



Provisional Life Expectancy Estimates for 2022

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Introduction

The National Center for Health Statistics (NCHS) collects and disseminates the nation's official vital statistics through the National Vital Statistics System. NCHS uses provisional vital statistics data for conducting public health surveillance and final data for producing annual national natality and mortality statistics. NCHS publishes annual life tables based on final vital statistics data. To assess the effects of excess mortality related to the COVID-19 pandemic on life expectancy, NCHS first published provisional life expectancy estimates for 2020 (1,2). Life expectancy estimates presented in this report are based on provisional mortality data for 2022 and final data for 2021. Provisional data are early estimates based on death certificates received, processed, and coded but not finalized by NCHS. These estimates are considered provisional because death certificate information may be revised, and additional death certificates may be received until about 6 months after the year's end.

This report presents life expectancy estimates calculated using complete period life tables based on provisional death counts for 2022 by sex and for the total, Hispanic, American Indian and Alaska Native non-Hispanic, Asian non-Hispanic, Black non-Hispanic, and White non-Hispanic populations. Estimates for the Native Hawaiian or Other Pacific Islander population were not produced because data needed to evaluate race and ethnicity

misclassification on death certificates for this population are not available (3).

Life tables are of two types: the cohort (or generation) and the period (or current) life table. The cohort life table presents the mortality experience of a particular birth cohort from the moment of birth through consecutive ages in successive calendar years. The period life table, instead of representing the mortality experience of an actual birth cohort, presents what would happen to a hypothetical cohort if it experienced throughout its entire life the mortality conditions of a particular period. This report also presents contributions of causes of death to the changes in life expectancy using a life table partitioning technique (Technical Notes).

Keywords: Hispanic origin • race • cause of death • National Vital Statistics System

Data and Methods

Provisional life expectancy estimates were calculated using complete period life tables based on provisional death counts for 2022 from death records received and processed by NCHS as of July 2, 2023; final numbers of births for 2022; July 1, 2022, postcensal population estimates; and age-specific death and population counts for Medicare beneficiaries ages 66–99 for 2022 from the Centers for Medicare & Medicaid Services. Population estimates are based on the blended base produced by the U.S. Census Bureau in place of the

April 1, 2020, decennial population count. The blended base consists of Vintage 2020 Population Estimates for April 1, 2020 (based on the April 1, 2010, decennial census), blended with the 2020 Demographic Analysis Estimates and the 2020 Census Edited File (see <https://www2.census.gov/programs-surveys/popest/technical-documentation/methodology/2020-2022/methods-statement-v2022.pdf>). Mortality data used in this report include more than 99% of the deaths that occurred in 2022, but certain jurisdictions and age groups may be underrepresented for later months (4,5). Deaths requiring investigation, including infant deaths and those from external injuries and drug overdoses, may be underestimated (6). See Technical Notes for more information about the calculation of the complete period life tables and life table partitioning by cause of death. Provisional 2022 life expectancy estimates are compared with final estimates for 2021.

Results

Life expectancy in the United States

The [Table](#) summarizes life expectancy by age, Hispanic origin and race, and sex. Life expectancy at birth represents the average number of years a group of infants would live if they were to experience throughout life the age-specific death rates prevailing during a



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Table. Provisional life expectancy, by age, Hispanic origin and race, and sex: United States, 2022

Age	Non-Hispanic																	
	All races and origins			Hispanic ¹			American Indian and Alaska Native			Asian			Black			White		
	Total	Male	Female	Total	Male	Female	Total	Male	Female	Total	Male	Female	Total	Male	Female	Total	Male	Female
0	77.5	74.8	80.2	80.0	77.0	82.8	67.9	64.6	71.3	84.5	82.4	86.3	72.8	69.1	76.5	77.5	75.1	80.1
1	76.9	74.3	79.6	79.4	76.4	82.2	67.4	64.2	70.8	83.7	81.6	85.6	72.6	68.9	76.3	76.9	74.4	79.4
5	73.0	70.4	75.7	75.4	72.5	78.3	63.6	60.4	67.0	79.8	77.7	81.6	68.8	65.1	72.4	73.0	70.5	75.5
10	68.0	65.4	70.7	70.5	67.6	73.3	58.7	55.5	62.1	74.8	72.7	76.6	63.9	60.2	67.5	68.0	65.6	70.5
15	63.1	60.5	65.8	65.5	62.6	68.4	53.8	50.6	57.2	69.8	67.8	71.7	58.9	55.3	62.6	63.0	60.6	65.6
20	58.3	55.7	60.9	60.7	57.8	63.5	49.2	46.1	52.6	64.9	62.9	66.7	54.3	50.7	57.8	58.2	55.8	60.7
25	53.5	51.1	56.1	56.0	53.2	58.6	44.8	41.8	48.0	60.1	58.0	61.8	49.8	46.4	53.0	53.4	51.1	55.8
30	48.9	46.6	51.3	51.3	48.7	53.8	40.8	38.0	43.7	55.2	53.2	56.9	45.3	42.2	48.4	48.8	46.6	51.0
35	44.3	42.1	46.5	46.7	44.2	49.0	37.0	34.4	39.7	50.4	48.4	52.0	41.0	38.0	43.8	44.2	42.1	46.3
40	39.8	37.7	41.9	42.1	39.8	44.2	33.4	31.1	35.8	45.6	43.7	47.1	36.7	33.8	39.3	39.7	37.7	41.7
45	35.3	33.4	37.3	37.6	35.4	39.5	29.9	27.8	31.9	40.8	38.9	42.2	32.5	29.8	34.9	35.2	33.3	37.1
50	31.0	29.1	32.8	33.1	31.0	34.9	26.7	24.9	28.4	36.1	34.3	37.4	28.4	25.9	30.6	30.8	29.1	32.6
55	26.7	25.0	28.4	28.7	26.8	30.3	23.6	21.9	25.1	31.4	29.8	32.7	24.4	22.1	26.5	26.6	25.0	28.2
60	22.7	21.1	24.2	24.5	22.7	25.9	20.7	19.3	21.9	26.9	25.4	28.0	20.8	18.7	22.6	22.6	21.1	24.0
65	18.9	17.5	20.2	20.5	19.0	21.7	17.8	16.8	18.7	22.5	21.2	23.4	17.4	15.5	19.0	18.8	17.5	20.0
70	15.3	14.2	16.3	16.8	15.4	17.7	15.0	14.2	15.5	18.4	17.2	19.1	14.4	12.8	15.6	15.2	14.1	16.2
75	12.0	11.0	12.8	13.2	12.1	13.9	12.4	12.0	12.6	14.5	13.6	15.0	11.5	10.2	12.4	11.8	10.9	12.6
80	8.9	8.1	9.5	10.0	9.1	10.4	9.9	9.6	10.0	10.8	10.1	11.1	8.9	7.8	9.5	8.8	8.0	9.4
85	6.4	5.8	6.8	7.2	6.5	7.4	7.9	7.8	7.8	7.7	7.2	7.8	6.6	5.8	7.0	6.3	5.7	6.7
90	4.4	3.9	4.6	5.0	4.4	5.0	6.2	6.1	6.0	5.1	4.8	5.1	4.8	4.2	5.0	4.3	3.8	4.5
95	3.0	2.7	3.1	3.4	3.0	3.3	4.9	4.9	4.6	3.4	3.2	3.2	3.4	3.1	3.5	2.9	2.6	3.0
100	2.1	1.9	2.2	2.4	2.2	2.3	3.9	4.0	3.6	2.3	2.2	2.1	2.5	2.3	2.5	2.0	1.8	2.1

¹People of Hispanic origin may be of any race.

NOTES: Life tables by race and Hispanic origin are based on death rates that have been adjusted for race and ethnicity misclassification on death certificates; see Technical Notes in this report. Estimates are based on provisional data for 2022. Provisional data are subject to change as additional data are received.

SOURCE: National Center for Health Statistics, National Vital Statistics System, mortality data file.

