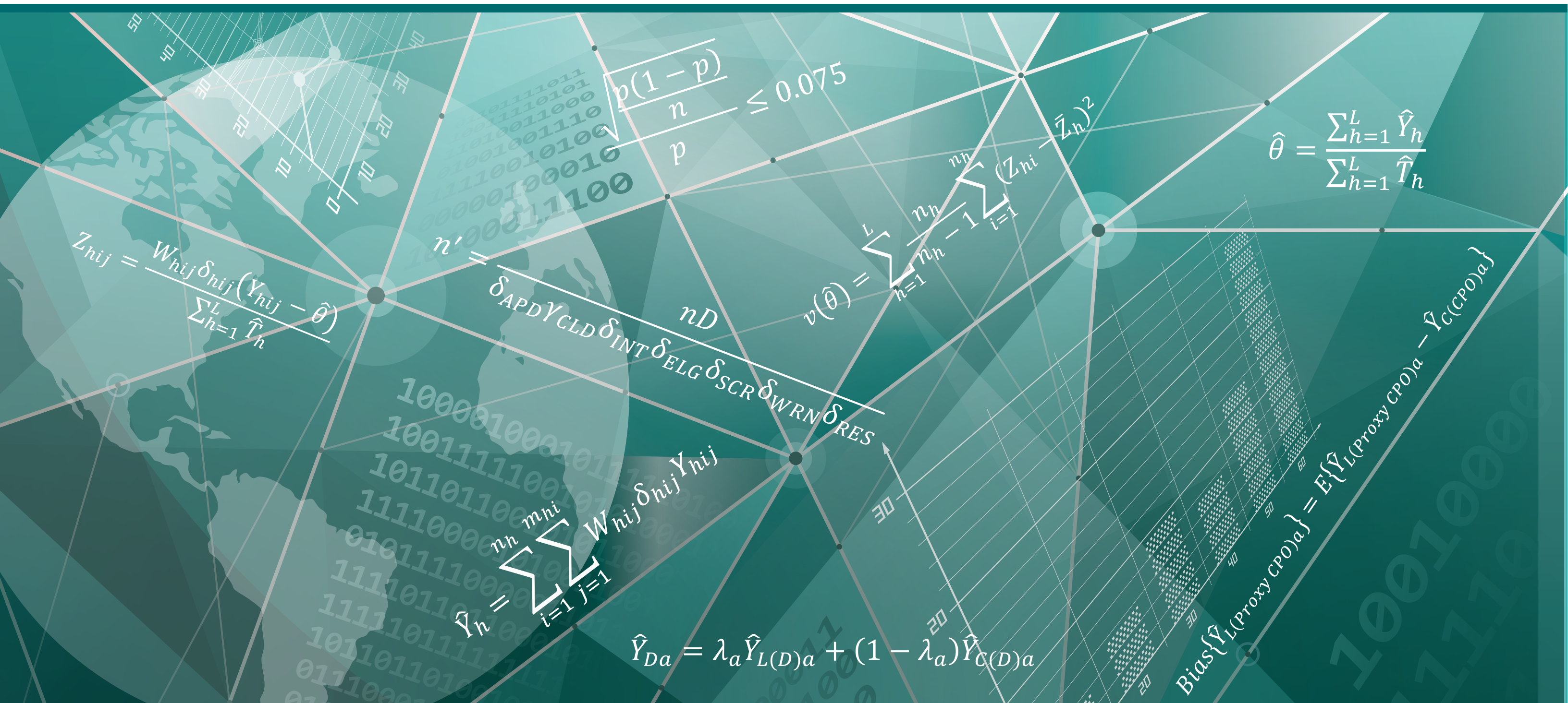
NATIONAL CENTER FOR HEALTH STATISTICS

Vital and Health Statistics

Series 2, Number 181 September 2018



U.S. Small-area Life Expectancy Estimates Project: Methodology and Results Summary

Data Evaluation and Methods Research

U.S. DEPARTMENT OF HEALTH AND HUMAN SERVICES
Centers for Disease Control and Prevention
National Center for Health Statistics

Suggested citation

Arias E, Escobedo LA, Kennedy J, Fu C, Cisewski J. U.S. small-area life expectancy estimates project: Methodology and results summary. National Center for Health Statistics. Vital Health Stat 2(181). 2018.

Library of Congress Cataloging-in-Publication Data

Names: National Center for Health Statistics (U.S.), issuing body.
Title: U.S. small-area life expectancy estimates project : methodology and results summary.
Other titles: Vital and health statistics. Series 2, Data evaluation and methods research ; no. 181. | DHHS publication ; no. (PHS) 2018-1381. 0276-4733
Description: Hyattsville, Maryland : U.S. Department of Health and Human Services, Centers for Disease Control and Prevention, National Center for Health Statistics, September 2018. | Series: Vital and health statistics. Series 2, Data evaluation and methods research ; number 181 | Series: DHHS pub ; number 2018-1381 | Includes bibliographical references.
Identifiers: LCCN 2018038892 | ISBN 0840606923 (pbk.)
Subjects: | MESH: Life Expectancy | Small-Area Analysis | United States Classification:
LCC QP85 | NLM W2 A N148vb no.181 2018 | DDC 612.6/8--dc23 LC record available at
https://lccn.loc.gov/2018038892

For sale by the U.S. Government Publishing Office
Superintendent of Documents
Mail Stop: SSOP
Washington, DC 20401–0001
Printed on acid-free paper.

NATIONAL CENTER FOR HEALTH STATISTICS

Vital and Health Statistics

Series 2, Number 181 September 2018

U.S. Small-area Life Expectancy Estimates Project: Methodology and Results Summary

Data Evaluation and Methods Research

U.S. DEPARTMENT OF HEALTH AND HUMAN SERVICES
Centers for Disease Control and Prevention
National Center for Health Statistics

Hyattsville, Maryland
September 2018
DHHS Publication No. 2018–1381

Contents

Text Figures

Contents—Con.

Detailed Tables

Acknowledgments

The authors would like to thank Paul Sutton, Deputy Director of the Division of Vital Statistics (DVS), National Center for Health Statistics (NCHS), and members of the National Association for Public Health Statistics and Information Systems (NAPHSIS), state vital registration offices, and the U.S. Small-area Life Expectancy Project (USALEEP) advisory panel for their leadership and oversight of this project. Financial support for this project was provided in part by the Robert Wood Johnson Foundation through a grant (73395) to NCHS. The authors are grateful for the insightful reviews and comments provided by Jennifer Madans, Office of the Director, NCHS; Hanyu Ni, DVS; and, Robert N. Anderson, Mortality Statistics Branch (MSB) of DVS. We would also like to thank Brigham Bastian, MSB, for technical support; Sally Curtin, MSB, for content review; Van Parsons, Office of Research Methodology, NCHS, for statistical consultation; David A. Raglin and his team, ACS Survey Analytics and Measures Branch, U.S. Census Bureau, for population estimates consultation; and Jon Sperling and Robert N. Renner, U.S. Department of Housing and Urban Development, for technical assistance on the geospatial data.

U.S. Small-area Life Expectancy Estimates Project: Methodology and Results Summary

by Elizabeth Arias, Ph.D., and Loraine A. Escobedo, Ph.D., National Center for Health Statistics; and Jocelyn Kennedy, M.S., Chunxia Fu, M.S., and Jodi Cisewski, M.P.H., Northrop Grumman Corporation

Abstract

Objectives

This report describes the methodology developed to produce the first set of abridged period life tables for U.S. census tracts for the 2010–2015 period and presents a summary of results.

Methods

The methodology used to calculate the U.S. census-tract abridged life tables consisted of several stages. First, through a collaboration between the National Vital Statistics System registration areas and the National Center for Health Statistics, death records of U.S. residents (excluding residents of Maine and Wisconsin) for deaths occurring in 2010 through 2015 were geocoded using decedents' residential addresses to identify and code census tracts. Second, population estimates were produced based on the 2010 decennial census and the 2011–2015 American Community Survey 5-year survey. Third, a methodology that combined standard demographic techniques and statistical modeling was developed to address challenges posed by small population sizes and small and missing age-specific death counts. Last, standard, abridged life table methods were adjusted to account for error introduced by population estimates based on sample data.

Results

Statistically reliable, abridged, period life tables were produced for 88.7% of U.S. census tracts (65,662). A battery of tests revealed that the census-tract life table functions followed expected patterns; their distribution about state and U.S. values showed no aberrations; and their weighted mean values compared well with state- and national-level estimates. The weighted mean life expectancy at birth for the 65,662 census tracts was 78.7 years compared with the official U.S. estimate of 78.8 years in midyear 2013. The results of this study concur with previous research showing that a minimum population size of 5,000 is acceptable, with the caveat that missing age-specific death counts cannot be ignored. The methodology developed for this study addressed the issues of small populations and zero deaths as robustly as possible, although it is not without error.

Keywords: census tract • life tables • mortality disparities • National Vital Statistics System • American Community Survey • 2010 Decennial Census

Introduction

A growing body of research is recognizing the importance of measuring mortality outcomes in small geographic areas, such as U.S. census tracts, to identify health disparities within a population (1–5). The indicator most widely identified as the ideal measure of a population's mortality experience is life expectancy at birth. The concept of life expectancy is intuitive and easily understood by both policymakers and the lay public (6,7). Life expectancy is estimated for national populations by most developed countries, including the United States, which has produced the estimate annually since 1945 and decennially since 1900 (8). However, its calculation is relatively complex compared with that of other summary mortality measures, because it entails the calculation of six distinct functions and requires a minimum number of age groups and total population size, below which the estimates become unstable and unreliable (9,10).

For geographic areas with relatively small populations, such as U.S. census tracts, several data and methodological challenges need to be resolved to produce reliable and useful life expectancy estimates. The two most important data issues are the availability of death counts and population estimates for small geographic areas. In the United States, the smallest geographic identifier available nationally for mortality data is the county of residence of decedents. Similarly, the U.S. Census Bureau does not produce annual population estimates for geographic areas smaller than counties. Methodologically, small numbers of deaths and populations pose another set of difficulties. Below a certain minimum death count and population size, death rates and, by extension, life expectancy estimates become unstable and unreliable. Selecting a methodological strategy that can reliably address these issues is a challenge.

This report presents the first set of abridged U.S. census-tract life tables for 2010–2015 for the District of Columbia (D.C.) and all states excluding Maine and Wisconsin. The strategy used to produce these tables consisted of three stages. First, in collaboration with National Vital Statistics System (NVSS) registration areas, death records of U.S. residents for deaths occurring in 2010 through 2015 were geocoded using decedents' residential addresses to identify and code census tracts. Second, because Census Bureau postcensal population estimates for census tracts are not available, alternative population estimates were generated based on a combination of 2010 decennial census counts and American Community Survey (ACS) 5-year data for 2011–2015. Finally, a combination of demographic methods and statistical modeling was used to address the challenges to the calculation of reliable life tables posed by small population sizes and small and missing age-specific death counts.

Background

The Life Table

There are two types of life tables, cohort and period. The cohort life table presents the mortality experience of a real birth cohort from birth through consecutive years until all members of the cohort have died. A period life table presents the mortality experience of a population during a particular point (period) in time and applies the age-specific death rates of an actual population to a hypothetical birth cohort. Under the assumption that the hypothetical cohort will experience at every age the mortality of a real population in a particular period, the period life table provides detailed mortality information such as the probability of dying and life expectancy by age. A further classification of life tables is the size of age intervals. A complete life table includes information for every single year of age except the final age group, which is usually open-ended. An abridged life table aggregates ages into 5- or 10-year intervals, with the exception of the first (ages 0 to 1 year) and second (ages 1–5 years) age categories and the final open-ended age interval (8). The selection of either a complete or abridged life table depends on the availability of age-specific mortality and population data.

For small areas, such as U.S. census tracts, it is impossible to estimate complete life tables due to the small number of people at each age and the resulting small or nonexistent death counts. It is difficult to estimate a reliable age-specific death rate, which is the first function needed to calculate a life table. As a result, the abridged life table is the most appropriate type for small populations. The most widely used method for the estimation of abridged life tables is that developed by Chiang (9,10). The method presumes no age-specific missing information. Indeed, one of the reasons Chiang proposed for the construction of an abridged rather than a complete life table is that the latter is more likely to have missing age-specific information (i.e., deaths or populations) unless the population is very large (10).

More recently, Silcocks et al. proposed a different methodology for estimating abridged life tables for small areas. The Silcocks method differed from Chiang's method with respect to the assumed shape of mortality within age groups and in the measurement of the variance of life expectancy in the final age interval (6). Chiang assumed deaths were distributed evenly throughout an age interval except for the first age group (10). Silcocks, on the other hand, assumed that the death rate was constant throughout an age interval and, therefore, the number of survivors decreased exponentially (6). Chiang assumed no variance in the life expectancy of the final age interval because the probability of death was 1 and survival 0 in this age category. The Silcocks method assumed the factor of relevance was the length of survival, not its probability, and estimated a variance based on this assumption (11). Comparisons of the two methods concurred that the Chiang method was the most accurate, although estimation of the variance of life expectancy in the oldest age group, which Chiang omits, was recommended (7,11–13).

Minimum Population Sizes and Death Counts

No universal standard exists for the minimum population size or death count required to estimate a reliable small-area life table. In the case of crude, age-specific and age-adjusted death rates, the National Center for Health Statistics (NCHS) has established guidelines that preclude the release of estimates with coefficients of variation (CV) greater than 23%, or based on fewer than 20 deaths (14). With respect to life tables, NCHS has alternatively relied on the use of the CV and smoothing techniques to determine the minimum number of deaths required to produce reliable complete life tables. The 1969–1971 decennial life table series, for example, excluded state-specific life tables for the black population that had crude death rates with CVs of more than 2.5% (15). The 1989–1991 series excluded tables based on fewer than 700 deaths using a manual smoothing technique (16). The latest decennial tables exclude tables with fewer than 300 deaths based on a statistical smoothing method that borrows information from past mortality data (17).

Experimental work investigating methods for calculating small-area life expectancy estimates, published by the United Kingdom's Office for National Statistics and the South East Public Health Observatory, concluded that a minimum population size of 5,000 was necessary for reliable estimates (7,11,12,18).

Missing Age-specific Deaths (Zero Cells)

Besides the problem of small population sizes and death counts, there is also the issue of missing deaths in some age groups. Missing deaths in an abridged life table estimated using Chiang's method causes the calculation of standard errors of the probability of death to fail and, therefore, leads to underestimation of the variance of life expectancy at birth. The Silcocks method allows for missing age-specific deaths; however, as already noted, some comparative research of the two methods consistently found that the Chiang method produced more accurate estimates. Further, missing age-specific deaths present other problems beyond the effects on variances of the life table functions. A significant problem rarely discussed in previous research on small-area life expectancy estimation is the biasing effect of missing age-specific deaths on overall life expectancy estimates and the underlying mortality profile of a population. The focus has been solely on the effect of missing deaths on the standard error of life expectancy at birth. Because of the seemingly small impact of zero age bands on the standard errors of life expectancy at birth for populations of 5,000 or larger, several authors have recommended refraining from any form of imputation, except for the oldest age interval to avoid assigning an infinite mean life expectancy for the oldest age band (11,12,19). Leaving age bands with zero deaths, however, ignores the underlying age-specific mortality pattern, or schedule, of a population. The underlying true mortality pattern can be misidentified when age-specific information is missing, particularly when the numbers of age categories with missing information are large.

Several methods of imputation have been proposed and tested (6,20) that include using death rates from larger geographic units, applying weights that are inversely proportional to the standard error of the census tract and adjacent units, and substituting zero cells with small positive values. Other tested methods include standard regression analyses that model relationships between death rates and population demographic and socioeconomic characteristics; graduation techniques that smooth crude mortality rates; and Bayesian random effects models that pool strength over geographic areas, age, time, and population groups (4,5,21–27). A more recent study supplemented the Bayesian framework with principal component methods that capture typical age patterns of mortality to estimate small-area death rates (1).

Data Availability for Small Areas

Mortality data

NCHS agreements with the 57 vital registration areas that form part of the official NVSS for the collection of mortality data do not include the requirement to produce geographic identifiers below the county level. As a result, county of residence is the smallest geographic identifier available in official NVSS mortality data files created by NCHS. To produce census tract-level life tables for this project, it was necessary to first geocode death records (28).

Population data

Census tracts typically have 1,200–8,000 people, with an average population size of 4,000 people, and were designed to be homogenous with respect to demographic characteristics, economic status, and living conditions when first delineated using local committees (29). In 2010, 70% of U.S. census tracts had populations of less than 5,000 (30).

To prepare the annual U.S. life tables, NCHS uses census counts and post- and intercensal population estimates based on the decennial census, produced under a collaborative agreement with the Census Bureau (8). As with mortality data, population estimates based on census data are not available for geographic areas below the county level. Although not intended for this purpose, ACS is the only source of population estimates at the census-tract level for intercensal years. Conducted by the Census Bureau, ACS is an ongoing survey implemented during and between decennial census years. It has been designed to measure the changing social, economic, demographic, and housing characteristics of the U.S. population since 2005 (31).

Data and Methods

Data

The data used to produce the abridged life tables combine 6 years of NVSS mortality data (2010–2015) and use 2010 decennial census population counts and ACS 5-year estimates (2011–2015).

