Changes in U.S. Life Expectancy in the Wake of COVID-19: Differences by Race/Ethnicity and Relative to Other High-Income Countries

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CHANGES IN U.S. LIFE EXPECTANCY IN THE WAKE OF COVID-19: DIFFERENCES BY RACE/ETHNICITY AND RELATIVE TO OTHER HIGH-INCOME COUNTRIES

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ABSTRACT

Objective: To estimate changes in life expectancy from 2010 through 2020 across U.S. population groups and peer nations.

Design: Life expectancy in 2010-2018 and 2020 was estimated for the U.S. population, by sex and race-ethnicity, and for 16 high-income countries. The analysis excluded 2019 because life table data were lacking for a sufficient number of peer countries. Data for the United States and peer countries were obtained from the National Center for Health Statistics and Human Mortality Database, respectively. Life expectancy in 2020 was estimated by simulating life tables from estimated age-specific mortality rates in 2020 and allowing for 10% random error.

Main Outcome Measures: Life expectancy at birth and ages 25 and 65 years. Estimates for 2020 are reported as medians along with 5th and 95th percentiles.

Results: Between 2010 and 2018, the gap in life expectancy between the United States and the peer-country average increased from 1.88 years (78.66 vs. 80.54 years, respectively) to 3.05 years (78.74 years vs. 81.78 years). Between 2018 and 2020, U.S. life expectancy decreased by 1.87 years (to 76.87 years), 8.5 times the average decrease in peer countries (0.22 years), widening the gap to 4.69 years. U.S. life expectancy decreased disproportionately among people of color between 2018 and 2020, declining by 3.88, 3.25, and 1.36 years, respectively, in Hispanic, non-Hispanic Black, and non-Hispanic White populations. Among Hispanic and non-Hispanic Black populations, respectively, declines were 15 and 18 times the average in peer countries. Progress since 2010 in reducing the U.S. Black-White life expectancy gap was erased between 2018 and 2020, life expectancy in Black men reached its lowest level since 1998, and the longstanding Hispanic life expectancy advantage was almost eliminated.

Conclusions: The United States experienced a much larger decrease in life expectancy between 2018 and 2020 than did other high-income nations, with pronounced losses among people of color. A longstanding and widening U.S. health disadvantage, high death rates in 2020, and continued inequitable impacts on people of color are products of policy choices and systemic racism.

INTRODUCTION

In 2020, COVID-19 became the third leading cause of death in the United States[1] and was thus expected to substantially lower life expectancy for that year (see **Box**). The United States experienced more deaths from COVID-19 than any other country in the world and among the highest per capita mortality rates.[2] This prompted speculation that the United States would experience a larger decrease in life expectancy in 2020 than peer nations, but empirical evidence has not been published. Americans entered the pandemic at a distinct disadvantage relative to other high-income peer nations: improvements in overall life expectancy have not kept pace with those in peer countries since the 1980s[3], and in 2011 U.S. life expectancy plateaued and then decreased for 3 consecutive years, further widening the mortality gap with peer countries.[4]

The meaning of life expectancy during a pandemic

Life expectancy is a widely used statistic for summarizing a population's mortality rates at a given time. It reflects how long a group of people can expect to live were they to experience at each age the prevailing age-specific mortality rates of that year.[2] Life expectancy estimates are sometimes misunderstood. We cannot know what *future* age-specific mortality rates will be for people born or living today, but we do know the *current* rates. Computing life expectancy (at birth, or age 25, or age 65) based on those rates is valuable for understanding and comparing a country's mortality profile over time or across places at a given point in time. Estimates of life expectancy during the COVID-19 pandemic, such as those reported here, can help clarify which people or places were most affected, but they do not predict how long a group of people will live. This study estimates life expectancy for 2020. Determinations of life expectancy for 2021 and subsequent years—and how quickly life expectancy will rebound—cannot occur until data for those years become available. Although life expectancy is expected to recover in time to pre-pandemic levels, past pandemics have demonstrated that survivors can be left with lifelong consequences, depending on their age and other socio-economic circumstances.[3]

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The impact of the pandemic on life expectancy extends beyond deaths attributed directly to COVID-19.[5] Studies have found an even larger number of excess deaths during the pandemic, inflated by undocumented COVID-19 deaths and by deaths from non-COVID-19 causes resulting from disruptions caused by the pandemic (e.g., diminished access to health care, economic pressures, behavioral crises).[6,7,8,9] Certain races, ethnicities, and age groups have been disproportionately affected.[10,11,12] Research on how the pandemic is affecting life expectancy is only just emerging.[13,14] Few studies have examined declines in 2020 life expectancy across racial-ethnic groups, and none have compared the U.S. decline with that of other countries.

METHODS

The study estimated life expectancy at birth and at ages 25 and 65 years, examining the U.S. population (in aggregate and by sex and race-ethnicity) and the average for 16 high-income countries (in aggregate and by sex). Life expectancy estimates for 2010-2018 were calculated from official life tables and were modeled for 2020. Estimates for 2019 would have been preferable to isolate the effect of the COVID-19 pandemic but life tables for a sufficient number of countries were lacking. However, U.S. life expectancy is estimated to have increased by only 0.1 years between 2018 and 2019,[15] and therefore observed changes in life expectancy between 2018 and 2020 are largely attributable to the events of 2020.

Peer country data did not include information on race or ethnicity. U.S. data were examined for three racial-ethnic groups that constitute more than 90% of the total population: Hispanic, non-Hispanic Black, and non-Hispanic white populations. Although many U.S. individuals self-identify as Latino or Latina, this study uses “Hispanic” to maintain consistency with data sources. “White” and “Black” hereafter refer to people in these racial groups who do not identify as Hispanic or Latinx.[16] Estimates for other important racial groups, such as Asians and Pacific Islanders and American Indians and Alaskan Natives, could not be calculated because the National Center for Health Statistics (NCHS) does provide official life tables for these groups.

U.S. life tables for 2010-2018 were obtained from the NCHS.[17,18,19.20,21,22,23,24,25] Weekly age-specific death counts among the total U.S. male and female populations and among the U.S. Black, White, and Hispanic male and female populations for years 2018 and 2020 were obtained from the NCHS *AH Excess Deaths by Sex, Age, and Race* file.[26] Mid-year population estimates by age, sex, and race-ethnicity for U.S. male and female populations in years 2015-2019 were obtained from the U.S. Census Bureau.[27] Population counts for 2020 were estimated from age-specific trends in U.S. population estimates across years 2015-2019. The NCHS and U.S. Census data were merged at ages 0-14,15-19, … 80-84, 85+ years to calculate age-specific death rates (m_x) for 2018 and 2020 among U.S. male and female populations in aggregate and by race-ethnicity.

Peer countries included 16 high-income democracies with adequate data for analysis: Austria, Belgium, Denmark, Finland, France, Israel, Netherlands, New Zealand, Norway, South Korea, Portugal, Spain, Sweden, Switzerland, Taiwan, and the United Kingdom. Australia, Canada, Germany, Italy, and Japan were omitted because of incomplete mortality data. To estimate life expectancy in these countries, 5-year abridged life tables for male and female populations of the peer countries were obtained for 2010-2018 from the Human Mortality Database (HMD)[28] (direct sources[29,30] were used for Israel and New Zealand, for which sufficiently current data were lacking in the Human Mortality Database). Weekly death counts by country for ages 0-14, 15-64, 65-74, 75-84, and 85+ years were obtained from the Human Mortality Database *Short Term Mortality Fluctuations* (HMD-STMF) files.

To arrive at life expectancy estimates for 2020, age-specific mortality rate ratios between 2020 m_x and 2018 m_x in the NCHS-Census data were estimated for U.S. populations. For populations in peer countries, average 2020 m_x and 2018 m_x in the HMD-STMF data were estimated for ages 0-14, 15-64, 65-74, 75-84, and 85+ years. Age-specific mortality rate ratios between 2020 m_x and 2018 m_x in the HMD-STMF data were estimated for each peer country in aggregate and by sex. The 2020 probabilities of death, q_x, for ages 0-1, 1-4, 5-9, … 90-94, 95-99, 100+ years were estimated separately for U.S. male and female populations and for male and female race-ethnic-specific populations in 2020 by multiplying the 2018 official m_x[25] by the 2020-2018 rate ratio estimates derived from the NCHS-U.S. Census data, and calculating $q_x = (m_x*n)/(1+m_x*a_x)$ where n is the width of the age interval.[31] Probabilities of death, q_x, for each peer country in 2020 were estimated by multiplying q_x in HMD life tables by the 2020-2018 rate ratios in the HMD-STMF data.

Using Python (version 3.9.1), 50,000 5-year abridged 2020 life tables were simulated for each U.S. sub-population using q_x derived from the estimated 2020 m_x, a_x derived from 2018 official life tables[25], and random 10% error in the q_x estimate. For peer country populations, 50,000 5-year abridged 2020 life tables were simulated using the estimated 2020 q_x, average 2018 a_x values in the HMD 2018 life tables, and random 10% error in the q_x estimates. Although the text only presents median estimates of 2020 life expectancy at birth and at ages 25 and 65 years, the tables also provide the 5th (P_5) and 95th (P_{95}) percentiles. An online supplement provides further details on methods.

RESULTS

United States

After a small increase of 0.08 years between 2010 and 2018, U.S. life expectancy at birth decreased by an estimated 1.87 years (or 2.4%) between 2018 and 2020 (**Figure 1**). The proportional decrease in life expectancy at ages 25 and 65 years was even greater (3.4% and 5.7%, respectively) (**Table 1**). U.S. men experienced a larger decrease in overall life expectancy than women, in both absolute (2.16 years vs. 1.50 years) and relative terms (2.8% vs. 1.8%).

Between 2018 and 2020, U.S. life expectancy decreased disproportionately among people of color (**Table 2**). In the Black population, it decreased by 3.25 years (4.4%), 2.4 times the decrease in the White population (1.36 years, 1.7%), with larger reductions among men (3.56 years, 5.0%) than women (2.65 years, 3.4%). In 2020, life expectancy among Black men was only 67.73 years. The decrease in life expectancy among Hispanic individuals was even larger (3.88 years, 4.7%), 2.9 times the decrease among Whites, with larger reductions among men (4.58 years, 5.8%) than women (2.94 years, 3.5%).

The disproportionate decrease in life expectancy in the U.S. Black population during 2018-2020 reversed years of progress in reducing the Black-White mortality gap. Although the gap in life expectancy between Black and White populations decreased from 4.02 years in 2010 to 3.54 years in 2014, it increased to 3.92 years in 2018, and to 5.81 years in 2020. Historically, the U.S. Hispanic population has had a higher life expectancy than the White population.[32,33] Although that advantage widened between 2010 and 2017, from 2.91 years to 3.30 years, it decreased to 3.20 years in 2018 and then decreased sharply to 0.68 years in 2020 (**Table 2**); the advantage reversed entirely among Hispanic men (from 2.88 years in 2018 to -0.20 years in 2020).

United States versus Peer Countries

Figure 1 present life expectancy estimates for 2010-2018 and 2020 for the United States and the average for 16 high-income countries. The United States began the decade with a 1.88-year deficit in life expectancy relative to peer countries. This gap increased steadily over the decade, as U.S. life expectancy declined and peer-country life expectancy increased, reaching 3.05 years in 2018. Between 2018 and 2020, the gap widened substantially to 4.69 years: the 1.87-year decrease in U.S. life expectancy was 8.5 times the average decrease in peer countries (0.22 years). **Table 3** presents the peer-country estimates of life expectancy at birth, age 25, and age 65 in 2010, 2018, and 2020.

Changes in life expectancy varied significantly across peer countries. In fact, six countries (Denmark, Finland, New Zealand, Norway, South Korea, and Taiwan) experienced *increases* in life expectancy between 2018 and 2020. Among the other 12 peer countries, decreases in life expectancy ranged from 0.12 years in Sweden to 1.09 years in Spain, but none approached the 1.87-year loss experienced by the United States.

Figure 2 contrasts changes in U.S. life expectancy in 2010-2018 and 2018-2020 with those of peer countries, based on sex and race-ethnicity. **Figure 3** shows how those changes contributed to the gap between the U.S. and peer countries. For example, Figure 2 shows that life expectancy for U.S. women increased by 0.21 years in 2010-2018 but—because female life expectancy in the peer countries increased even more (0.98 years)—the gap increased by 0.77 years (Figure 3). The gap increased an additional 1.36 years during 2018-2020, largely because of the pandemic. Altogether, the gap between U.S. and peer women increased by 2.14 years (Figure 3), from 1.97 years in 2010 (81.04 vs 83.01 years) to 4.11 years (79.75 vs. 83.86 years) in 2020 (Tables 1 and 3). The gap between U.S. and peer men increased even more (3.37 years) (Figure 3). In 2020, life expectancy for U.S. men was 5.27 years (74.06 vs 79.33 years) shorter than the peer country average for men.

The demographic composition and ethnic inequities of peer countries vary considerably, making it difficult to identify analogous reference populations to compare with U.S. racial-ethnic groups. However, the peer country average provides a useful benchmark for demonstrating the disproportionately large decreases in life expectancy that people of color experienced in the United States **(Figures 1-3)**. For example, among U.S. Black men and women, the decrease in life expectancy between 2018 and 2020 was 12.3 times and 20.3 times greater, respectively, than the average decrease for men and women in peer countries. The corresponding figures are even larger for the U.S. Hispanic population, with declines in life expectancy an estimated 15.9 times and 22.5 times higher among men and women, respectively, compared to their counterparts in peer countries.