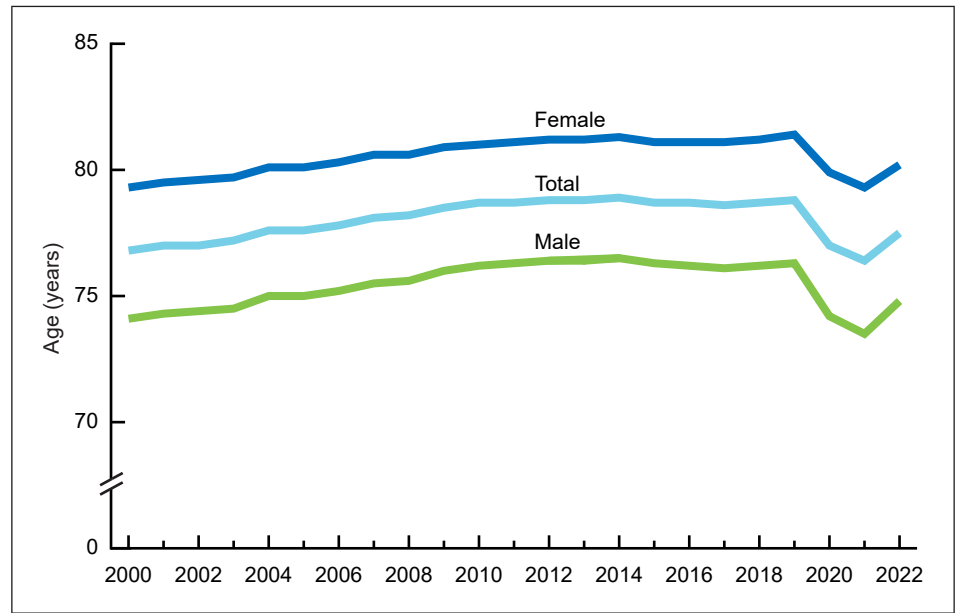
period. In 2022, life expectancy at birth was 77.5 years, increasing by 1.1 years from 76.4 in 2021 (3). Life expectancy at birth for males in 2022 was 74.8 years, representing an increase of 1.3 years from 73.5 in 2021. For females, life expectancy increased to 80.2 years, increasing 0.9 year from 79.3 in 2021 (Figure 1).

The difference in life expectancy between the sexes was 5.4 years in 2022, decreasing from 5.8 in 2021. Between 2000 and 2010, the difference in life expectancy between the sexes narrowed from 5.2 years to its lowest level of 4.8, but then increased in 2020 and 2021 to levels not seen since 1996, when the difference was 6.0 years (Figure 1).

Life expectancy by Hispanic origin and race

From 2021 to 2022, life expectancy increased by 2.3 years for the American Indian and Alaska Native non-Hispanic population (from 65.6 to 67.9) (Figure 2) (3). It increased by 2.2 years for the Hispanic population (from 77.8 to 80.0), 1.6 years for the Black non-Hispanic population (71.2 to 72.8), 1.0 year for the Asian non-Hispanic population (83.5 to 84.5), and 0.8 year for the White

Figure 1. Life expectancy at birth, by sex: United States, 2000–2022



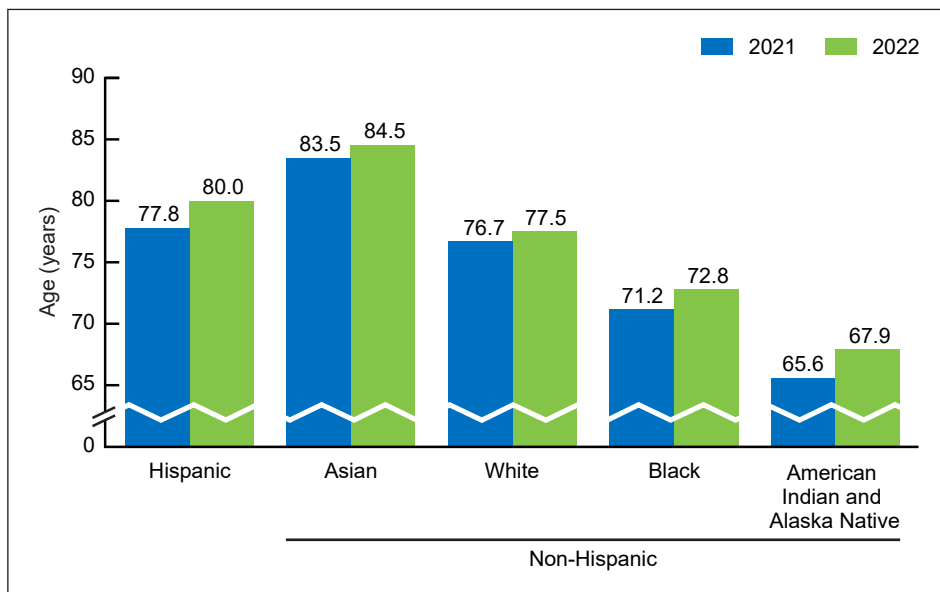
NOTES: Estimates are based on provisional data for 2022. Provisional data are subject to change as additional data are received. Estimates for 2000–2021 are based on final data.
SOURCE: National Center for Health Statistics, National Vital Statistics System, mortality data file.

non-Hispanic population (76.7 to 77.5).

Among the 10 Hispanic-origin and race–sex groups (Figure 3), the increase in life expectancy from 2021 to 2022 was greatest for American Indian and Alaska Native non-Hispanic and Hispanic males, whose life expectancy increased by 2.4 years each (62.2 to 64.6 and 74.6 to

77.0, respectively), followed by American Indian and Alaska Native non-Hispanic females with an increase of 2.1 years (69.2 to 71.3), Hispanic females with an increase of 1.7 years (81.1 to 82.8), Black non-Hispanic males and females with an increase of 1.5 years each (67.6 to 69.1 and 75.0 to 76.5, respectively), Asian non-Hispanic males with an increase of 1.2 years (81.2 to 82.4), White non-Hispanic males with an increase of 1.1 years (74.0 to 75.1), Asian non-Hispanic females with an increase of 0.7 year (85.6 to 86.3), and White non-Hispanic females with an increase of 0.6 year (79.5 to 80.1).

Figure 2. Life expectancy at birth, by Hispanic origin and race: United States, 2021-2022

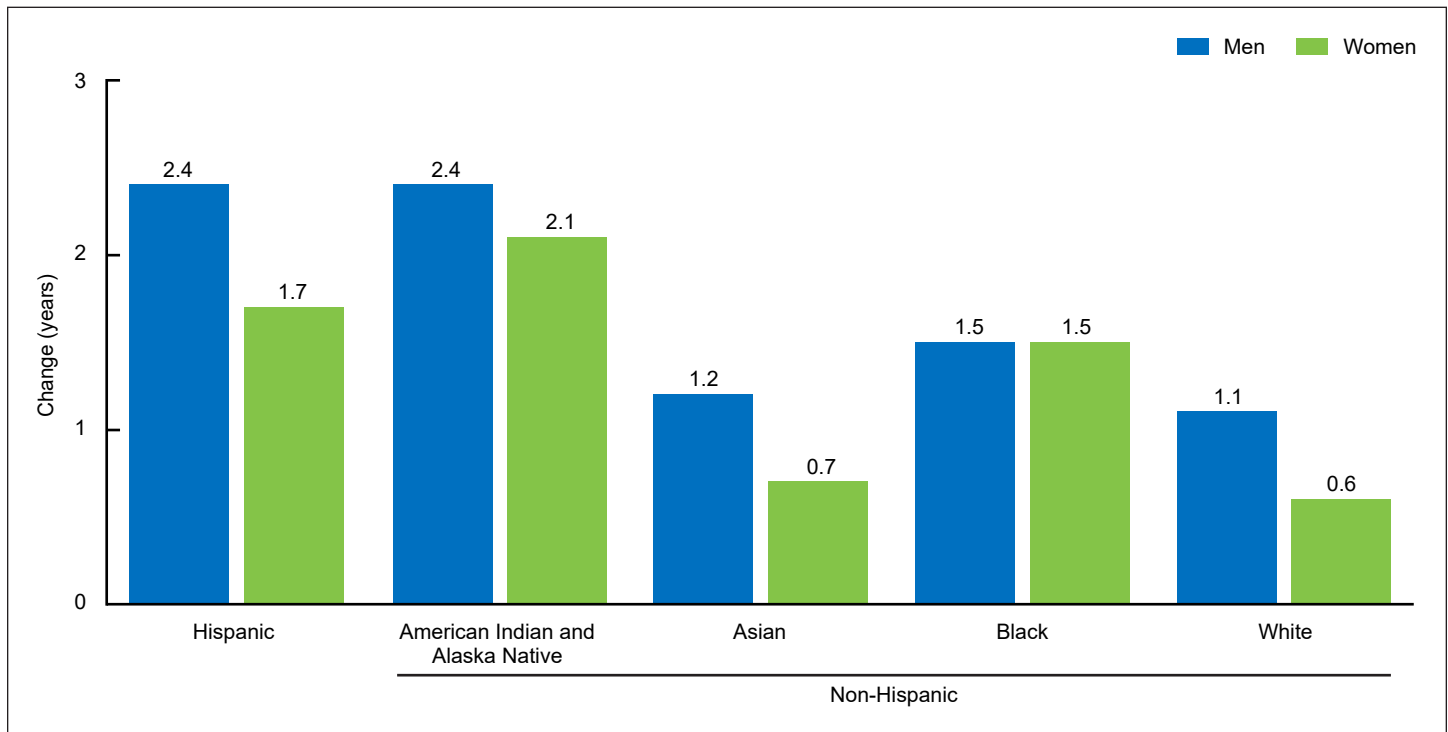


NOTES: Estimates are based on provisional data for 2022. Provisional data are subject to change as additional data are received. Estimates for 2021 are based on final data. Life tables by Hispanic origin and race are based on death rates that have been adjusted for Hispanic-origin and race misclassification on death certificates; see Technical Notes in this report.
SOURCE: National Center for Health Statistics, National Vital Statistics System, mortality data file.

