

Declines 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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DECLINES 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, 2017, and 2020 was estimated for the U.S. population, by sex and raceethnicity, and for 18 high-income 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: In 2010, 2017, and 2020, respectively, life expectancy at birth was 78.66, 78.61, and 76.90 (76.63, 77.08) years in the United States and averaged 80.60, 81.74, and 81.55 (81.40, 81.70) years in peer countries. The decrease in U.S. life expectancy between 2017 and 2020 was largely attributable to the COVID-19 pandemic. The decrease was nine times greater than that experienced by peer countries, widening the life expectancy gap from 3.13 in 2017 to 4.65 years in 2020. U.S. life expectancy decreased disproportionately among people of color, declining by 3.87, 3.12, and 1.18 years, respectively, in Hispanic, non-Hispanic Black, and non-Hispanic White populations. Among Hispanic and non-Hispanic Black populations, declines were 16-20 times the average in peer countries. Progress since 2010 in

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reducing the U.S. Black-White life expectancy gap was erased between 2017 and 2020, and a longstanding Hispanic life expectancy advantage was almost eliminated.

<text><text> Conclusions: The United States experienced a much larger decrease in life expectancy between 2017 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

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In 2020, COVID-19 became the third leading cause of death in the United States¹ 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 That the United States would experience a larger decrease in life expectancy in 2020 than peer nations has been suspected but not established empirically. 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 1980s³, 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 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} People of color and certain age groups have been disproportionately affected.^{9,10,11} Research on how the pandemic affected life expectancy is only just emerging^{12,13} and few studies have examined declines in 2020 life expectancy across racial-ethnic groups or how these declines compare to those of peer nations.

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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 18 high-income countries (in aggregate and by sex). Data were calculated for three years: 2010, 2017 (the most recent year for which peer nation data were widely available), and 2020. Estimates for 2019 would have been preferable to isolate the effect of the COVID-19 pandemic but reliable data were lacking. However, observed changes in life expectancy between 2017 and 2020 were largely attributable to the events of 2020. Peer country data did not include information on race or ethnicity. 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 those who do not identify as Hispanic or Latinx.¹⁴

U.S. life tables for 2010¹⁵ and 2017¹⁶ provided life expectancy estimates for the United States. 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 2017 and 2020 were obtained from the National Center for Health Statistics (NCHS) AH Excess Deaths by Sex, Age, and Race file.¹⁷ 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.¹⁸ 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 2017 and 2020 among U.S. male and female populations in aggregate and by sex and by race-ethnicity.

To derive life expectancy estimates for 2010 and 2017, 5-year abridged life tables for male and female populations of the peer countries were obtained for those years from the Human Mortality Database¹⁹

(direct sources^{20,21} were used for Israel and New Zealand). 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. Peer countries included 18 high-income democracies with adequate HMD data for analysis: Austria, Belgium, Denmark, Finland, France, Germany, Israel, Italy, Netherlands, New Zealand, Norway, Republic of South Korea, Portugal, Spain, Sweden, Switzerland, Taiwan, and the United Kingdom. Australia, Canada, and Japan were omitted because of incomplete mortality data.

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To arrive at life expectancy estimates for 2020, age-specific mortality rate ratios between 2020 m_x and 2017 m_x in the NCHS-Census data were estimated for U.S. populations. For populations in peer countries, average 2020 m_x and 2017 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 2017 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 2017 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 2017 official m_x¹⁶ by the 2020-2017 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.²² Probabilities of death, q_x, for each peer country in 2020 were estimated by multiplying q_x in HMD life tables by the 2020-2017 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. subpopulation using q_x derived from the estimated 2020 m_x , a_x derived from 2017 official life tables¹⁶ 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 2017 a_x values in the HMD 2017 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 (P₅) and 95th (P₉₅) percentiles. The online supplement provides further details on methods.