NVSS data

The mortality data used to compute the abridged life tables by census tracts are the final death counts for each year of the 2010–2015 period, collected from death certificates filed in state vital statistics offices and reported to NCHS as part of NVSS. Fifty-one registration areas—all U.S. states (excluding Maine and Wisconsin), New York City, D.C., and Puerto Rico—provided NCHS with usable residential address information for all deaths that occurred in their jurisdictions in 2010 through 2015. Through a collaborative agreement between NCHS and the U.S. Department of Housing and Urban Development (HUD), residential addresses of decedents were sent to the HUD Geocode Service Center for geocoding. The geocoded information was used to identify their corresponding census tract codes. Death records that were successfully geocoded to census tract were matched back to NVSS mortality data files for 2010–2015, and those considered of high quality—records whose census-tract codes were based on street address or 9-digit zip code matches—were used to produce the abridged life tables by census tracts.

Census and ACS data

The population data used to compute the 2010–2015 abridged life tables by census tracts include counts of the population residing in the United States and enumerated as of April 1, 2010, by the decennial census conducted by the Census Bureau; and population estimates based on ACS combined 2011–2015 samples. The primary focus of ACS is not the provision of official post- or intercensal population estimates (31). However, the Census Bureau's Population Estimates Program does not produce population estimates for geographic areas below the county level and, therefore, ACS was the only available source of estimates for 2011–2015 census tract-level populations.

The strategy of combining decennial census counts with ACS survey-based estimates resulted from an exploration of the benefits and drawbacks of pooling 5 or 6 years of data. Pooling over a shorter time span increases the accuracy of the life expectancy estimates (20). However, the reliability of these estimates diminishes when death counts are too small or missing and population estimates have sampling error. Adding an additional year of data increased the number of deaths while simultaneously reducing the variance of the population estimates, because the decennial census counts are not affected by sampling error; only the 2011–2015 ACS 5-year population estimates are affected by sampling error. As a result, the 6-year population estimate is affected by only 5 years of sampling error.

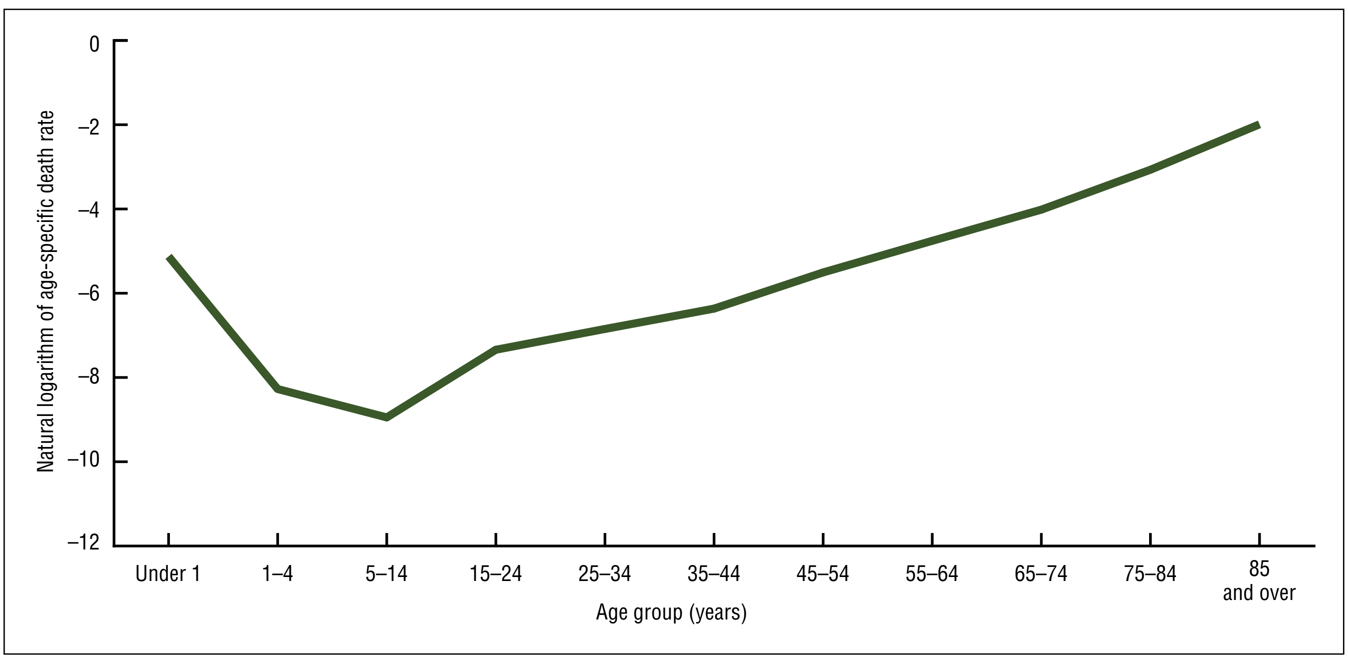
Methods

The final stage of this project, the methodology, consisted of three phases. Phase 1 entailed the estimation of age-specific death rates for census tracts with minimum pooled population sizes of 5,000 people over the 6-year period (2010–2015) and no missing age-specific death counts. Tracts with acceptable age patterns, or schedules, of mortality (defined below) served as models from which to borrow information for tracts with missing age-specific death counts. In Phase 2, zero-truncated Poisson and negative binomial models were fitted to Phase 1 model tracts. Resulting model parameter estimates were used to predict age-specific death rates. Missing observed age-specific death rates due to zero death counts in tracts with minimum pooled population sizes of 5,000 over the 6-year period were replaced with predicted values based on their combinations of demographic, socioeconomic, and geographic characteristics included in the models. In Phase 3, abridged life tables were calculated for all tracts with minimum pooled population sizes of 5,000; complete age-specific death counts, either observed or predicted; and acceptable age patterns of mortality. Results were evaluated for reliability using various demographic and statistical techniques.

Selection of Phase 1 tracts for modeling

The selection of Phase 1 census tract-data for the generation of predicted death rates depended on whether the observed age-specific death rates were consistent with the age-specific mortality pattern universally observed in human populations (Figure 1). Figure 1 displays the age-specific

Figure 1. Age pattern (schedule) of mortality: United States, 2013



NOTE: Values are based on official statistics published in "Deaths: Final Data for 2013," available from: https://www.cdc.gov/nchs/data/nvsr/nvsr64/nvsr64_02.pdf.
SOURCE: NCHS, National Vital Statistics System, Mortality.

death rates on the logarithmic scale for the U.S. population in 2013, selected as the midpoint of the 2010–2015 period. Three components of the mortality curve stand out. First, mortality at birth is higher than in subsequent ages into middle adulthood. Second, mortality is at its lowest point in middle childhood, around ages 5–14. Third, the rate of change in mortality increases with age and may decelerate in very old ages. Smoothing was undertaken in the adult age range when very small counts made the rates erratic, making it difficult to observe the rate of change across age-specific death rates. Phase 1 census tracts with age-specific mortality curves that had these three basic characteristics were considered acceptable and selected for modeling regardless of overall mortality levels or other variations, such as the existence or absence of accident humps.

Predicted age-specific death rates

Under the assumption that the underlying distribution of deaths follows a Poisson process, age-specific zero-truncated Poisson or negative binomial models were fitted to the model Phase 1 census tract—tracts with a minimum population of 5,000 over the 6-year period, no missing age-specific death counts, and age patterns of mortality that met the characteristics described above. Predicted age-specific death rates, ${}_n\overline{M}_x$, were estimated from the model results. The models included seven covariates that describe the socioeconomic and demographic characteristics of the tract-level populations, obtained from the 2010 decennial census data and the 2011–2015 ACS 5-year sample. They included quartiles of median household income, population density, and the proportions of the population that are non-Hispanic black, Hispanic, and had a 4-year college degree or higher in the census tract; and a binary variable indicating whether the census tract belonged to a Purchased/Referred Care Service Delivery Area (PRCSDA). PRCSDAs are counties that include all or part of a reservation or share a boundary with a reservation and, as a result, have high proportions of American Indian and Alaska Native populations who have significantly higher mortality than all other race and Hispanic-origin groups in the United States (32).

A control for geographic region (Northeast, Midwest, South, and West) of the country was also included to reduce the potential biasing effects of regional concentration of census tracts in Phase 1 on the predicted values. The Northeast region comprises 9 states: Connecticut, Maine, Massachusetts, New Hampshire, New Jersey, New York, Pennsylvania, Rhode Island, and Vermont. The 12 states that make up the Midwest region are Illinois, Indiana, Iowa, Kansas, Michigan, Minnesota, Missouri, Nebraska, North Dakota, Ohio, South Dakota, and Wisconsin. The South region includes D.C. and 16 states: Alabama, Arkansas, Delaware, Florida, Georgia, Kentucky, Louisiana, Maryland, Mississippi, North Carolina, Oklahoma, South Carolina, Tennessee, Texas, Virginia, and West Virginia. The West region consists of 13 states: Alaska, Arizona, California, Colorado, Hawaii, Idaho, Montana, Nevada, New Mexico, Oregon, Utah, Washington, and Wyoming.

The choice of a Poisson model compared with a negative binomial model is dictated by the variance of the count variable—in this case, the age-specific number of deaths, ${}_nD_x$. In cases where the variance is not equal to the expected value of the count variable (i.e., overdispersion), a negative binomial model is preferred, because it accounts for the extra variation of a Poisson-distributed count variable. Deviance goodness-of-fit tests were used to determine whether a Poisson process with no overdispersion generated the data. The negative binomial model includes an overdispersion parameter, α. A likelihood ratio test of α = 0 is used to determine if the negative binomial model is preferable.

The predicted death rate, ${}_n\overline{M}_x$, was estimated as:

$$ {}_n\overline{M}_x = e^{\beta_0+\beta_1 Y_1+\ldots+\beta_k Y_k} \quad [1] $$

where β_0, β_i, *and* Y_i are the model constant, coefficients, and independent covariates, respectively. The age-specific exposure is the observed age-specific population count, ${}_nP_x$, and the age-specific predicted number of deaths, ${}_n\overline{D}_x$, is defined as:

$$ {}_n\overline{D}_x = e^{\ln({}_nP_x)+\beta_0+\beta_1 Y_1+\ldots+\beta_k Y_k} \quad [2] $$

Abridged life tables

Census-tract abridged life tables were constructed using the methodology developed by Chiang with the modifications described below (10). The life table columns include:

Age

The age interval between two exact ages, x and $x + n$. For this study, the 11 age groups used were: 0, 1–4, 5–14, 15–24, 25–34, 35–44, 45–54, 55–64, 65–74, 75–84, and 85 and over.

Probability of dying, ${}_nq_x$

The probability of dying between two exact ages, x and $x + n$, is defined as:

$$ {}_nq_x = \frac{n_x * {}_nM_x}{1+(1-a_x) * n_x * {}_nM_x} \quad [3] $$

where ${}_nM_x$ is the age-specific period death rate, $\frac{{}_nD_x}{{}_nP_x}$, and

$$ {}_nD_x = \sum_{y=2010}^{y=2015} {}_nD_x{}^y \,,\ {}_nP_x = {}_nP_x{}^{DCP} + (5 * {}_nP_x{}^{ACSP}),\ {}_nP_x^{DCP} $$

is the 2010 decennial census population count; ${}_nP_x{}^{ACSP}$ is the average ACS 2011–2015 population estimate; n_x is the size of the age interval in years; and a_x is the fraction of life lived by those who died in the age interval.

Number surviving, l_x

The number of persons surviving to the beginning of the age interval from the original 100,000 hypothetical live births is defined as:

$$l_{x+n} = l_x - {}_nd_x \qquad [4]$$

where the radix of the table l_0 = 100,000.

Number dying, ${}_nd_x$

The number of persons dying in the age-interval x and $x + n$ is defined as:

$${}_nd_x = l_x \ * \ {}_nq_x \qquad [5]$$

Person-years lived, ${}_nL_x$

The number of person-years lived by the hypothetical life table cohort within an age interval x and $x + n$ is defined as:

$${}_nL_x = n_x * (l_x - {}_nd_x) + a_x * n_x * {}_nd_x \qquad [6]$$

where ${}_\infty L_x$, the person-years lived in the final open-ended age interval, is defined as:

$${}_\infty L_x = \frac{l_x}{{}_\infty M_x}$$

Total number of person-years lived, T_x

The number of person-years that would be lived after the beginning of the age interval x and $x + n$ is defined as:

$${}_nT_x = \sum_{x=0}^{x=\infty} {}_nL_x \qquad [7]$$

Expectation of life, e_x

The average number of years to be lived by those surviving to age x is defined as:

$$e_x = \frac{T_x}{l_x} \qquad [8]$$

Variances and standard errors of the probability of dying and life expectancy

Variance of ${}_nq_x$

The variance of the age-specific probability of dying, $Var({}_nq_x)$, is a function of the variance of the age-specific death rate, $Var({}_nM_x)$. The standard definition of $Var({}_nM_x)$ is based on the assumption that ${}_nP_x$ is a constant and, as a result, only the random error of ${}_nD_x$ affects $Var({}_nM_x)$. However, because ACS population estimates are based on sample data, the denominator of ${}_nM_x$ is affected by sampling error. As a result, $Var({}_nM_x)$ is a function of both the variance of ${}_nD_x$, $Var({}_nD_x)$, and the variance of ${}_nP_x$, $Var({}_nP_x)$. The delta method was used to approximate $Var({}_nM_x)$ and $Var({}_nq_x)$ as:

$$Var({}_nM_x) \approx \left(\frac{1}{{}_nP_x^{\,2}} \ * \ Var({}_nD_x)\right) + \left(\frac{{}_nD_x^{\,2}}{{}_nP_x^{\,4}} \ * \ Var({}_nP_x)\right) \qquad [9]$$

and

$$Var({}_nq_x) \approx \left(\frac{n_x}{(1+(1-a_x) \ * \ n_x \ * \ {}_nM_x)^2}\right)^2 \ * \ Var({}_nM_x) \qquad [10]$$

where $Var({}_n\bar{M}_x)$ and $Var({}_m\bar{D}_x)$ are used in place of the observed values as needed for Phase 2 tracts.

Variance of e_x

The variance of the age-specific expectation of life, e_x, is a function of the variance of the age-specific probability of death, $Var({}_nq_x)$. Chiang assumed that because q_{85+} = 1.00 and, equivalently, the probability of survival, p_{85+}, is equal to zero, then $Var(q_{85+})$ is equal to zero, and as a result, so is $Var(e_{85})$. Silcocks et al. proposed that in the final age group, life expectancy is dependent on the mean length of survival and not on the probability of survival, and, therefore, the assumption of no variance is incorrect (6). This proposition has been determined to have merit and, as a result, the variance of the last age interval is accounted for in this study (11,13). For ages 0 through 75–84:

$$Var(e_x) \approx \frac{\sum_{x=0}^{x=75-84} l_x^{\,2} * [(1-a_x) \ * n_x + e_{x+n}]^2 * Var({}_nq_x)}{l_x^{\,2}} \qquad [11]$$

and for ages 85 and over:

$$Var(e_{85+}) \approx \frac{l_{85+}^{\,2}}{M_{85+}^{\,4}} \ * \ Var(M_{85+})$$

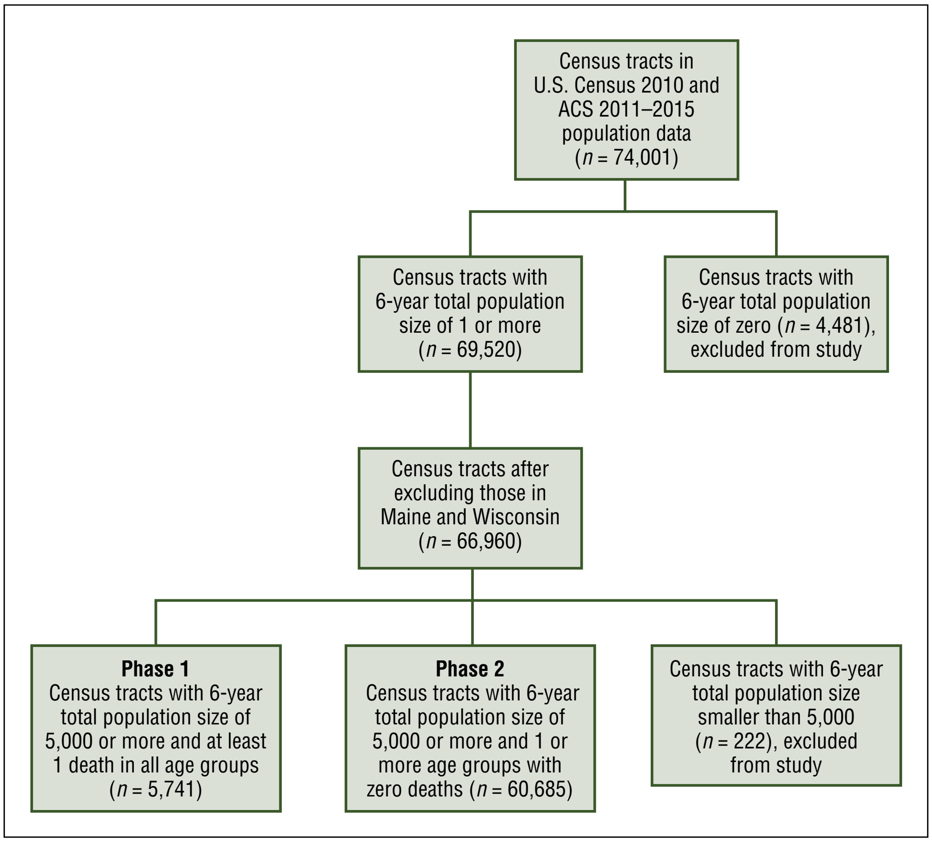
Results

The total number of census tracts identified in both the decennial U.S. Census 2010 and the 5-year 2011–2015 ACS population data sets was 74,001 (Figure 2). Of these, 69,520 (93.9%) had a minimum resident population of at least one over the 6-year period of 2010–2015. After excluding census tracts in Maine and Wisconsin, which had only 5 years of geocoded death records (2011–2015), the majority of tracts with at least one resident, 66,960, had a pooled population of 5,000 or more over the 6-year period and, therefore, were eligible for inclusion in the study. Phase 1 census tracts—those that met the population size requirement and had no missing age-specific death counts or age-specific death counts smaller than the population size—included 5,741 (8.6%) of the eligible tracts. Census tracts that met the population size criterion, had no age groups where the number of deaths were more than the population or where there was no population at all, but had one or more age groups with missing deaths (Phase 2), included 60,685 (90.6%) of eligible tracts.