Effect on life expectancy of changes in cause-specific mortality

Increases or decreases in life expectancy represent the sum of positive and negative contributions of cause-specific death rates. Declines in cause-specific mortality contribute to increases in life expectancy, while increases contribute to decreases in life expectancy. If the negative contributions (increases in cause-specific death rates) are greater than the positive

Figure 3. Change in life expectancy at birth, by Hispanic origin and race and sex: United States, 2021–2022



NOTES: Estimates are based on provisional data for 2022. Provisional data are subject to change as additional data are received. Estimates for 2021 are based on final data. Life tables by Hispanic origin and race are based on death rates that have been adjusted for Hispanic-origin and race misclassification on death certificates; see Technical Notes in this report. SOURCE: National Center for Health Statistics, National Vital Statistics System, mortality data file.

contributions (decreases in cause-specific deaths rates), then the result is a decline in life expectancy. If negative and positive contributions offset each other, then life expectancy would be unchanged (see Technical Notes for a description of the partitioning method).

The increase of 1.1 years in life expectancy from 2021 to 2022 primarily resulted from decreases in mortality due to COVID-19 (84.2% of the positive contribution), heart disease (3.6%), unintentional injuries (2.6%), cancer (2.2%), and homicide (1.5%) (Figure 4). The increase in life expectancy would have been even greater if not for the offsetting effects of increases in mortality due to influenza and pneumonia (25.5%), perinatal conditions (21.5%), kidney disease (13.0%), nutritional deficiencies (12.6%), and congenital malformations (5.9%).

For the male population, the 1.3-year increase in life expectancy mostly resulted from decreases in mortality due to COVID-19 (81.2%), heart disease (4.6%), unintentional injuries (2.9%),

cancer (2.4%), and homicide (2.3%). The increase in life expectancy was offset by increases in mortality due to perinatal conditions (35.2%), influenza and pneumonia (19.8%), kidney disease (13.5%), nutritional deficiencies (10.0%), and congenital malformations (7.9%).

For females, the increase in life expectancy of 0.9 year primarily resulted from decreases in mortality due to COVID-19 (86.6%), unintentional injuries (2.7%), heart disease (2.1%), cancer (1.6%), and diabetes (1.6%). The increase in life expectancy was offset by increases in mortality due to influenza and pneumonia (24.8%), nutritional deficiencies (12.0%), chronic lower respiratory diseases (11.3%), kidney disease (10.4%), and perinatal conditions (9.9%).

The American Indian and Alaska Native non-Hispanic population experienced the greatest increase in life expectancy (2.3 years), primarily resulting from decreases in mortality due to COVID-19 (70.0%), chronic liver disease and cirrhosis (10.4%), suicide

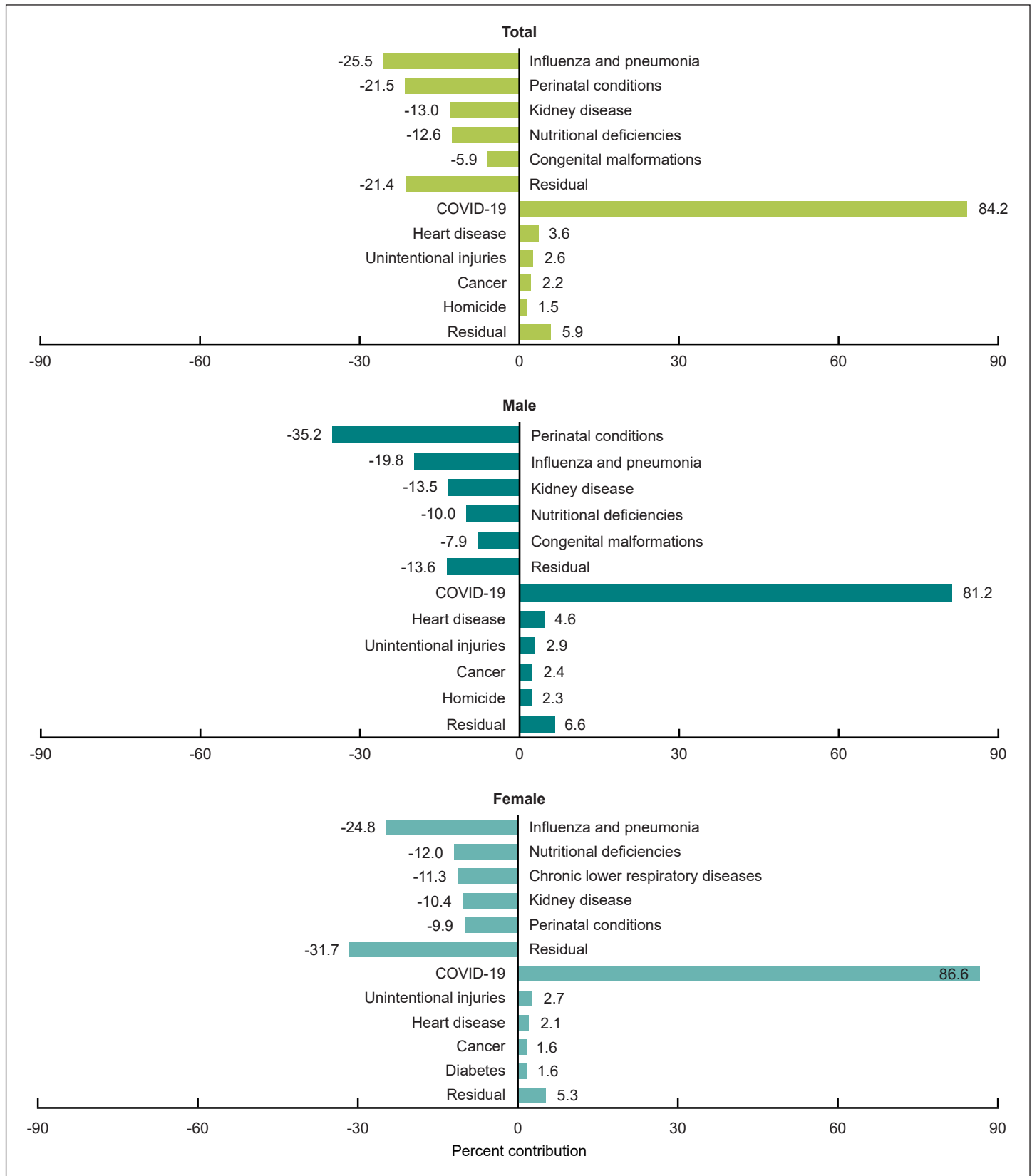
(1.8%), cancer (1.7%), and diabetes (1.6%) (Figure 5). The increase in life expectancy would have been greater if not for the offsetting increases in mortality due to unintentional injuries (31.9%), homicide (22.8%), perinatal conditions (14.3%), influenza and pneumonia (6.8%), and legal intervention (4.4%).

The Hispanic population experienced the second greatest increase (2.2 years), primarily due to declines in mortality from COVID-19 (92.4%), heart disease (3.2%), diabetes (0.9%), cancer (0.7%), and complications of medical care (0.4%) (Figure 5). The positive effects of these causes were offset by increases in mortality due to unintentional injuries (29.5%), perinatal conditions (12.0%), influenza and pneumonia (11.6%), congenital malformations (11.4%), and nutritional deficiencies (2.9%).