DISCUSSION

Long before COVID-19 appeared, the United States was at a distinct disadvantage relative to other high-income nations in terms of health and survival.[3,34,35,36,37,38] A 2013 report by the National Research Council and Institute of Medicine demonstrated that the United States began losing ground relative to other high-income countries in the 1980s, with higher rates of morbidity and mortality for multiple conditions.[3] A recent report by the National Academies of Sciences, Engineering, and Medicine found that this gap widened further through 2017 and that the greatest relative increase in U.S. mortality occurred among young and middle-aged U.S. adults (ages 25-64 years). Increased mortality in this age group was due largely to deaths from drug use, suicide, cardiometabolic diseases, and other chronic illnesses and injuries.[39] Between 2015 and 2017, while life expectancy continued to increase in other countries, U.S. life expectancy decreased by 0.3 years,[4] a three-year decline that generated considerable public concern[40] but is now eclipsed by the large 2020 declines reported here. Even countries with much lower per capita incomes now outperform the United States.[41,42,43,44] According to data for 36 OECD member countries, the gap in life expectancy between the United States and the OECD average increased from 0.9 to 2.2 years between 2010 and 2017.[45,46]

This study shows that the U.S. life expectancy gap increased dramatically between 2018 and 2020. The decrease in U.S. life expectancy was 8.5 times the average loss experienced by 16 high-income peer nations and the largest decrease since 1943 during World War II.[47] The conditions that produced a U.S. health disadvantage prior to the arrival of COVID-19 are still in place, but the predominant cause for this large decline was the COVID-19 pandemic: in 2020, all-cause mortality in the United States increased by 23%.[9]

The large decreases in life expectancy reported here, and the excess deaths reported in several studies of 2020 death counts[6,7,8,9], reflect the combined effects of: (a) deaths directly attributable to COVID-19, (b) deaths in which COVID-19 infection was unrecognized or undocumented; and (c) deaths from non-COVID-19 health conditions, exacerbated by limited access to health care and by widespread social and economic disruptions produced by the pandemic (e.g., unemployment, food insecurity, homelessness).[5,48] Many of these are products of national, state, and local policy decisions and (in)actions that influenced viral transmission and management of the pandemic.[49,50,51,52,53,54] These policies span healthcare, public health, employment, education, and social protection systems. A variety of organizations are tracking these decisions internationally for ongoing research and development.[55,56,57,58]

The extraordinary consequences of COVID-19 in the United States reflect not only the country's policy choices and mishandling of the pandemic[49,51,52,53.54] but also deeply rooted factors that have put the country at a health disadvantage for decades.[3,4,59,60] For much of the public, it was the pandemic itself that drew attention to these longstanding conditions, including major deficiencies in the U.S. health care and public health systems, widening social and economic inequality, and stark inequities and injustices experienced by Black, Brown, and Indigenous Americans and other systematically marginalized and excluded groups. Many studies have documented that rates of COVID-19 infections, hospitalizations, and deaths are significantly higher among communities of color compared to White people, due to heightened viral exposure, a higher prevalence of comorbid conditions (e.g., diabetes), and diminished access to healthcare and other protective resources.[61,62]

This study adds to this growing body of evidence, revealing extreme differences in life expectancy reductions during the COVID-19 pandemic based on race-ethnicity. Decreases in life expectancy among Black and Hispanic men and women were approximately 2-3 times greater than losses among White people, and far larger than those experienced in peer countries. Decreases among U.S. Black and Hispanic men were 12-16 times greater than that of men in other high-income countries and decreases among U.S. Black and Hispanic women were 20-23 times greater. Progress made between 2010 and 2018 in reducing the Black-White gap in life expectancy in the United States was erased between 2018 and 2020. Life expectancy among Black men fell to 67.73 years, a level not seen since 1998.[63] The U.S. Hispanic life expectancy advantage was fully erased among men and nearly erased among women.

Evidence of disproportionate reductions in life expectancy among people of color comes at a time of increasing attention to the root causes of racial inequities in health, wealth, and wellbeing. Chief among these is systemic racism; extensive research has shown that systems of power in the United States structure opportunity and assign value in ways that unfairly disadvantage Black, Brown and Indigenous people, while unfairly advantaging White people. [64,65,66,67,68,69,70] Many of the same factors placed people of color at greater risk from COVID-19.[10,11,12,71,72,73,74,75] The higher prevalence of comorbid conditions among many racialized or marginalized groups is itself a reflection of unequal access to the social determinants of health (e.g., education, income, justice) and not their race/ethnicity or other socially-determined constructs. Low-income communities and women have also been disproportionately affected by the social, familial, and economic disruptions of the pandemic.[76,77] Diminished access to COVID-19 vaccines, and vaccine hesitancy rooted in a community's distrust of systems that have mistreated them, may exacerbate these disparities. These affect not only Black and Hispanic populations but other marginalized people and places. American Indian and Alaska Native people, for example, have some of the worst health outcomes of any group in the United States, but data limitations preclude separate calculations for this important population.

This study has several other limitations. First, 2020 life expectancies were simulated using preliminary mortality data, which are subject to errors (e.g., undercounting, mismatching between death and population counts) and often vary across racial-ethnic populations and countries. Second, the 2020 q_x values used to generate life tables for peer populations could have been biased by the wide age ranges used in the HMD-STMF. Third, definitions for peer countries vary; this study's list differs slightly from the 16 high-income countries used in several cross-national comparisons.[3,34,35] Five large high-income democracies—Australia, Canada, Germany, Italy, and Japan—were excluded because of incomplete data. Fourth, this study compared 2020 life expectancy with 2018 values; the pandemic's effect would be better isolated by comparisons with 2019 life expectancy, but data for a number of peer countries were lacking for this calculation. Fifth, for reasons explained in the online supplement, race-ethnicity data for the U.S. population and for 2020 deaths were incomplete,[78] likely underestimating racial inequalities. Reports suggest that COVID-19 and all-cause mortality in 2020 were alarmingly high in American Indian and Alaskan Native populations.[79] Finally, this study uses the average for peer countries; values for individual countries varied.

This study aligns closely with prior research. In an analysis of deaths between January and June 2020, Arias et al. found that U.S. life expectancy decreased by 1.0 years between 2019 and 2020, including reductions of 0.8 years among White people and reductions of 2.7 years and 1.9 years, respectively, among Black and Hispanic individuals.[14] Andrasfay and Goldman estimated that life expectancy from January to mid-October 2020 was 1.1 years below expected values, including a reduction of 0.7 years among White populations and 2.1 and 3.1 years, respectively, among Black and Hispanic populations.[13] Neither study examined changes in life expectancy in other countries nor estimated U.S. life expectancy for the entirety of 2020.

The mortality outcomes examined here, in the research literature, and in the daily news represent only part of the burden of COVID-19; for every death, a larger number of infected individuals experience acute illness, and many face long-term health and life complications.[80] It remains unclear whether some of these long-term complications will affect how quickly U.S. life expectancy will rebound in the coming years. Morbidity and mortality during the pandemic have ripple effects through families, neighborhoods, and communities. One study estimated that each death leaves behind an average of nine bereaved family members.[81] The pandemic will have short- and long-term effects on the social determinants of health, changing living conditions in many communities and altering life-course trajectories across age groups. Fully understanding the health consequences of these changes poses a daunting but important challenge for future research.

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COMPETING INTEREST

All authors have completed the ICMJE uniform disclosure form and declare: no support from any organisation for the submitted work, no financial relationships with any organisations that might have an interest in the submitted work in the previous three years, and no other relationships or activities that could appear to have influenced the submitted work.

PATIENT AND PUBLIC INVOLVEMENT

It was not possible to involve patients or the public in the design, conduct, reporting, or dissemination plans of our research. We hope to disseminate the findings to the public.

Ethics approval was not required because human subjects were not involved.

Table 1. U.S. Life Expectancy at Birth, Age 25 Years, and Age 65 Years: 2010, 2018, and 2020					
				Change in life expectancy (y, P_5, P_{95})	
	2010	**2018**	**2020 (y, P_5, P_{95})**	**2018 vs 2010**	**2020 vs 2018**
Life expectancy at birth					
Total	78.66	78.74	76.87 (76.70, 77.04)	0.08	-1.87 (-2.04; -1.70)
Women	81.04	81.25	79.75 (79.59, 79.92)	0.21	-1.50 (-1.66; -1.33)
Men	76.20	76.22	74.06 (73.88, 74.24)	0.02	-2.16 (-2.34; -1.98)
Life expectancy at age 25					
Total	54.71	54.76	52.91 (52.74, 53.09)	0.05	-1.84 (-2.02, -1.67)
Women	56.87	57.04	55.54 (55.37, 55.71)	0.17	-1.51 (-1.67, -1.34)
Men	52.44	52.43	50.32 (50.14, 50.50)	-0.01	-2.12 (-2.29, -1.93)
Life expectancy at age 65					
Total	19.13	19.47	18.37 (18.19, 18.55)	0.34	-1.11 (-1.28, -0.93)
Women	20.33	20.69	19.67 (19.50, 19.84)	0.36	-1.02 (-1.19, -0.85)
Men	17.70	18.10	16.93 (16.75, 17.12)	0.40	-1.16 (-1.34, -0.98)

Authors' analysis of data from the National Center for Health Statistics-U.S. Census Bureau and Human Mortality Database. Sums may differ from text due to rounding.
P_5, P_{95}: 5th and 95th percentiles of 50,000 simulated life expectancies using 10% random uncertainty around the 2020 q_x estimates.

Table 2. U.S. Life Expectancy at Birth, Age 25 Years, and Age 65 Years, by Race-Ethnicity: 2010, 2018, and 2020

	Life expectancy (y)			Change in life expectancy (P_5, P_{95})	
	2010	**2018**	**2020 (P_5, P_{95})**	**2018 vs. 2010**	**2020 vs. 2018**
LIFE EXPECTANCY AT BIRTH					
Total					
Hispanic	81.68	81.83	77.95 (77.78, 78.12)	0.15	-3.88 (-4.05, -3.71)
Non-Hispanic Black	74.75	74.71	71.46 (71.27, 71.65)	-0.04	-3.25 (-3.44, -3.06)
Non-Hispanic White	78.76	78.63	77.27 (77.10, 77.44)	-0.13	-1.36 (-1.53, -1.19)
Female					
Hispanic	84.26	84.32	81.38 (81.22, 81.54)	0.06	-2.94 (-3.10, -2.78)
Non-Hispanic Black	77.70	77.99	75.34 (75.16, 75.52)	0.29	-2.65 (-2.83, -2.47)
Non-Hispanic White	81.12	81.10	79.99 (79.83, 80.16)	-0.02	-1.11 (-1.27, -0.94)
Male					
Hispanic	78.84	79.08	74.50 (74.33, 74.68)	0.24	-4.58 (-4.75, -4.40)
Non-Hispanic Black	71.51	71.29	67.73 (67.54, 67.93)	-0.22	-3.56 (-3.75, -3.36)
Non-Hispanic White	76.35	76.20	74.70 (74.52, 74.87)	-0.15	-1.50 (-1.68, -1.33)
LIFE EXPECTANCY AT AGE 25 YEARS					
Total					
Hispanic	57.57	57.71	53.85 (53.68, 54.03)	0.14	-3.86 (-4.03, -3.68)
Non-Hispanic Black	51.42	51.43	48.34 (48.15, 48.53)	0.01	-3.09 (-3.28, -2.90)
Non-Hispanic White	54.72	54.54	53.16 (52,99, 53.33)	-0.18	-1.38 (-1.55, -1.21)
Female					
Hispanic	59.97	60.06	57.12 (56.96, 57.29)	0.09	-2.94 (-3.10, -2.77)
Non-Hispanic Black	54.00	54.28	51.69 (51.51, 51.87)	0.28	-2.59 (-2.77, -2.41)
Non-Hispanic White	56.86	56.80	55.66 (55.49, 55.82)	-0.06	-1.14 (-1.31, -0.98)
Male					
Hispanic	54.88	55.11	50.62 (50.44, 50.80)	0.23	-4.49 (-4.67, -4.31)
Non-Hispanic Black	48.47	48.33	44.99 (44.79, 45.19)	-0.14	-3.34 (-3.54, -3.14)
Non-Hispanic White	52.50	52.29	50.77 (50.59, 50.95)	-0.21	-1.52 (-1.70, -1.34)
LIFE EXPECTANCY AT AGE 65 YEARS					
Total					
Hispanic	21.15	21.44	18.85 (18.67, 19.03)	0.29	-2.59 (-2.77, -2.41)
Non-Hispanic Black	17.71	18.02	16.13 (15.93, 16.32)	0.31	-1.89 (-2.09,-1.70)
Non-Hispanic White	19.11	19.38	18.50 (18.33, 18.68)	0.27	-0.88 (-1.05, -0.70)
Female					
Hispanic	22.62	22.70	20.54 (20.38, 20.72)	0.08	-2.16 (-2.32, -1.98)
Non-Hispanic Black	19.15	19.52	17.76 (17.57, 17.94)	0.37	-1.76 (-1.95, -1.58)
Non-Hispanic White	20.28	20.58	19.77 (19.60, 19.94)	0.30	-0.81 (-0.98, -0.64)
Male					
Hispanic	19.23	19.73	16.86 (16.68, 17.05)	0.50	-2.87 (-3.05, -2.68)
Non-Hispanic Black	15.79	16.11	14.24 (14.04, 14.44)	0.32	-1.87 (-2.07, -1.67)
Non-Hispanic White	17.72	18.06	17.16 (16.98, 17.34)	0.34	-0.90 (-1.08, -0.72)

Authors' analysis of data from the National Center for Health Statistics-U.S. Census Bureau and Human Mortality Database. Sums may differ from text due to rounding. P_5, P_{95}: 5th and 95th percentiles of 50,000 simulated life expectancies using 10% random uncertainty around the 2020 q_x estimates.

Table 3. Peer Country Average for Life Expectancy at Birth, Age 25 Years, and Age 65 Years: 2010, 2018, and 2020					
				Change in life expectancy (P_5, P_{95})	
	2010	**2018**	**2020 (P_5, P_{95})**	**2018 vs 2010**	**2020 vs. 2018**
Life expectancy at birth					
Total	80.54	81.78	81.56 (81.40, 81.71)	1.24	-0.22 (-0.38, -0.07)
Women	83.01	83.99	83.86 (83.71, 84.01)	0.98	-0.13 (-0.28, 0.02)
Men	78.10	79.62	79.33 (79.17, 79.49)	1.52	-0.29 (-0.45, -0.13)
Life expectancy at age 25					
Total	56.21	57.35	57.08 (56.93, 57.24)	1.14	-0.27 (-0.42, -0.11)
Women	58.56	59.47	59.29 (59.14, 59.44)	0.91	-0.18 (-0.33, -0.03)
Men	53.86	55.26	54.94 (54.78, 55.10)	1.40	-0.32 (-0.48, -0.16)
Life expectancy at age 65					
Total	19.53	20.31	20.05 (19.89, 20.21)	0.78	-0.26 (-0.42, -0.10)
Women	21.00	21.69	21.50 (21.35, 21.66)	0.69	-0.19 (-0.34, 0.03)
Men	17.88	18.82	18.53 (18.36, 18.69)	0.94	-0.29 (-0.46, -0.13)

Authors' analysis of data from the National Center for Health Statistics-U.S. Census Bureau and Human Mortality Database. Sums may differ from text due to rounding.

P_5, P_{95}: 5th and 95th percentiles of 50,000 simulated life expectancies using 10% random uncertainty around the 2020 q_x estimates.