RESULTS

United States

After a small decrease of 0.05 years between 2010 and 2017, U.S. life expectancy at birth decreased by an estimated 1.71 years (or 2.2%) between 2017 and 2020 (**Table 1**). The proportional decrease in life expectancy at ages 25 and 65 years was even greater (3.1% and 5.3%, respectively). U.S. men experienced a larger decrease in overall life expectancy than women, in both absolute (1.99 years vs. 1.32 years) and relative terms (2.6% vs. 1.6%).

Between 2017 and 2020, U.S. life expectancy decreased disproportionately among people of color (**Table 2**). In the Black population, it decreased by 3.12 years (4.2%), 2.6 times the decrease in the White population (1.18 years, 1.5%). The decrease was even larger among Hispanic individuals (3.87 years, 4.7%), 3.3 times the decrease among Whites, and the ratio was greater among men (3.5) than women (3.0).

The disproportionate decrease in life expectancy in the U.S. Black population during 2017-2020 reversed years of progress in reducing the Black-White mortality gap (**Figure 1**). Although the gap in life expectancy at birth between Black and White populations decreased from 4.07 years in 2010 to 3.64 years in 2017, the gap increased to 5.58 years in 2020. Historically, the U.S. Hispanic population has had

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a higher life expectancy than the White population.^{23,24} Although that advantage widened between 2010 and 2017 (from 2.61 years to 3.30 years, respectively), it decreased to 0.61 years in 2020 (**Table 2**) and was entirely reversed among Hispanic men (-0.22 years).

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United States versus Peer Countries

In both 2010 and 2017, the average life expectancy at birth in 18 high-income countries (80.60 and 81.74 years, respectively) exceeded that of the United States (78.66 and 78.61 years, respectively). These peer countries also experienced much smaller declines in life expectancy between 2017 and 2020 (**Tables 1 and 3**). The overall decrease in life expectancy in the United States (1.71 years) was 9.0 times greater than the average of these peer countries (0.19 years) (**Figure 2**). The gap in life expectancy between the United States and the peer country average grew from 1.94 years in 2010, to 3.13 years in 2017 and 4.65 years in 2020. By 2020, life expectancy at birth was 5.20 and 4.08 years shorter for U.S. males and females, respectively, than the peer country average for their sex (**Tables 1 and 3**).

These disparities were even starker for people of color (Figure 3). Among U.S. Black men and women, the decrease in life expectancy at birth was 15.5 times and 25.5 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 at birth an estimated 20.6 times and 28.5 times higher among men and women, respectively, compared to their counterparts in peer countries. Between 2010 and 2020, gaps in the life expectancy of U.S. Black and Hispanic women and that of women in peer countries grew by 2.99 years and 3.16 years, respectively. Among men, the corresponding figures are 4.50 years and 5.33 years, respectively.

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DISCUSSION

Long before COVID-19 appeared, the United States was at a distinct disadvantage relative to other highincome nations in terms of health and survival.^{3,25,26,27,28} 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.²⁹ 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 concern³⁰ but is now eclipsed by the large 2020 declines reported here. Even countries with much lower per capita incomes now outperform the United States.^{31,32,33,44} According to data for 36 OECD member countries, the gap in life expectancy between the United States and the OECD increased from 0.9 to 2.2 years between 2010 and 2017,^{35,36}

This study shows that the life expectancy gap widened further after 2017. U.S. life expectancy fell dramatically between 2017 and 2020, a drop 9 times the average loss experienced by 18 high-income peer nations and the largest decrease since 1943 during World War II.³⁷ 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 more than 20 percent.⁸

The large decreases in life expectancy reported here, and the excess deaths reported in several studies of 2020 death counts^{6,7,8}, 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).^{5,38} Many of these are products of national, state, and local policy decisions and (in)actions that influenced viral transmission and management of the pandemic.³⁹ 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.^{40,41,42,43}