The Black non-Hispanic population had the third greatest increase in life expectancy (1.6 years), resulting primarily from decreases in mortality due to COVID-19 (71.9%), heart disease

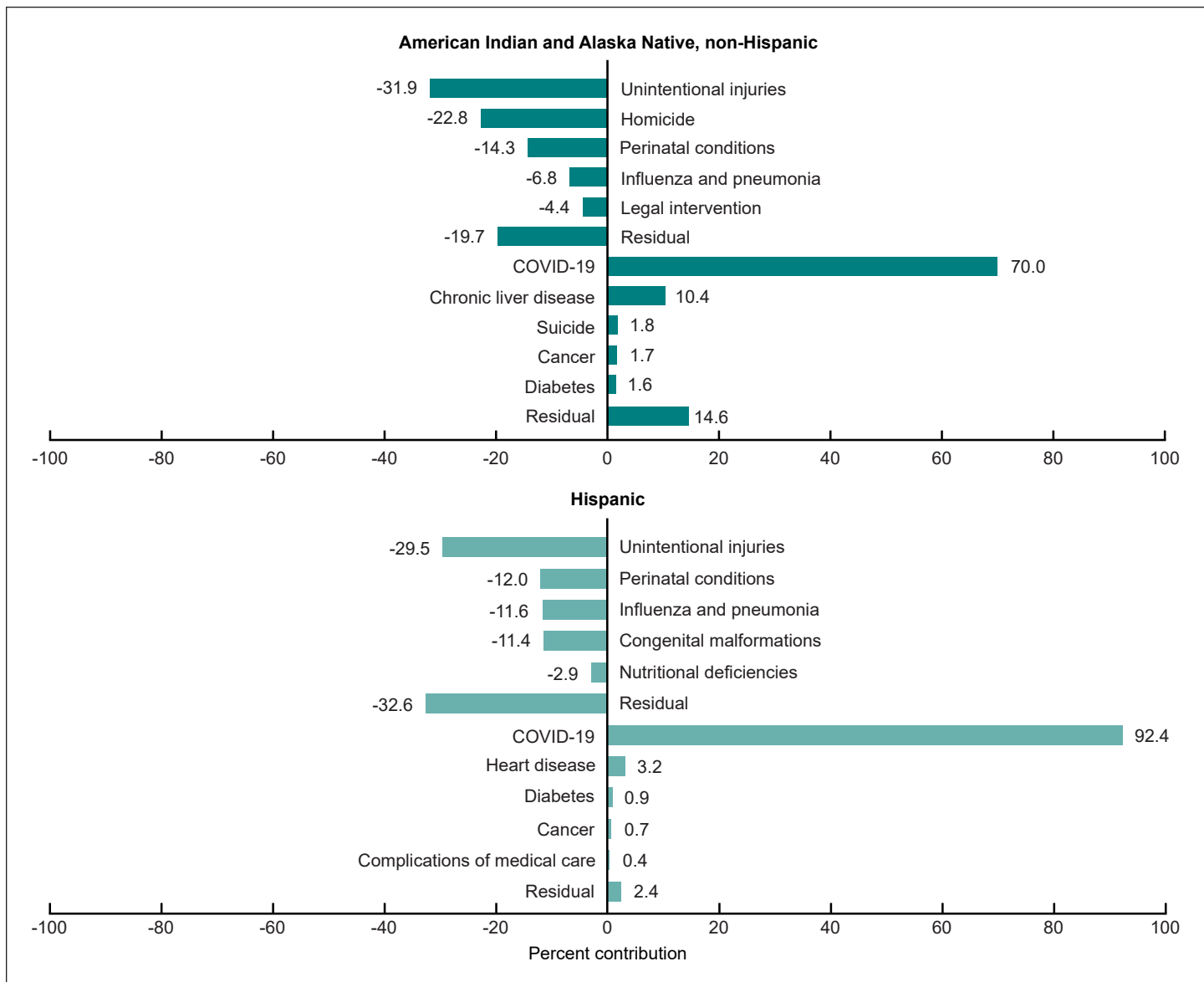
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Figure 4. Contribution of leading causes of death to change in life expectancy, by total population and sex: United States, 2021–2022



NOTES: Estimates are based on provisional data for 2022. Provisional data are subject to change as additional data are received. Estimates for 2021 are based on final data. Life tables by Hispanic origin and race are based on death rates that have been adjusted for Hispanic-origin and race misclassification on death certificates; see Technical Notes in this report.
SOURCE: National Center for Health Statistics, National Vital Statistics System, mortality data file.

Figure 5. Contribution of leading causes of death to change in life expectancy, by Hispanic origin and race: American Indian and Alaska Native non-Hispanic and Hispanic populations, 2021–2022



NOTES: Estimates are based on provisional data for 2022. Provisional data are subject to change as additional data are received. Estimates for 2021 are based on final data. Life tables by Hispanic origin and race are based on death rates that have been adjusted for Hispanic-origin and race misclassification on death certificates; see Technical Notes in this report.
SOURCE: National Center for Health Statistics, National Vital Statistics System, mortality data file.

(7.3%), homicide (5.7%), diabetes (2.6%), and cancer (1.5%) (Figure 6). The increase in life expectancy was offset by increases in mortality due to perinatal conditions (58.9%), congenital malformations (13.8%), kidney disease (11.6%), nutritional deficiencies (3.3%), and legal intervention (3.2%).

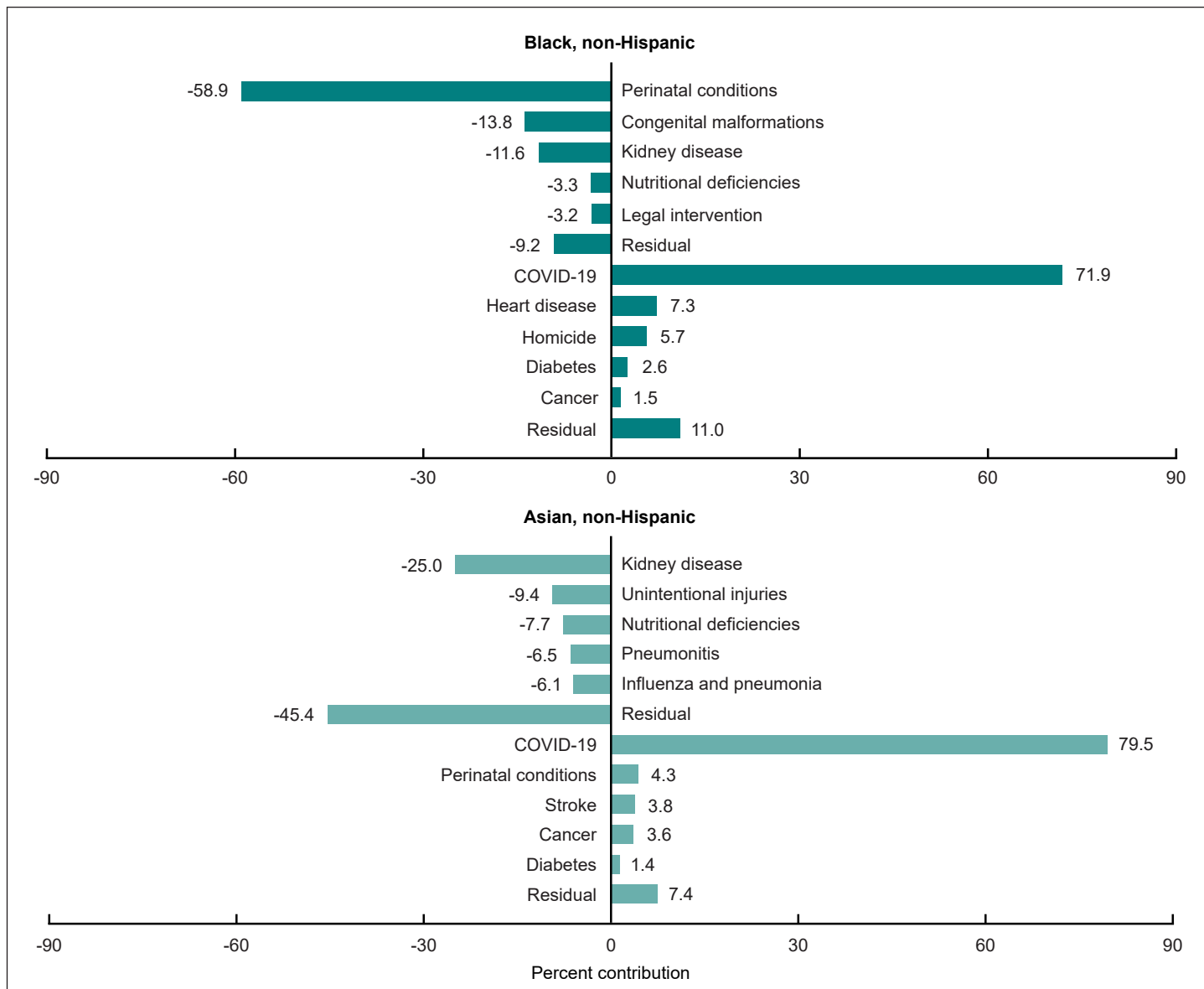
The Asian non-Hispanic population had the fourth largest increase in life expectancy (1.0 year), primarily due to decreases in mortality from COVID-19 (79.5%), perinatal conditions (4.3%),

stroke (3.8%), cancer (3.6%), and diabetes (1.4%) (Figure 6). The increase in life expectancy would have been greater if not for the offsetting effects of increases in mortality due to kidney disease (25.0%), unintentional injuries (9.4%), nutritional deficiencies (7.7%), pneumonitis (6.5%), and influenza and pneumonia (6.1%).