Phase 1—Model Tracts

Of the total 5,741 Phase 1 tracts, 4,639 (80.4%) had age-specific mortality patterns consistent with the standard age-specific mortality schedule (Figure 3). Figure 3 presents the age-specific death rates on the log scale. Each of the 4,639

Figure 2. Distribution of U.S. census tracts, by study phases



NOTE: ACS is American Community Survey, U.S. Census Bureau.
SOURCE: NCHS, National Vital Statistics Systems, Mortality.

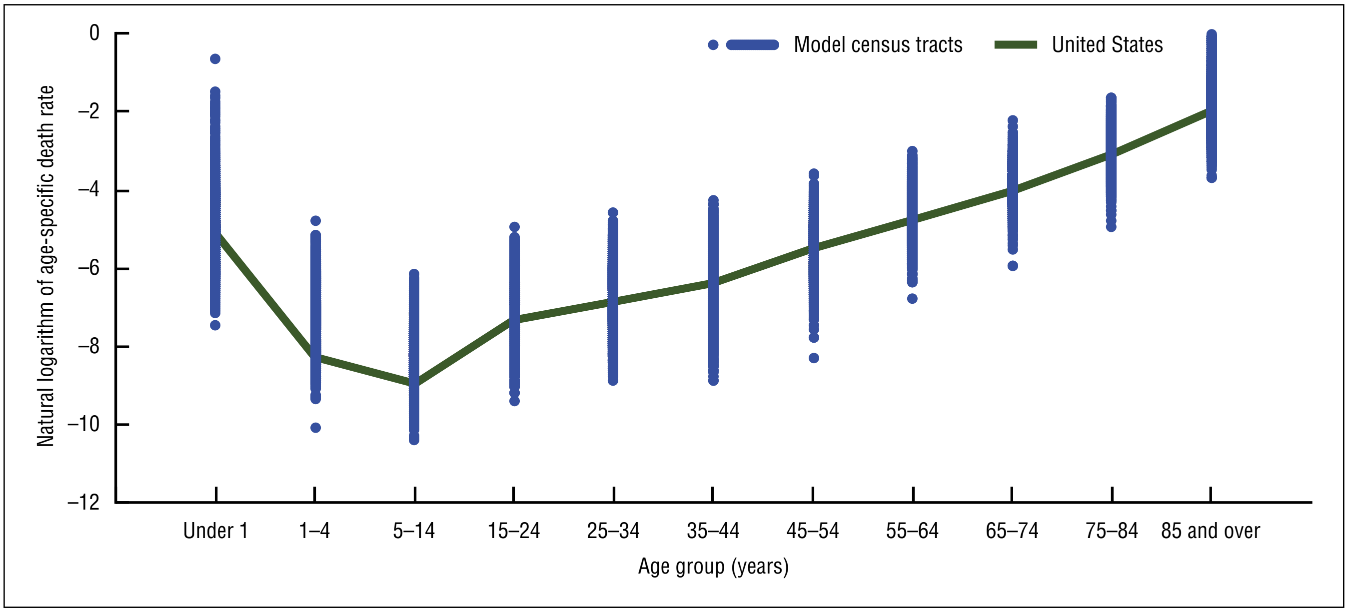
tracts is indicated by a dark blue circle. The circles appear as vertical blue bars where they overlay each other. The equivalent values for the United States in 2013 are shown as an intersecting connected green line. The census-tract values for most age groups are distributed evenly around each age-specific U.S. value. The census-tract distribution is somewhat skewed toward the higher mortality ends in the first three age groups, that is, more tracts have values above the U.S. total than below it. This is likely a function of several factors. One is the population data source. The ACS population estimates are affected by relatively large variances, particularly in the younger age groups. Birth data, the more accurate denominator for the estimation of the probability of death at birth, is not available at the tract level. The other bias factor may be the regional distribution of the tracts in Phase 1. Fifty-one percent of Phase 1 census tracts are in the South (Table 1), where mortality is generally higher than in other regions of the country (15%, 12%, and 2% higher than in the West, Northeast, and Midwest, respectively). Finally, tracts with no missing deaths in any age group may have higher mortality overall (see Table 1 for descriptive characteristics of tracts by study phase). It is not possible to correct for the data problems posed by the use of the ACS population estimates or the lack of birth data. However, it is possible to mitigate some of these issues as well as regional effects through inclusion in the models of geographic, socioeconomic, and demographic indicators known to be closely associated with mortality outcomes.

Statistical Model Results

Tables 2 and 3 show the results of the age-specific zero-truncated negative binomial models fitted to the 4,639 Phase 1 tracts that met the mortality schedule criterion. Table 2 contains estimates for the models that included all covariates, and Table 3 contains the results for models that excluded census tract-level household income. Household income information was not available for 103 tracts in Phase 2. For all age groups, both zero-truncated Poisson and negative binomial models were estimated, and the latter was found to fit the data better, as indicated by the likelihood ratio tests of the overdispersion parameter, alpha (α). The likelihood ratio tests showed that α was statistically different from zero. The parameter estimates show a strong correlation between most of the selected covariates and mortality, and the direction of the relationship between each covariate and mortality was as expected. Higher percentages of Hispanic and college-educated populations and higher household incomes were associated with significantly lower mortality at the census-tract level, net of all other covariates. On the other hand, higher proportions of non-Hispanic black populations were associated with higher mortality. The relationship between mortality outcomes and population density, region, or counties designated as PRCSDA was observed for some age groups but was of much smaller consequence.

Figure 4 shows the age distribution of observed ${}_nM_x$ and predicted ${}_n\bar{M}_x$ on the log scale for each model Phase 1 census tract against the U.S. 2013 schedule. The observed rates for the model tracts are shown as dark blue circles, the predicted rates as light blue circles, and the U.S. rates as an intersecting connected green line. The circles appear as vertical bars where they overlap. The distributions suggest that the models performed rather well in predicting age-specific mortality at the census-tract level. The spread of the predicted death rates, ${}_n\bar{M}_x$, about the U.S. values is much tighter than the observed rates and varies as expected by age. For example, the spread declines with increasing age and is at its smallest in the oldest age group, 85 and over.

Figure 3. Age patterns of mortality for Phase 1 model census tracts, 2010–2015, compared with United States, 2013 schedule



NOTES: Census tracts from Maine and Wisconsin are excluded. Values for the United States, 2013, are based on official statistics published in "Deaths: Final Data for 2013," available from: https://www.cdc.gov/nchs/data/nvsr/nvsr64/nvsr64_02.pdf.
SOURCE: NCHS, National Vital Statistics System, Mortality.

This result is consistent with previous findings that show mortality disparities across groups decline with age (8,32,33).

Phase 2

Table 4 shows the distribution of census tracts by the number of age categories without deaths and by the age categories missing deaths. The majority of these census tracts (89.0%) had one to three age groups with missing deaths, and 10% had four or more age groups with missing deaths (Table 4). The majority of census tracts (84.5%) were missing deaths in the 0–1, 1–4, and 5–14 age categories, at 13.6%, 37.0%, and 33.9%, respectively. The high percentages in the second and third age categories are consistent with universally lower mortality in childhood ages.

Missing age-specific death rates resulting from zero death counts were replaced with predicted values in Phase 2 tracts that had one to five age groups missing deaths, based on the zero-truncated negative binomial models fitted to Phase 1 data and extrapolated to the entire sample. For census tracts with six or more age groups missing deaths, all were replaced with predicted values. Each tract with missing age-specific information received a predicted value based on its particular combination of socioeconomic and demographic characteristics included in the models. For example, tract x with missing death counts in the age group 1–4 years received a predicted estimate such as:

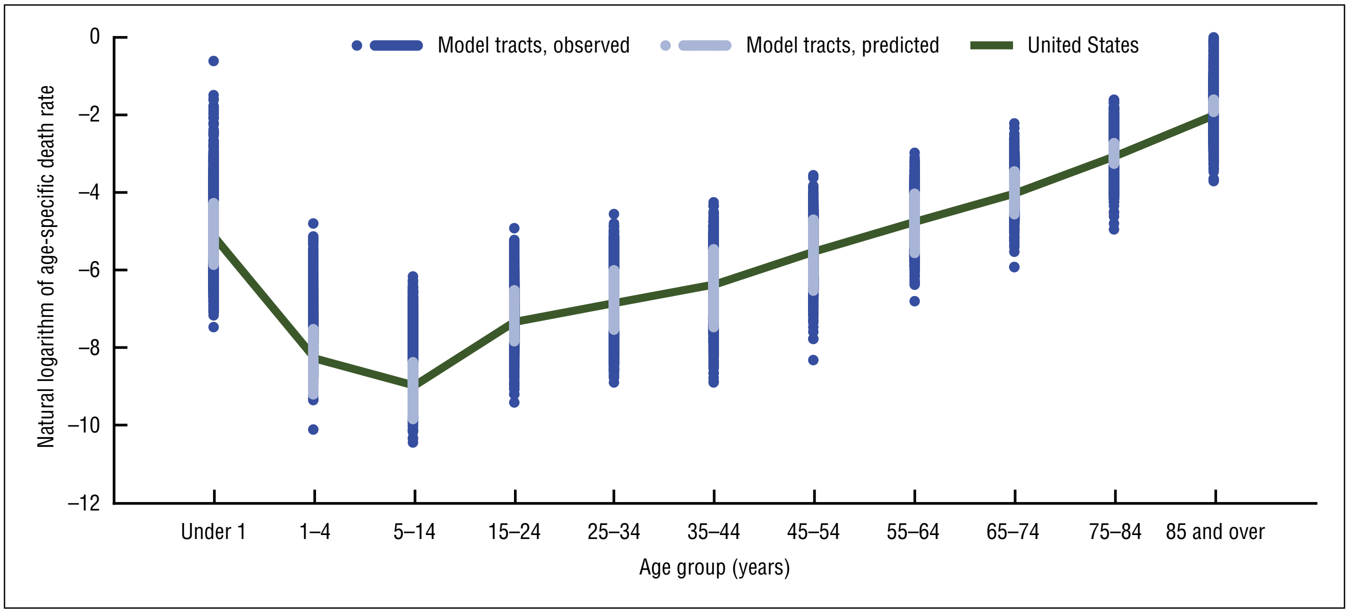
$$_4\overline{M}_1 = e^{\beta_0 + \beta_1 quartile\%Hispanic + \cdots + \beta_k quartile\ Population\ density}$$

Figure 5 shows the age distribution of observed $_nM_x$ and predicted $_n\overline{M}_x$ on the log scale for each Phase 2 tract about the U.S. 2013 schedule. The observed rates for the Phase 2 tracts are shown as dark blue circles, the predicted rates as light blue circles, and the U.S. rates as an intersecting connected green line. The circles appear as vertical bars where they overlap. The distributions show large spreads in the observed values about U.S. values, but mortality schedules consistent with the expected pattern. Similar to Phase 1 tracts, observed $_nM_x$ values for the youngest age groups were somewhat skewed toward higher mortality. In this case, it is not likely a result of regional bias because Phase 2 contains the bulk of all tracts (Table 1), and regional distribution is almost identical to the national distribution. The skewed distributions for the youngest age groups are most likely a result of large variances in population data quality and the lack of birth data for the first age group. The predicted values are much tighter about and equidistant to the U.S. values.

Evaluation and Selection of Final Abridged Life Tables

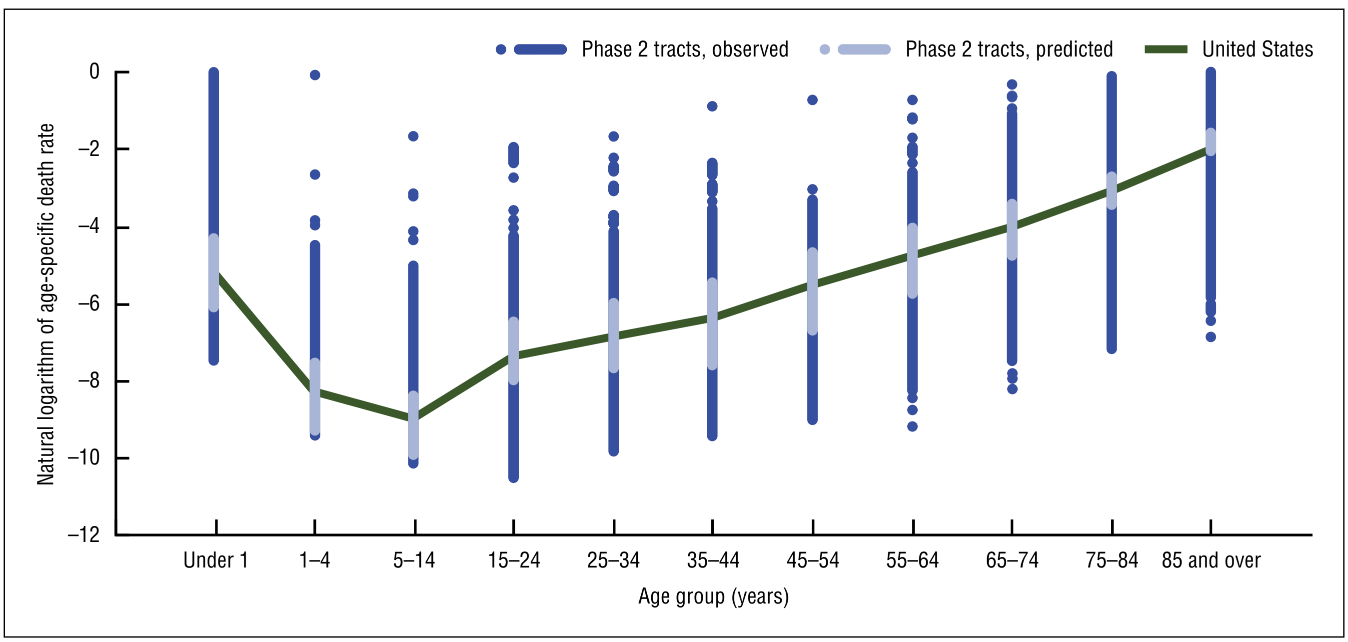
Abridged life tables were calculated for a total of 66,426 Phase 1 and Phase 2 census tracts that met the mortality schedule criterion. Among the 5,741 Phase 1 census tracts, 4,639 abridged life tables were based exclusively on observed age-specific death rates (known as model tracts), and 1,102 were based on predicted death rates for all ages. Among the 60,685 Phase 2 census tracts, 56,915 abridged life tables were based on a combination of observed and predicted death rates, and 3,770 were based only on predicted death rates. Those based exclusively on predicted death rates were census tracts with mortality schedules that

Figure 4. Age patterns of mortality for Phase 1 model census tracts, 2010–2015, based on observed and predicted age-specific death rates, compared with United States, 2013 schedule



NOTES: Census tracts from Maine and Wisconsin are excluded. Values for the United States, 2013, are based on official statistics published in "Deaths: Final Data for 2013," available from: https://www.cdc.gov/nchs/data/nvsr/nvsr64/nvsr64_02.pdf.
SOURCE: NCHS, National Vital Statistics System, Mortality.

Figure 5. Age patterns of mortality for Phase 2 census tracts with observed and predicted age-specific death rates, compared with United States, 2013 schedule



NOTES: Census tracts from Maine and Wisconsin are excluded. Values for the United States, 2013, are based on official statistics published in "Deaths: Final Data for 2013," available from: https://www.cdc.gov/nchs/data/nvsr/nvsr64/nvsr64_02.pdf.
SOURCE: NCHS, National Vital Statistics System, Mortality.

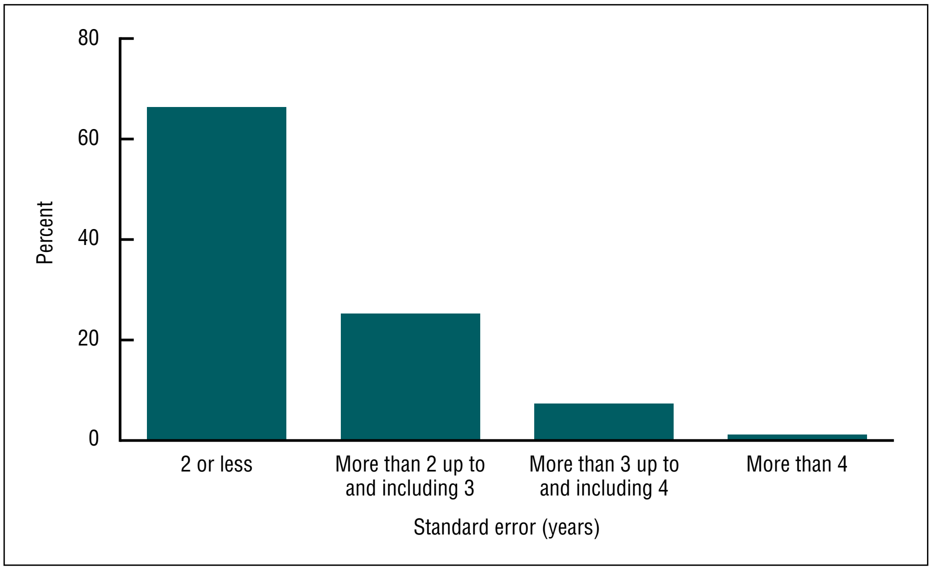
did not meet the age-specific mortality pattern criterion or had more than five age groups with zero death counts.