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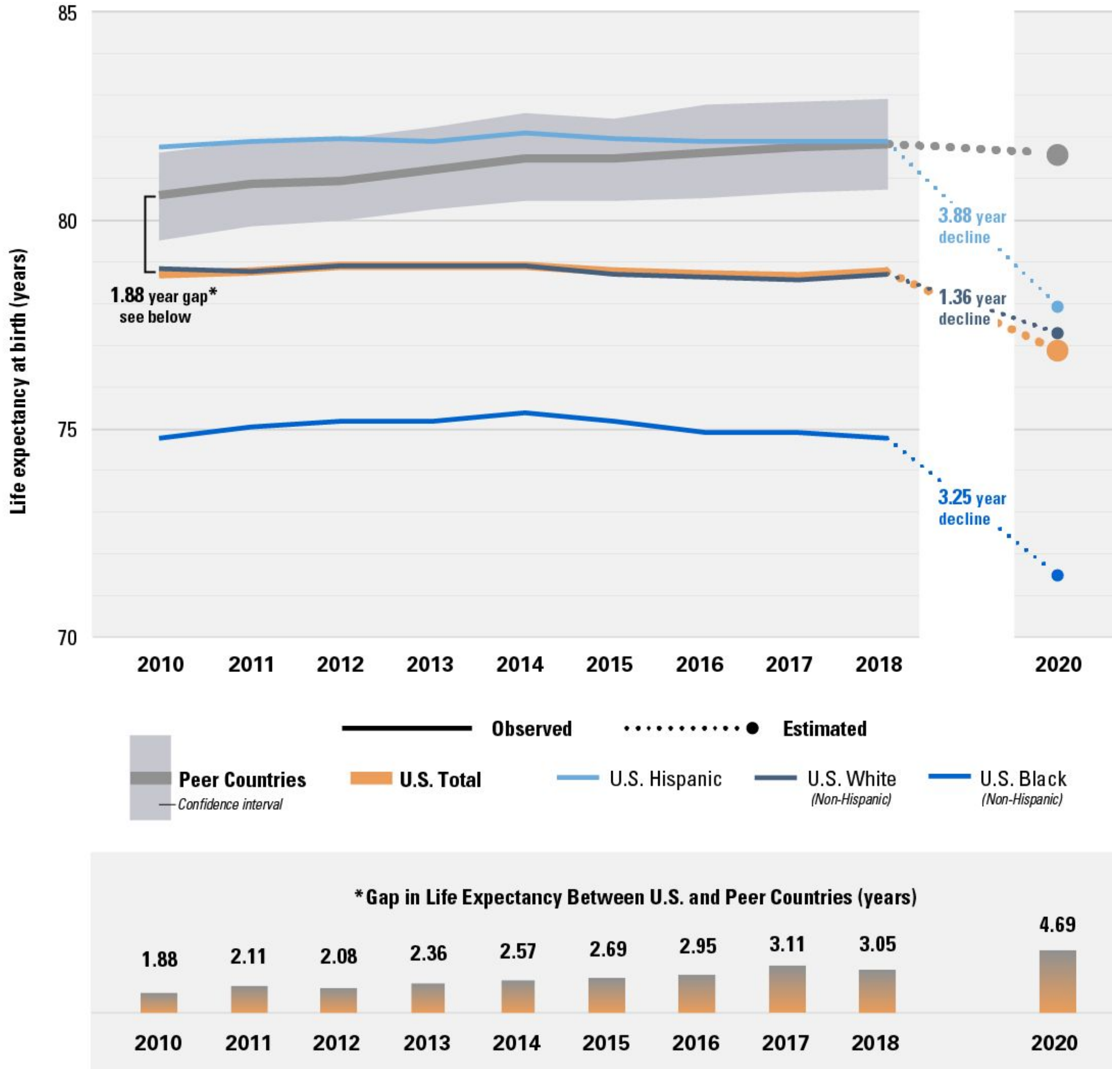
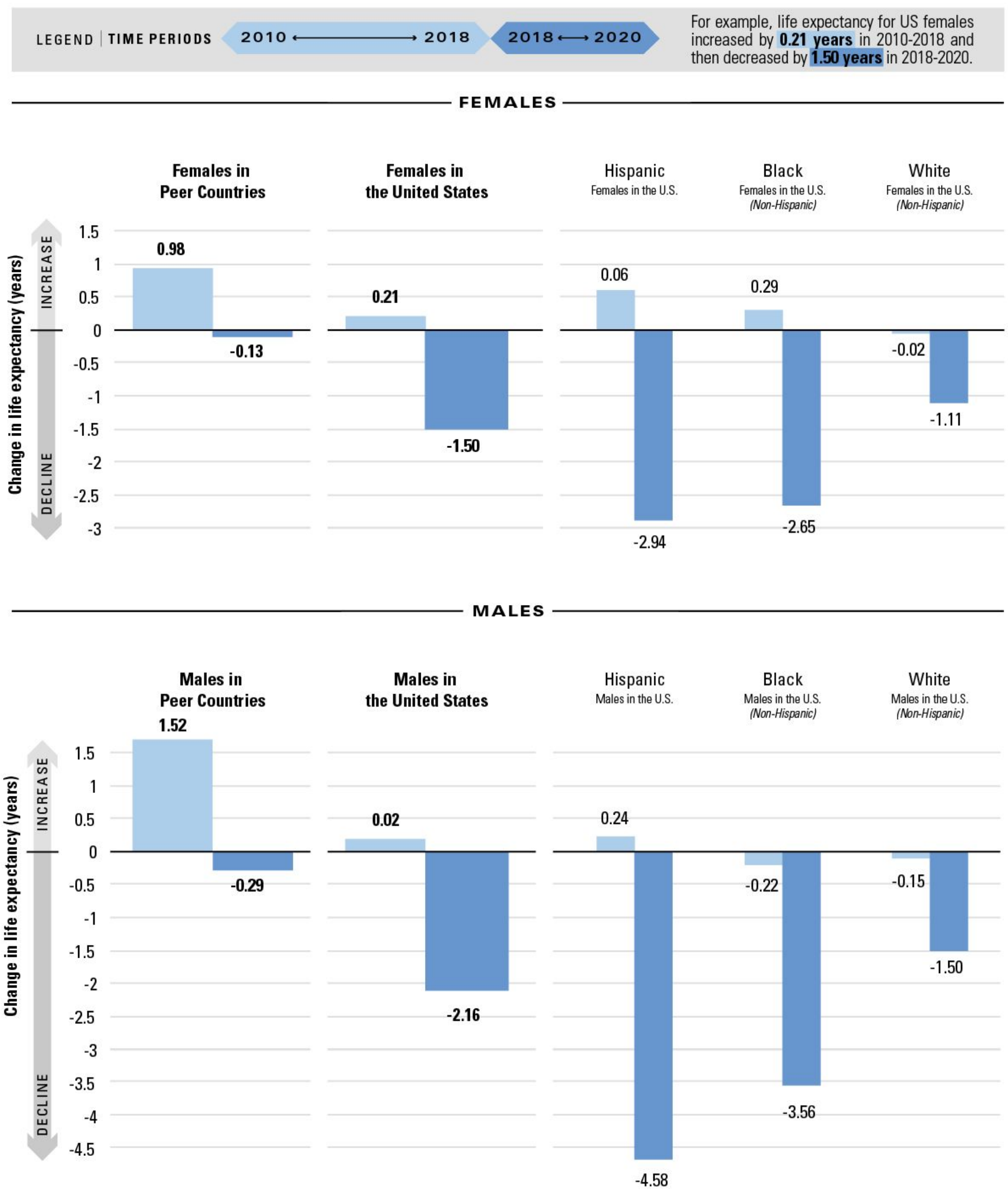
Figure 1. Life expectancy at Birth in the United States, by Race-Ethnicity, and in Peer Countries: 2010-2018 and 2020



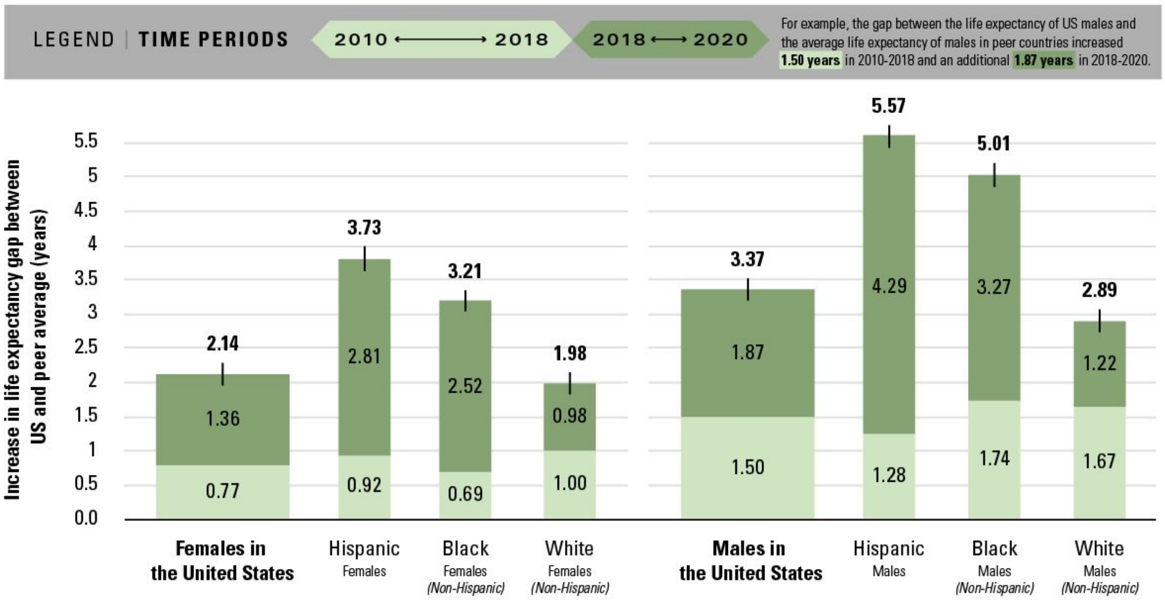
Source: Authors' analysis of data from the National Center for Health Statistics-U.S. Census Bureau and Human Mortality Database. Data for 2019 could not be calculated because life tables for a sufficient number of peer countries were not available. Grey band denotes the range of error for peer average estimates.

Figure 2. Changes in Life Expectancy at Birth, U.S. Populations and Peer Country Average: 2010 to 2018, and 2018 to 2020



Authors' analysis of data from the National Center for Health Statistics-U.S. Census Bureau and Human Mortality Database.

Figure 3. Increasing Gap in Life Expectancy Between the United States and Peer Country Average; 2010–2018 and 2018–2020



Authors' analysis of data from the National Center for Health Statistics-U.S. Census Bureau and Human Mortality Database. Sums may differ due to rounding.

SUMMARY BOX

What is already known on this topic

- Due to systemic factors in the United States, the gap between U.S. life expectancy and that of other high-income countries has been widening for decades.
- In 2020, the United States experienced more deaths from the COVID-19 pandemic than any other country, but no study has quantified the impact on U.S. life expectancy or on the gap with peer countries.

What this study adds

- Between 2018 and 2020, due largely to the COVID-19 pandemic, U.S. life expectancy decreased by 1.87 years, a decrease 8.5 times the average decrease in peer countries, and this widened the life expectancy gap with peer countries to 4.69 years.
- The decreases in life expectancy among U.S. Hispanic and non-Hispanic black people were 2-3 times that of the U.S. non-Hispanic white population, reversing years of progress in reducing racial-ethnic disparities and lowering the life expectancy of black men to levels not seen since 1998.

Print abstract

Study question:

What changes in life expectancy occurred in the United States and 16 other high-income countries during 2010-2018 and 2018-2020, and how did changes in U.S. life expectancy differ across racial-ethnic groups?

Methods: Life expectancy (at birth and at ages 25 and 65 years) was calculated for 2010-2018 from life tables obtained from the National Center for Health Statistics and the Human Mortality Database. Life expectancy in 2020 was estimated by simulating life tables from estimated age-specific mortality rates in 2020 and allowing for 10% random error. Estimates for 2019 were not possible because life tables were unavailable for many peer countries. Results for the United States and peer countries were analyzed by sex, and U.S. results were also analyzed for Hispanic, non-Hispanic Black, and non-Hispanic white populations.

Study answer and limitations: During 2010-2018, life expectancy decreased in the United States while increasing in peer countries. The resulting gap in life expectancy widened much further (to 4.69 years) in 2020. Between 2018 and 2020, U.S. life expectancy decreased by 1.87 years, 8.5 times the average decrease in peer countries. The decrease in life expectancy among U.S. Hispanic and non-Hispanic black people was 2-3 times that of non-Hispanic white people. The study relied on simulations of provisional mortality data for 2020 and could not include all high-income countries or all U.S. racial groups.

What this study adds: The study suggests that the COVID-19 pandemic of 2020 produced an extraordinary decrease in U.S. life expectancy relative to peer countries, disproportionately affecting people of color and deepening the health divide between the United States and its peers. The findings call attention to the root causes of the U.S. health disadvantage and persistent racial-ethnic inequities.

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1. Data Sources

US Populations

1. Total US Population
2. Total Female Population
3. Total Male Population
4. Total Non-Hispanic Black Population
5. Total Non-Hispanic White Population
6. Total Hispanic Population
7. Non-Hispanic Black Female Population
8. Non-Hispanic White Female Population
9. Hispanic Female Population
10. Non-Hispanic Black Male Population
11. Non-Hispanic White Male Population
12. Hispanic Male Population

Life expectancies for U.S. race/ethnic populations (Hispanic, non-Hispanic Black [NHB], and non-Hispanic white [NHW]) in 2010-2018, total and by sex, were recorded from life tables obtained from the National Center for Health Statistics (NCHS).[1,2,3.4,5,6,7,8,9]

<u>Comparison Group Populations for 16 Peer Countries</u>

Countries comprising the peer country comparison group were: Austria, Belgium, Denmark, Finland, France, Israel, Netherlands, New Zealand, Norway, Portugal, South Korea, Spain, Sweden, Switzerland, Taiwan, United Kingdom (data for England/Wales, Northern Ireland, and Scotland reported separately).

Criteria for inclusion in the peer country comparison group were: (1) high-income, (2) advanced democracy, and (3) data availability for 2010 – 2018 in the Human Mortality Database[10] (HMDB) 5 x 1 period life tables and data availability in the HMDB-Short Term Mortality Fluctuations (STMF) reports of weekly deaths in 2020. Data for each country's total population, female population, and male population in years 2010 – 2018 were obtained from 5-year age x 1-year time period abridged period life tables taken from the Human Mortality Database. (Direct sources[11,12] were used for Israel and New Zealand 2017 and 2018 life tables, which were not available in the HMDB.) In total, 54 separate data sets were downloaded and analyzed for the peer country life expectancies.

2. Average Life Expectancies among Peer Country Populations, 2010-2018

Life expectancy for each peer country's total population, female population, and male population for years 2010-2018 were saved separately as well as appended together. The ***average life expectancy*** at birth (***e_0***), at age 25 (***e_{25}***) and age 65 (***e_{65}***), the *average* ***age-specific probability of death (q_x)***, and the average ***age-specific person-years lived by the deceased (a_x)*** were calculated. The individual countries and the averages were also collapsed into year-specific datasets for total populations, female populations, and male populations of the peer countries.