The White non-Hispanic population experienced the smallest increase in life expectancy (0.8 year), primarily as a result of decreases in mortality due

to COVID-19 (80.6%), unintentional injuries (6.9%), heart disease (3.2%), cancer (2.3%), and chronic liver disease and cirrhosis (1.3%) (Figure 7). The increase in life expectancy was offset by increases in mortality due to influenza and pneumonia (30.4%), nutritional deficiencies (13.9%), perinatal conditions (13.3%), kidney disease (11.1%), and chronic lower respiratory diseases (10.1%).

Figure 6. Contribution of leading causes of death to change in life expectancy, by Hispanic-origin and race: Black non-Hispanic and Asian non-Hispanic populations, 2021–2022



NOTES: Estimates are based on provisional data for 2022. Provisional data are subject to change as additional data are received. Estimates for 2021 are based on final data. Life tables by Hispanic origin and race are based on death rates that have been adjusted for Hispanic-origin and race misclassification on death certificates; see Technical Notes in this report.
SOURCE: National Center for Health Statistics, National Vital Statistics System, mortality data file.

Discussion and Conclusions

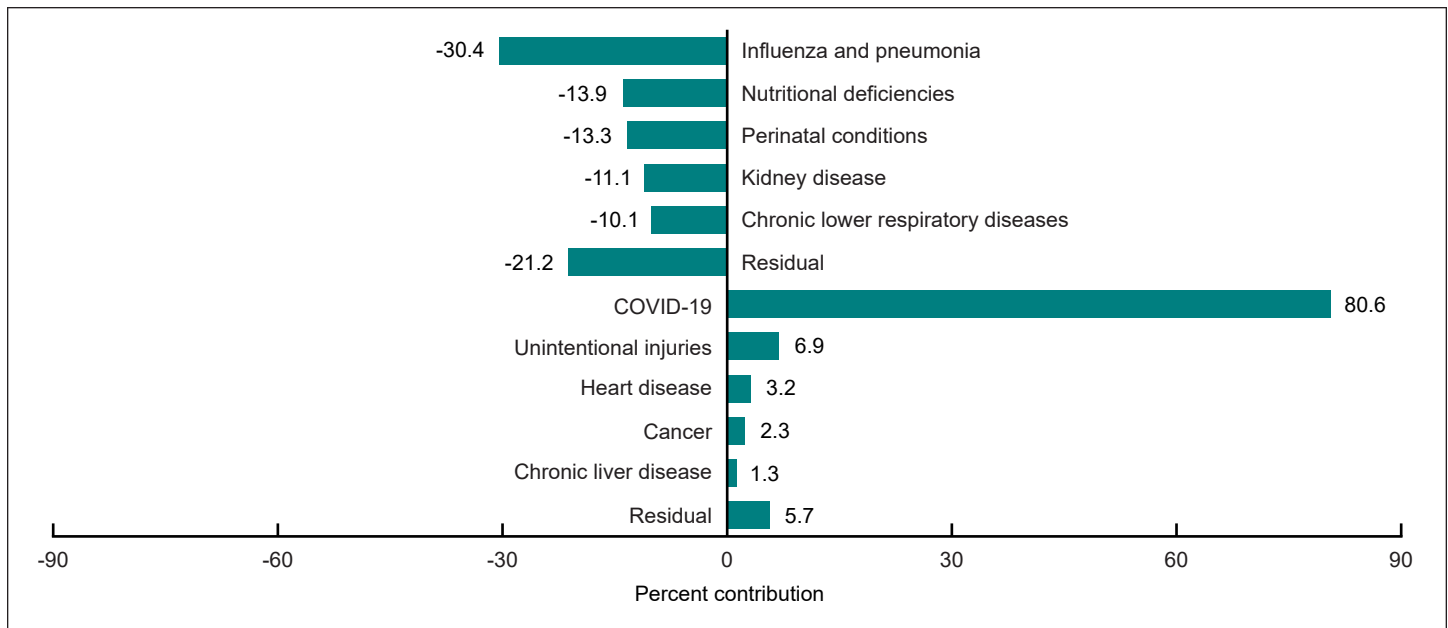
U.S. life expectancy at birth for 2022, based on near-final data, was 77.5 years, an increase of 1.1 years from 2021 (76.4 years). This increase does not fully offset the loss of 2.4 years of life expectancy between 2019 and 2021 that resulted mostly from increases in excess deaths due to the COVID-19 pandemic (Internet Table I–21) (3). In 2022, males regained 1.3 years of the 2.8-year life

expectancy loss and females regained 0.9 year of the 2.1-year life expectancy loss between 2019 and 2021. The American Indian and Alaska Native non-Hispanic population experienced the greatest increase in life expectancy in 2022, regaining 2.3 years of the 6.2-year life expectancy loss between 2019 and 2021. The Hispanic population had the next largest gain at 2.2 years after having lost 4.1 years during the same period, followed by the Black non-Hispanic population with a gain of 1.6 years out of 3.6 years lost, the Asian non-Hispanic

population with 1.0 year regained from 2.1 years lost, and the White non-Hispanic population with 0.8 year regained from a loss of 2.1 years between 2019 and 2021.

From 2021 to 2022, racial and ethnic disparities in life expectancy increased for some groups and declined for others. For example, the White non-Hispanic life expectancy advantage over the American Indian and Alaska Native non-Hispanic population decreased by 13.5% from 2021 (11.1 years) to 2022 (9.6). The White non-Hispanic advantage over the

Figure 7. Contribution of leading causes of death to change in life expectancy, by Hispanic-origin and race: White non-Hispanic population, 2021–2022



NOTES: Estimates are based on provisional data for 2022. Provisional data are subject to change as additional data are received. Estimates for 2021 are based on final data. Life tables by Hispanic origin and race are based on death rates that have been adjusted for Hispanic-origin and race misclassification on death certificates; see Technical Notes in this report.
SOURCE: National Center for Health Statistics, National Vital Statistics System, mortality data file.

Black non-Hispanic population declined by 14.5% from 2021 (5.5 years) to 2022 (4.7). Regardless of Hispanic origin, life expectancy for the Black population has consistently been lower than that of the White population, but the gap had been narrowing during nearly the past 3 decades (from 7.1 years in 1993 to 4.0 in 2019) (7).

The Hispanic life expectancy advantage over the White non-Hispanic population increased by 127.3% from 2021 (1.1 years) to 2022 (2.5). Between 2019 and 2021, the Hispanic population lost most of the life expectancy advantage it had experienced relative to the White non-Hispanic population (3.1 years to 1.1) since it was first recorded in 2006 (7). The Asian non-Hispanic life expectancy advantage over the White non-Hispanic population increased by 2.9% from 2021 (6.8 years) to 2022 (7.0).

Declines in mortality due to COVID-19 were the primary reason for the increases in life expectancy from 2021 to 2022 observed for the total population and each of the five Hispanic-origin and race groups shown in this report. Decreases in mortality due to COVID-19 accounted for 92.4% of the

life expectancy increase for the Hispanic population. They also accounted for much of the life expectancy increases for the White (80.6%), Asian (79.5%), Black (71.9%), and American Indian and Alaska Native (70.0%) non-Hispanic populations.

The provisional mortality data that the life tables are based on have several limitations. First, the timeliness of death certificate data varies by jurisdiction and time. Some jurisdictions have historically taken longer to submit death certificates because of paper records, staffing shortages, or other local issues. The effects of recent changes in timeliness will not be clear until data are finalized. Another limitation is the variation in timeliness due to age and cause of death. Certain age groups, particularly younger than 5 years, may be underrepresented (5). Death certificates for deaths requiring investigation, including infant deaths, deaths involving external injuries, and drug overdose deaths take longer to complete; these deaths may be underreported in the 3–6 months after the deaths occurred. Lastly, the timeliness of death certificate data by race and ethnicity has not been studied. Differences in timeliness by these factors

may result in underestimation of deaths for specific groups. The underestimation of infant deaths, for example, will have a disproportionate effect on life expectancy at birth, given the latter’s sensitivity to infant mortality, which is generally higher than mortality at all other ages up to generally the mid-50s.