To select the most reliable census tract-level abridged life tables, a battery of tests was performed. First, the distributions of age-specific life expectancy estimates and their standard errors were examined to identify obvious outliers. Second, mean values of tract-level life table functions were compared with national and state-level estimates to identify outliers not found through the previous evaluation. Third, the patterns of other life table functions were compared with those of the United States and individual states as a further check for implausible values. The relationship between life expectancy at birth and select demographic, socioeconomic, and geographic indicators was explored as a final check on the validity of the estimates.

Life expectancy

Of the 66,426 census tracts for which abridged life tables were calculated, 44,066 had life expectancy at birth that ranged from 56.3 to 89.9 years, with a weighted mean standard error (SE) of 1.46 years (Table 5). For 16,768 census tracts, life expectancy at birth ranged from 59.0 to 94.2 years, with a mean SE of 2.39 years. For 4,828 census tracts, life expectancy at birth ranged from 60.7 to 97.5 years, with a mean SE of 3.41 years. Finally, for 764 census tracts, life expectancy at birth ranged from 71.2 to 83.4 years, with SE values of 4 years or more and a mean of 24.04 years (Figure 6, Table 5). The group of tracts with SE at birth greater than 4 years contains clearly unacceptable SE estimates, despite having been based exclusively on predicted age-specific death rates. This group of life tables was dropped from the sample, leaving a final set of 65,662 abridged life tables. Of these, 87.0% were based on a combination of observed and predicted values of ${}_nM_x$, and 13.0% were based exclusively on predicted values. Of the first group (87.0%) in the final set, 88.6% were made up of tracts with zero to three age groups missing death counts. The final 65,662 census-tract abridged life tables are available from: https://www.cdc.gov/nchs/nvss/usaleep/usaleep.html.

Figure 6. Distribution of standard error of life expectancy at birth, Phases 1 and 2 census tracts



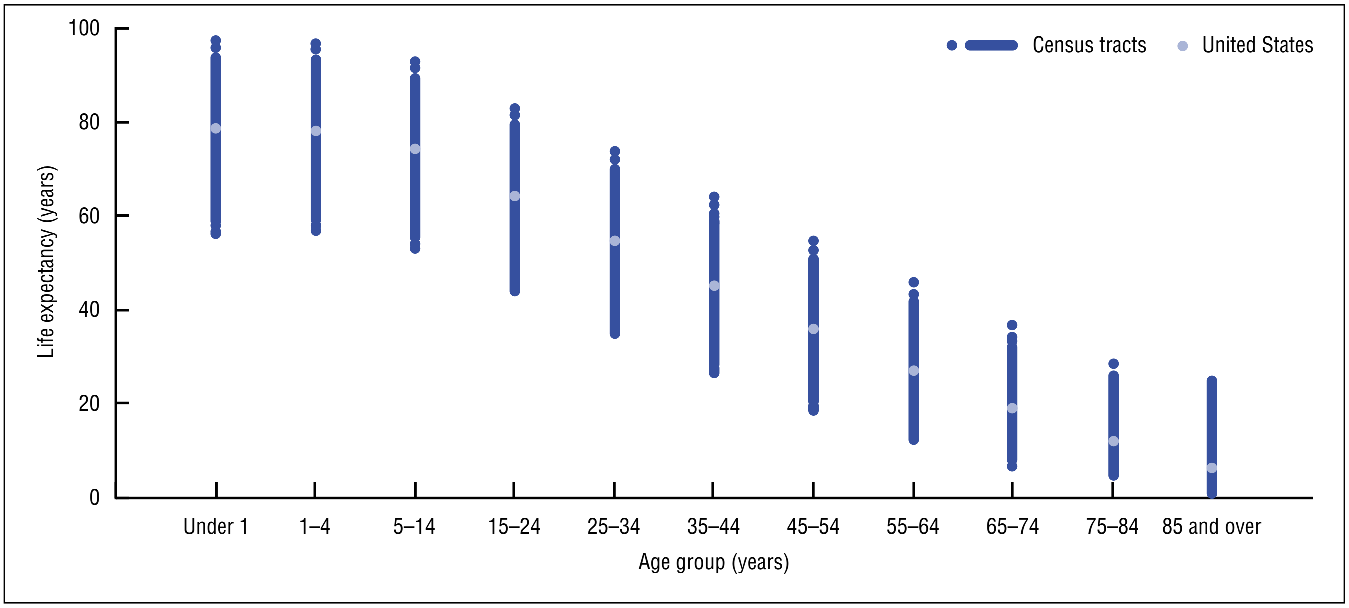
NOTE: Maine and Wisconsin are excluded.
SOURCE: NCHS, National Vital Statistics System, Mortality.

Life expectancy at birth ranges and associated SEs for the first three groups outlined above are plausible and acceptable (Table 5). Mean life expectancy at birth for the 65,662 census tracts was 78.7 years, with a minimum of 56.3 years, a maximum of 97.5 years, and a weighted mean SE of 1.80 years. Comparable small-area life expectancy at birth estimates include United Kingdom ward-level life expectancy at birth estimates based on 1999–2003 data. These estimates ranged from 65.4 to 93.4 years (18). Life expectancy at birth worldwide ranged from 52.9 years in Lesotho to 84.2 years in Japan in 2016 (34).

The top panel of Table 6 presents mean abridged life table functions, weighted by census-tract population size, for the 65,662 census tracts. For comparison, the bottom panel shows the 2013 U.S. abridged life table. The weighted mean life expectancy at birth for the 65,662 census tracts was 78.7 years. Life expectancy at birth for the total U.S. population in 2013 was 78.8 years. The difference of 0.1 year was well within a 95% confidence interval, based on a weighted mean SE for the census-tract estimates of 1.80 years. For all other age groups, differences between the census-tract estimates and the United States were concentrated in the youngest ages. This appears to be mostly a result of the very small numbers of deaths in these age groups, the large variances of the ACS population estimates, and the unavailability of birth data for the denominator of the probability of death at birth. Figure 7 presents age-specific life expectancy estimates for each census tract about the 2013 U.S. values. The estimates for the census tracts are shown as dark blue circles, which appear as vertical bars where they overlap, and the U.S. values are shown as light blue circles. The census-tract estimates fall mostly about the U.S. values with no aberrant outliers. Skewness in the oldest age group is consistent with the larger variance for this estimate (Table 6).

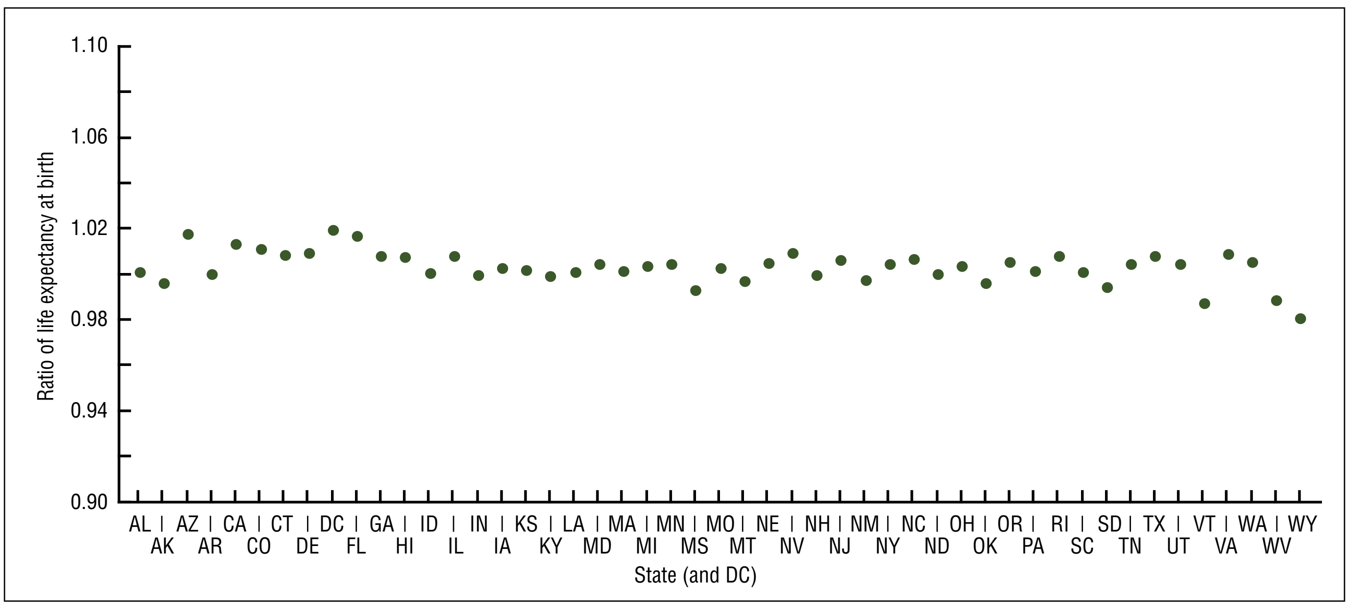
Table 7 shows the mean life expectancy at birth, standard deviation (SD), and minimum and maximum values, weighted by census-tract population size for each state, based on the tract-level abridged life tables compared with life expectancy at birth estimated for the entire population of each state. The state estimates are based on abridged life tables, calculated using pooled death counts for 2011–2015 and midperiod 2013, postcensal population estimates for ages 1 and over, and birth counts for ages 0 to 1. Figure 8 presents the ratio of the state-level weighted means of the tract-level life expectancy at birth to the direct state-level estimates. The ratios fall slightly above but are very close to 1.00 for most states, suggesting that the census-tract estimates are robust but overestimate mortality to some degree. The absolute differences between the census-tract weighted means and state values range from no difference for several states to 1.5 years for D.C. and Wyoming.

Figure 7. Age-specific life expectancy estimates: Census tracts, 2010–2015, and United States, 2013



NOTES: Census tracts from Maine and Wisconsin are excluded. Values for the United States, 2013, are based on official life tables in "United States Life Tables, 2013," available from: https://www.cdc.gov/nchs/data/nvsr/nvsr66/nvsr66_03.pdf.
SOURCE: NCHS, National Vital Statistics System, Mortality.

Figure 8. Ratio of state-level weighted means of census tract-level life expectancy at birth to direct state-level life expectancy at birth estimates, 2010–2015

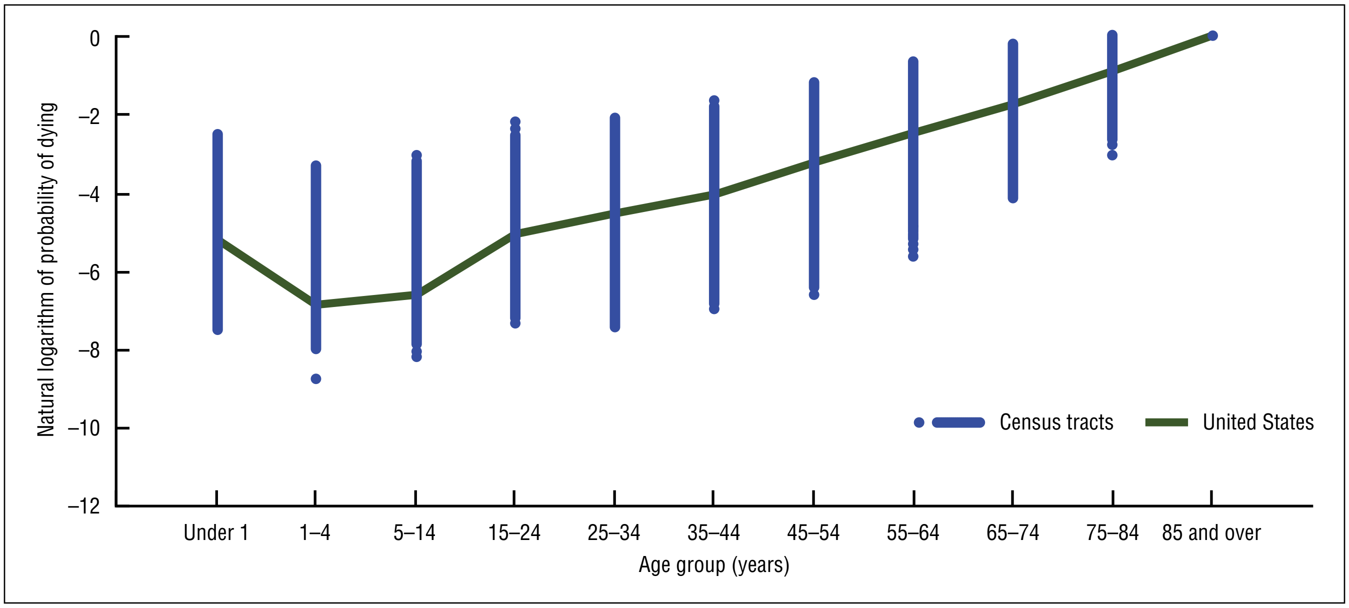


NOTE: Maine and Wisconsin are excluded; DC is District of Columbia.
SOURCE: NCHS, National Vital Statistics System, Mortality.

Probability of dying

Figure 9 shows the age-specific probability of dying, ${}_nq_x$, estimates for each of the final 65,662 census tracts compared with the values for the United States in 2013. The observed probabilities for the tracts are shown as dark blue circles, which appear as vertical bars where they overlap, and the U.S. probabilities are shown as an intersecting connected green line. The census-tract estimates fall about the U.S. values as expected, with some skewness toward higher mortality in the younger age groups. As with ${}_nM_x$, the skewness in the younger ages is predominantly a function of the very small number of deaths, relatively large ACS-based population variances, and lack of birth data. Figure 10 shows the distributions of census tract-level ${}_nq_x$ about the state values. In all cases, the census-tract ${}_nq_x$ distributions behave as expected, with wider spreads for some states.

Figure 9. Probability of dying, by age: Census tracts, 2010–2015, and United States, 2013



NOTES: Census tracts from Maine and Wisconsin are excluded. Values for the United States, 2013, are based on official life tables in "United States Life Tables, 2013," available from: https://www.cdc.gov/nchs/data/nvsr/nvsr66/nvsr66_03.pdf.
SOURCE: NCHS, National Vital Statistics System, Mortality.

Survivorship

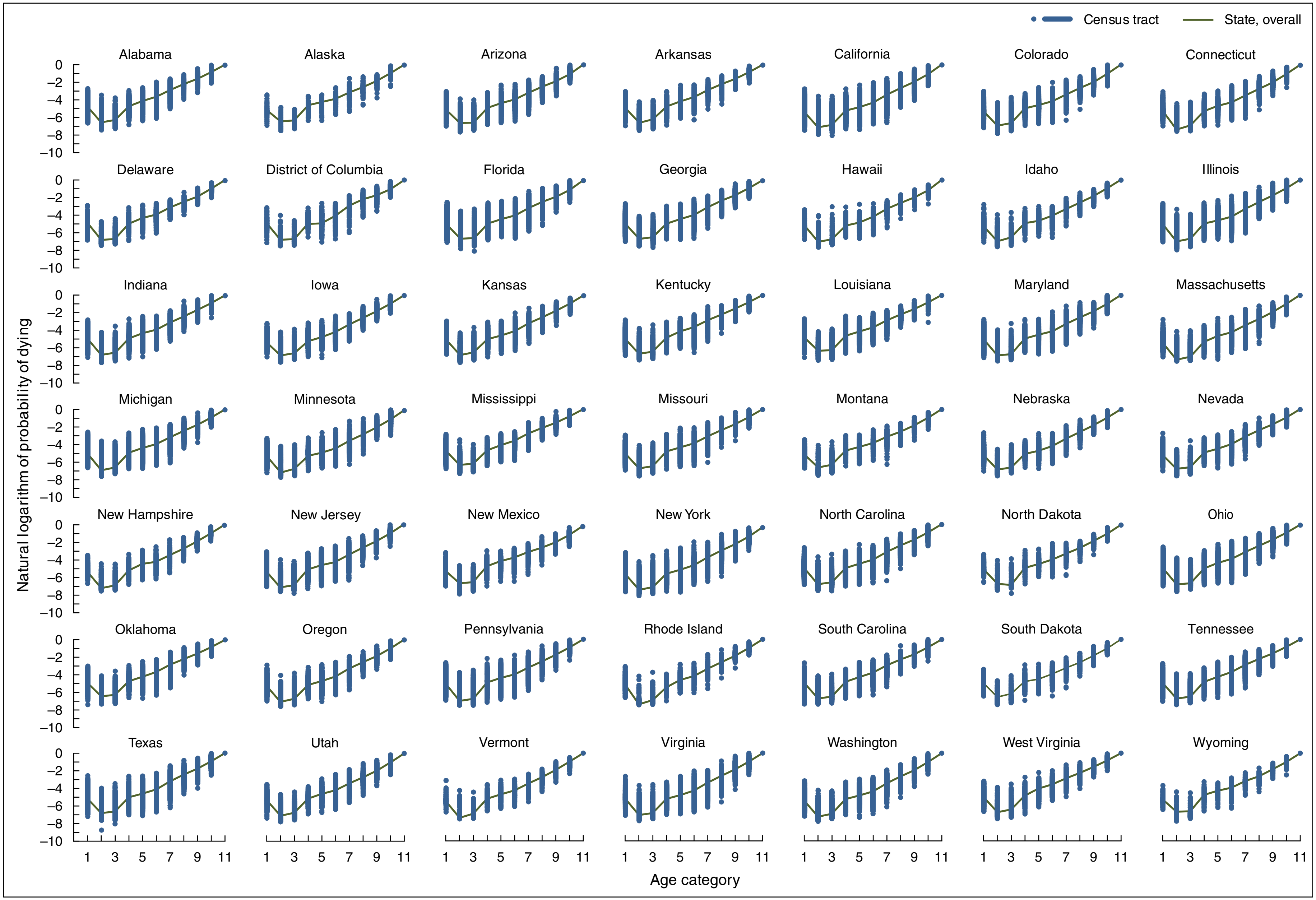
Figure 11 presents the age-specific percentage surviving for each of the final census tracts compared with the 2013 U.S. values. The observed percentages for the tracts are shown as dark blue circles, which appear as vertical bars where they overlap, and the U.S. percentages are shown as an intersecting connected green line. The shape of the survival curves is as expected. The spread about the U.S. values increases with age and is consistent with the distributions of the age-specific life expectancy and probabilities of death. Figure 12 shows the census tract-level percentage surviving in each state compared with the state-level values. The distributions of tract-level survival curves have acceptable patterns about each state-level value, with no aberrant outliers.