3a. Estimated 2020 Life Expectancy for U.S. Populations

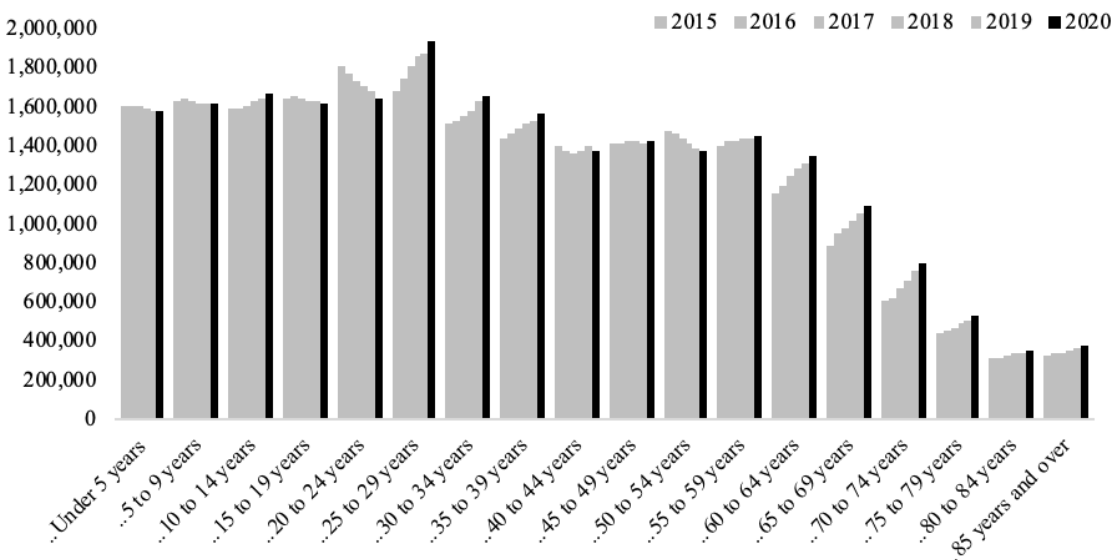
To calculate 2020 life tables for each U.S. population, we estimated 2020 age-specific death rates (m_x) for each U.S. population using (1) official life tables for 2018[9] (2) estimates of age-specific death counts among US populations in 2017, 2018 and 2020[8,9,13] and (3) estimates of age-specific population counts in 2017, 2018, and 2020.[14] The analytic steps are described below.

<u>*Estimated age-specific death rates in 2017, 2018, 2020 from NCHS-Census data*</u>

Age-specific death rates for US populations in 2017, 2018, and 2020 were calculated by merging estimates of age-specific counts of death with estimates of age-specific population counts. The counts of death were obtained from the March 28, 2021 release of the NCHS Center for Disease

Control and Prevention, file, *AH Excess Deaths by Sex, Age, and Race*. These NCHS data are composed of weekly death counts for ages 0-14; 15-19; …; 80-84; and 85+ years. We summed the weekly counts for years 2017, 2018, and 2020 separately for each age group and for each of the twelve U.S. populations.

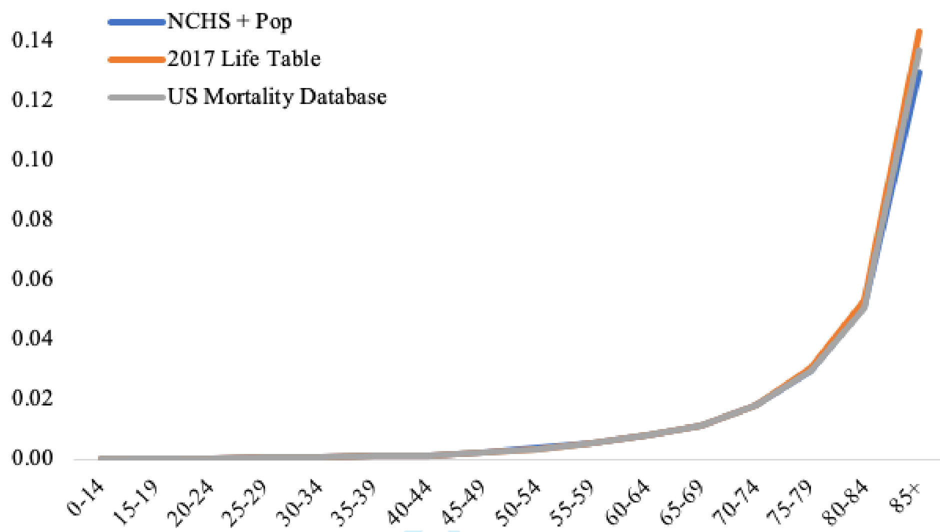
Mid-year population estimates were obtained from the U.S. Census Bureau file, *2019 Population Estimates by Age, Sex, Race, and Hispanic Origin*.[13] Tables *NC-EST2019-ASR5H* and *NC-EST2019-ASR6H* provide estimated annual counts of mid-year populations for ages 0-4; 5-9; …; 80-84; 85+ years for 2015-2019. Estimated population counts for ages 0-4; 5-9; and 10-14 are summed to approximate mid-year populations for ages 0-14 and to match the age structure of the death counts in the NCHS data. For year 2020, the estimated population counts for ages 0-4; 5-9; …; 80-84; 85+ years are estimated from the linear trends of age-specific populations between years 2015 and 2019. For example, below are the estimated age-specific population counts for the U.S. non-Hispanic Black female population:



The yearly age-specific death counts were merged with the yearly age-specific population counts, separately by race/ethnicity and sex, to estimate 2017 age-specific mortality rates (m_x), 2018 m_x, and 2020 m_x for the 12 separate U.S. populations.

The 2017 m_x and 2018 m_x estimated in these NCHS-Census data were compared with the m_x derived from the official 2017 and 2018 U.S. life tables to validate the accuracy of the data. This validation was performed to assess the validity of the 2020 m_x estimated in the NCHS-Census data. Specifically, we compared the 2017 m_x estimated in the NCHS-Census data with the 2017 m_x derived from official 2017 U.S. life tables,[8] and we also compared the 2018 m_x estimated in the NCHS-Census data with the 2018 m_x derived from official 2018 U.S. life tables.[9] To derive the m_x in the official life tables, we simply use the sum of d_x and the sum of L_x across age groups 0-14; 15-19; …; 80-84; 85+ years to match the age structure of the NCHS-Census data.

We contrast the 2017 m_x estimated from the NCHS-Census linked data with the 2017 m_x derived from official U.S. life tables to assess the validity of the m_x estimates in the NCHS-Census linked data. Below, for example, we contrast our estimated 2017 m_x for the U.S. total female population with the 2017 m_x derived from Arias et al. 2019[8] and the 2017 m_x reported by the US Mortality Database, *5X1 Female Period Life* Table[10] (after combining d_x and L_x for age group 0-14 years and for ages 85+ years).



The rate ratios (RR) between the estimated 2017 m_x using the NCHS-Census linked data and the 2017 m_x derived from Arias et al. 2019 are reported below, separately by U.S. male and female populations.

Rate Ratios: Estimated 2017 mx from NCHS-Census Linked Data vs. 2017 mx Reported by Arias et al. 2019

	US Female Population				US Male Population			
	Total	NHB	Latina	NHW	Total	NHB	Latino	NHW
0-14	0.90	0.83	0.86	0.87	0.90	0.86	0.89	0.81
15-19	1.01	0.89	0.96	0.97	1.01	0.92	1.09	0.96
20-24	1.01	0.90	0.95	0.98	1.01	0.93	1.10	0.97
25-29	1.00	0.95	0.98	0.97	1.01	0.99	0.98	0.97
30-34	1.00	0.97	0.99	0.98	1.00	0.99	0.98	0.98
35-39	1.00	0.97	1.00	0.98	1.00	0.97	0.96	0.99
40-44	1.00	0.98	1.00	0.99	1.01	0.98	0.96	0.99
45-49	1.01	0.99	0.92	0.99	1.01	0.99	0.98	1.00
50-54	1.00	0.99	0.92	1.00	1.01	1.00	0.98	1.00
55-59	1.00	0.98	0.94	0.99	1.00	1.00	0.96	1.00
60-64	1.00	0.98	0.95	0.99	1.00	0.99	0.96	0.99
65-69	0.99	0.98	1.00	0.99	1.00	0.99	0.96	0.99
70-74	0.98	0.97	1.00	0.99	0.99	0.98	0.96	0.99
75-79	0.97	0.96	0.98	0.98	0.97	0.96	0.97	0.98
80-84	0.96	0.93	0.95	0.97	0.96	0.92	0.92	0.97
85+	0.90	0.85	0.76	0.93	0.87	0.80	0.72	0.90

Although the estimated m_x from the NCHS-Census linked data are quite close to the reported m_x in Arias et al. 2019[8], two concerns are apparent. First, the m_x estimates are smaller than the reported m_x for the two pooled age groups at the youngest ages and the oldest ages (i.e., ages 0-14 and ages 85+ years). Second, m_x estimates smaller than the reported m_x are more common for non-Hispanic Black and Hispanic populations than for the non-Hispanic white and total populations. Both of these concerns about the m_x estimates are also evident in the 2018 data:

Rate Ratios: Estimated 2018 mx from NCHS-Census Linked Data vs. 2018 mx Reported by Arias 2020

	US Female Population				US Male Population			
	Total	NHB	Latina	NHW	Total	NHB	Latino	NHW
0-14	0.89	0.81	0.80	0.86	0.89	0.81	0.87	0.81
15-19	1.00	0.85	0.95	0.96	1.01	0.87	1.08	0.95
20-24	1.01	0.88	0.95	0.97	1.01	0.89	1.10	0.96
25-29	1.01	0.93	0.99	0.97	1.01	0.96	0.98	0.96
30-34	1.00	0.94	0.99	0.97	1.01	0.97	0.99	0.97
35-39	1.00	0.95	1.00	0.98	1.01	0.95	0.96	0.98
40-44	1.00	0.96	1.00	0.98	1.00	0.96	0.95	0.98
45-49	1.00	0.97	0.91	0.99	1.01	0.97	0.98	0.99
50-54	1.00	0.98	0.92	0.99	1.01	0.98	0.97	1.00
55-59	1.00	0.97	0.94	0.99	1.00	0.98	0.95	0.99
60-64	1.00	0.97	0.94	0.99	1.00	0.98	0.96	0.99
65-69	0.99	0.97	1.00	0.99	1.00	0.97	0.96	0.99
70-74	0.98	0.96	1.00	0.98	0.99	0.97	0.96	0.98
75-79	0.97	0.95	0.97	0.97	0.97	0.95	0.97	0.97
80-84	0.95	0.92	0.94	0.97	0.96	0.92	0.92	0.97
85+	0.90	0.84	0.75	0.94	0.86	0.80	0.71	0.89

Because concerns about bias in m_x estimates are evident in both the 2017 and 2018 NCHS-Census linked data, we assume the 2020 estimates are biased as well. Further, we assume that the degree of bias remains unchanged across 2017, 2018, and 2020 by age, sex, and race/ethnicity. That is, we assume the degree of bias is consistent across the years, such that rate ratios in the estimated 2017, 2018, and 2020 NCHS-Census linked data are due to *actual* changes in the m_x and not changes in bias across the years. This assumption is validated in the table below, which shows the absolute differences between the rate ratios reported in the two tables above:

Difference in Difference in Rate Ratios: 2018 Difference - 2017 Difference								
	US Female Population				US Male Population			
	Total	NHB	Latina	NHW	Total	NHB	Latino	NHW
0-14	-0.01	-0.02	-0.06	0.00	-0.01	-0.05	-0.03	0.00
15-19	0.00	-0.04	-0.01	-0.02	0.00	-0.06	-0.01	-0.01
20-24	0.00	-0.02	0.00	-0.01	0.00	-0.04	0.00	-0.01
25-29	0.00	-0.02	0.01	-0.01	0.00	-0.03	0.00	-0.01
30-34	0.00	-0.03	0.00	0.00	0.00	-0.02	0.01	-0.01
35-39	0.00	-0.02	0.00	-0.01	0.00	-0.02	0.00	-0.01
40-44	0.00	-0.02	0.00	-0.01	0.00	-0.02	0.00	-0.01
45-49	0.00	-0.02	-0.01	-0.01	0.00	-0.02	0.00	-0.01
50-54	0.00	-0.01	0.00	0.00	0.00	-0.02	0.00	0.00
55-59	0.00	-0.01	0.00	0.00	0.00	-0.01	0.00	0.00
60-64	0.00	-0.01	0.00	0.00	0.00	-0.01	-0.01	0.00
65-69	0.00	-0.01	0.00	0.00	0.00	-0.01	-0.01	0.00
70-74	0.00	-0.01	0.00	0.00	0.00	-0.01	0.00	0.00
75-79	0.00	-0.01	0.00	0.00	0.00	-0.01	-0.01	0.00
80-84	0.00	-0.01	-0.01	0.00	0.00	-0.01	0.00	0.00
85+	0.00	-0.01	-0.01	0.00	-0.01	-0.01	-0.01	0.00

The degree of bias in m_x estimates in the NCHS-Census data are consistent between 2017 and 2018, although some differences exist for m_x estimates at the youngest ages (0-14; 15-19; and 20-24 years) for the non-Hispanic Black population and the youngest age group (0-14 years) for the Latina population. Because deaths at these ages minimally affect changes in disparities in life expectancy at birth across the years, these differences in rate ratios are less concerning for estimates of life expectancy overall. At all other ages for all other U.S. populations, the differences between the rate ratios are minimal, suggesting that any difference in the rate ratios for year 2020 should overwhelmingly reflect actual changes in mortality rates, not discrepancies due to errors in reporting.