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Technical Notes

The methodology used to estimate provisional 2022 complete period life tables (Internet Tables I-1 through I-21) on which the life expectancy estimates presented in this report are based is the same as that used to produce annual U.S. life tables, with some modifications (3). First, the life tables presented in this report are based on provisional death counts rather than on final death counts. Final death counts for 2022 will not be available until late in 2023. Another difference is the use of final birth counts from the standard birth file and provisional infant death counts, because linked birth and infant death data used for life tables by Hispanic origin and race are not yet available (Tables I-1 through I-18).

Standard errors of the two most important functions, the probability of dying and life expectancy (Tables I-19 and I-20), are estimated under the assumption that the data are affected only by random error because more than 99% of deaths that occurred in 2022 are included. However, the possibility that certain jurisdictions and age groups may be underrepresented for later months could potentially lead to biases not accounted for by the estimated standard errors. Other possible errors, including age and Hispanic-origin and race misreporting on death certificates, also are not considered in the calculation of the variances or standard errors of the life table functions.

Data for calculating life table functions

Vital statistics data

Mortality data used to estimate the life tables presented in this report include more than 99% of the deaths that occurred in 2022, although certain jurisdictions and age groups may be underrepresented for later months. Death data are typically more than 99% complete 3 months after the date of death, but this can vary by jurisdiction, age of the decedent, and cause of death.

Most jurisdictions submit more than 90% of death data by 3 months after the date of death, but some jurisdictions take longer to submit death records. Death data for decedents younger than age 5 years are 90% complete 3 months after the date of death, and 95% complete by 6 months. Provisional estimates of infant mortality are typically presented with a 9-month lag, because infant deaths require additional investigation and death certificates take longer to complete. Timeliness also varies by cause of death, with deaths due to external causes taking additional time to investigate and complete death certificates. Provisional estimates for most external causes of death (for example, falls, suicides, unintentional injuries, and others) are presented with a 6-month lag, while drug overdose deaths are presented with a 9-month lag.

Beginning with the 2018 data year, all 50 states and the District of Columbia reported deaths based on the 2003 revision of the U.S. Standard Certificate of Death for the entire year (3). The revision is based on the 1997 Office of Management and Budget standards (8), which allow individuals to report more than one race and increase the race choices from four to five by separating the Asian and Pacific Islander groups. The Hispanic category did not change, remaining consistent with previous reports.

The Hispanic-origin and race groups in this report follow the 1997 standards and differ from the race categories used in reports for data years before 2018. From 2003 through 2017, not all deaths were reported using the 2003 certificate revision that allowed multiple-race reporting (8). As a result, during those years, multiple-race data were bridged to the 1977 Office of Management and Budget standards' single-race categories (9). Use of the bridged-race process was discontinued for the reporting of mortality statistics in 2018 when all states collected data on race according to the 1997 Office of Management and Budget guidelines for the full data year.

Census population data

The population data used to estimate the life tables shown in this report are July 1, 2022, postcensal population estimates based on the so-called blended base produced by the U.S. Census Bureau instead of the April 1, 2020, decennial population count. The blended base consists of the blended Vintage 2020 Population Estimates for April 1, 2020 (based on the April 1, 2010, decennial census), 2020 Demographic Analysis Estimates, and 2020 Census Edited File (see <https://www2.census.gov/programs-surveys/popest/technical-documentation/methodology/2020-2022/methods-statement-v2022.pdf>).

Preliminary adjustment of the data

Adjustment for unknown age

An adjustment is made to account for the small proportion of deaths for which age is not reported on the death certificate. The number of deaths in each age category is adjusted proportionally to account for those with not-stated ages. The following factor (F) is used to make the adjustment. F is calculated for the total and for each sex group within a racial and ethnic population for which life tables are constructed:

$$F = \frac{D}{D^a} \quad [1]$$

where D is the total number of deaths and D^a is the total number of deaths for which age is stated. F is then applied by multiplying it by the number of deaths in each age group.

Adjustment for misclassification of Hispanic origin and race on death certificates

Two data sources were used to adjust for race and ethnicity misclassification on death certificates. For the Hispanic, Asian non-Hispanic, Black non-Hispanic, and White non-Hispanic populations, the National Longitudinal Mortality Study was used to produce classification ratios (or correction factors) to adjust observed sex- and age-specific death rates for

misclassification on death certificates (10). The National Longitudinal Mortality Study consists of a series of Current Population Surveys (1979–2011) linked to vital statistics mortality data through the National Death Index (10). For the American Indian and Alaska Native non-Hispanic population, an extract of the 2010 Census Edited File–Census Unedited File Match File (referred to as the CEF–CUF Match) that contained records for people classified as American Indian and Alaska Native alone or in combination with another race in the 2010 decennial census was linked to the National Death Index to identify decedents for the period April 1, 2010, to December 31, 2011 (11). The resulting 34,366 CEF–CUF Match American Indian and Alaska Native Extract–Mortality Linked Data decedent records were used to estimate classification ratios to correct for race and ethnicity misclassification on death certificates for the American Indian and Alaska Native non-Hispanic population (11).

The classification ratios compare self-reported Hispanic origin and race on Current Population Surveys or the decennial census with Hispanic origin and race reported on the death certificates of the samples of decedents in the National Longitudinal Mortality Study who died during 1999–2011 as well as decedents in the CEF–CUF Match American Indian and Alaska Native Extract who died between April 1, 2010, and December 31, 2011 (10,11). Linked records are used to estimate sex–age-specific ratios of survey or census Hispanic-origin and race counts to death certificate counts (10,11).

The survey or census death certificate ratio (or classification ratio) is the ratio of the count (weighted in the case of Current Population Surveys) of self-reported race and ethnicity on the survey or census to the count (weighted in the case of Current Population Surveys) of the same racial or ethnic category on the death certificates of the sample of National Longitudinal Mortality Study (CEF–CUF Match American Indian and Alaska Native Extract) decedents described previously. It can

be interpreted as the net difference in assignment of a specific Hispanic-origin and race category between the two classification systems and can be used as a correction factor for race and ethnicity misclassification (10,11). The race and ethnicity reported by a survey or census respondent is assumed to be more reliable than proxy reporting of race and ethnicity by a funeral director who has little personal knowledge of the decedent. The 1997 Office of Management and Budget standards also mandate that self-identification be the standard used for the collection and recording of race and ethnicity information (8).

Classification ratios discussed previously are used to adjust the age-specific number of deaths for ages 1–95 and older for the total Hispanic, American Indian and Alaska Native non-Hispanic, Asian non-Hispanic, Black non-Hispanic, and White non-Hispanic populations, and by sex for each group, as:

$${}_nD_x = {}_nD_x^F \cdot {}_nCR_x \quad [2]$$

where ${}_nD_x^F$ is the age-specific number of deaths adjusted for unknown age as described above, ${}_nCR_x$ is the sex- and age-specific classification ratios used to correct for the misclassification of Hispanic origin and race on death certificates, and ${}_nD_x$ is the final age-specific counts of death adjusted for age and race and ethnicity misclassification.

Classification ratios for infant deaths are unreliable due to small sample sizes. Corrections for racial and ethnic misclassification of infant deaths are addressed by using infant death counts and live birth counts from linked birth and infant death data files rather than the traditional birth and death data files (3). In the linked file, each infant death record is linked to its corresponding birth record so that the race and ethnicity of the mother reported on the birth record can be ascribed to the infant death record. Due to the unavailability of linked birth and infant death, standard final birth and provisional death data

were used to estimate infant mortality for 2022 provisional life tables. Typically, infant mortality rates based on linked birth and infant death data show that using the traditional files overestimates the infant mortality rate by 5.0% for Hispanic and 4.0% for Black non-Hispanic infants, and underestimates the infant mortality rate by 20.3% for Asian non-Hispanic and 3.7% for White non-Hispanic infants (3).

Interpolation of P_x and D_x

Anomalies—both random and those associated with reporting age at death—can be problematic when using vital statistics and census data by single years of age to estimate the probability of death (1,3). Graduation techniques are often used to eliminate these anomalies and derive a smooth curve by age. Beers' ordinary minimized fifth difference formula is used to obtain smoothed values of population counts (P_x) and death counts (D_x) from 5-year age groupings of ${}_n P_x$ from age 0 to 99 and ${}_n D_x$ from age 5 to 99, and where ${}_n D_x$ has first been adjusted for not-reported age and race and ethnicity misclassification on the death certificate (12).