Demographic, Socioeconomic, and Geographic Correlates of Life Expectancy

Table 8 presents the number and percentage of census tracts for each quartile of life expectancy at birth by each of the demographic, geographic, and socioeconomic variables used in the statistical models. Among census tracts that belong to the lowest quartile of life expectancy at birth (56.3–75.7 years), more than one-half are found in the southern U.S. region (52.2%), have predominantly non-Hispanic black populations (51.0%), and consist of populations with low educational attainment (56.7%) and low median income (60.9%). Among census tracts that belong to the highest quartile group (81.0–97.5 years), more than one-half have highly educated populations (56.3%) and high median income (56.8%). Figure 13 shows the ratio of the means of the fourth quartile group's probability of dying, ${}_nq_x$, to each of the first three quartile groups, for median household income and the percentages of the tract-level population that are non-Hispanic black, Hispanic, and had 4 or more years of college education.

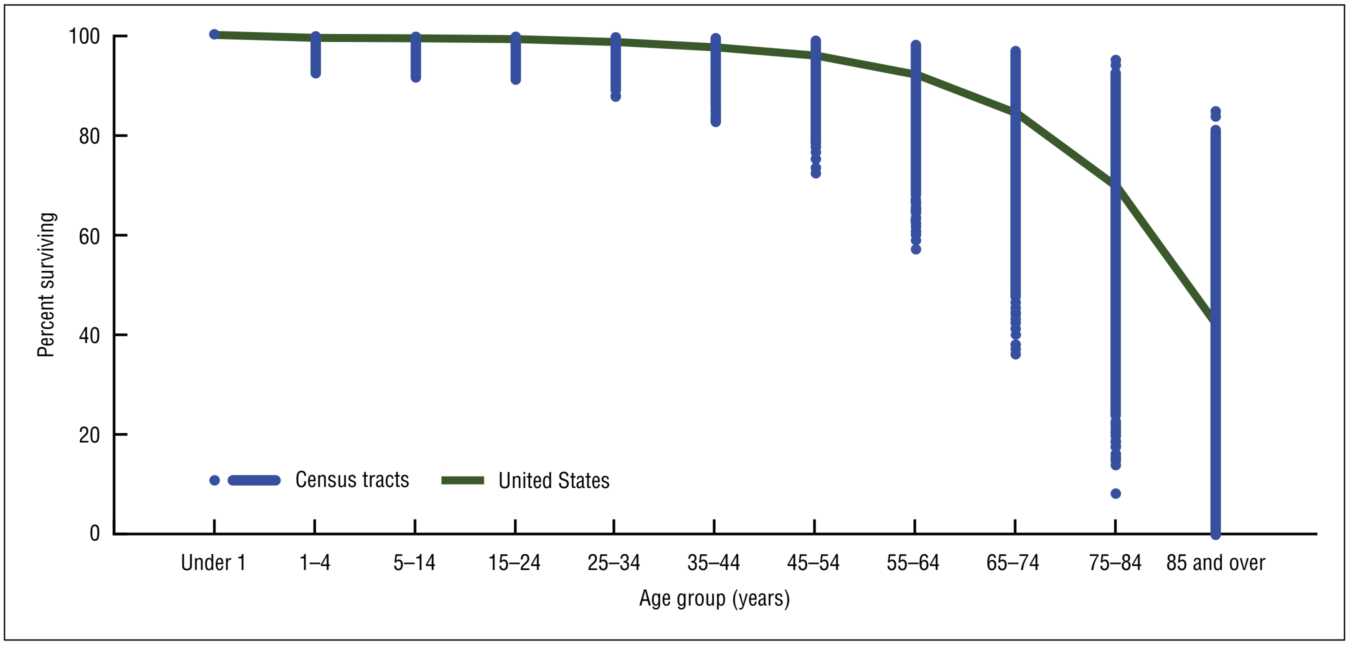
Generally, census tracts belonging to the highest quartile of a socioeconomic variable have lower ${}_nq_x$ estimates than those census tracts belonging to the lower 75% of the percentile, resulting in ratios greater than 1.00 (Figure 13). These disparities in ${}_nq_x$ are substantial for educational attainment and median household income and, although observed in all age groups, are largest for age groups 35–44 and 55–64. As expected, the larger the gaps are in educational attainment and median income, the larger the differences in ${}_nq_x$. Census tracts having a predominantly non-Hispanic black population have consistently higher ${}_nq_x$ estimates than census tracts with smaller non-Hispanic black populations, resulting in ratios greater than 1.00 across all age groups, but the relative differences disappear in the older age groups where the ratios between the fourth quartile and each of the first two quartiles merge. On the other hand, having a predominantly Hispanic population appears to be protective (lower ${}_nq_x$ estimates), especially for age groups under 1 year to 25–34, which is consistent with previous findings showing a Hispanic mortality advantage (35). In the older age groups, census tracts that are predominantly Hispanic have roughly similar ${}_nq_x$ estimates compared with census tracts with smaller Hispanic populations, resulting in ratios equal or close to 1.00. Differences in ${}_nq_x$ between the most and least densely populated census tracts that are substantial in the younger age groups also disappear in the older age groups (figure not shown).

Figure 10. Age pattern of mortality, by census tracts within each state compared with overall state patterns, 2010–2015



NOTES: Census tracts from Maine and Wisconsin are excluded. Age categories are 1 = Less than 1 year, 2 = 1–4 years, 3 = 5–14 years, 4 = 15–24, 5 = 25–34, 6 = 35–44, 7 = 45–54, 8 = 55–64, 9 = 65–74, 10 = 75–84, and 11 = 85 and over.
SOURCE: NCHS, National Vital Statistics System, Mortality.

Figure 11. Percentage surviving, by age: Census tracts, 2010–2015, and United States, 2013



NOTES: Census tracts from Maine and Wisconsin are excluded. Values for the United States, 2013, are based on official life tables in "United States Life Tables, 2013, available from: https://www.cdc.gov/nchs/data/nvsr/nvsr66/nvsr66_03.pdf.
SOURCE: NCHS, National Vital Statistics System, Mortality.

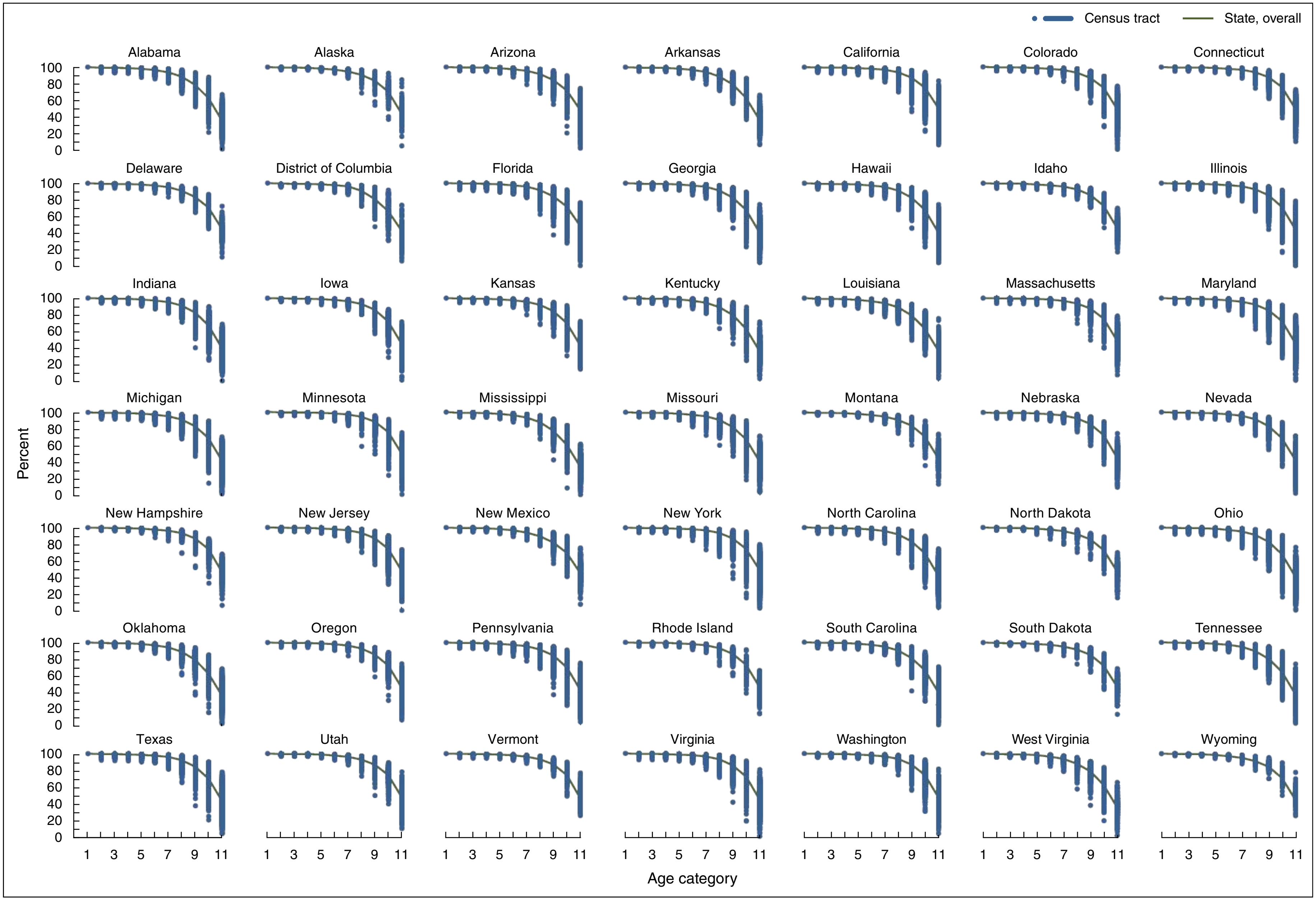
Aside from demographic and socioeconomic disparities, geographic disparities in ${}_nq_x$ and life expectancy at birth also exist. The largest differences in ${}_nq_x$ are observed between the Southern and Western regions of the United States (Table 8). The relatively low life expectancy at birth estimates for the Southern region are prominent in Figure 14, where the geographic distribution of life expectancy at birth, categorized into quartile groups, for the census tracts in 48 states (Maine and Wisconsin are excluded) are presented. When the higher or lower median of life expectancy at birth is paired with either the higher or lower median of educational attainment, 37.0% (n = 24,559) of the census tracts are found to have both low life expectancy at birth and populations that have lower educational attainment. Another 37.0% (n = 24,494) have both high life expectancy at birth and populations that have higher educational attainment; 13.0% (n = 8,676) have high life expectancy at birth but populations that have lower educational attainment; and 13.0% (n = 8,697) have low life expectancy at birth despite having highly educated populations (Figure 15).

Summary and Conclusions

Statistically reliable, abridged, period life tables were calculated for a total of 65,662 (88.7%) U.S. census tracts (excluding tracts in Maine and Wisconsin) for 2010–2015. Small-area estimation challenges were addressed in the most statistically robust manner possible. Through a collaborative effort between state vital registration areas and NCHS, mortality data were geocoded using decedents' address information to identify census tracts. Census tract-level population estimates were generated through an innovative technique that combined decennial census data with ACS sample data. The problem of small numbers of deaths, missing age-specific death counts, and small population sizes was addressed through a unique combination of statistical and demographic methods.

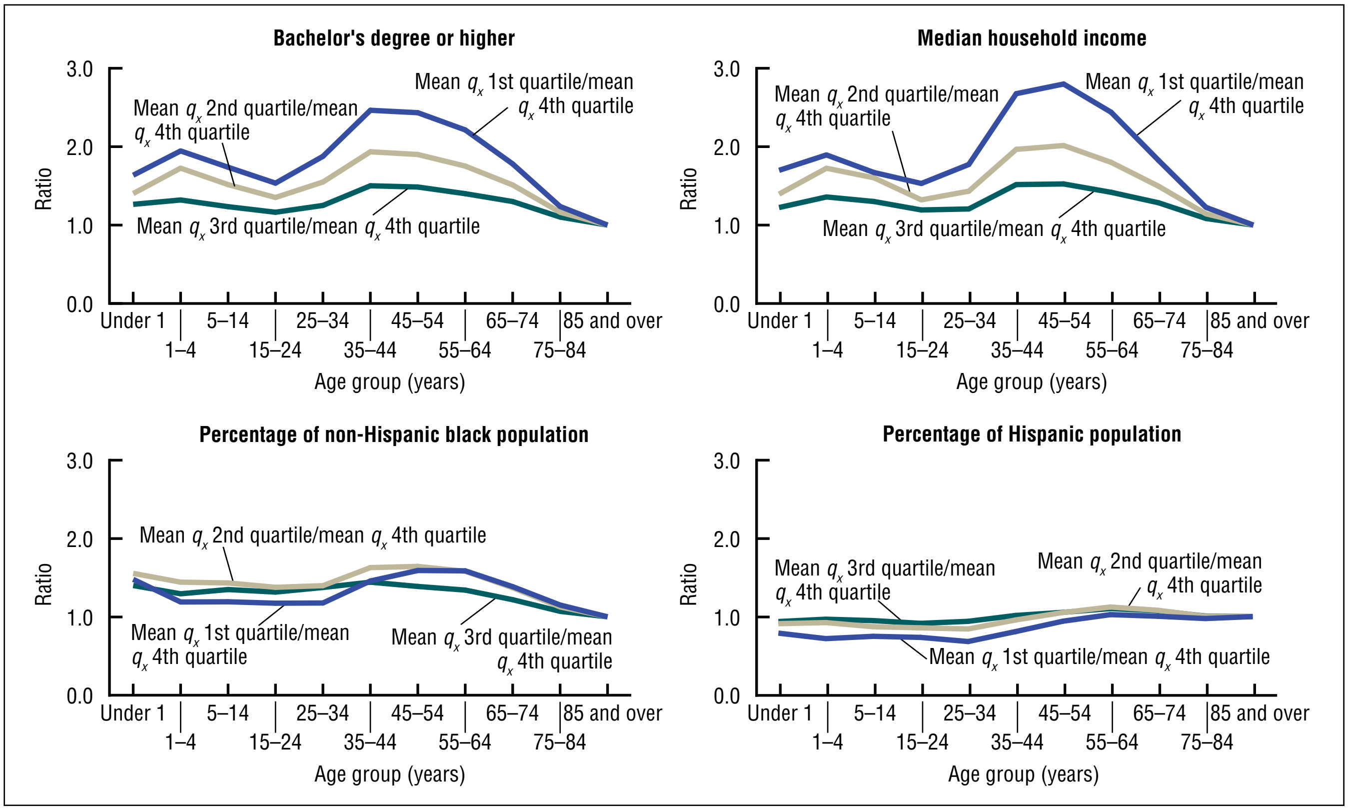
The results of this study concur with the findings of previous research showing that a minimum population size of 5,000 is acceptable for the estimation of abridged life tables, with a caveat (7,11,12,19). This study showed that the proportion of census tracts with a minimum population size of 5,000 over a 6-year period that also had at least one age group with zero deaths was rather high, at 90.6%. To date, the most robust abridged life table methodology is that developed by Chiang, and it fails to produce reliable estimates when there are zero death counts in any age group. Further, ignoring missing deaths can lead to misidentification of the underlying mortality pattern of a population, something that life table functions are designed to estimate (10). The methodology developed for this study addressed this issue using standard statistical modeling to fill in missing information. Final results suggest that the methodology was successful. The census-tract life table functions followed expected patterns, their distributions about state and U.S. values showed no aberrant patterns, and their weighted mean values compared exceedingly well with state- and national-level estimates. Finally, the associations between life expectancy and the probability of dying, and select socioeconomic, demographic, and geographic characteristics of census-tract populations, were found to be consistent with the large body of research on mortality in the United States.

Figure 12. Percentage surviving, by census tracts within each state compared with overall state values, 2010–2015



NOTES: Census tracts from Maine and Wisconsin are excluded. Age categories are 1 = Less than 1 year, 2 = 1–4 years, 3 = 5–14 years, 4 = 15–24, 5 = 25–34, 6 = 35–44, 7 = 45–54, 8 = 55–64, 9 = 65–74, 10 = 75–84, and 11 = 85 and over.
SOURCE: NCHS, National Vital Statistics System, Mortality.