Because of the slight differences between the NCHS-Census estimated m_x and the m_x derived in the official US life tables, we do not use the 2020 m_x estimated in the NCHS-Census linked data to calculate 2020 U.S. life tables. Rather, we instead use the estimated rate ratios between the 2020 m_x estimates in the NCHS-Census data and the 2018 m_x estimates in the NCHS-Census data (below), and multiply these rate ratios by the 2018 m_x derived in the official 2018 US life tables.[9]

Estimated Rate Ratios: 2020 m_x vs. 2018 m_x Estimated in NCHS-Census Linked Data

	US Female Population				US Male Population			
	Total	NHB	Latina	NHW	Total	NHB	Latino	NHW
0-14	0.94	0.95	0.96	0.92	0.93	0.95	0.96	0.92
15-19	1.11	1.38	1.19	0.97	1.22	1.41	1.41	1.07
20-24	1.20	1.51	1.31	1.06	1.23	1.47	1.34	1.09
25-29	1.16	1.24	1.27	1.09	1.18	1.28	1.36	1.08
30-34	1.22	1.34	1.41	1.12	1.31	1.44	1.52	1.20
35-39	1.19	1.25	1.33	1.14	1.27	1.35	1.51	1.19
40-44	1.27	1.37	1.42	1.21	1.36	1.39	1.63	1.28
45-49	1.16	1.23	1.41	1.09	1.23	1.33	1.56	1.13
50-54	1.17	1.22	1.35	1.12	1.23	1.30	1.53	1.16
55-59	1.12	1.19	1.37	1.07	1.16	1.24	1.53	1.09
60-64	1.16	1.21	1.44	1.12	1.18	1.24	1.52	1.12
65-69	1.17	1.25	1.44	1.12	1.20	1.26	1.59	1.14
70-74	1.14	1.26	1.39	1.10	1.17	1.32	1.52	1.11
75-79	1.14	1.26	1.38	1.10	1.17	1.26	1.48	1.13
80-84	1.15	1.24	1.34	1.13	1.17	1.25	1.36	1.14
85+	1.13	1.23	1.23	1.12	1.14	1.24	1.29	1.12

Thus, the 2020 m_x used to calculate 2020 life tables for US populations are the official 2018 NCHS m_x[9] inflated by the 2020:2018 mortality rate ratios estimated from the NCHS-Census data (i.e., in above table). These calculations assume a constant rate ratio for ages 0, 1-4, 5-9, and 10-14 years (i.e., 0-14 year rate ratios in the NCHS-Census data are used to inflate the 2018 m_x at these ages) and a constant rate ratio for ages 85-89, 90-94, 95-99, and 100+ years (i.e., the 85+ rate ratio in the NCHS-Census data are used to inflate the 2018 m_x at these ages).

To calculate 2020 five-year q_x, we use the standard equation of Preston et al.[15]

$$q_x = (m_x*n)/(1+(a_x*m_x))$$

where *n* is the width of the age interval (i.e., 1 year, 4 years, or 5 years) and a_x is derived from the official 2018 US life tables for each US population.

Estimates of 2018 U.S. life expectancy at birth from five-year abridged life tables using q_x from this equation approximate the official reported 2018 life expectancy at birth with remarkable accuracy (see table below). Thus, using five-year q_x should not seriously bias estimates of 2020 life expectancy.

2018 Life Expectancy at Birth by US Population		
	Official	Abridged q_x
Total	78.74	78.74
Female	81.25	81.24
Male	76.22	76.22
Hispanic	81.83	81.83
NHB	74.71	74.68
NHW	78.63	78.62
Hispanic female	84.32	84.32
NHB female	77.99	77.98
NHW female	81.10	81.10
Hispanic male	79.08	79.08
NHB male	71.29	71.28
NHW male	76.20	76.20

Note: life expectancies in "Official" column from Arias 2020[9]

To account for possible error in 2020 death counts, possible error in 2020 population estimates, and possible error in estimated mortality rate ratios between 2020 m_x and 2018 m_x, we used Python (3.9.1) to simulate 50,000 life tables with 10% uncertainty added to the 2020 estimated q_x. Specifically, we simulated life tables using random (i.e., uniform) draws of q_x ranging from $0.95*q_x$ to $1.05*q_x$ and a_x from official 2018 life tables.[9] We report the 5th percentiles, medians, and 95th percentiles of 2020 life expectancies at birth, at age 25, and at age 65 for all US populations.

3b. Estimated Average 2020 Life Expectancy for Peer Populations

To calculate average 2020 life expectancies among peer populations, we separately estimate 2020 q_x among each peer country's total population, male population, and female population using (a) the country's reported q_x in the 2018 life tables in the Human Mortality Database[10] (and CBS-reported 2018 life table for Israel[11] and StatsNZ-reported 2017-2019 life table for New Zealand[12]) and (b) the mortality rate ratio between the country's reported m_x in the 2018 life tables and the country's reported 2020 m_x for ages 0-14; 15-64; 65-74; 75-84; and 85+ years in the *Human Mortality Database-Short Term Mortality Fluctuation* data. Weekly estimates of peer countries' mortality rates at ages 0-14; 15-64; 65-74; 75-84; and 85+ (m_x) were obtained from the *Human Mortality Database-Short Term Mortality Fluctuations* files. The rate ratios (RR) between the 2020 m_x and the 2018 m_x and the mortality risk ratios between the 2020 q_x and the 2018 q_x were calculated for each country.

To calculate 2020 five-year q_x among each peer country's total population and by sex, we use each country's 2018 q_x, 2018 a_x, and 2020:2018 mortality risk . As an illustration of the strong correspondence between countries' m_x ratios and q_x ratios, the table below shows the differences between the q_x ratios between 2018 and 2016 and the mx ratios between 2018 and 2016 for the female populations of Switzerland and Portugal. We compare the ratios between 2018 and 2016 because it is the same time difference as between 2020 and 2018 (i.e., two years). The average differences between the ratios for all 16 peer countries' female populations are also included, as well as the differences between the 2018 q_x and the estimated 2018 q_x using a) 2016 q_x and b) the 2018:2016 m_x ratio.

Age-specific Mortality Rate Ratios and Mortality Risk Ratios between 2018 and 2016 for Switzerland and Portugal Female Populations, and Average Ratio among 16 Peer Countries.

	Switzerland			Portugal			Average	
Age	2018:2016 m_x	2018:2016 q_x	Ratio	2018:2016 m_x	2018:2016 q_x	Ratio	Ratio	q_x est - q_x
0	0.836	0.836	1.00	1.065	1.065	1.00	1.00	0.00
1-4	1.800	1.707	0.95	1.357	1.382	1.02	0.99	0.00
5-9	1.200	1.148	0.96	1.500	1.419	0.95	1.02	0.00
10-14	1.000	1.047	1.05	1.250	1.333	1.07	1.01	0.00
15-19	1.308	1.273	0.97	0.882	0.881	1.00	0.99	0.00
20-24	1.063	1.049	0.99	1.063	1.088	1.02	1.01	0.00
25-29	0.864	0.880	1.02	1.933	1.934	1.00	1.00	0.00
30-34	0.867	0.860	0.99	1.444	1.419	0.98	1.00	0.00
35-39	0.795	0.813	1.02	0.763	0.762	1.00	1.00	0.00
40-44	0.969	0.969	1.00	0.967	0.969	1.00	1.00	0.00
45-49	0.934	0.936	1.00	0.972	0.972	1.00	1.00	0.00
50-54	1.049	1.044	1.00	0.949	0.948	1.00	1.00	0.00
55-59	0.982	0.984	1.00	0.965	0.965	1.00	1.00	0.00
60-64	1.009	1.009	1.00	0.970	0.969	1.00	1.00	0.00
65-69	0.966	0.967	1.00	0.947	0.948	1.00	1.00	0.00
70-74	0.979	0.980	1.00	0.938	0.940	1.00	1.00	0.00
75-79	0.982	0.982	1.00	0.977	0.978	1.00	1.00	0.00
80-84	0.978	0.982	1.00	0.972	0.975	1.00	1.00	0.00
85-89	0.992	0.993	1.00	0.932	0.946	1.02	1.00	0.00
90-94	1.006	1.004	1.00	1.053	1.032	0.98	1.00	0.00
95-99	1.000	1.000	1.00	1.039	1.016	0.98	0.94	0.00
100-104	1.003	1.001	1.00	1.048	1.009	0.96	0.93	0.01
105-109	1.004	1.000	1.00	1.043	1.004	0.96	0.93	0.01
110+	1.004	1.000	1.00	1.034	1.000	0.97	0.93	0.00

Note: "q_x est – q_x" indicates the average size of the difference between the true 2018 q_x reported in the HMDB data and the 2018 qx estimated from the 2016 HMDB data.

The ratios between m_x 2018:2016 ratios and q_x 2018:2016 ratios are remarkably similar for all countries. Further, on average, the estimated 2018 q_x using the m_x 2018:2016 ratios and the 2016 life tables match the actual 2018 q_x with remarkable accuracy. While there are some differences between the estimated 2018 q_x and the actual 2018 q_x at ages 100-104 and 105-109 (last column on the right), these have minimal to no effect on life expectancy estimates. Indeed, the average difference between the estimated 2018 life expectancies using the estimated 2018 q_x and the actual 2018 life expectancies is only .005 years. This exercise shows that combining each country's 2018 q_x with the countries' m_x estimated 2020:2018 ratios likely approximates each country's true 2020 q_x.

To account for possible error in 2020 m_x reported in the STMF data and possible error in estimated mortality rate ratios between 2020 m_x and 2018 m_x, we used Python (3.9.1) to simulate 50,000 life tables with 10% uncertainty added to the 2020 estimated q_x. Specifically, we simulated life tables using random (i.e., uniform) draws of q_x ranging from .95* q_x to 1.05* q_x and each country's 2018 a_x as reported in the HMDB 2018 life tables. We report the 5th percentiles, medians, and 95th percentiles of life expectancies at birth, and at ages 25 and 65, for total peer populations and by sex.

4. Analytic Scripts

a. Stata files merging death counts in NCHS data and population counts from Census estimates

```
********* All US Pop ************
*** 2020 NCHS Mortality Data, by Week ***

import delimited "/…/NCHS
Data/AH_Excess_Deaths_by_Sex__Age__and_Race_3_28.csv",
encoding(ISO-8859-1)

drop footnote geography numberaboveaverageweighted
percentaboveaverageweighted numberaboveaverageunweighted
percentaboveaverageunweighted timeperiod analysisdate weekending
covid19weighted covid19unweighted averagenumberofdeathsweighted
averagenumberofdeathsunweighted

keep if mmwryear == 2020
keep if raceethnicity == "All Race/Ethnicity Groups"

keep if sex == "All Sexes"
encode agegroup, gen(age)
drop if age == 17 | age == 18


*** Sum Deaths for Entire 2020 by Age ***

sort age
collapse (sum) mort = deathsunweighted, by(age)

save "/…/total pop_age specific death counts_2020.dta", replace


****** Import 2020 Pop Estimates ******
```

```
* Linear Trend Approximations from Age-specific Populations
2015-2019
* All US Pop, 0-14, 15-19, 80-84, 85+

import excel "/…/total pop_age.xlsx", sheet("2020 pop") firstrow
clear

encode age, gen(agecat)
drop age
rename agecat age

merge using "/…/total pop_age specific death counts_2020.dta"

gen mx = mort/pop

save "/…/total pop_2020 mx.dta", replace
```