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The extraordinary consequences of COVID-19 in the United States reflect not only the country's mishandling of the pandemic^{39,44,45,46} but also deeply rooted factors that put the country at a health disadvantage long ago.⁴⁷ 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 Black and Hispanic individuals compared to White people, due to heightened viral exposure, a higher prevalence of comorbid conditions (e.g., diabetes), and diminished access to healthcare.^{48,49}

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 people were approximately 2-3 times greater than losses among White people, and

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far larger than those experienced in peer countries. Decreases among U.S. Black and Hispanic men were approximately 16-21 times greater than that of men in other high-income countries and decreases among U.S. Black and Hispanic women were 26-29 times greater. Progress made between 2010 and 2017 in reducing the Black-White gap in life expectancy in the United States was erased between 2017 and 2020. Life expectancy among Black men fell to 68.10 years, a level not seen since 1999.⁵⁰ 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 are the systems of power in the United States that structure opportunity and assign value in ways that unfairly disadvantage Black, Brown and Indigenous people, while unfairly advantaging White people. ^{51,5253,54,55,56,57} Many of the same factors placed people of color at greater risk from COVID-19. ^{58,59,60,61} 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 pandemic. ^{62,63} Diminished access to COVID-19 vaccines and vaccine hesitancy, rooted in a community's mistrust of systems that have mistreated them, could exacerbate these disparities. These affect not only Black and Hispanic populations but other marginalized groups. 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 did not allow 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 HMDB-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 25 26 Three large high-income democracies—Australia, Canada, and Japan—were excluded because of incomplete data. Fourth, this study compared 2020 life expectancy with 2017 values; the pandemic's effect would be better isolated by comparisons with 2019 life expectancy, but data were lacking for this calculation. Fifth, race-ethnicity data for the U.S. population and for 2020 deaths were incomplete,⁶⁴ likely underestimating the extent and size of racial inequalities. Reports suggest that COVID-19 and all-cause mortality in 2020 were alarmingly high in American Indian and Alaskan Native populations.⁶⁵ Finally, this study uses the average for peer countries; values for individual countries could vary.

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This study aligns closely with prior research. In a recent 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.¹³ 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 below expected values.

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.⁶⁶ It remains unclear whether some of these long-term complications will affect how quickly U.S. life expectancy will rebound in the coming

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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.⁶⁷ 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, no other relationships or activities that could appear to have influenced the submitted work.

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TEXT BOX

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. 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 offer predictions of how long any group of people will live. Although life expectancy is likely 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.²

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Table 1. U.S. Life Expectancy at Birth, Age 25 Years, and Age 65 Years: 2010, 2017, and 2020								
	•			Change in	life expectancy			
				(y, P ₅ , P ₉₅)				
	2010	2017	2020 (y, P ₅ , P ₉₅)	2017 vs 2010	2020 vs 2017			
Life expectancy at	Life expectancy at birth							
Total	78.66	78.61	76.90 (76.73, 77.08)	-0.05	-1.71 (-1.88; -1.53)			
Females	81.04	81.10	79.78 (79.61, 79.95)	0.06	-1.32 (-1.49; -1.15)			
Males	76.20	76.10	74.11 (73.93, 74.29)	-0.10	-1.99 (-2.17; -1.81)			
		Life	expectancy at age 25					
Total	54.71	54.66	52.94 (52.76, 53.11)	-0.05	-1.72 (-1.90, -1.55)			
Females	56.87	56.92	55.56 (55.39, 55.73)	0.05	-1.36 (-1.53, -1.19)			
Males	52.44	52.36	50.36 (50.19, 50.54)	-0.08	-2.00 (-2.17, -1.82)			
Life expectancy at age 65								
Total	19.13	19.40	18.38 (18.20 – 18.56)	0.27	-1.02 (-1.20, -0.84)			
Females	20.33	20.60	19.67 (19.50 – 19.85)	0.27	-0.93 (-1.10, -0.75)			
Males	17.70	18.04	16.96 (16.78 – 17.14)	0.34	-1.08 (-1.26, -0.90)			
Authors' analysis of data from the National Center for Health Statistics-U.S. Census Bureau and Human Mortality								

Database.