Calculation of the probability of dying (q_x)

The first step in the calculation of a complete period life table is the estimation of the age-specific probability of dying, q_x , which is derived from the age-specific death rate, m_x (3,13). In the life table cohort,

$$m_x = \frac{d_x}{L_x}$$

where d_x is the number of deaths occurring between ages x and $x + 1$, and L_x is the number of person-years lived by the life table cohort between ages x and $x + 1$. The conversion of the age-specific death rate, m_x , to the age-specific probability of death, q_x , is:

$$q_x = \frac{m_x}{1 + (1 - a_x)m_x} \quad [3]$$

where a_x is the fraction of the number

of person-years lived in the age interval by members of the life table cohort who died in the interval. When the age interval is 1 year, except at infancy, $a_x = 1/2$; in other words, deaths occur on average midway through the age interval. As a result,

$$q_x = \frac{m_x}{1 + \frac{1}{2}m_x} \quad [4]$$

Because the complete period life table is based on the age-specific death rates of a current population observed for a specific calendar year, the life table death rate is equivalent to the observed death rates of the current population:

$$m_x = \frac{d_x}{L_x} = M_x = \frac{D_x}{P_x}$$

where D_x is the Beers' smoothed number of deaths adjusted for not-stated age and race and ethnicity misclassification on the death certificate (for the Hispanic, American Indian and Alaska Native non-Hispanic, Asian non-Hispanic, Black non-Hispanic, and White non-Hispanic populations), and P_x is the Beers' smoothed population at risk of dying between ages x and $x + 1$.

Then,

$$q_x = \frac{M_x}{1 + \frac{1}{2}M_x} = \frac{D_x}{P_x + \frac{1}{2}D_x} \quad [5]$$

This procedure is used to estimate vital statistics age-specific probabilities of death for ages 1–99.

Calculation of q_x at age 0

The higher mortality observed in infancy is associated with a high concentration of deaths occurring at the beginning of the age interval rather than in the middle. As a result, whenever possible, it is best to assign deaths to the appropriate birth cohorts. Consequently, the probability of death at birth, q_0 , is calculated using a birth cohort method that uses a separation factor (f) defined as the proportion of infant deaths in year t occurring in infants born in the previous year ($t - 1$). The value f is estimated by categorizing infant deaths

by date of birth. The probability of death is then calculated as:

$$q_0 = \frac{D_0(1-f)}{B^t} + \frac{D_0(f)}{B^{t-1}} \quad [6]$$

where D_0 is the number of infant deaths adjusted for not-stated age in 2021, B^t is the number of live births in 2021, and B^{t-1} is the number of live births in 2020.

Probabilities of dying at the oldest ages for total, Black non-Hispanic, and White non-Hispanic populations

Medicare data are used to supplement vital statistics data for the estimation of q_x at the oldest ages because these data are more accurate, as proof of age is required for enrollment in the Medicare program. Medicare data are used to estimate the probability of dying for ages 66 and older for the total, Black non-Hispanic, and White non-Hispanic populations.

The method consists of the following steps. First, vital statistics and Medicare death rates are blended in the age range 66–99. Second, a logistic model is used to smooth the blended death rates in the age range 85–99 and predict death rates for ages 100–120. Third, final resulting death rates, M_x , are converted to q_x .

For ages 66–94, vital statistics death rates, M_x^V , and Medicare death rates, M_x^M , are blended with a weighting process that gives gradually declining weight to vital statistics data and gradually increasing weight to Medicare data. For ages 95–99, M_x^M is used exclusively. Blended M_x is then obtained as:

$$M_x = \frac{1}{30} \left[(95-x)M_x^V + (x-65)M_x^M \right] \quad [7]$$

when $x = 66, \dots, 94$, and

$$M_x = M_x^M$$

when $x = 95, \dots, 99$.

M_x^M is estimated as:

$$M_x^M = \frac{D_x^M}{P_x^M}$$

where D_x^M is the age-specific Medicare death count, and P_x^M is the age-specific Medicare midyear population count.

A logistic model proposed by Kannisto is then used to smooth M_x in the age range 85–99 and predict M_x in the age range 100–120 (14). The start of the modeled age range varies by race- and ethnicity-specific population because it is a function of the age at which the rate of change in the age-specific death rates peaks. Currently, the rate of change in the age-specific death rate rises steadily up to generally ages 80–85 and then begins to decline. As a result, modeling a large age span, such as 65–100, with one simple model is difficult without oversmoothing and, as a result, changing the underlying mortality pattern seen in the population of interest (15). Further, the observed data for the age range 65–85 or so is reliable and robust, as indicated by the very close similarity between vital statistics and Medicare death rates, so modeling (smoothing) the entire age span (65–100) is unnecessary.

The Kannisto model is a simple form of a logistic model in which the logit of u_x (or the natural log of the odds of u_x) is a linear function of age, x (14), expressed as:

$$\ln\left(\frac{u_x}{1-u_x}\right) = \ln(\alpha) + \beta x \quad [8]$$

where u_x , the force of mortality (or instantaneous death rate), is defined as:

$$u_x = \frac{\alpha e^{\beta x}}{1 + \alpha e^{\beta x}}$$

Because u_x is not directly observed but is closely approximated by m_x , and $m_x = M_x$, then the logit of M_x is modeled instead. A maximum-likelihood generalized linear model estimation procedure is used to fit the following model in the age range 85–99:

$$\ln\left(\frac{M_x}{1-M_x}\right) = \ln(\alpha) + \beta x \quad [9]$$

Then, the estimated parameters are used to predict \bar{M}_x as:

$$\bar{M}_x = \frac{e^a e^{bx}}{1 + e^a e^{bx}}$$

or, equivalently,

$$\bar{M}_x = \frac{e^{a+bx}}{1 + e^{a+bx}} \quad [10]$$

where a and b are the predicted values of parameters $\ln(\alpha)$ and β , respectively, given by fitting model 10.

Finally, the predicted probability of death, \bar{q}_x , for ages 85–120 is estimated by converting \bar{M}_x as:

$$\bar{q}_x = \frac{\bar{M}_x}{1 + \frac{1}{2}\bar{M}_x} \quad [11]$$

The probability of death is extrapolated to age 120 to estimate the life table population until no survivors remain. This information is then used to estimate L_x for ages 100–120, which is used to close the table with the age category 100 and older, combined (see following section).

Probability of dying at the oldest ages for Hispanic, American Indian and Alaska Native non-Hispanic, and Asian non-Hispanic populations

As noted previously, Medicare data are unreliable for the Hispanic, American Indian and Alaska Native non-Hispanic, and Asian non-Hispanic populations due to inconsistencies in the Medicare race and ethnicity classification system. As a result, other methods are used to estimate mortality at the oldest ages for these populations. Beyond age 80, mortality estimates based strictly on vital statistics data for the Hispanic, American Indian and Alaska Native non-Hispanic, and Asian non-Hispanic populations are too low, despite correction for ethnic misclassification on the death certificate.

A consistent finding across diverse studies has been that Hispanic mortality in the adult and advanced ages varies between about 80% and 89% relative

to that of the White non-Hispanic population (16–19). The Brass relational logit model takes advantage of the relationship between Hispanic and White non-Hispanic mortality previously identified and has been widely and successfully used to predict the mortality of one population relative to another at the older ages (20,21). Using the age-specific mortality pattern of the White non-Hispanic population as the standard, the Brass relational logit model is used to predict Hispanic mortality in the older ages. The standard is fit to Hispanic data in the age interval 45–80, and the predicted parameters are used to estimate the probabilities of death for ages 76–100. This method allows the relationship between the two populations in the younger ages to be extended to the older ages (16,20,21).

Although similar information is not available for the American Indian and Alaska Native non-Hispanic and Asian non-Hispanic populations, with a slight modification, the Brass relational logit model was successfully used to produce reliable complete period life tables for the American Indian and Alaska Native non-Hispanic population in Indian Health Service's Contract Health Service Delivery Area counties (22). The choice of the White non-Hispanic population as the standard population is based on several factors. First, it is the most widely used comparison population in the study of racial and ethnic disparities given its social and economic privilege. Second, it is the largest population in the United States and has the most reliable mortality data. Third, the relationship of the age-specific mortality patterns of the American Indian and Alaska Native non-Hispanic and Asian non-Hispanic populations compared with that of the White non-Hispanic population remains constant throughout the age span 45–80 (45–84 for the American Indian and Alaska Native non-Hispanic population). Assuming that this pattern continues to the oldest ages is reasonable because the final results are consistent with expected age-specific mortality patterns at the oldest ages.