b. Stata files appending peer country data. Female HMDB as Example

```
*******************
****  Austria ****
*******************

import delimited "/.../HMDB data/women/Austria_Women.txt",
delimiter(space, collapse) varnames(1) encoding(ISO-8859-1)
clear

keep if   year >= 2010 & year <= 2018

gen country = "Austria"

save "/.../HMDB data/women/austria_paper1.dta", replace


*******************
****  Belgium ****
*******************

import delimited "/.../HMDB data/women/Belgium_Women.txt",
delimiter(space, collapse) varnames(1) encoding(ISO-8859-1)
clear

keep if   year >= 2010 & year <= 2018

gen country = "Belgium"
```

```
save "/.../HMDB data/women/belgium_paper1.dta", replace


*****************
****  Israel ****
*****************

import delimited "/.../HMDB data/women/Israel_Women.txt",
delimiter(space, collapse) varnames(1) encoding(ISO-8859-1)
clear

keep if   year == 2010 & year <= 2016

gen country = "Israel"

save "/.../HMDB data/women/israel_paper1.dta", replace


* Data from Central Bureau of Statistics, State of Israel 2017 &
2018 Life Tables
import excel "/…/HMDB data/Israel/Israel_2017_2018.xlsx",
sheet("female") firstrow clear

append using "/.../HMDB data/women/israel_paper1.dta"

replace country = "Israel" if country == ""

* USE Data Editor to change String Variable Coding of Age
* *(1 variable, 24 observations pasted into data editor)

* save "/.../HMDB data/women/israel_paper1.dta", replace

save "/.../HMDB data/women/israel_paper1.dta", replace


******************
****  S Korea ****
******************

import delimited "/.../HMDB data/women/Korea_Women.txt",
delimiter(space, collapse) varnames(1) encoding(ISO-8859-1)
clear

keep if   year >= 2010 & year <= 2018

gen country = "S Korea"
```

```
save "/.../HMDB data/women/korea_paper1.dta", replace


*****************
****  Denmark ****
*****************

import delimited "/.../HMDB data/women/Denmark_Women.txt",
delimiter(space, collapse) varnames(1) encoding(ISO-8859-1)
clear

keep if   year >= 2010 & year <= 2018

gen country = "Denmark"

save "/.../HMDB data/women/denmark_paper1.dta", replace

*****************
****  Finland ****
*****************

import delimited "/.../HMDB data/women/Finland_Women.txt",
delimiter(space, collapse) varnames(1) encoding(ISO-8859-1)
clear

keep if   year >= 2010 & year <= 2018

gen country = "Finland"

save "/.../HMDB data/women/finland_paper1.dta", replace


****************
****  France ****
****************

import delimited "/.../HMDB data/women/France_Women.txt",
delimiter(space, collapse) varnames(1) encoding(ISO-8859-1)
clear

keep if   year >= 2010 & year <= 2018

gen country = "France"

save "/.../HMDB data/women/france_paper1.dta", replace
```

```
*********************
****  Netherlands ****
*********************

import delimited "/.../HMDB data/women/Netherlands_Women.txt",
delimiter(space, collapse) varnames(1) encoding(ISO-8859-1)
clear

keep if   year >= 2010 & year <= 2018

gen country = "Netherlands"

save "/.../HMDB data/women/netherlands_paper1.dta", replace


*********************
****  New Zealand ****
*********************

import delimited "/.../HMDB data/women/New Zealand_Women.txt",
delimiter(space, collapse) varnames(1) encoding(ISO-8859-1)
clear

keep if   year == 2010 & year <= 2013

gen country = "New Zealand"

save "/.../HMDB data/women/nz_paper1.dta", replace

* Data from Stats NZ, 2014-2016, 2015-2016, 2016-2018, 2017-2019
Life Tables. Missing 2014.
import excel "/…/HMDB data/New Zealand/NZ_2015_2018.xlsx",
sheet("female") firstrow clear

append using "/.../HMDB data/women/nz_paper1.dta"

replace country = "New Zealand" if country == ""

drop if year == .
replace age = "90-94" if age == "90-95"
* Change ax

save "/.../HMDB data/women/nz_paper1.dta", replace
```

```
*********************
****  Taiwan ****
*********************

import delimited "/.../HMDB data/women/Taiwan_Women.txt",
delimiter(space, collapse) varnames(1) encoding(ISO-8859-1)
clear

keep if   year >= 2010 & year <= 2018

gen country = "Taiwan"

save "/.../HMDB data/women/taiwan_paper1.dta", replace


****************
****  Norway ****
****************

import delimited "/.../HMDB data/women/Norway_Women.txt",
delimiter(space, collapse) varnames(1) encoding(ISO-8859-1)
clear

keep if   year >= 2010 & year <= 2018

gen country = "Norway"

save "/.../HMDB data/women/norway_paper1.dta", replace


******************
****  Portugal ****
******************

import delimited "/.../HMDB data/women/Portugal_Women.txt",
delimiter(space, collapse) varnames(1) encoding(ISO-8859-1)
clear

keep if   year >= 2010 & year <= 2018

gen country = "Portugal"

save "/.../HMDB data/women/portugal_paper1.dta", replace


***************
****  Spain ****
```

```
****************

import delimited "/.../HMDB data/women/Spain_Women.txt",
delimiter(space, collapse) varnames(1) encoding(ISO-8859-1)
clear

keep if   year >= 2010 & year <= 2018

gen country = "Spain"

save "/.../HMDB data/women/spain_paper1.dta", replace


****************
****  Sweden ****
****************

import delimited "/.../HMDB data/women/Sweden_Women.txt",
delimiter(space, collapse) varnames(1) encoding(ISO-8859-1)
clear

keep if   year >= 2010 & year <= 2018

gen country = "Sweden"

save "/.../HMDB data/women/sweden_paper1.dta", replace


*********************
****  Switzerland ****
*********************

import delimited "/.../HMDB data/women/Switzerland_Women.txt",
delimiter(space, collapse) varnames(1) encoding(ISO-8859-1)
clear

keep if   year >= 2010 & year <= 2018

gen country = "Switzerland"

save "/.../HMDB data/women/swiss_paper1.dta", replace



*************************
****  United Kingdom ****
```

```
************************

import delimited "/.../HMDB data/women/England_Wales_Women.txt",
delimiter(space, collapse) varnames(1) encoding(ISO-8859-1)
clear

keep if   year >= 2010 & year <= 2018

gen country = "England & Wales"

save "/.../HMDB data/women/england_wales_paper1.dta", replace

import delimited "/.../HMDB data/women/Scotland_Women.txt",
delimiter(space, collapse) varnames(1) encoding(ISO-8859-1)
clear

keep if   year >= 2010 & year <= 2018

gen country = "Scotland"

save "/.../HMDB data/women/scotland_paper1.dta", replace


import delimited "/.../HMDB data/women/Northern
Ireland_Women.txt", delimiter(space, collapse) varnames(1)
encoding(ISO-8859-1) clear

keep if   year >= 2010 & year <= 2018

gen country = "Northern Ireland"

save "/.../HMDB data/women/northern ireland_paper1.dta", replace




************************
* Append Peer Countries *
************************

* 16 Country Comparison Group

use "/.../HMDB data/women/swiss_paper1.dta", clear

append using "/.../HMDB data/women/sweden_paper1.dta"
append using "/.../HMDB data/women/spain_paper1.dta"
```

```
append using “/.../HMDB data/women/portugal_paper1.dta"
append using “/.../HMDB data/women/norway_paper1.dta"
append using “/.../HMDB data/women/netherlands_paper1.dta"
append using “/.../HMDB data/women/france_paper1.dta"
append using “/.../HMDB data/women/finland_paper1.dta"
append using “/.../HMDB data/women/denmark_paper1.dta"
append using “/.../HMDB data/women/austria_paper1.dta"
append using “/.../HMDB data/women/belgium_paper1.dta"
append using “/.../HMDB data/women/nz_paper1.dta"
append using “/.../HMDB data/women/korea_paper1.dta"
append using “/.../HMDB data/women/israel_paper1.dta"
append using “/.../HMDB data/women/taiwan_paper1.dta"
append using “/.../HMDB data/women/england_wales_paper1.dta"
append using “/.../HMDB data/women/scotland_paper1.dta"
append using “/.../HMDB data/women/northern ireland_paper1.dta"


save "/…/peer_paper1sep.dta", replace


* Variation in LE at Birth

set scheme s1manual

kdensity ex if nage==1 & year==2010
kdensity ex if nage==1 & year==2018

sum ex if nage==1 & year==2010, detail
sum ex if nage==1 & year==2018, detail


* Individual LT Kept for Merging with STMF RR

gen id = .
replace id = 1 if country == "Austria"
replace id = 2 if country == "Belgium"
replace id = 3 if country == "Denmark"
replace id = 4 if country == "Finland"
replace id = 5 if country == "France"
replace id = 6 if country == "Israel"
replace id = 7 if country == "Netherlands"
replace id = 8 if country == "New Zealand"
replace id = 9 if country == "Norway"
replace id = 10 if country == "Portugal"
replace id = 11 if country == "Spain"
replace id = 12 if country == "Sweden"
replace id = 13 if country == "Switzerland"
```

```
replace id = 14 if country == "Taiwan"
replace id = 15 if country == "England & Wales"
replace id = 16 if country == "Scotland"
replace id = 17 if country == "Northern Ireland"
replace id = 18 if country == "S Korea"

sort id year

save "/…/peer_paper1_sepLT.dta", replace

merge id using "/…/paper1_rr_female.dta"

sort id year nage

drop lx dx Lx Tx countrycode sex _merge

bysort nage: gen mx20 = mx*rr_0 if year == 2018
bysort nage: replace mx20 = mx*rr_15 if nage >= 5 & nage < 15 &
year == 2018
bysort nage: replace mx20 = mx*rr_65 if nage >= 15 & nage < 17 &
year == 2018
bysort nage: replace mx20 = mx*rr_75 if nage >= 17 & nage < 19 &
year == 2018
bysort nage: replace mx20 = mx*rr_85 if nage >= 19 & year ==
2018

bysort nage: gen qx20 = qx*rr_0 if year == 2018
bysort nage: replace qx20 = qx*rr_15 if nage >= 5 & nage < 15 &
year == 2018
bysort nage: replace qx20 = qx*rr_65 if nage >= 15 & nage < 17 &
year == 2018
bysort nage: replace qx20 = qx*rr_75 if nage >= 17 & nage < 19 &
year == 2018
bysort nage: replace qx20 = qx*rr_85 if nage >= 19 & year ==
2018

save "/…/peer_paper1_sepLT.dta", replace

sort id year nage

export excel using "/…/peer_sepLT_female.xls",
firstrow(variables) nolabel replace
```

c. Stata files estimating 2018 and 2020 death rates in peer country data.

```
* Use Rate Ratios*Mx to estimate age-specific Mx for 2020 from
2018 Life Table*RR
* Generate 2020 life table with the assumptions


import delimited "/Users…/peer_STMF/pooled_stmf_4_9_21.csv",
encoding(ISO-8859-1)

drop split splitsex forecast rtotal dtotal d85p d75_84 d65_74
d15_64 d0_14

keep if sex == "b"

drop if inlist(country,"AUS2","BGR","CAN",
"CHL","CZE","EST","GRC","HRV","HUN")
drop if inlist(country,"ISL","LTU","LUX","LVA","POL","RUS")
drop if inlist(country,"SVK","SVN","USA", "DEUTNP","ITA")

keep if year == 2018 | year == 2020


* Estimate Yearly Average ASRD - Mean across the 52 weeks

sort countrycode year

collapse (mean) r0=r0_14 r15=r15_64 r65=r65_74 r75=r75_84
r85=r85p, by(countrycode year)



* RR b/w 2020 and 2018
* Compute Average of 2018

tempfile a b c

sort countrycode

save `a'

keep if year == 2018

collapse (mean) r018=r0 r1518=r15 r6518=r65 r7518=r75 r8518=r85,
by(countrycode)

sort countrycode

save `b'
```

```
use `a', clear

sort countrycode

keep if year == 2020

sort countrycode

save `c'

merge using `b'

drop _merge

* Data are now Country/Sex-specific ASDRs in 2020 and average
ASDRs in 2018

* Estimate RR
* Take Average for peers by sex
* Combine with the 2018 Peer Life Table to Estimate ASDRs for
2020 Life Table


gen rr_0 = r0/r018
gen rr_15 = r15/r1518
gen rr_65 = r65/r6518
gen rr_75 = r75/r7518
gen rr_85 = r85/r8518

* Heterogeneity in countries RR

set scheme s1manual

kdensity rr_0
kdensity rr_15
kdensity rr_65
kdensity rr_75
kdensity rr_85

sum rr_0 rr_15 rr_65 rr_75 rr_85


**** Save File to Merge with Appended HMDB Life Tables ****

save "/Users…/peer_STMF/paper1_2018rr_total.dta", replace
```

```
use "/Users…/peer_STMF/paper1_2018rr_total.dta", clear

gen id = .
replace id = 1 if countrycode == "AUT"
replace id = 2 if countrycode == "BEL"
replace id = 3 if countrycode == "DNK"
replace id = 4 if countrycode == "FIN"
replace id = 5 if countrycode == "FRATNP"
replace id = 6 if countrycode == "ISR"
replace id = 7 if countrycode == "NLD"
replace id = 8 if countrycode == "NZL_NP"
replace id = 9 if countrycode == "NOR"
replace id = 10 if countrycode == "PRT"
replace id = 11 if countrycode == "ESP"
replace id = 12 if countrycode == "SWE"
replace id = 13 if countrycode == "CHE"
replace id = 14 if countrycode == "TWN"
replace id = 15 if countrycode == "GBRTENW"
replace id = 16 if countrycode == "GBR_SCO"
replace id = 17 if countrycode == "GBR_NIR"
replace id = 18 if countrycode == "KOR"


drop r0 r15 r65 r75 r85 r018 r1518 r6518 r7518 r8518

sort id

save "/Users…/peer_STMF/paper1_2018rr_total.dta", replace
```