P₅, P₉₅: 5th and 95th percentiles of 50,000 simulated life expectancies using 10% random uncertainty around the 2020 qx estimates.

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	Life expectancy (y) Change in life expectancy (P					
	2010 2017 2020 (<i>P</i> ₅ , <i>P</i> ₉₅)			2017 vs. 2010 2020 vs. 2017		
LIFE EXPECTANCY AT BIRT	Ή					
Total						
Hispanic	81.40	81.82	77.95 (77.78, 78.13)	0.42	-3.87 (-4.04, -3.	
Non-Hispanic Black	74.72	74.88	71.76 (71.57, 71.95)	0.16	-3.12 (-3.31, -2.	
Non-Hispanic White	78.79	78.52	77.34 (77.17, 77.51)	-0.27	-1.18 (-1.35, -1.	
Female					•·	
Hispanic	83.82	84.31	81.46 (81.30, 81.63)	0.49	-2.85 (-3.01, -2.	
Non-Hispanic Black	77.72	78.08	75.53 (75.35, 75.71)	0.36	-2.55 (-2.73, -2.	
Non-Hispanic White	81.11	80.98	80.03 (79.86, 80.20)	-0.13	-0.95 (-1.12, -0.	
Male						
Hispanic	78.72	79.10	74.56 (74.39, 74.74)	0.38	-4.54 (-4.71, -4.	
Non-Hispanic Black	71.43	71.51	68.10 (67.90, 68.29)	0.08	-3.41 (-3.61, -3.	
Non-Hispanic White	76.41	76.09	74.78 (74.64, 74.96)		-1.31 (-1.45, -1.	
LIFE EXPECTANCY AT AGE	25 YEARS				, ,	
Total						
Hispanic	57.30	57.73	53.87 (53.70, 54.04)	0.43	-3.86 (-4.03, -3.	
Non-Hispanic Black	51.38	51.59	48.56 (48.37, 48.75)	0.21	-3.03 (-3.22, -2.	
Non-Hispanic White	54.75	54.46	53.22 (53.05, 53.39)	-0.29	-1.24 (-1.41, -1.	
Female	1 1					
Hispanic	59.51	60.05	57.12 (56.96, 57.28)	0.54	-2.93 (-3.09, -2.	
Non-Hispanic Black	54.00	54.39	51.83 (51.66, 52.02)	0.39	-2.56 (-2.73, -2.	
Non-Hispanic White	56.87	56.69	55.69 (55.52, 55.85)	-0.18	-1.00 (-1.17, -0.	
Male						
Hispanic	54.78	55.16	50.65 (50.48, 50.84)	0.38	-4.51 (-4.68, -4.	
Non-Hispanic Black	48.39	48.52	45.23 (45.04, 45.43)	0.13	-3.29 (-3.48, -3.	
Non-Hispanic White	52.54	52.22	50.84 (50.67, 51.02)	-0.32	-1.38 (-1.55, -1.	
LIFE EXPECTANCY AT AGE	65 YEARS		· · · · · ·		••	
Total						
Hispanic	20.80	21.44	18.85 (18.68, 19.04)	0.64	-2.58 (-2.76, -2	
Non-Hispanic Black	17.72	18.09	16.22 (16.03, 16.42)	0.37	-1.87 (-2.06,-1	
Non-Hispanic White	19.12	19.32	18.53 (18.35, 18.71)	0.20	-0.79 (-0.97, -0	
Female						
Hispanic	22.08	22.69	20.53 (20.36, 20.70)	0.61	-2.16 (-2.33, -1.	
Non-Hispanic Black	19.14	19.55	17.80 (17.62, 17.99)	0.41	-1.75 (-1.93, -1.	
Non-Hispanic White	20.30	20.49	19.77 (19.60, 19.95)	0.19	-0.72 (-0.89, -0.	
Male			, -,			
Hispanic	19.06	19.73	16.88 (16.70, 17.07)	0.67	-2.85 (-3.03, -2.	
Non-Hispanic Black	15.82	16.21	14.33 (14.13, 14.53)	0.39	-1.88 (-2.08, -1.	
Non-Hispanic White	17.73	18.01	17.20 (17.02, 17.38)	0.28	-0.81 (-0.99, -0.	
Authors' analysis of data fror						

