial/ethnic groups compared to the White population, 2000–2010



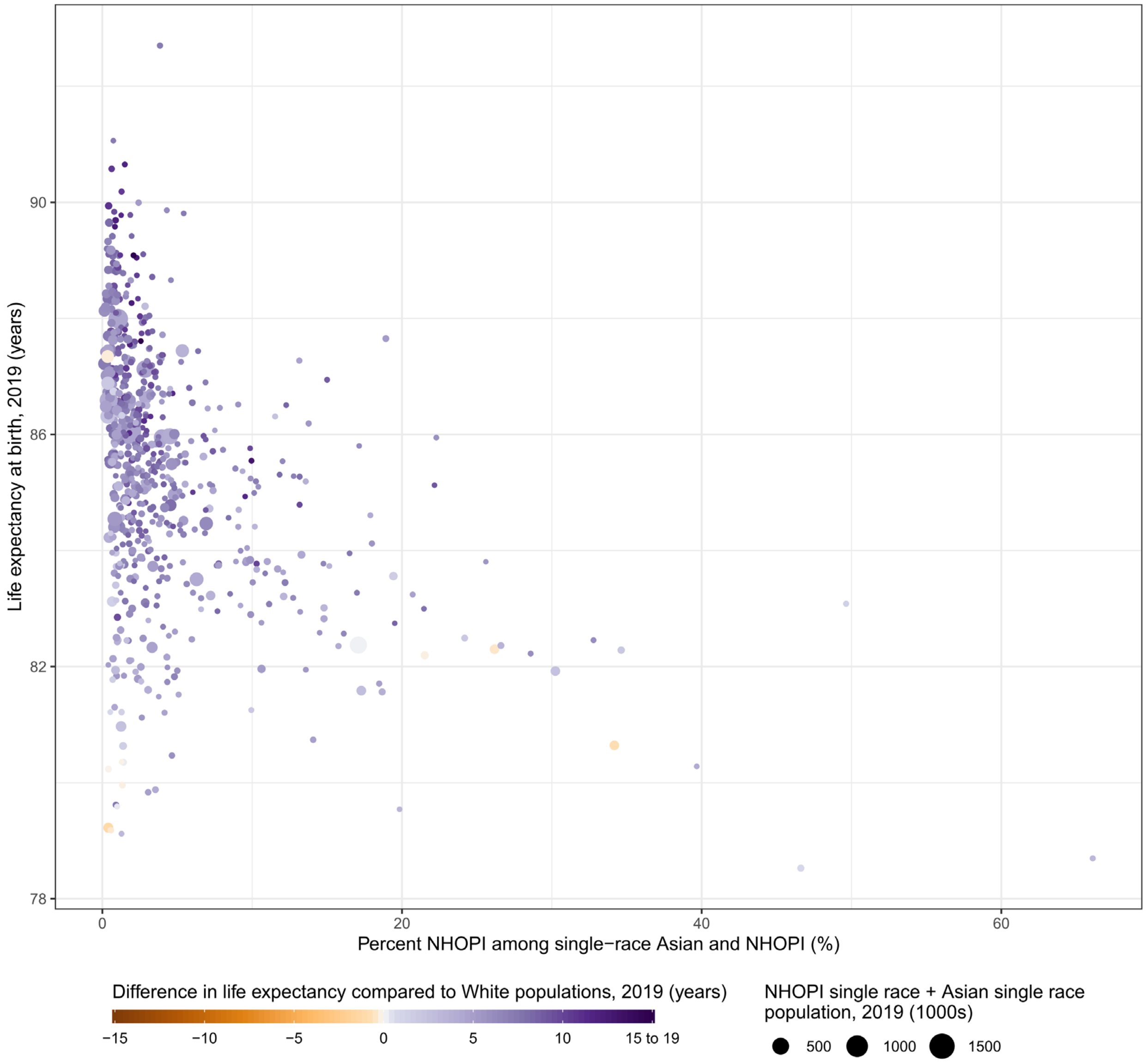
Absolute difference in county life expectancy at birth by racial/ethnic group in 2000 and 2010, relative to life expectancy for the White population in the same county. Each arrow corresponds to a county and the arrow starts at the difference in life expectancy between the racial/ethnic group specified in the panel title and the White population in that county in 2000 and ends at the same quantity in 2010. The colour of each arrow indicates the change in life expectancy over this period in a given county for the specified racial/ethnic group, and the size of the arrow indicates the population of this racial/ethnic group in 2010. The colour scale is truncated at an absolute difference of –6 and 6 years, as indicated by the ranges in the legend. Estimates of life expectancy in county-racial/ethnic group combinations with an average annual population less than 1000 people and/or estimates with an uncertainty interval width greater than ten years are not displayed.

5.10 Change in differences in county life expectancy among racial/ethnic groups compared to the White population, 2010–2019



Absolute difference in county life expectancy at birth by racial/ethnic group in 2010 and 2019, relative to life expectancy for the White population in the same county. Each arrow corresponds to a county and the arrow starts at the difference in life expectancy between the racial/ethnic group specified in the panel title and the White population in that county in 2010 and ends at the same quantity in 2019. The colour of each arrow indicates the change in life expectancy over this period in a given county for the specified racial/ethnic group, and the size of the arrow indicates the population of this racial/ethnic group in 2019. The colour scale is truncated at an absolute difference of –6 and 6 years, as indicated by the ranges in the legend. Estimates of life expectancy in county-racial/ethnic group combinations with an average annual population less than 1000 people and/or estimates with an uncertainty interval width greater than ten years are not displayed.

5.11 County life expectancy and the composition of the API population



County-level life expectancy at birth in 2019 among the API population versus the proportion of the single-race Asian and NHOPI population that is NHOPI based on county-level population estimates by race and ethnicity from the census bureau. This population proportion excludes multiracial individuals, as population estimates are not available for specific combinations of racial/ethnic groups. Estimates in this paper use a combined API category due to data constraints, but these estimates likely mask differences in life expectancy between Asian and NHOPI populations.