The Brass relational logit model expresses the age-specific mortality pattern of a population of interest as a function of the age-specific mortality pattern of a standard population and is expressed as:

$$\bar{Y}_x = \alpha + \beta Y_x^S \quad [12]$$

where \bar{Y}_x is the predicted logit of the probability of death, q_x , in the population of interest, that is,

$$\text{logit}[q_x] = \ln \left[\frac{q_x}{1 - q_x} \right]$$

Y_x^S is the logit of the probability of death in the standard population, q_x^S , that is,

$$\text{logit}[q_x^S] = \ln \left[\frac{q_x^S}{1 - q_x^S} \right]$$

α is the predicted parameter that measures the level of mortality of the population of interest relative to the standard population, and β is the predicted parameter that measures the slope of the mortality function of the population of interest relative to the standard population (16,20,21).

A maximum-likelihood generalized linear model estimation procedure was used to fit equation 12 in the age range 45–80 (45–84 for the American Indian and Alaska Native non-Hispanic population). The resulting predicted parameters α and β were then used to estimate the predicted probability of death for ages 76–120 (80–120 for the American Indian and Alaska Native non-Hispanic population). The value q_x was predicted to age 120 to estimate the life table population until no survivors remain, as was done for the other population groups. This information was then used to estimate L_x for ages 100–120, which was used to close the table with the age category 100 and older, combined (see next section).

Predicted \bar{q}_x is estimated by transforming its logit, \bar{Y}_x , back as:

$$\bar{q}_x = \frac{\exp[\bar{Y}_x]}{1 + \exp[\bar{Y}_x]} = \frac{\exp[\alpha + \beta Y_x^S]}{1 + \exp[\alpha + \beta Y_x^S]} \quad [13]$$

To ensure a smooth transition from vital q_x^V and predicted \bar{q}_x , the two

were blended for ages 76–80 (80–84 for the American Indian and Alaska Native non-Hispanic population) with a graduating process as:

$$q_x = \frac{1}{6} \left[(81-x)q_x^V + (x-75)\bar{q}_x \right] \quad [14]$$

when $x = 76, \dots, 80$, and

$$q_x = \frac{1}{6} \left[(85-x)q_x^V + (x-79)\bar{q}_x \right]$$

when $x = 80, \dots, 84$.

Finally, to close the table at age 100 and older (combined), ${}_{\infty}q_{100}$ is set equal to 1.0 because all survivors to this age will die at some point in the open-ended age interval. Once q_x is obtained for each single year of age, the other life table functions are easily calculated.

Calculation of remaining life table functions for all groups

Survivor function (l_x)

The life table radix, l_0 , is set at 100,000. For ages greater than 0, the number of survivors remaining at exact age x is calculated as:

$$l_x = l_{x-1}(1 - q_{x-1}) \quad [15]$$

Decrement function (d_x)

The number of deaths occurring between ages x and $x + 1$ is calculated from the survivor function:

$$d_x = l_x - l_{x+1} = l_x q_x \quad [16]$$

Note that ${}_{\infty}d_{100} = {}_{\infty}l_{100}$ because ${}_{\infty}q_{100} = 1.0$.

Person-years lived (L_x)

Person-years lived for ages 1–99 are calculated assuming that the survivor function declines linearly between ages x and $x + 1$. This gives the formula:

$$L_x = \frac{1}{2}(l_x + l_{x+1}) = l_x - \frac{1}{2}d_x \quad [17]$$

For $x = 0$, the separation factor f is used to calculate L_0 :

$$L_0 = fl_0 + (1-f)l_1 \quad [18]$$

Finally, ${}_{\infty}L_{100}$ is estimated as the sum of the extrapolated L_x values for ages 100–120.

Person-years lived at and above age x (T_x)

T_x is calculated by summing L_x values at and above age x :

$$T_x = \sum_{x=0}^{\infty} L_x \quad [19]$$

Life expectancy at age x (e_x)

Life expectancy at exact age x is calculated as:

$$e_x = \frac{T_x}{l_x} \quad [20]$$

Variances and standard errors of probability of dying and life expectancy

Variances are estimated under the assumption that the mortality data on which the life tables are based are not affected by sampling error and are subject only to random variation. However, although more than 99% of deaths that occurred from January through December 2022 are included, the data may be biased by the possibility that certain jurisdictions and age groups may be underrepresented for later months. These errors as well as those resulting from age and Hispanic-origin and race misreporting on death certificates are not considered in the calculation of the variances or standard errors of the life table functions.

The methods used to estimate the variances of q_x and e_x are based on Chiang (23), with some necessary modifications due to the use of Medicare data and statistical modeling for smoothing and prediction of older age death rates. Based on the assumption that deaths are binomially distributed, Chiang proposed the following equation for the variance of q_x :

$$Var(q_x) = \frac{q_x^2(1-q_x)}{D_x} \quad [21]$$

where D_x is the age-specific number of deaths. For the total, Black non-Hispanic, and White non-Hispanic populations, this equation is used to estimate $Var(q_x)$ throughout the age span, with a modification where for ages younger than 66, D_x is the deaths from vital statistics data, smoothed by interpolation and adjusted for the number of deaths with age not stated and for the Black non-Hispanic and White non-Hispanic populations adjusted for race and ethnicity misclassification. For ages 66 and older, D_x was obtained by treating the population as a cohort population and calculated from q_x (12,24):

$$P_x = \frac{(P_{x-1} - 0.5D_{x-1})(2 - q_x)}{2} \quad [22]$$

$$D_x = \frac{q_x P_x}{1 - 0.5q_x}$$

For the Hispanic, American Indian and Alaska Native non-Hispanic, and Asian non-Hispanic populations, equation 21 was used for ages 0–75 (0–79 for the American Indian and Alaska Native non-Hispanic group). Because q_x was predicted based on the Brass relational logit model for ages 76–120 (80–120 for the American Indian and Alaska Native non-Hispanic group), the Delta method was used to approximate its variance for these ages as:

$$Var(\bar{q}_x) = \left(\frac{\exp(\alpha + \beta Y_x^S)}{[\exp(\alpha + \beta Y_x^S) + 1]^2} \right)^2 \cdot Var(\alpha + \beta Y_x^S) \quad [23]$$

For ages 76–80 (80–84 for the American Indian and Alaska Native non-Hispanic group), the variance of q_x is calculated as:

$$\frac{1}{6} [(81 - x) \cdot \text{Var}(q_x) + (x - 75) \cdot \text{Var}(\bar{q}_x)]$$

when $x = 76, \dots, 80$, and

$$\frac{1}{6} [(85 - x) \cdot \text{Var}(q_x) + (x - 79) \cdot \text{Var}(\bar{q}_x)]$$

when $x = 80, \dots, 84$.

Standard error of q_x

$$SE(q_x) = \sqrt{\text{Var}(q_x)} \quad [24]$$

For all groups, variances of the life expectancies for ages 0–99 years are estimated using Chiang's equation:

$$\text{Var}(e_x) = \frac{\sum_{x=0}^{x=99} l_x^2 \cdot [(1 - 0.5) + e_{x+n}]^2 \cdot \text{Var}(q_x)}{l_x^2} \quad [25]$$

Chiang assumed that because $q_{100+} = 1.00$, then $\text{Var}(q_{100+}) = 0$, and as a result, $\text{Var}(e_{100+}) = 0$. 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; therefore, the assumption of no variance is incorrect, and $\text{Var}(e_{100+})$ can be approximated as (25):

$$\text{Var}(e_{100+}) \approx \frac{\frac{l_{100+}^2}{M_{100+}^4} \cdot \text{Var}(M_{100+})}{l_{100+}^2}$$

Standard error of e_x

$$SE(e_x) = \sqrt{\text{Var}(e_x)} \quad [26]$$

Causes of death contributing to changes in life expectancy

To measure changes in mortality, a discrete method developed by Arriaga (26,27) was used to estimate the contribution of mortality change by causes of death based on changes in life expectancy, which is described as a procedure that “estimates the number of years added to or removed from life expectation because of the decrease or increase (respectively) of the central mortality rates of life tables” (26). With this method, the change in life expectancy can be partitioned over time or between two separate groups of populations. In this report, Arriaga's technique is used to partition changes in life expectancy at birth in the United States from 2021 to 2022 by cause of death.

The method partitions changes into component additive parts and identifies the causes of death having the greatest influence, positive or negative, on changes in life expectancy based on rankable causes of death (28). This is the same method used by the National Center for Health Statistics annually to analyze changes in life expectancy (29).

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