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			10, 2017, and 2020	Change in life	expectancy (P ₅ , I		
	2010	2017	2020 (P ₅ , P ₉₅)	2017 vs 2010	2020 vs. 201		
Life expectancy a	birth						
Total	80.60	81.74	81.55 (81.40, 81.70)	1.14	-0.19 (-0.34, 0.		
Females	83.06	83.96	83.86 (83.71, 84.01)	0.90	-0.10 (-0.25, 0.		
Males	78.14	79.53	79.31 (79.15, 79.47)	1.39	-0.22 (-0.38, -0.		
Life expectancy a	age 25						
Total	56.26	57.30	57.06 (56.91, 57.22)	1.04	-0.24 (-0.39, -0.		
Females	58.61	59.42	59.27 (59.12, 59.42)	0.81	-0.15 (-0.30, 0.		
Males	53.89	55.17	54.90 (54.74, 55.06)	1.28	-0.27 (-0.43, -0.		
Life expectancy a	age 65				· · ·		
Total	19.54	20.26	20.00 (19.84, 20.16)	0.72	-0.26 (-0.42, -0.		
Females	21.03	21.61	21.45 (21.30, 21.60)	0.58	-0.16 (-0.31, 0.0		
Males	17.87	18.72	18.47 (18.31, 18.64)	0.85	-0.25 (-0.41, -0.		
			or per				