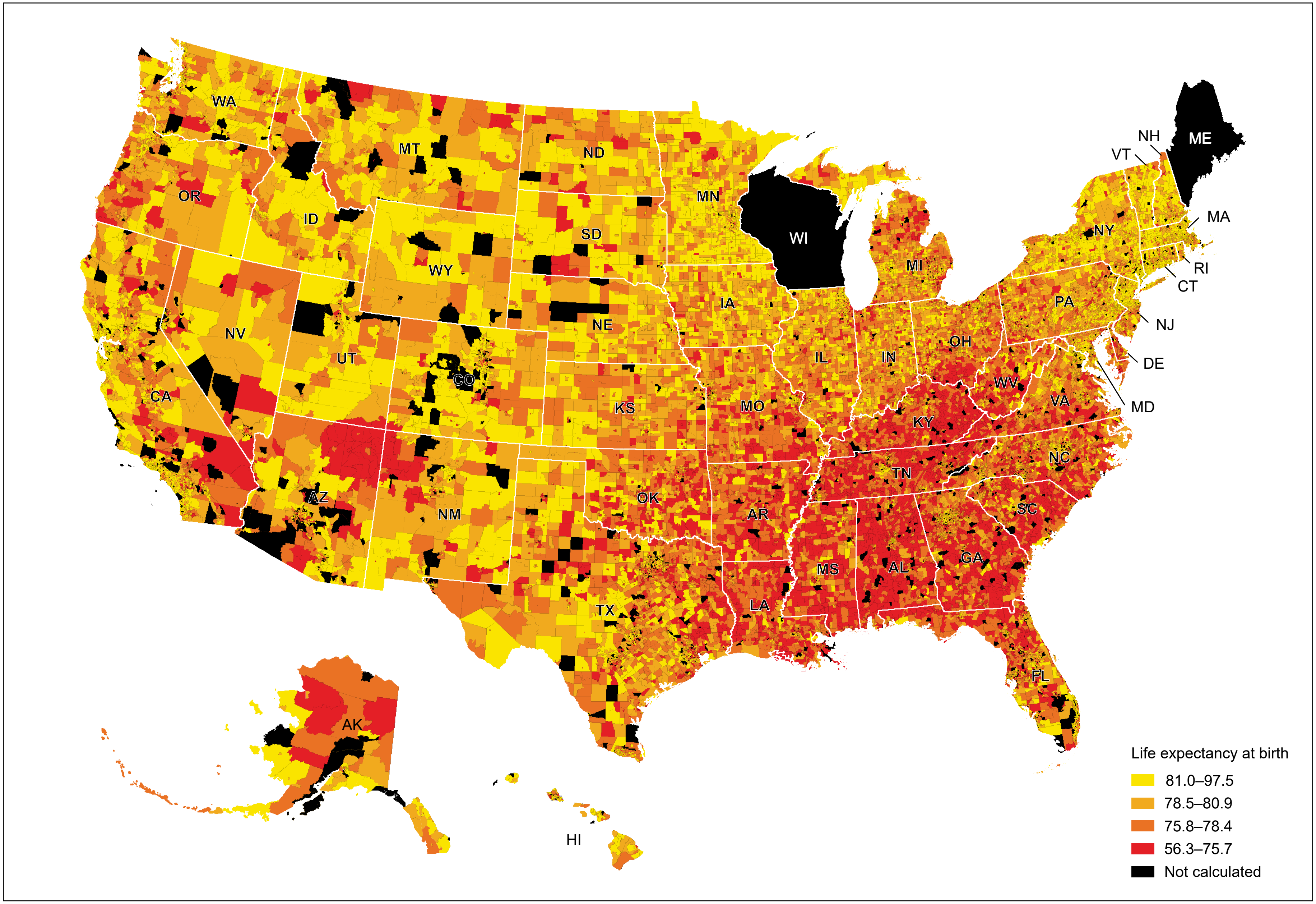
Figure 13. Ratio of mean probability of dying for quartile groups of select statistical model covariates, by age group: United States, 2010–2015



NOTES: q_x is probability of dying. Census tracts from Maine and Wisconsin are excluded.
SOURCE: NCHS, National Vital Statistics System, Mortality.

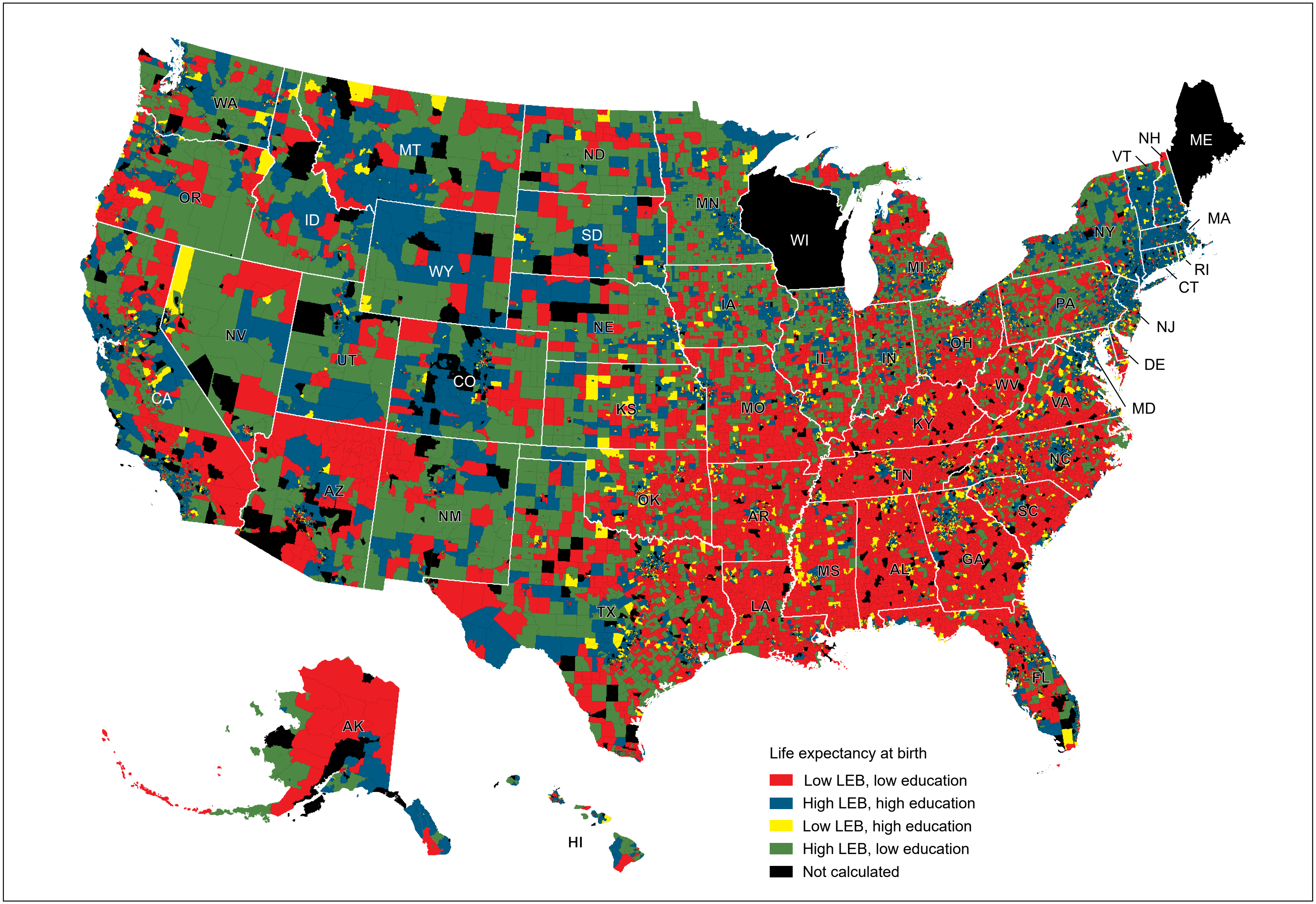
Despite the successful production of the first-ever census tract-level life expectancy estimates, this study has important limitations. The most significant is the lack of census tract-level post- or intercensal population estimates based on decennial census counts. The use of population estimates derived from sample data introduces additional error into the estimates of life table functions. If the production of decennial census-based population estimates at the tract level remains beyond the scope of the Census Bureau's population estimates program, census tract-level mortality data and construction of future census tract-level life tables need to be centered on a decennial census year. Another limitation of the study is the lack of birth data for the estimation of the probability of death at birth. Because mortality in infancy is concentrated in the beginning of the age interval, assigning deaths to the appropriate birth cohort is preferable (8). The lack of birth data combined with the large variances of the ACS population estimates led to overestimation of mortality in the younger ages, as comparisons with state and national estimates indicated. An additional limitation of this study was the omission of the states of Maine and Wisconsin. Abridged life tables will be estimated for these states using the available 5 years of geocoded mortality data for 2011–2015 and ACS population estimates. Estimates found to be acceptable will be published as an addendum to this report. Finally, as more reliable population data become available for small geographic areas in the United States, the methodology presented here may be revised.

Figure 14. Life expectancy at birth, by census tract: United States, 2010–2015



NOTE: Census tracts from Maine and Wisconsin were excluded.
SOURCE: NCHS, National Vital Statistics Systems, Mortality.

Figure 15. Life expectancy at birth and population educational attainment, by census tract: United States, 2010–2015



NOTES: Census tracts from Maine and Wisconsin are excluded. LEB is life expectancy at birth.
SOURCE: NCHS, National Vital Statistics Systems, Mortality.

References

1. Alexander M, Zagheni E, Barbieri M. A flexible Bayesian model for estimating subnational mortality. Demography 54(6):2025–41. 2017.
2. Dwyer-Lindgren L, Bertozzi-Villa A, Stubbs RW, Morozoff C, Mackenbach JP, van Lenthe FJ, et al. Inequalities in life expectancy among US counties, 1980 to 2014: Temporal trends and key drivers. JAMA Intern Med 177(7):1003–11. 2017.
3. Chetty R, Stepner M, Abraham S, Lin S, Scuderi B, Turner N, et al. The association between income and life expectancy in the United States, 2001–2014. JAMA 315(16):1750–66. 2016.
4. Wang H, Schumacher AE, Levitz CE, Mokdad AH, Murray CJ. Left behind: Widening disparities for males and females in US county life expectancy, 1985–2010. Popul Health Metr 11(1):8. 2013.
5. Kulkarni SC, Levin-Rector A, Ezzati M, Murray CJ. Falling behind: Life expectancy in US counties from 2000 to 2007 in an international context. Popul Health Metr 9(1):16. 2011.
6. Silcocks PB, Jenner DA, Reza R. Life expectancy as a summary of mortality in a population: Statistical considerations and suitability for use by health authorities. J Epidemiol Community Health 55(1):38–43. 2001.
7. Grayer MP. "Achieving closure": Improving the estimation of life expectancy for small populations. European Population Conference. 2010.
8. Arias E, Heron M, Xu JQ. United States life tables, 2014. National Vital Statistics Reports; vol 66 no 4. Hyattsville, MD: National Center for Health Statistics. 2017. Available from: https://www.cdc.gov/nchs/data/nvsr/nvsr66/nvsr66_04.pdf.
9. Chiang CL. Introduction to stochastic processes in biostatistics. New York, London, Sydney: Wiley & Sons, Inc. 1968.
10. Chiang CL. The life table and its applications. Malabar, FL: R.E. Krieger Publishing Company. 1984.
11. Toson B, Baker A. Life expectancy at birth: methodological options for small populations. Norwich, UK: Office for National Statistics.
12. Williams T, Dinsdale H, Eayres D, Tahzib F. Technical report—Calculating life expectancy in small areas. South East England Public Health Observatory. 2005.
13. Lo E, Vatnik D, Benedetti A, Bourbeau R. Variance models of the last age interval and their impact on life expectancy at subnational scales. Demogr Res 35:399–454. 2016.
14. Murphy SL, Xu JQ, Kochanek KD, Curtin S, Arias E. Deaths: Final data for 2015. National Vital Statistics Reports; vol 66 no 6. Hyattsville, MD: National Center for Health Statistics. 2017. Available from: https://www.cdc.gov/nchs/data/nvsr/nvsr66/nvsr66_06.pdf.
15. Greville TNE. U.S. decennial life tables for 1969–71. Methodology of the National and State Life Tables for the United States: 1969–71 1(3). Hyattsville, MD: National Center for Health Statistics. 1975. Available from: https://www.cdc.gov/nchs/data/lifetables/life69_1_3.pdf.
16. National Center for Health Statistics. U.S. decennial life tables for 1989–91. Methodology of the National and State Life Tables 1(2). Hyattsville, MD: National Center for Health Statistics. 1998. Available from: https://www.cdc.gov/nchs/data/lifetables/life89_1_2.pdf.
17. Wei R, Anderson RN, Curtin LR, Arias E. U.S. decennial life tables for 1999–2001: State life tables. National Vital Statistics Reports; vol 60 no 9. Hyattsville, MD: National Center for Health Statistics. 2012. Available from: https://www.cdc.gov/nchs/data/nvsr/nvsr60/nvsr60_09.pdf.
18. Office for National Statistics. Life expectancy at birth for wards in England and Wales, 1999–2003 (experimental), results. 2006. Available from: http://webarchive.nationalarchives.gov.uk/20120327052242/http://www.ons.gov.uk/ons/rel/subnational-health4/life-expec-birth-wards-eng-wal/results/index.html?format=hi-vis.
19. Eayres D, Williams ES. Evaluation of methodologies for small area life expectancy estimation. J Epidemiol Community Health 58(3):243–9. 2004.
20. Woolf S, Chapman D, Cohen SA, Johnson R, Sabo R, Wheeler D, Kelly L. Technical report: Calculating life expectancy by U.S. census tracts [unpublished]. Virginia Commonwealth University Center on Society and Health, Urban Institute. 2015.
21. Swanson DA. A state-based regression model for estimating substate life expectancy. Demography 26(1):161–70. 1989.
22. Choudhury L, Sarma R. Indirect estimation of life expectancy at birth for the districts of the major states of India (2001–05). Indian J Public Health Res Dev 5(3):220–5. 2014.
23. Ranjana K. Estimation of life expectancy from infant mortality rate at districts level. Int Res J Soc Sci 4(6):52–63. 2015.
24. Bravo JM, Malta J. Estimating life expectancy in small population areas. Conference of European Statisticians. 2010.

25. Stephens AS, Purdie S, Yang B, Moore H. Life expectancy estimation in small administrative areas with non-uniform population sizes: Application to Australian New South Wales local government areas. BMJ Open 3(12):e003710. 2013.

26. Jonker MF, van Lenthe FJ, Congdon PD, Donkers B, Burdorf A, Mackenbach JP. Comparison of Bayesian random-effects and traditional life expectancy estimations in small-area applications. Am J Epidemiol 176(10):929–37. 2012.

27. Congdon P. Chapter 2: Estimating life expectancy in small areas, with an application to recent changes in life expectancy in US counties. In: Anson J, Luy M, editors. Mortality in an international perspective. Switzerland: Springer International Publishing. 15–24. 2014.

28. Hadler JL, Lampkins R, Lemmings J, Lichtenstein M, Huang M, Engel J, Centers for Disease Control and Prevention. Assessment of epidemiology capacity in state health departments—United States, 2013. MMWR Morb Mortal Wkly Rep 64(14):394–8. 2015. Available from: https://www.cdc.gov/mmwr/preview/mmwrhtml/mm6414a6.htm.

29. U.S. Census Bureau. Geographic areas reference manual. 1994. Available from: https://www.census.gov/geo/reference/garm.html.

30. U.S. Census Bureau. Census 2010, Summary File 1, Table P12. 2010. Available from: https://www2.census.gov/census_2010/04-Summary_File_1/.

31. U.S. Census Bureau. A compass for understanding and using American Community Survey data: What general data users need to know. Washington, DC: U.S. Government Printing Office. 2008. Available from: https://www.census.gov/content/dam/Census/library/publications/2008/acs/ACSGeneralHandbook.pdf.

32. Arias E, Xu J, Jim MA. Period life tables for the non-Hispanic American Indian and Alaska Native population, 2007–2009. Am J Public Health 104 Suppl 3:S312–9. 2014.

33. Wing S, Manton KG, Stallard E, Hames CG, Tryoler HA. The black/white mortality crossover: Investigation in a community-based study. J Gerontol 40(1):78–84. 1985.

34. United Nations. World mortality 2017—Data booklet. 2017. Available from: http://www.un.org/en/development/desa/population/publications/pdf/mortality/World-Mortality-2017-Data-Booklet.pdf.

35. Arias E. United States life tables by Hispanic origin. National Center for Health Statistics. Vital Health Stat 2(152). 2010. Available from: https://www.cdc.gov/nchs/data/series/sr_02/sr02_152.pdf.

Table 1. Selected population characteristics at census tract level, 2011–2015

Characteristic	Census tracts		
	Phases 1 and 2	Phase 1	Phase 2
Number (percent)	66,426 (100)	5,741 (8.6)	60,685 (91.4)
Geographic distribution by region (percent)			
Northeast	18.7	9.5	19.6
Midwest	22.4	18.4	22.7
South	36.4	50.8	35.1
West	22.5	21.3	22.6
Socioeconomic and demographic characteristics			
Mean percentage of population[1] with bachelor's degree or higher	27.8	19.4	28.5
Mean household median income during past 12 months (U.S. dollars)	67,771	53,855	69,089
Mean percentage of population that is Hispanic	16.0	21.4	15.5
Mean percentage of population that is non-Hispanic black	13.5	21.1	12.7
Mean population density	5,311.8	4,825.4	5,357.8
Percentage of census tracts in PRCSDA counties	24.0	24.0	24.0
Summary vital statistics			
Mean number of deaths per census tract (min)(max)	210 (0)(1,825)	264 (28)(1,825)	205 (0)(1,556)
Mean population size per census tract (min)(max)	26,440 (5,013)(302,261)	35,616 (5,324)(302,261)	25,572 (5,013)(219,222)

[1]Aged 25 and over.

NOTES: Maine and Wisconsin are excluded. PRCSDA is Purchased/Referred Care Service Delivery Area; min is minimum value; and max is maximum value.