d. Python files simulating life tables, Norway's female population as an example.

```
"""
```

```
Peer 2020 Life Tables from 2018 qx*2020:2018RR and 2018 ax

@author: …

"""
#import packages
import random

# importing in the qx and error and ax
nor_f = r"/…/nor_f.txt"
# change as needed for input files

# read in the file
textFile = open(nor_f,'r')
text = textFile.readlines()
# split into different age categories
a0=text[1]
a1=text[2]
a5=text[3]
a10=text[4]
a15=text[5]
a20=text[6]

a25=text[7]
a30=text[8]
a35=text[9]
a40=text[10]
a45=text[11]
a50=text[12]
a55=text[13]
a60=text[14]
a65=text[15]
a70=text[16]
a75=text[17]
a80=text[18]
a85=text[19]
a90=text[20]
a95=text[21]
a100=text[22]
a105=text[23]
a110=text[24]

a0_sp = a0.split(",")
a1_sp = a1.split(",")
```

```
a5_sp = a5.split(",")
a10_sp = a10.split(",")
a15_sp = a15.split(",")
a20_sp = a20.split(",")
a25_sp = a25.split(",")
a30_sp = a30.split(",")
a35_sp = a35.split(",")
a40_sp = a40.split(",")
a45_sp = a45.split(",")
a50_sp = a50.split(",")
a55_sp = a55.split(",")
a60_sp = a60.split(",")
a65_sp = a65.split(",")
a70_sp = a70.split(",")
a75_sp = a75.split(",")
a80_sp = a80.split(",")
a85_sp = a85.split(",")
a90_sp = a90.split(",")
a95_sp = a95.split(",")
a100_sp = a100.split(",")
a105_sp = a105.split(",")
a110_sp = a110.split(",")

# qx
a0_qx = float(a0_sp[1])
a1_qx = float(a1_sp[1])
a5_qx = float(a5_sp[1])
a10_qx = float(a10_sp[1])
a15_qx = float(a15_sp[1])
a20_qx = float(a20_sp[1])
a25_qx = float(a25_sp[1])
a30_qx = float(a30_sp[1])
a35_qx = float(a35_sp[1])
a40_qx = float(a40_sp[1])
a45_qx = float(a45_sp[1])
a50_qx = float(a50_sp[1])
a55_qx = float(a55_sp[1])
a60_qx = float(a60_sp[1])
a65_qx = float(a65_sp[1])
a70_qx = float(a70_sp[1])
a75_qx = float(a75_sp[1])
a80_qx = float(a80_sp[1])
a85_qx = float(a85_sp[1])
a90_qx = float(a90_sp[1])
```

```
a95_qx = float(a95_sp[1])
a100_qx = float(a100_sp[1])
a105_qx = float(a105_sp[1])
a110_qx = float(a110_sp[1])

# qx - lower bound
a0_qxl = float(a0_sp[2])
a1_qxl = float(a1_sp[2])
a5_qxl = float(a5_sp[2])
a10_qxl = float(a10_sp[2])
a15_qxl = float(a15_sp[2])
a20_qxl = float(a20_sp[2])
a25_qxl = float(a25_sp[2])
a30_qxl = float(a30_sp[2])
a35_qxl = float(a35_sp[2])
a40_qxl = float(a40_sp[2])
a45_qxl = float(a45_sp[2])
a50_qxl = float(a50_sp[2])
a55_qxl = float(a55_sp[2])
a60_qxl = float(a60_sp[2])
a65_qxl = float(a65_sp[2])
a70_qxl = float(a70_sp[2])
a75_qxl = float(a75_sp[2])
a80_qxl = float(a80_sp[2])
a85_qxl = float(a85_sp[2])
a90_qxl = float(a90_sp[2])
a95_qxl = float(a95_sp[2])
a100_qxl = float(a100_sp[2])
a105_qxl = float(a105_sp[2])
a110_qxl = float(a110_sp[2])
# qx - Upper bound
a0_qxu = float(a0_sp[3])
a1_qxu = float(a1_sp[3])
a5_qxu = float(a5_sp[3])
a10_qxu = float(a10_sp[3])
a15_qxu = float(a15_sp[3])
a20_qxu = float(a20_sp[3])
a25_qxu = float(a25_sp[3])
a30_qxu = float(a30_sp[3])
a35_qxu = float(a35_sp[3])
a40_qxu = float(a40_sp[3])
a45_qxu = float(a45_sp[3])
a50_qxu = float(a50_sp[3])
a55_qxu = float(a55_sp[3])
```

```
a60_qxu = float(a60_sp[3])
a65_qxu = float(a65_sp[3])
a70_qxu = float(a70_sp[3])
a75_qxu = float(a75_sp[3])
a80_qxu = float(a80_sp[3])
a85_qxu = float(a85_sp[3])
a90_qxu = float(a90_sp[3])
a95_qxu = float(a95_sp[3])
a100_qxu = float(a100_sp[3])
a105_qxu = float(a105_sp[3])
a110_qxu = float(a110_sp[3])

# ax
a0_ax = float(a0_sp[4])
a1_ax = float(a1_sp[4])
a5_ax = float(a5_sp[4])
a10_ax = float(a10_sp[4])
a15_ax = float(a15_sp[4])
a20_ax = float(a20_sp[4])
a25_ax = float(a25_sp[4])
a30_ax = float(a30_sp[4])
a35_ax = float(a35_sp[4])
a40_ax = float(a40_sp[4])
a45_ax = float(a45_sp[4])
a50_ax = float(a50_sp[4])
a55_ax = float(a55_sp[4])
a60_ax = float(a60_sp[4])
a65_ax = float(a65_sp[4])
a70_ax = float(a70_sp[4])
a75_ax = float(a75_sp[4])
a80_ax = float(a80_sp[4])
a85_ax = float(a85_sp[4])
a90_ax = float(a90_sp[4])
a95_ax = float(a95_sp[4])
a100_ax = float(a100_sp[4])
a105_ax = float(a105_sp[4])
a110_ax = float(a110_sp[4])



count = 0
while count < 50000: #5000: #50000

    a0_rand_qx = random.uniform(a0_qxl,a0_qxu)
```

```
    a1_rand_qx = random.uniform(a1_qxl,a1_qxu)
    a5_rand_qx = random.uniform(a5_qxl,a5_qxu)
    a10_rand_qx = random.uniform(a10_qxl,a10_qxu)
    a15_rand_qx = random.uniform(a15_qxl,a15_qxu)
    a20_rand_qx = random.uniform(a20_qxl,a20_qxu)
    a25_rand_qx = random.uniform(a25_qxl,a25_qxu)
    a30_rand_qx = random.uniform(a30_qxl,a30_qxu)
    a35_rand_qx = random.uniform(a35_qxl,a35_qxu)
    a40_rand_qx = random.uniform(a40_qxl,a40_qxu)
    a45_rand_qx = random.uniform(a45_qxl,a45_qxu)
    a50_rand_qx = random.uniform(a50_qxl,a50_qxu)
    a55_rand_qx = random.uniform(a55_qxl,a55_qxu)
    a60_rand_qx = random.uniform(a60_qxl,a60_qxu)
    a65_rand_qx = random.uniform(a65_qxl,a65_qxu)
    a70_rand_qx = random.uniform(a70_qxl,a70_qxu)
    a75_rand_qx = random.uniform(a75_qxl,a75_qxu)
    a80_rand_qx = random.uniform(a80_qxl,a80_qxu)
    a85_rand_qx = random.uniform(a85_qxl,a85_qxu)
    a90_rand_qx = random.uniform(a90_qxl,a90_qxu)
    a95_rand_qx = random.uniform(a95_qxl,a95_qxu)
    a100_rand_qx = random.uniform(a100_qxl,a100_qxu)
    a105_rand_qx = random.uniform(a105_qxl,a105_qxu)
    a110_rand_qx = 1

    # without randomization
#   a0_rand_qx = a0_qx
#   a1_rand_qx = a1_qx
#   a5_rand_qx = a5_qx
#   a10_rand_qx = a10_qx
#   a15_rand_qx = a15_qx
#   a20_rand_qx = a20_qx
#   a25_rand_qx = a25_qx
#   a30_rand_qx = a30_qx
#   a35_rand_qx = a35_qx
#   a40_rand_qx = a40_qx
#   a45_rand_qx = a45_qx
#   a50_rand_qx = a50_qx
#   a55_rand_qx = a55_qx
#   a60_rand_qx = a60_qx
#   a65_rand_qx = a65_qx
#   a70_rand_qx = a70_qx
#   a75_rand_qx = a75_qx
#   a80_rand_qx = a80_qx
#   a85_rand_qx = a85_qx
```

```
#    a90_rand_qx = a90_qx
#    a95_rand_qx = a95_qx
#    a100_rand_qx = a100_qx
#    a105_rand_qx = a105_qx
#    a110_rand_qx = 1
#


### calculate life table variables
   radix = 1000000.0000000

   # calculate the number of deaths age0
   a0_dx = a0_rand_qx*radix
   # calculate survivors
   a0_lx=radix
   a0_sx=a0_lx/radix # this is 1?
   a1_lx=(radix-a0_dx)
   a1_sx = a1_lx/radix

   # calculate the number of deaths age1
   a1_dx = a1_rand_qx*a1_lx
   # calculate survivors
   a5_lx=(a1_lx-a1_dx)
   a5_sx = a5_lx/radix

   # calculate the number of deaths age5
   a5_dx = a5_rand_qx*a5_lx
   # calculate survivors
   a10_lx=(a5_lx-a5_dx)
   a10_sx = a10_lx/radix

   # calculate the number of deaths age10
   a10_dx = a10_rand_qx*a10_lx
   # calculate survivors
   a15_lx=(a10_lx-a10_dx)
   a15_sx = a15_lx/radix

   # calculate the number of deaths age15
   a15_dx = a15_rand_qx*a15_lx
   # calculate survivors
   a20_lx=(a15_lx-a15_dx)
   a20_sx = a20_lx/radix

   # calculate the number of deaths age20
```

```
a20_dx = a20_rand_qx*a20_lx
# calculate survivors
a25_lx=(a20_lx-a20_dx)
a25_sx = a25_lx/radix

# calculate the number of deaths age25
a25_dx = a25_rand_qx*a25_lx
# calculate survivors
a30_lx=(a25_lx-a25_dx)
a30_sx = a30_lx/radix

# calculate the number of deaths age30
a30_dx = a30_rand_qx*a30_lx
# calculate survivors
a35_lx=(a30_lx-a30_dx)
a35_sx = a35_lx/radix

# calculate the number of deaths age35
a35_dx = a35_rand_qx*a35_lx
# calculate survivors
a40_lx=(a35_lx-a35_dx)
a40_sx = a40_lx/radix

# calculate the number of deaths age40
a40_dx = a40_rand_qx*a40_lx
# calculate survivors
a45_lx=(a40_lx-a40_dx)
a45_sx = a45_lx/radix

# calculate the number of deaths age45
a45_dx = a45_rand_qx*a45_lx
# calculate survivors
a50_lx=(a45_lx-a45_dx)
a50_sx = a50_lx/radix

# calculate the number of deaths age50
a50_dx = a50_rand_qx*a50_lx
# calculate survivors
a55_lx=(a50_lx-a50_dx)
a55_sx = a55_lx/radix

# calculate the number of deaths age55
a55_dx = a55_rand_qx*a55_lx
# calculate survivors
```

```
a60_lx=(a55_lx-a55_dx)
a60_sx = a60_lx/radix

# calculate the number of deaths age60
a60_dx = a60_rand_qx*a60_lx
# calculate survivors
a65_lx=(a60_lx-a60_dx)
a65_sx = a65_lx/radix

# calculate the number of deaths age65
a65_dx = a65_rand_qx*a65_lx
# calculate survivors
a70_lx=(a65_lx-a65_dx)
a70_sx = a70_lx/radix

# calculate the number of deaths age70
a70_dx = a70_rand_qx*a70_lx
# calculate survivors
a75_lx=(a70_lx-a70_dx)
a75_sx = a75_lx/radix

# calculate the number of deaths age75
a75_dx = a75_rand_qx*a75_lx
# calculate survivors
a80_lx=(a75_lx-a75_dx)
a80_sx = a80_lx/radix

# calculate the number of deaths age80
a80_dx = a80_rand_qx*a80_lx
# calculate survivors
a85_lx=(a80_lx-a80_dx)
a85_sx = a85_lx/radix

# calculate the number of deaths age85
a85_dx = a85_rand_qx*a85_lx
# calculate survivors
a90_lx=(a85_lx-a85_dx)
a90_sx = a90_lx/radix

# calculate the number of deaths age90
a90_dx = a90_rand_qx*a90_lx
# calculate survivors
a95_lx=(a90_lx-a90_dx)
a95_sx = a95_lx/radix
```

```
# calculate the number of deaths age95
a95_dx = a95_rand_qx*a95_lx
# calculate survivors
a100_lx=(a95_lx-a95_dx)
a100_sx = a100_lx/radix

# calculate the number of deaths age100
a100_dx = a100_rand_qx*a100_lx
# calculate survivors
a105_lx=(a100_lx-a100_dx)
a105_sx = a105_lx/radix

# calculate the number of deaths age105
a105_dx = a105_rand_qx*a105_lx
# calculate survivors
a110_lx=(a105_lx-a105_dx)
a110_sx = a110_lx/radix

# calculate the number of deaths age110
a110_dx = a110_rand_qx*a110_lx
# No Survivors - top-coded

#calculate Lx
a0_Lx = (a1_lx*1)+(a0_dx*a0_ax)
a1_Lx = (a5_lx*4)+(a1_dx*a1_ax)
a5_Lx = (a10_lx*5)+(a5_dx*a5_ax)
a10_Lx = (a15_lx*5)+(a10_dx*a10_ax)
a15_Lx = (a20_lx*5)+(a15_dx*a15_ax)
a20_Lx = (a25_lx*5)+(a20_dx*a20_ax)
a25_Lx = (a30_lx*5)+(a25_dx*a25_ax)
a30_Lx = (a35_lx*5)+(a30_dx*a30_ax)
a35_Lx = (a40_lx*5)+(a35_dx*a35_ax)
a40_Lx = (a45_lx*5)+(a40_dx*a40_ax)
a45_Lx = (a50_lx*5)+(a45_dx*a45_ax)
a50_Lx = (a55_lx*5)+(a50_dx*a50_ax)
a55_Lx = (a60_lx*5)+(a55_dx*a55_ax)
a60_Lx = (a65_lx*5)+(a60_dx*a60_ax)
a65_Lx = (a70_lx*5)+(a65_dx*a65_ax)
a70_Lx = (a75_lx*5)+(a70_dx*a70_ax)
a75_Lx = (a80_lx*5)+(a75_dx*a75_ax)
a80_Lx = (a85_lx*5)+(a80_dx*a80_ax)
a85_Lx = (a90_lx*5)+(a85_dx*a85_ax)
a90_Lx = (a95_lx*5)+(a90_dx*a90_ax)
```

```
  a95_Lx = (a100_lx*5)+(a95_dx*a95_ax)
  a100_Lx = (a105_lx*5)+(a100_dx*a100_ax)
  a105_Lx = (a110_lx*5)+(a105_dx*a105_ax)
  a110_Lx = (a110_dx*a110_ax)

  ####
  # calculate Tx
  a0_Tx =
a0_Lx+a1_Lx+a5_Lx+a10_Lx+a15_Lx+a20_Lx+a25_Lx+a30_Lx+a35_Lx+a40_Lx+a45_Lx+a50_Lx+
a55_Lx+a60_Lx+a65_Lx+a70_Lx+a75_Lx+a80_Lx+a85_Lx+a90_Lx+a95_Lx+a100_Lx+a105_Lx+a1
10_Lx
  a1_Tx =
a1_Lx+a5_Lx+a10_Lx+a15_Lx+a20_Lx+a25_Lx+a30_Lx+a35_Lx+a40_Lx+a45_Lx+a50_Lx+a55_Lx
+a60_Lx+a65_Lx+a70_Lx+a75_Lx+a80_Lx+a85_Lx+a90_Lx+a95_Lx+a100_Lx+a105_Lx+a110_Lx
  a5_Tx =
a5_Lx+a10_Lx+a15_Lx+a20_Lx+a25_Lx+a30_Lx+a35_Lx+a40_Lx+a45_Lx+a50_Lx+a55_Lx+a60_L
x+a65_Lx+a70_Lx+a75_Lx+a80_Lx+a85_Lx+a90_Lx+a95_Lx+a100_Lx+a105_Lx+a110_Lx
  a10_Tx =
a10_Lx+a15_Lx+a20_Lx+a25_Lx+a30_Lx+a35_Lx+a40_Lx+a45_Lx+a50_Lx+a55_Lx+a60_Lx+a65_
Lx+a70_Lx+a75_Lx+a80_Lx+a85_Lx+a90_Lx+a95_Lx+a100_Lx+a105_Lx+a110_Lx
  a15_Tx =
a15_Lx+a20_Lx+a25_Lx+a30_Lx+a35_Lx+a40_Lx+a45_Lx+a50_Lx+a55_Lx+a60_Lx+a65_Lx+a70_
Lx+a75_Lx+a80_Lx+a85_Lx+a90_Lx+a95_Lx+a100_Lx+a105_Lx+a110_Lx
  a20_Tx =
a20_Lx+a25_Lx+a30_Lx+a35_Lx+a40_Lx+a45_Lx+a50_Lx+a55_Lx+a60_Lx+a65_Lx+a70_Lx+a75_
Lx+a80_Lx+a85_Lx+a90_Lx+a95_Lx+a100_Lx+a105_Lx+a110_Lx
  a25_Tx =
a25_Lx+a30_Lx+a35_Lx+a40_Lx+a45_Lx+a50_Lx+a55_Lx+a60_Lx+a65_Lx+a70_Lx+a75_Lx+a80_
Lx+a85_Lx+a90_Lx+a95_Lx+a100_Lx+a105_Lx+a110_Lx
  a30_Tx =
a30_Lx+a35_Lx+a40_Lx+a45_Lx+a50_Lx+a55_Lx+a60_Lx+a65_Lx+a70_Lx+a75_Lx+a80_Lx+a85_
Lx+a90_Lx+a95_Lx+a100_Lx+a105_Lx+a110_Lx
  a35_Tx =
a35_Lx+a40_Lx+a45_Lx+a50_Lx+a55_Lx+a60_Lx+a65_Lx+a70_Lx+a75_Lx+a80_Lx+a85_Lx+a90_
Lx+a95_Lx+a100_Lx+a105_Lx+a110_Lx
  a40_Tx =
a40_Lx+a45_Lx+a50_Lx+a55_Lx+a60_Lx+a65_Lx+a70_Lx+a75_Lx+a80_Lx+a85_Lx+a90_Lx+a95_
Lx+a100_Lx+a105_Lx+a110_Lx
  a45_Tx =
a45_Lx+a50_Lx+a55_Lx+a60_Lx+a65_Lx+a70_Lx+a75_Lx+a80_Lx+a85_Lx+a90_Lx+a95_Lx+a100
_Lx+a105_Lx+a110_Lx
  a50_Tx =
a50_Lx+a55_Lx+a60_Lx+a65_Lx+a70_Lx+a75_Lx+a80_Lx+a85_Lx+a90_Lx+a95_Lx+a100_Lx+a10
5_Lx+a110_Lx
```

```
a55_Tx =
a55_Lx+a60_Lx+a65_Lx+a70_Lx+a75_Lx+a80_Lx+a85_Lx+a90_Lx+a95_Lx+a100_Lx+a105_Lx+a1
10_Lx
a60_Tx =
a60_Lx+a65_Lx+a70_Lx+a75_Lx+a80_Lx+a85_Lx+a90_Lx+a95_Lx+a100_Lx+a105_Lx+a110_Lx
a65_Tx =
a65_Lx+a70_Lx+a75_Lx+a80_Lx+a85_Lx+a90_Lx+a95_Lx+a100_Lx+a105_Lx+a110_Lx
a70_Tx = a70_Lx+a75_Lx+a80_Lx+a85_Lx+a90_Lx+a95_Lx+a100_Lx+a105_Lx+a110_Lx
a75_Tx = a75_Lx+a80_Lx+a85_Lx+a90_Lx+a95_Lx+a100_Lx+a105_Lx+a110_Lx
a80_Tx = a80_Lx+a85_Lx+a90_Lx+a95_Lx+a100_Lx+a105_Lx+a110_Lx
a85_Tx = a85_Lx+a90_Lx+a95_Lx+a100_Lx+a105_Lx+a110_Lx
a90_Tx = a90_Lx+a95_Lx+a100_Lx+a105_Lx+a110_Lx
a95_Tx = a95_Lx+a100_Lx+a105_Lx+a110_Lx
a100_Tx = a100_Lx+a105_Lx+a110_Lx
a105_Tx = a105_Lx+a110_Lx
a110_Tx = a110_Lx

###### estimate qx: 15-64, 65-84, 85-99

a1564_qx =
(a15_dx+a20_dx+a25_dx+a30_dx+a35_dx+a40_dx+a45_dx+a50_dx+a55_dx+a60_dx)/a15_lx
a6584_qx = (a65_dx+a70_dx+a75_dx+a80_dx)/a65_lx
a8599_qx = (a85_dx+a90_dx+a95_dx)/a85_lx


###### estimate life expectancy

a0_ex = a0_Tx/radix
a1_ex = a1_Tx/a1_lx
a5_ex = a5_Tx/a5_lx
a10_ex = a10_Tx/a10_lx
a15_ex = a15_Tx/a15_lx
a20_ex = a20_Tx/a20_lx
a25_ex = a25_Tx/a25_lx
a30_ex = a30_Tx/a30_lx
a35_ex = a35_Tx/a35_lx
a40_ex = a40_Tx/a40_lx
a45_ex = a45_Tx/a45_lx
a50_ex = a50_Tx/a50_lx
a55_ex = a55_Tx/a55_lx
a60_ex = a60_Tx/a60_lx
a65_ex = a65_Tx/a65_lx
a70_ex = a70_Tx/a70_lx
a75_ex = a75_Tx/a75_lx
```

```
    a80_ex = a80_Tx/a80_lx
    a85_ex = a85_Tx/a85_lx
    a90_ex = a90_Tx/a90_lx
    a95_ex = a95_Tx/a95_lx
    a100_ex = a100_Tx/a100_lx
    a105_ex = a105_Tx/a105_lx
    a110_ex = a110_Tx/a110_lx

# this outputs the probabilities of each estimate as a check
    nor_f_filenm = r"/…/nor_f_qx.txt"
    opened_file = open(nor_f_filenm, 'a')

    if count==0:
        opened_file.write('{0} {1} {2} {3}\n'.format("sim_num","qx1564","qx6584","qx8599"))

    else:
        opened_file.write('{0} {1} {2} {3}\n'.format(count,a1564_qx,a6584_qx,a8599_qx))

    # save data

    tot_file_name = r"/…/nor_f_ex.txt"
#   file_name = r"C:\... .txt"
    tot_opened_file = open(tot_file_name, 'a')
    #opened_file.write("%r\n" %age45_ex_total)
    if count==0:
        tot_opened_file.write('{0} {1} {2} {3}\n'.format("sim_num","age","sx", "ex"))
        tot_opened_file.write('{0} {1} {2} {3}\n'.format(count,"0",a0_sx,a0_ex))
        tot_opened_file.write('{0} {1} {2} {3}\n'.format(count,"1",a1_sx,a1_ex))
        tot_opened_file.write('{0} {1} {2} {3}\n'.format(count,"5",a5_sx,a5_ex))
        tot_opened_file.write('{0} {1} {2} {3}\n'.format(count,"10",a10_sx,a10_ex))
        tot_opened_file.write('{0} {1} {2} {3}\n'.format(count,"15",a15_sx,a15_ex))
        tot_opened_file.write('{0} {1} {2} {3}\n'.format(count,"20",a20_sx,a20_ex))
        tot_opened_file.write('{0} {1} {2} {3}\n'.format(count,"25",a25_sx,a25_ex))
        tot_opened_file.write('{0} {1} {2} {3}\n'.format(count,"30",a30_sx,a30_ex))
        tot_opened_file.write('{0} {1} {2} {3}\n'.format(count,"35",a35_sx,a35_ex))
        tot_opened_file.write('{0} {1} {2} {3}\n'.format(count,"40",a40_sx,a40_ex))
        tot_opened_file.write('{0} {1} {2} {3}\n'.format(count,"45",a45_sx,a45_ex))
        tot_opened_file.write('{0} {1} {2} {3}\n'.format(count,"50",a50_sx,a50_ex))
        tot_opened_file.write('{0} {1} {2} {3}\n'.format(count,"55",a55_sx,a55_ex))
        tot_opened_file.write('{0} {1} {2} {3}\n'.format(count,"60",a60_sx,a60_ex))
        tot_opened_file.write('{0} {1} {2} {3}\n'.format(count,"65",a65_sx,a65_ex))
        tot_opened_file.write('{0} {1} {2} {3}\n'.format(count,"70",a70_sx,a70_ex))
        tot_opened_file.write('{0} {1} {2} {3}\n'.format(count,"75",a75_sx,a75_ex))
        tot_opened_file.write('{0} {1} {2} {3}\n'.format(count,"80",a80_sx,a80_ex))
```

```
        tot_opened_file.write('{0} {1} {2} {3}\n'.format(count,"85",a85_sx,a85_ex))
        tot_opened_file.write('{0} {1} {2} {3}\n'.format(count,"90",a90_sx,a90_ex))
        tot_opened_file.write('{0} {1} {2} {3}\n'.format(count,"95",a95_sx,a95_ex))
        tot_opened_file.write('{0} {1} {2} {3}\n'.format(count,"100",a100_sx,a100_ex))
        tot_opened_file.write('{0} {1} {2} {3}\n'.format(count,"105",a105_sx,a105_ex))
        tot_opened_file.write('{0} {1} {2} {3}\n'.format(count,"110",a110_sx,a110_ex))

    else:
        tot_opened_file.write('{0} {1} {2} {3}\n'.format(count,"0",a0_sx,a0_ex))
        tot_opened_file.write('{0} {1} {2} {3}\n'.format(count,"1",a1_sx,a1_ex))
        tot_opened_file.write('{0} {1} {2} {3}\n'.format(count,"5",a5_sx,a5_ex))
        tot_opened_file.write('{0} {1} {2} {3}\n'.format(count,"10",a10_sx,a10_ex))
        tot_opened_file.write('{0} {1} {2} {3}\n'.format(count,"15",a15_sx,a15_ex))
        tot_opened_file.write('{0} {1} {2} {3}\n'.format(count,"20",a20_sx,a20_ex))
        tot_opened_file.write('{0} {1} {2} {3}\n'.format(count,"25",a25_sx,a25_ex))
        tot_opened_file.write('{0} {1} {2} {3}\n'.format(count,"30",a30_sx,a30_ex))
        tot_opened_file.write('{0} {1} {2} {3}\n'.format(count,"35",a35_sx,a35_ex))
        tot_opened_file.write('{0} {1} {2} {3}\n'.format(count,"40",a40_sx,a40_ex))
        tot_opened_file.write('{0} {1} {2} {3}\n'.format(count,"45",a45_sx,a45_ex))
        tot_opened_file.write('{0} {1} {2} {3}\n'.format(count,"50",a50_sx,a50_ex))
        tot_opened_file.write('{0} {1} {2} {3}\n'.format(count,"55",a55_sx,a55_ex))
        tot_opened_file.write('{0} {1} {2} {3}\n'.format(count,"60",a60_sx,a60_ex))
        tot_opened_file.write('{0} {1} {2} {3}\n'.format(count,"65",a65_sx,a65_ex))
        tot_opened_file.write('{0} {1} {2} {3}\n'.format(count,"70",a70_sx,a70_ex))
        tot_opened_file.write('{0} {1} {2} {3}\n'.format(count,"75",a75_sx,a75_ex))
        tot_opened_file.write('{0} {1} {2} {3}\n'.format(count,"80",a80_sx,a80_ex))
        tot_opened_file.write('{0} {1} {2} {3}\n'.format(count,"85",a85_sx,a85_ex))
        tot_opened_file.write('{0} {1} {2} {3}\n'.format(count,"90",a90_sx,a90_ex))
        tot_opened_file.write('{0} {1} {2} {3}\n'.format(count,"95",a95_sx,a95_ex))
        tot_opened_file.write('{0} {1} {2} {3}\n'.format(count,"100",a100_sx,a100_ex))
        tot_opened_file.write('{0} {1} {2} {3}\n'.format(count,"105",a105_sx,a105_ex))
        tot_opened_file.write('{0} {1} {2} {3}\n'.format(count,"110",a110_sx,a110_ex))

    print(count)
    count += 1  # This is the same as count = count + 1

tot_opened_file.close()
opened_file.close()
print("simulation completed")
```