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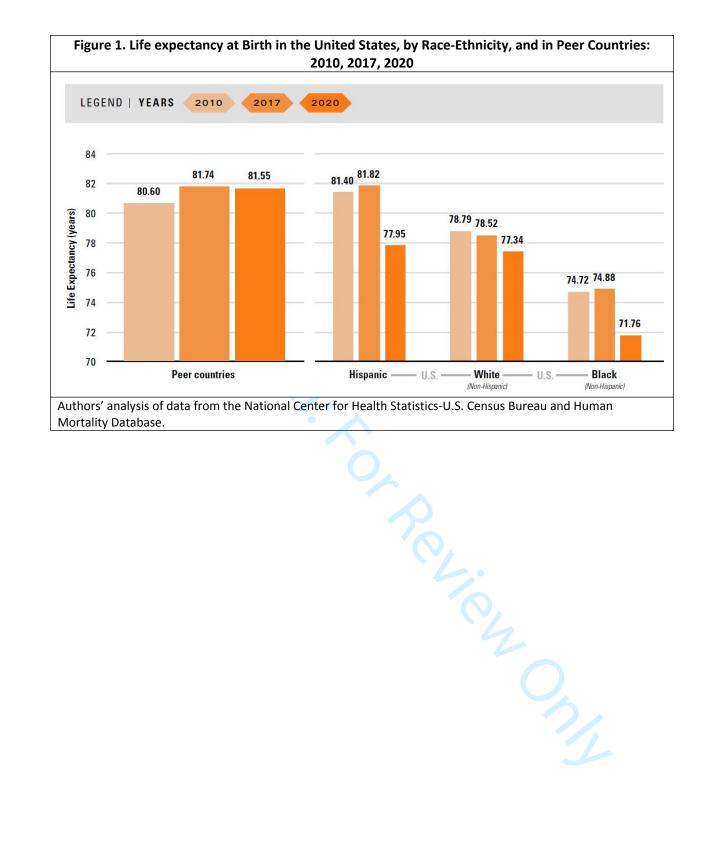
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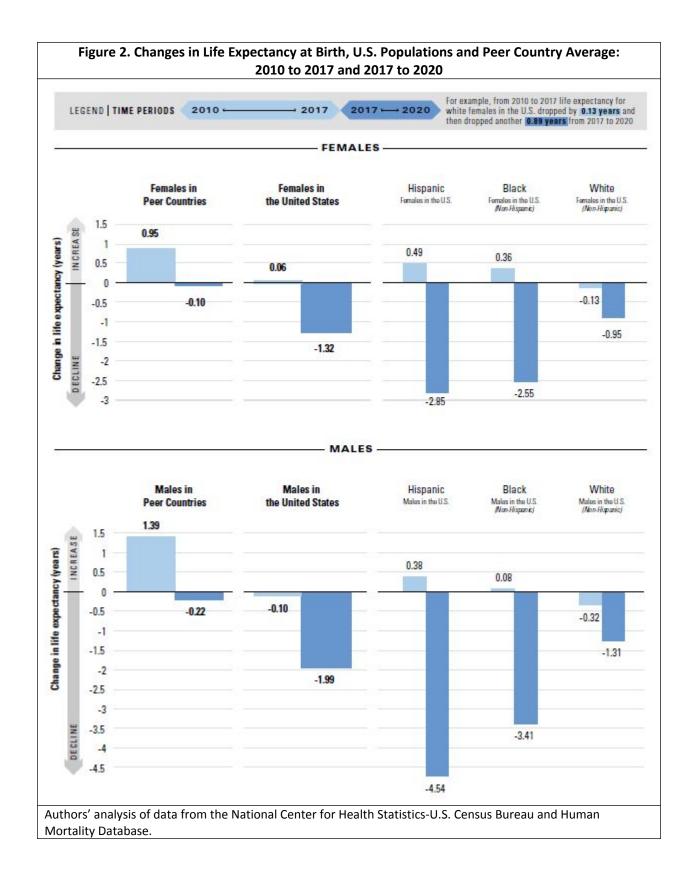
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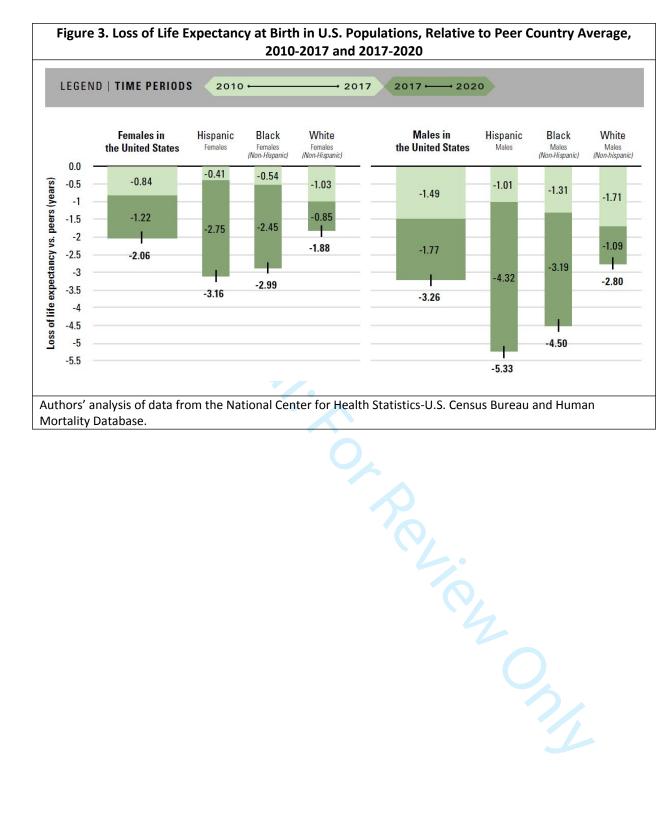
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DECLINES IN U.S. LIFE EXPECTANCY IN THE WAKE OF COVID-19: ONLINE SUPPLEMENT