SOURCES: NCHS, National Vital Statistics Systems, Mortality, and U.S. Census Bureau, American Community Survey 5-year survey, 2011–2015.

Table 2. Estimated parameters β_0 and β_i of zero-truncated negative binomial models used for predicting $_nM_x$, by age group (years)

	Under 1 year		1–4		5–14		15–24		25–34		35–44	
Parameter (β_i)	β_i	SE	β_i	SE	β_i	SE	β_i	SE	β_i	SE	β_i	SE
Region:												
Northeast	ref	ref	ref	ref	ref	ref	ref	ref	ref	ref	ref	ref
Midwest	0.203452	0.0546	–0.144519	0.1133	0.075771	0.1095	0.160638	0.0380	–0.008660	0.0351	–0.007919	0.0305
South	0.172910	0.0506	0.064959	0.1015	0.107234	0.1002	0.107280	0.0350	0.041436	0.0321	0.049817	0.0281
West	0.082675	0.0562	–0.145568	0.1136	0.020038	0.1105	0.054163	0.0388	0.020086	0.0356	0.006390	0.0313
Percentage of census-tract population that is non-Hispanic black:												
First quartile	ref	ref	ref	ref	ref	ref	ref	ref	ref	ref	ref	ref
Second quartile	0.070776	0.0466	–0.003567	0.0914	–0.015040	0.0844	–0.036040	0.0312	–0.005275	0.0291	0.068348	0.0250
Third quartile	0.164937	0.0438	0.081118	0.0847	0.060002	0.0787	0.035798	0.0295	0.034339	0.0276	0.096969	0.0240
Fourth quartile	0.382905	0.0426	0.091568	0.0831	0.242931	0.0769	0.134604	0.0290	0.125224	0.0273	0.182708	0.0237
Percentage of census-tract population that is Hispanic:												
First quartile	ref	ref	ref	ref	ref	ref	ref	ref	ref	ref	ref	ref
Second quartile	–0.127480	0.0399	–0.194160	0.0808	0.002361	0.0739	–0.082038	0.0271	–0.155961	0.0254	–0.091987	0.0220
Third quartile	–0.183334	0.0399	–0.258767	0.0815	–0.111131	0.0762	–0.140210	0.0276	–0.274603	0.0258	–0.186853	0.0223
Fourth quartile	–0.389853	0.0410	–0.410884	0.0826	–0.237287	0.0778	–0.385009	0.0285	–0.493275	0.0267	–0.442902	0.0232
Percentage of census-tract population[1] with bachelor's degree or higher:												
First quartile	ref	ref	ref	ref	ref	ref	ref	ref	ref	ref	ref	ref
Second quartile	–0.118984	0.0324	–0.064155	0.0638	–0.140464	0.0608	–0.109842	0.0224	–0.136966	0.0208	–0.124658	0.0181
Third quartile	–0.135035	0.0435	–0.271147	0.0895	–0.251134	0.0825	–0.174976	0.0299	–0.314067	0.0279	–0.276770	0.0243
Fourth quartile	–0.399614	0.0676	–0.387918	0.1419	–0.389258	0.1278	–0.386323	0.0472	–0.528940	0.0437	–0.604580	0.0386
Median household income during past 12 months:												
First quartile	ref	ref	ref	ref	ref	ref	ref	ref	ref	ref	ref	ref
Second quartile	–0.115686	0.0340	–0.031584	0.0668	0.031636	0.0627	–0.107703	0.0234	–0.135468	0.0218	–0.194542	0.0189
Third quartile	–0.194314	0.0438	–0.218736	0.0886	–0.131273	0.0820	–0.153498	0.0298	–0.163583	0.0278	–0.379358	0.0243
Fourth quartile	–0.236463	0.0648	–0.306894	0.1369	–0.171343	0.1207	–0.197976	0.0445	–0.276002	0.0420	–0.646025	0.0369
Population density:												
First quartile	ref	ref	ref	ref	ref	ref	ref	ref	ref	ref	ref	ref
Second quartile	0.109944	0.0374	–0.151726	0.0725	–0.178901	0.0659	–0.026143	0.0252	–0.017696	0.0237	0.030676	0.0204
Third quartile	0.130396	0.0418	–0.118947	0.0828	–0.206592	0.0771	–0.035178	0.0288	0.009396	0.0268	0.073357	0.0233
Fourth quartile	0.143639	0.0474	–0.075182	0.0946	–0.214300	0.0895	0.007503	0.0328	–0.029662	0.0307	–0.000135	0.0269
PRCSDA:												
Outside PRCSDA	ref	ref	ref	ref	ref	ref	ref	ref	ref	ref	ref	ref
Within PRCSDA	–0.032818	0.0326	0.082211	0.0645	0.035702	0.0609	0.070591	0.0223	0.051928	0.0209	0.028223	0.0183
Constant (β_0)	–5.030287	0.0638	–7.772357	0.1322	–8.806323	0.1268	–6.841273	0.0432	–6.227108	0.0400	–5.795418	0.0348
Likelihood ratio test of alpha = 0, chi-square (d.f.)	994.82 (1)	…	21.55 (1)	…	12.34 (1)	…	179.36 (1)	…	726.23 (1)	…	1,374.51 (1)	…
Probability > chi-square	0.000	…	0.000	…	0.000	…	0.000	…	0.000	…	0.000	…

See footnotes at end of table.

Table 2. Estimated parameters β_0 and β_i of zero-truncated negative binomial models used for predicting ${}_nM_x$, by age group (years)—Con.

Parameter (β_i)	45–54		55–64		65–74		75–84		85 and over	
	β_i	SE	β_i	SE	β_i	SE	β_i	SE	β_i	SE
Region:										
Northeast	ref	ref	ref	ref	ref	ref	ref	ref	ref	ref
Midwest	−0.024619	0.0237	0.055719	0.0202	0.073666	0.0190	0.054644	0.0207	0.041026	0.0318
South	0.027591	0.0219	0.098626	0.0187	0.054119	0.0176	0.061518	0.0193	0.081979	0.0297
West	−0.034924	0.0245	0.041198	0.0209	0.036260	0.0197	0.049549	0.0215	0.015272	0.0331
Percentage of census-tract population that is non-Hispanic black:										
First quartile	ref	ref	ref	ref	ref	ref	ref	ref	ref	ref
Second quartile	0.118887	0.0196	0.119931	0.0165	0.117090	0.0153	0.080075	0.0168	0.044223	0.0260
Third quartile	0.151288	0.0189	0.151729	0.0160	0.150741	0.0149	0.097182	0.0164	0.022133	0.0253
Fourth quartile	0.178645	0.0188	0.212471	0.0159	0.187507	0.0149	0.097124	0.0163	0.049113	0.0253
Percentage of census-tract population that is Hispanic:										
First quartile	ref	ref	ref	ref	ref	ref	ref	ref	ref	ref
Second quartile	−0.011402	0.0173	−0.013505	0.0147	0.009952	0.0137	0.016513	0.0152	−0.013033	0.0235
Third quartile	−0.084658	0.0176	−0.054120	0.0149	−0.032400	0.0140	−0.039618	0.0155	0.010965	0.0239
Fourth quartile	−0.308649	0.0184	−0.189761	0.0156	−0.128922	0.0148	−0.107886	0.0163	0.004116	0.0250
Percentage of census-tract population[1] with bachelor's degree or higher:										
First quartile	ref	ref	ref	ref	ref	ref	ref	ref	ref	ref
Second quartile	−0.110537	0.0145	−0.107614	0.0123	−0.102601	0.0116	−0.058889	0.0128	−0.043102	0.0199
Third quartile	−0.237630	0.0193	−0.254500	0.0163	−0.199248	0.0153	−0.130700	0.0168	−0.027018	0.0261
Fourth quartile	−0.519075	0.0300	−0.505537	0.0252	−0.449159	0.0235	−0.200751	0.0258	0.046845	0.0397
Median household income during past 12 months:										
First quartile	ref	ref	ref	ref	ref	ref	ref	ref	ref	ref
Second quartile	−0.247024	0.0152	−0.198726	0.0129	−0.123342	0.0122	−0.020817	0.0134	−0.010179	0.0208
Third quartile	−0.437035	0.0193	−0.338829	0.0163	−0.185057	0.0154	−0.046365	0.0169	0.035474	0.0261
Fourth quartile	−0.697164	0.0287	−0.524344	0.0242	−0.296670	0.0226	−0.071032	0.0248	0.013578	0.0382
Population density:										
First quartile	ref	ref	ref	ref	ref	ref	ref	ref	ref	ref
Second quartile	0.067035	0.0162	0.081802	0.0137	0.058422	0.0128	0.060178	0.0142	0.002392	0.0220
Third quartile	0.094491	0.0185	0.094397	0.0157	0.061365	0.0147	0.059457	0.0162	0.013964	0.0251
Fourth quartile	0.049652	0.0213	0.074759	0.0181	0.019054	0.0171	0.027402	0.0188	0.031639	0.0291

See footnotes at end of table.

Table 2. Estimated parameters β_0 and β_i of zero-truncated negative binomial models used for predicting ${}_nM_x$, by age group (years)—Con.

Parameter (β_i)	45–54		55–64		65–74		75–84		85 and over	
	β_i	SE	β_i	SE	β_i	SE	β_i	SE	β_i	SE
PRCSDA:										
Outside PRCSDA	ref	ref	ref	ref	ref	ref	ref	ref	ref	ref
Within PRCSDA	0.019481	0.0146	0.007113	0.0124	–0.018466	0.0116	–0.017072	0.0128	–0.019707	0.0196
Constant (β_0)	–5.025023	0.0273	–4.458481	0.0232	–3.788808	0.0217	–2.991029	0.0237	–1.859557	0.0367
Likelihood ratio test of alpha = 0, chi-square (d.f.)	4,445.07 (1)	…	7,318.61 (1)	…	8,487.56 (1)	…	16,000.00 (1)	…	43,000.00 (1)	…
Probability > chi-square	0.000	…	0.000	…	0.000	…	0.000	…	0.000	…

… Category not applicable.
[1]Aged 25 and over.

NOTES: Maine and Wisconsin are excluded. SE is standard error of β_i; ref is reference category; PRCSDA is Purchased/Referred Care Service Delivery Area; and d.f. is degrees of freedom. Sample size is 4,639.

SOURCES: NCHS, National Vital Statistics System, Mortality, and U.S. Census Bureau, American Community Survey 5-year survey, 2011–2015.

Table 3. Estimated parameters β_0 and β_i of zero-truncated negative binomial models used for predicting ${}_nM_x$ without household income information, by age group (years)

Parameter (β_i)	Under 1 year		1–4		5–14		15–24		25–34		35–44	
	β_i	SE	β_i	SE	β_i	SE	β_i	SE	β_i	SE	β_i	SE
Region:												
Northeast	ref	ref	ref	ref	ref	ref	ref	ref	ref	ref	ref	ref
Midwest	0.211348	0.0547	–0.134860	0.1135	0.083612	0.1097	0.164833	0.0381	–0.002444	0.0353	0.011713	0.0317
South	0.189087	0.0506	0.088957	0.1014	0.124770	0.1001	0.119934	0.0350	0.055031	0.0322	0.091432	0.0291
West	0.070512	0.0563	–0.153042	0.1138	0.018516	0.1105	0.044704	0.0389	0.007997	0.0358	–0.011321	0.0326
Percentage of census-tract population that is non-Hispanic black:												
First quartile	ref	ref	ref	ref	ref	ref	ref	ref	ref	ref	ref	ref
Second quartile	0.060353	0.0466	–0.015129	0.0916	–0.020430	0.0845	–0.044039	0.0313	–0.015424	0.0293	0.043643	0.0260
Third quartile	0.157320	0.0439	0.069051	0.0849	0.053998	0.0787	0.027435	0.0296	0.025936	0.0278	0.079374	0.0249
Fourth quartile	0.400435	0.0426	0.103328	0.0833	0.247508	0.0771	0.148266	0.0290	0.145018	0.0274	0.222185	0.0246
Percentage of census-tract population that is Hispanic:												
First quartile	ref	ref	ref	ref	ref	ref	ref	ref	ref	ref	ref	ref
Second quartile	–0.134904	0.0400	–0.196647	0.0811	0.004442	0.0741	–0.088674	0.0272	–0.163028	0.0256	–0.102491	0.0229
Third quartile	–0.189662	0.0400	–0.260572	0.0819	–0.107664	0.0763	–0.145748	0.0277	–0.281751	0.0260	–0.198153	0.0232
Fourth quartile	–0.389438	0.0411	–0.407067	0.0830	–0.234272	0.0781	–0.385255	0.0287	–0.491762	0.0269	–0.438894	0.0242
Percentage of census-tract population[1] with bachelor's degree or higher:												
First quartile	ref	ref	ref	ref	ref	ref	ref	ref	ref	ref	ref	ref
Second quartile	–0.176094	0.0301	–0.112085	0.0594	–0.163926	0.0563	–0.158714	0.0208	–0.193349	0.0194	–0.234728	0.0174
Third quartile	–0.257462	0.0352	–0.415896	0.0738	–0.343765	0.0664	–0.271498	0.0243	–0.427518	0.0229	–0.541487	0.0206
Fourth quartile	–0.569595	0.0517	–0.625961	0.1065	–0.540968	0.0940	–0.522615	0.0361	–0.707813	0.0341	–1.057623	0.0307
Population density:												
First quartile	ref	ref	ref	ref	ref	ref	ref	ref	ref	ref	ref	ref
Second quartile	0.130761	0.0372	–0.141215	0.0724	–0.178742	0.0657	–0.010413	0.0251	–0.000038	0.0237	0.058961	0.0211
Third quartile	0.167321	0.0412	–0.091949	0.0818	–0.199537	0.0761	–0.004589	0.0285	0.044161	0.0266	0.138004	0.0239
Fourth quartile	0.194924	0.0463	–0.032579	0.0923	–0.199005	0.0873	0.051830	0.0320	0.020735	0.0302	0.095342	0.0273
PRCSDA:												
Outside PRCSDA	ref	ref	ref	ref	ref	ref	ref	ref	ref	ref	ref	ref
Within PRCSDA	–0.021208	0.0326	0.092311	0.0646	0.040057	0.0609	0.078612	0.0223	0.063177	0.0210	0.052141	0.0191
Constant (β_0)	–5.107398	0.0618	–7.837337	0.1290	–8.829011	0.1237	–6.907504	0.0418	–6.306727	0.0387	–5.943230	0.0349
Likelihood ratio test of alpha = 0, chi-square (d.f.)	1,007.74 (1)	...	23.46 (1)		13.23 (1)	...	189.50 (1)	...	775.53 (1)	...	1,745.95 (1)	...
Probability > chi-square	0.000	...	0.000		0.000	...	0.000	...	0.000	...	0.000	...

See footnotes at end of table.

Table 3. Estimated parameters β_0 and β_i of zero-truncated negative binomial models used for predicting ${}_nM_x$ without household income information, by age group (years)—Con.

	45–54		55–64		65–74		75–84		85 and over	
Parameter (β_i)	β_i	SE	β_i	SE	β_i	SE	β_i	SE	β_i	SE
Region:										
Northeast	ref	ref	ref	ref	ref	ref	ref	ref	ref	ref
Midwest	–0.003386	0.0255	0.069999	0.0214	0.080671	0.0194	0.056966	0.0207	0.039075	0.0319
South	0.068335	0.0235	0.129599	0.0197	0.070092	0.0180	0.066285	0.0193	0.078190	0.0297
West	–0.055931	0.0263	0.025836	0.0221	0.026249	0.0201	0.047725	0.0215	0.012930	0.0331
Percentage of census-tract population that is non-Hispanic black:										
First quartile	ref	ref	ref	ref	ref	ref	ref	ref	ref	ref
Second quartile	0.094525	0.0210	0.101642	0.0175	0.107684	0.0157	0.077604	0.0168	0.044421	0.0260
Third quartile	0.137284	0.0203	0.138938	0.0170	0.144265	0.0152	0.095597	0.0164	0.021357	0.0254
Fourth quartile	0.230193	0.0200	0.253240	0.0168	0.210986	0.0151	0.102250	0.0163	0.046474	0.0252
Percentage of census-tract population that is Hispanic:										
First quartile	ref	ref	ref	ref	ref	ref	ref	ref	ref	ref
Second quartile	–0.024923	0.0186	–0.023508	0.0156	0.003404	0.0140	0.015317	0.0152	–0.012997	0.0235
Third quartile	–0.094421	0.0189	–0.064061	0.0158	–0.039267	0.0143	–0.040545	0.0155	0.010809	0.0239
Fourth quartile	–0.303455	0.0197	–0.186699	0.0165	–0.127966	0.0151	–0.107307	0.0163	0.003981	0.0250
Percentage of census-tract population[1] with bachelor's degree or higher:										
First quartile	ref	ref	ref	ref	ref	ref	ref	ref	ref	ref
Second quartile	–0.239770	0.0143	–0.208229	0.0120	–0.161978	0.0109	–0.071934	0.0118	–0.036714	0.0183
Third quartile	–0.533440	0.0169	–0.479765	0.0141	–0.325240	0.0127	–0.161680	0.0137	–0.009329	0.0213
Fourth quartile	–1.002467	0.0244	–0.867089	0.0202	–0.651256	0.0181	–0.251607	0.0194	0.065605	0.0297
Population density:										
First quartile	ref	ref	ref	ref	ref	ref	ref	ref	ref	ref
Second quartile	0.104769	0.0172	0.113855	0.0144	0.076123	0.0130	0.063880	0.0141	0.001386	0.0218
Third quartile	0.170084	0.0195	0.155228	0.0164	0.094897	0.0148	0.066509	0.0160	0.011468	0.0247
Fourth quartile	0.160587	0.0224	0.163435	0.0187	0.067787	0.0171	0.038133	0.0183	0.026066	0.0285
PRCSDA:										
Outside PRCSDA	ref	ref	ref	ref	ref	ref	ref	ref	ref	ref
Within PRCSDA	0.047633	0.0156	0.028551	0.0131	–0.006257	0.0119	–0.014432	0.0128	–0.019722	0.0196
Constant (β_0)	–5.201248	0.0283	–4.598712	0.0237	–3.868962	0.0214	–3.008588	0.0228	–1.855458	0.0352
Likelihood ratio test of alpha = 0, chi-square (d.f.):	5,874.93 (1)	...	8,967.87 (1)	...	9,103.02 (1)		16,000.00 (1)		43,000.00 (1)	...
Probability > chi-square	0.000	...	0.000	...	0.000		0.000		0.000	...