e. Stata files estimating life expectancy distributions from simulated life tables (peer female populations as examples).

```
* Input Simulation Results into Stata

* Austria, Female

import delimited "/.../aut_f_ex.txt", delimiter(space) encoding(ISO-
8859-1) clear

gen country="Austria"

keep if age==0 | age==25 | age==65
drop sx

save "/.../aut_f.dta", replace



* Belgium, Female

import delimited "/.../bel_f_ex.txt", delimiter(space) encoding(ISO-
8859-1) clear

gen country="Belgium"

keep if age==0 | age==25 | age==65
drop sx

save "/.../bel_f.dta", replace


* Denmark, Female

import delimited "/.../den_f_ex.txt", delimiter(space) encoding(ISO-
8859-1) clear

gen country="Denmark"

keep if age==0 | age==25 | age==65
drop sx

save "/.../den_f.dta", replace


* Finland, Female

import delimited "/.../fin_f_ex.txt", delimiter(space) encoding(ISO-
8859-1) clear

gen country="Finland"

keep if age==0 | age==25 | age==65
```

```
drop sx

save "/.../fin_f.dta", replace



* England, Female

import delimited "/.../engw_f_ex.txt", delimiter(space) encoding(ISO-
8859-1) clear

gen country="England & Wales"

keep if age==0 | age==25 | age==65
drop sx

save "/.../engw_f.dta", replace


* Spain, Female

import delimited "/.../esp_f_ex.txt", delimiter(space) encoding(ISO-
8859-1) clear

gen country="Spain"

keep if age==0 | age==25 | age==65
drop sx

save "/.../esp_f.dta", replace


* France, Female

import delimited "/.../fra_f_ex.txt", delimiter(space) encoding(ISO-
8859-1) clear

gen country="France"

keep if age==0 | age==25 | age==65
drop sx

save "/.../fra_f.dta", replace



* Israel, Female

import delimited "/.../isr_f_ex.txt", delimiter(space) encoding(ISO-
8859-1) clear

gen country="Israel"
```

```
keep if age==0 | age==25 | age==65
drop sx

save "/.../isr_f.dta", replace


* S Korea, Female

import delimited "/.../kor_f_ex.txt", delimiter(space) encoding(ISO-
8859-1) clear

gen country="Korea"

keep if age==0 | age==25 | age==65
drop sx

save "/.../kor_f.dta", replace


* Northern Ireland, Female

import delimited "/.../nir_f_ex.txt", delimiter(space) encoding(ISO-
8859-1) clear

gen country="Northern Ireland"

keep if age==0 | age==25 | age==65
drop sx

save "/.../nir_f.dta", replace


* Netherlands, Female

import delimited "/.../nld_f_ex.txt", delimiter(space) encoding(ISO-
8859-1) clear

gen country="Netherlands"

keep if age==0 | age==25 | age==65
drop sx

save "/.../nld_f.dta", replace


* Norway, Female

import delimited "/.../nor_f_ex.txt", delimiter(space) encoding(ISO-
8859-1) clear
```

```
gen country="Norway"

keep if age==0 | age==25 | age==65
drop sx

save "/.../nor_f.dta", replace


* Portugal, Female

import delimited "/.../por_f_ex.txt", delimiter(space) encoding(ISO-
8859-1) clear

gen country="Portugal"

keep if age==0 | age==25 | age==65
drop sx

save "/.../por_f.dta", replace


* Scotland, Female

import delimited "/.../sco_f_ex.txt", delimiter(space) encoding(ISO-
8859-1) clear

gen country="Scotland"

keep if age==0 | age==25 | age==65
drop sx

save "/.../sco_f.dta", replace


* Sweden, Female

import delimited "/.../swe_f_ex.txt", delimiter(space) encoding(ISO-
8859-1) clear

gen country="Sweden"

keep if age==0 | age==25 | age==65
drop sx

save "/.../swe_f.dta", replace


* Switzerland, Female

import delimited "/.../swz_f_ex.txt", delimiter(space) encoding(ISO-
8859-1) clear
```

```
gen country="Switzerland"

keep if age==0 | age==25 | age==65
drop sx

save "/.../swz_f.dta", replace


* Taiwan, Female

import delimited "/.../twn_f_ex.txt", delimiter(space) encoding(ISO-8859-1) clear

gen country="Taiwan"

keep if age==0 | age==25 | age==65
drop sx

save "/.../twn_f.dta", replace


* New Zealand, Female

import delimited "/.../nz_f_ex.txt", delimiter(space) encoding(ISO-8859-1) clear

gen country="New Zealand"

keep if age==0 | age==25 | age==65
drop sx

save "/.../nz_f.dta", replace



*******************************************************************
********************** Append all Countries **********************
***** Distributions of Sim LE at birth for 16 peer countries *****
*******************************************************************

use "/.../aut_f.dta", clear

append using "/.../bel_f.dta"

append using "/.../den_f.dta"

append using "/.../fin_f.dta"

append using "/.../engw_f.dta"

append using "/.../esp_f.dta"
```

```
append using "/.../fra_f.dta"

append using "/.../isr_f.dta"

append using "/.../kor_f.dta"

append using "/.../nir_f.dta"

append using "/.../nld_f.dta"

append using "/.../nor_f.dta"

append using "/.../por_f.dta"

append using "/.../sco_f.dta"

append using "/.../swe_f.dta"

append using "/.../swz_f.dta"

append using "/.../twn_f.dta"

append using "/.../nz_f.dta"

save "/.../female_2020ex_sim.dta", replace


tabstat ex if age==0, statistics( p5 p50 p95 ) by(country)
tabstat ex if age==25, statistics( p5 p50 p95 ) by(country)
tabstat ex if age==65, statistics( p5 p50 p95 ) by(country)


bysort country: egen med_ex = median(ex) if age==0
bysort country: egen med_ex25 = median(ex) if age==25
bysort country: egen med_ex65 = median(ex) if age==65
sum med_ex med_ex25 med_ex65
```

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