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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
- ale r ... ; Black Male , c White Male Popula... de Population 11. Non-Hispanic White Male Population
- 12. Hispanic Male Population

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Life expectancies for 12 U.S. populations in 2010 were recorded from *National Vital Statistics Reports* Volume 63, Number 7, "United States Life Tables, 2010"¹ and 2017 life expectancies for these 12 US populations were recorded from *National Vital Statistics Reports* Volume 68, Number 7, "United States Life Tables, 2017."²

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Comparison Group Populations for 18 Peer Countries

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

Criteria for inclusion in the peer country comparison group were: (1) high-income, (2) advanced democracy, and (3) data availability in both the Human Mortality Database (HMDB) 5 x 1 period life tables and 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 2010 and 2017 were obtained from 5-year age x 1-year time period abridged period life tables taken from the Human Mortality Database. (Direct sources^{3,4} were used for Israel and New Zealand 2017 life tables.) In total, 60 separate data sets were downloaded and analyzed.

2. Average 2010 and 2017 Life Expectancies among Peer Populations

Life expectancy for each peer country's total population, female population, and male population were saved separately as well as appended together. The *average life expectancy* at birth (e_0), at age 25 (e_{25}), at 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 collapsed into 2010 and 2017 datasets for total populations among peer countries, female populations among peer countries, and male populations among 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 2017^2 (2) estimates of age-specific death counts among US populations in 2017, 2018, and 2020⁵, and (3) estimates of age-specific population counts in 2017, 2018, and 2020.⁶ The analytic steps are described below.

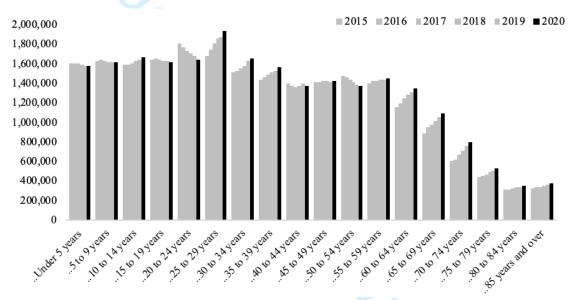
Estimated age-specific death rates in 2017, 2018, 2020 from NCHS-Census data

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 February 17, 2021 release of the National Center for Health Statistics (NCHS), Center for Disease Control and Prevention, file, *AH Excess Deaths by Sex, Age, and Race.*⁵ These NCHS data are composed of weekly death counts for ages 0-14; 15-

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19; ...; 80-84; and 85+ years. We summed the weekly counts for years 2017, 2018, and 2020 separately for each age group, separately for 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.*⁶ 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 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:

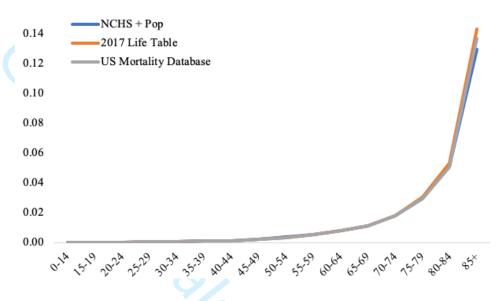


The yearly age-specific death counts were merged with the yearly age-specific population counts, separately by race/ethnicity and sex, to estimate 2017 age-specific mortality rates (m_x), 2018 m_x, and 2020 m_x for the 12 separate U.S. populations.

The 2017 m_x and 2018 m_x estimated in these NCHS-Census data were compared with the m_x derived from the 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.² We also compared the 2018 m_x estimated in the NCHS-Census data with the 2018 m_x derived from official 2017 U.S. life tables.² We also compared the 2018 m_x estimated in the NCHS-Census data with the 2018 m_x derived from official 2017 U.S. life tables.² 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.⁷ 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. 2019² and the 2017 m_x reported by the US Mortality Database, *5X1 Female Period Life Table⁸* (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.