... Category not applicable.
[1]Aged 25 and over.

NOTES: Maine and Wisconsin are excluded. SE is standard error of β_i; ref is reference category; PRCSDA is Purchased/Referred Care Service Delivery Area; and d.f. is degrees of freedom. Sample size is 4,639.

SOURCES: NCHS, National Vital Statistics System, Mortality, and U.S. Census Bureau, American Community Survey 5-year survey, 2011–2015.

Table 4. Distribution of Phase 2 census tracts with zero death counts by number of age groups, and by age group

Number of age groups with zero death counts	Number of census tracts	Percent	Age group (years)	Number of census tracts with zero deaths[1]	Percent
1	17,400	28.7	Under 1 year	18,033	13.6
2	23,643	39.0	1–4	49,120	37.0
3	12,942	21.3	5–14	45,081	33.9
4	4,911	8.1	15–24	11,425	8.6
5	1,398	2.3	25–34	5,853	4.4
6	276	0.5	35–44	2,624	2.0
7	44	0.1	45–54	272	0.2
8	12	0.0	55–64	89	0.1
9	15	0.0	65–74	81	0.1
10	16	0.0	75–84	100	0.1
11	28	0.1	85 and over	131	0.1
Total	60,685	100.0			

0.0 Quantity more than zero but less than 0.05.
[1]Not mutually exclusive.

NOTE: Maine and Wisconsin are excluded.

SOURCE: NCHS, National Vital Statistics System, Mortality.

Table 5. Distribution of census-tract life expectancy at birth, by standard error

Characteristic	Standard error of life expectancy at birth			
	2 years or less	More than 2 years up to and including 3 years	More than 3 years up to and including 4 years	More than 4 years
Number of census tracts	44,066	16,768	4,828	764
Life tables based on predicted ${}_n\bar{M}_x$	6,878	1,296	385	764
Weighted mean (LEB)	78.0	79.9	81.6	78.1
Min LEB	56.3	59.0	60.7	71.2
Max LEB	89.9	94.2	97.5	83.4
Weighted mean (SE)	1.4580	2.3866	3.4079	24.0400

NOTES: Maine and Wisconsin are excluded. LEB is life expectancy at birth; min is the minimum value; max is the maximum value; and SE is standard error.

SOURCE: NCHS, National Vital Statistics System, Mortality.

Table 6. Weighted mean abridged life table functions for census tracts, 2010–2015, compared with United States, 2013 abridged life table

Age group (years)	Probability of dying between ages x and $x + n$ ($_nq_x$)	Number surviving to age x (l_x)	Number dying between ages x and $x + n$ ($_nd_x$)	Person-years lived between ages x and $x + n$ ($_nL_x$)	Total number of person-years lived above age x (T_x)	Expectation of life at age x (e_x)	Standard error of e_x (SE)
Census tracts[1]							
Under 1 year	0.007451	100,000	745	99,329	7,868,455	78.7	1.8021
1–4	0.001520	99,256	151	396,723	7,768,638	78.3	1.9188
5–14	0.001735	99,105	172	990,194	7,371,915	74.4	1.9155
15–24	0.008147	98,934	805	985,308	6,381,721	64.5	1.9135
25–34	0.011898	98,128	1,165	975,457	5,396,412	55.0	1.9015
35–44	0.017813	96,963	1,720	961,035	4,420,954	45.6	1.8903
45–54	0.040411	95,244	3,818	933,345	3,459,919	36.3	1.8908
55–64	0.083300	91,425	7,508	876,712	2,526,574	27.6	1.9233
65–74	0.169839	83,917	13,967	769,337	1,649,862	19.6	2.0261
75–84	0.385691	69,950	26,565	566,677	880,525	12.5	2.2819
85 and over	1.000000	43,385	43,385	313,848	313,848	7.1	3.1331
United States[2]							
Under 1 year	0.005960	100,000	596	99,474	7,882,618	78.8	…
1–4	0.001016	99,404	101	397,371	7,783,144	78.3	…
5–14	0.001299	99,303	129	992,435	7,385,773	74.4	…
15–24	0.006373	99,174	632	989,187	6,393,338	64.5	…
25–34	0.010574	98,542	1,042	980,476	5,404,151	54.8	…
35–44	0.016944	97,500	1,652	967,654	4,423,675	45.4	…
45–54	0.039500	95,848	3,786	942,164	3,456,021	36.1	…
55–64	0.083846	92,062	7,719	885,908	2,513,857	27.3	…
65–74	0.172854	84,343	14,579	778,776	1,627,949	19.3	…
75–84	0.395218	69,764	27,572	572,263	849,173	12.2	…
85 and over	1.000000	42,192	42,192	276,910	276,910	6.6	…

… Category not applicable.
[1]Exclude Maine and Wisconsin; weighted using census-tract population sizes.
[2]Values based on official life tables published in "Deaths: Final Data for 2013," available from: https://www.cdc.gov/nchs/data/nvsr/nvsr64/nvsr64_02.pdf.

SOURCE: NCHS, National Vital Statistics System, Mortality.

Table 7. Weighted means of census tract-level life expectancy at birth, standard deviation, and minimum and maximum values, by state, compared with direct state-level estimates of life expectancy at birth, 2010–2015

	Census tract-level estimates[1,2]				State-level estimates[1]
Area	Weighted mean LEB	SD of mean LEB	Minimum LEB	Maximum LEB	LEB
Alabama	75.4	3.416	63.6	88.2	75.5
Alaska	79.1	3.326	65.7	86.9	78.8
Arizona	78.5	3.323	65.8	90.8	79.9
Arkansas	76.0	3.244	65.8	89.6	76.0
California	80.3	3.348	64.4	93.4	81.3
Colorado	79.7	3.334	67.3	89.5	80.5
Connecticut	80.3	3.119	68.9	89.1	80.9
Delaware	78.0	3.006	68.2	86.1	78.7
District of Columbia	77.0	5.389	63.2	90.7	78.5
Florida	78.8	3.822	61.1	91.6	80.1
Georgia	77.1	3.294	63.3	87.6	77.7
Hawaii	81.4	3.400	70.8	92.2	82.0
Idaho	79.4	2.759	70.1	89.2	79.4
Illinois	78.7	3.742	59.9	91.8	79.3
Indiana	77.5	3.755	62.0	90.7	77.4
Iowa	79.4	3.546	66.3	90.2	79.6
Kansas	78.5	3.436	62.5	89.7	78.6
Kentucky	76.0	3.435	62.4	88.9	75.9
Louisiana	75.9	3.464	62.3	88.1	76.0
Maryland	79.2	4.082	62.6	96.1	79.6
Massachusetts	80.6	3.041	68.1	94.2	80.7
Michigan	78.0	3.724	62.0	90.8	78.2
Minnesota	80.7	3.394	64.8	91.9	81.0
Mississippi	75.5	3.469	59.5	85.5	74.9
Missouri	77.4	3.692	60.7	89.2	77.6
Montana	78.9	3.432	66.4	89.2	78.6
Nebraska	79.2	3.284	67.3	89.6	79.6
Nevada	77.7	3.270	64.0	86.1	78.4
New Hampshire	80.1	3.001	63.9	88.3	80.1
New Jersey	80.0	3.491	65.8	91.6	80.5
New Mexico	78.6	3.393	67.9	89.2	78.4
New York	80.6	3.578	59.0	93.6	81.0
North Carolina	77.6	3.381	64.6	97.5	78.1
North Dakota	79.7	3.557	68.1	88.0	79.7
Ohio	77.3	3.825	60.0	89.2	77.6
Oklahoma	76.2	3.909	56.3	89.4	75.8
Oregon	79.2	3.031	66.2	89.1	79.6
Pennsylvania	78.5	3.585	62.0	91.9	78.6
Rhode Island	79.3	2.877	70.2	90.0	79.9
South Carolina	77.0	3.577	64.3	89.4	77.0
South Dakota	79.9	3.682	69.7	90.5	79.4
Tennessee	76.0	3.518	64.3	88.0	76.3
Texas	78.2	3.252	60.7	89.7	78.8
Utah	79.5	3.047	66.1	90.4	79.8
Vermont	81.0	3.387	70.8	90.8	80.0
Virginia	78.7	3.701	61.5	91.1	79.4
Washington	79.9	3.242	66.0	90.7	80.3
West Virginia	76.2	3.717	56.9	89.6	75.3
Wyoming	80.3	3.084	72.4	92.5	78.8

[1]Exclude Maine and Wisconsin.
[2]Weighted using census-tract population sizes.

NOTES: LEB is life expectancy at birth; SD is standard deviation. State-level estimates are based on pooled 2011–2015 National Vital Statistics System mortality and birth data, and midperiod 2013 postcensal population estimates.

SOURCE: NCHS, National Vital Statistics System, Mortality.

Table 8. Number and percentage of census tracts for each quartile of life expectancy at birth, by demographic, geographic, and socioeconomic characteristics of tracts

Characteristic	Life expectancy at birth (years), quartiles							
	56.3–75.7		75.8–78.4		78.5–80.9		81.0–97.5	
	Number of census tracts	Percent	Number of census tracts	Percent	Number of census tracts	Percent	Number of census tracts	Percent
Region:								
Northeast	1,798	10.8	2,473	15.1	3,469	20.9	4,607	27.4
Midwest	4,132	24.9	3,791	23.1	3,763	22.6	3,048	18.1
South	8,656	52.2	6,499	39.7	5,030	30.2	3,670	21.8
West	1,828	11.0	3,381	20.6	4,134	24.8	5,383	32.0
Percentage of census-tract population that is non-Hispanic black:								
First quartile	2,132	12.9	3,831	23.4	4,523	27.2	5,307	31.5
Second quartile	2,250	13.6	3,572	21.8	4,612	27.7	6,037	35.9
Third quartile	3,568	21.5	4,549	27.8	4,642	27.9	3,975	23.6
Fourth quartile	8,464	51.0	4,192	25.6	2,619	15.7	1,389	8.3
Percentage of census-tract population that is Hispanic:								
First quartile	5,261	31.7	4,015	24.5	3,805	22.9	3,417	20.3
Second quartile	3,938	23.7	3,673	22.4	4,092	24.6	4,816	28.6
Third quartile	3,672	22.1	3,761	23.0	4,322	26.0	4,913	29.2
Fourth quartile	3,543	21.4	4,695	28.7	4,177	25.1	3,562	21.2
Percentage of census-tract population[1] with bachelor's degree or higher:								
First quartile	9,400	56.7	4,342	26.5	1,856	11.2	1,005	6.0
Second quartile	4,758	28.7	5,668	34.6	3,801	22.8	2,108	12.5
Third quartile	1,805	10.9	4,673	28.5	5,729	34.4	4,120	24.5
Fourth quartile	451	2.7	1,461	8.9	5,010	30.1	9,475	56.3
Median household income during past 12 months:								
First quartile	10,101	60.9	3,897	23.8	1,441	8.7	908	5.4
Second quartile	4,596	27.7	6,014	36.7	3,718	22.3	2,029	12.1
Third quartile	1,490	9.0	4,687	28.6	5,999	36.1	4,122	24.5
Fourth quartile	224	1.4	1,544	9.4	5,235	31.5	9,557	56.8
Population density:								
First quartile	3,993	24.1	4,782	29.2	4,212	25.3	3,332	19.8
Second quartile	4,102	24.7	3,812	23.3	4,099	24.6	4,359	25.9
Third quartile	4,478	27.0	3,721	22.7	4,141	24.9	4,301	25.6
Fourth quartile	3,841	23.2	3,829	23.4	3,944	23.7	4,716	28.0
PRCSDA:								
Outside PRCSDA	13,161	79.3	12,211	74.5	12,145	73.0	12,367	73.5
Within PRCSDA	3,253	19.6	3,933	24.0	4,251	25.6	4,341	25.8

[1]Aged 25 and over.

NOTES: Maine and Wisconsin are excluded. PRCSDA is Purchased/Referred Care Service Delivery Area.

SOURCES: NCHS, National Vital Statistics System, Mortality, and U.S. Census Bureau, American Community Survey 5-year survey, 2011–2015.

Vital and Health Statistics Series Descriptions

Active Series

Series 1. Programs and Collection Procedures
Reports describe the programs and data systems of the National Center for Health Statistics, and the data collection and survey methods used. Series 1 reports also include definitions, survey design, estimation, and other material necessary for understanding and analyzing the data.

Series 2. Data Evaluation and Methods Research
Reports present new statistical methodology including experimental tests of new survey methods, studies of vital and health statistics collection methods, new analytical techniques, objective evaluations of reliability of collected data, and contributions to statistical theory. Reports also include comparison of U.S. methodology with those of other countries.

Series 3. Analytical and Epidemiological Studies
Reports present data analyses, epidemiological studies, and descriptive statistics based on national surveys and data systems. As of 2015, Series 3 includes reports that would have previously been published in Series 5, 10–15, and 20–23.

Discontinued Series

Series 4. Documents and Committee Reports
Reports contain findings of major committees concerned with vital and health statistics and documents. The last Series 4 report was published in 2002; these are now included in Series 2 or another appropriate series.

Series 5. International Vital and Health Statistics Reports
Reports present analytical and descriptive comparisons of U.S. vital and health statistics with those of other countries. The last Series 5 report was published in 2003; these are now included in Series 3 or another appropriate series.

Series 6. Cognition and Survey Measurement
Reports use methods of cognitive science to design, evaluate, and test survey instruments. The last Series 6 report was published in 1999; these are now included in Series 2.

Series 10. Data From the National Health Interview Survey
Reports present statistics on illness; accidental injuries; disability; use of hospital, medical, dental, and other services; and other health-related topics. As of 2015, these are included in Series 3.

Series 11. Data From the National Health Examination Survey, the National Health and Nutrition Examination Surveys, and the Hispanic Health and Nutrition Examination Survey
Reports present 1) estimates of the medically defined prevalence of specific diseases in the United States and the distribution of the population with respect to physical, physiological, and psychological characteristics and 2) analysis of relationships among the various measurements. As of 2015, these are included in Series 3.

Series 12. Data From the Institutionalized Population Surveys
The last Series 12 report was published in 1974; these reports were included in Series 13, and as of 2015 are in Series 3.

Series 13. Data From the National Health Care Survey
Reports present statistics on health resources and use of health care resources based on data collected from health care providers and provider records. As of 2015, these reports are included in Series 3.

Series 14. Data on Health Resources: Manpower and Facilities
The last Series 14 report was published in 1989; these reports were included in Series 13, and are now included in Series 3.

Series 15. Data From Special Surveys
Reports contain statistics on health and health-related topics from surveys that are not a part of the continuing data systems of the National Center for Health Statistics. The last Series 15 report was published in 2002; these reports are now included in Series 3.

Series 16. Compilations of Advance Data From Vital and Health Statistics
The last Series 16 report was published in 1996. All reports are available online; compilations are no longer needed.

Series 20. Data on Mortality
Reports include analyses by cause of death and demographic variables, and geographic and trend analyses. The last Series 20 report was published in 2007; these reports are now included in Series 3.

Series 21. Data on Natality, Marriage, and Divorce
Reports include analyses by health and demographic variables, and geographic and trend analyses. The last Series 21 report was published in 2006; these reports are now included in Series 3.

Series 22. Data From the National Mortality and Natality Surveys
The last Series 22 report was published in 1973. Reports from sample surveys of vital records were included in Series 20 or 21, and are now included in Series 3.

Series 23. Data From the National Survey of Family Growth
Reports contain statistics on factors that affect birth rates, factors affecting the formation and dissolution of families, and behavior related to the risk of HIV and other sexually transmitted diseases. The last Series 23 report was published in 2011; these reports are now included in Series 3.

Series 24. Compilations of Data on Natality, Mortality, Marriage, and Divorce
The last Series 24 report was published in 1996. All reports are available online; compilations are no longer needed.

For answers to questions about this report or for a list of reports published in these series, contact:

Information Dissemination Staff
National Center for Health Statistics
Centers for Disease Control and Prevention
3311 Toledo Road, Room 4551, MS P08
Hyattsville, MD 20782

Tel: 1–800–CDC–INFO (1–800–232–4636)
TTY: 1–888–232–6348
Internet: https://www.cdc.gov/nchs
Online request form: https://www.cdc.gov/info
For e-mail updates on NCHS publication releases, subscribe online at: https://www.cdc.gov/nchs/govdelivery.htm.

U.S. DEPARTMENT OF
HEALTH & HUMAN SERVICES

Centers for Disease Control and Prevention
National Center for Health Statistics
3311 Toledo Road, Room 4551, MS P08
Hyattsville, MD 20782–2064

For more NCHS Series Reports, visit:
https://www.cdc.gov/nchs/products/series.htm

DHHS Publication No. (PHS) 2018–1381, Series 2, No. 181
CS295028