	<u>U</u>	S Female Po	pulation		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. 2019², 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

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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:

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

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

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:

1 2	
3	Difference
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7	0-14
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9	20-24 25-29
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21	80-84
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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

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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,^{2,7} 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 2017 m_x estimates in the NCHS-Census data (below), and multiply these rate ratios by the 2017 m_x derived in the official 2017 US life tables.⁷

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	US Female Population				-			
	Total	NHB	Latina	NHW	Total	NHB	Latino	NHW
0-14	0.88	0.87	0.88	0.88	0.87	0.87	0.88	0.87
15-19	1.07	1.40	1.07	0.94	1.12	1.28	1.26	1.00
20-24	1.11	1.41	1.24	0.98	1.14	1.38	1.33	0.97
25-29	1.11	1.22	1.30	1.02	1.10	1.18	1.32	0.97
30-34	1.18	1.33	1.40	1.07	1.23	1.38	1.48	1.12
35-39	1.17	1.25	1.34	1.11	1.25	1.29	1.51	1.16
40-44	1.21	1.33	1.39	1.14	1.33	1.40	1.63	1.23
45-49	1.11	1.21	1.32	1.06	1.20	1.31	1.55	1.11
50-54	1.11	1.16	1.33	1.07	1.18	1.26	1.44	1.11
55-59	1.08	1.13	1.36	1.04	1.14	1.19	1.53	1.07
60-64	1.13	1.17	1.37	1.09	1.16	1.20	1.48	1.10
65-69	1.12	1.21	1.38	1.08	1.18	1.23	1.56	1.13
70-74	1.10	1.24	1.37	1.05	1.13	1.28	1.50	1.08
75-79	1.10	1.19	1.34	1.07	1.13	1.23	1.42	1.10
80-84	1.11	1.20	1.29	1.09	1.12	1.20	1.33	1.10
85+	1.11	1.19	1.21	1.11	1.11	1.20	1.26	1.09

Thus, the 2020 m_x used to calculate 2020 life tables for US populations are the official 2017 NCHS m_x^7 inflated by the 2020:2017 mortality rate ratios estimated from the NCHS-Census data. 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 2017 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 2017 m_x at these ages).

To calculate 2020 five-year q_x , we use the standard equation of Preston et al.⁹

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

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 2017 US life tables for each US population.

Estimates of 2017 life expectancy at birth from five-year abridged life tables using q_x from this equation approximate the official reported 2017 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.

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	Official	Abridged q _x
Total	78.61	78.59
Female	81.10	81.08
Male	76.10	76.10
Hispanic	81.82	81.85
Non-Hispanic Black	74.88	74.85
Non-Hispanic White	78.52	78.51
Hispanic female	84.31	84.33
Non-Hispanic Black female	78.08	78.04
Non-Hispanic White female	80.98	80.96
Hispanic male	79.10	79.08
Non-Hispanic Black male	71.51	71.50
Non-Hispanic White male	76.09	76.08

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 2017 m_x , we simulated 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 2017 life tables.² 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 2017 life tables in the Human Mortality Database (and CBS-reported 2017 life table for Israel and StatsNZ-reported 2016-2018 life table for New Zealand) and (b) the mortality rate ratio between the country's reported m_x in the 2017 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 2017 m_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 2017 q_x , each country's 2017 a_x , and each country's 2020:2017 RR. Generally, m_x

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ratios are slightly different from q_x ratios at older ages, but the differences are minimal and do not substantively affect e_x estimates. As an illustration of the strong correspondence between countries' m_x ratios and q_x ratios, below is a table showing the differences between the q_x ratios between 2017 and 2014 and the mx ratios between 2017 and 2014 for Switzerland's and Norway's female population. We compare the ratios between 2017 and 2014 because it is the same time difference as between 2020 and 2017. The average differences between the ratios for all 18 peer country's female populations are also included, as well as the differences between the 2017 qx and the estimated 2017 q_x using a) 2014 q_x and b) the 2017:2014 m_x ratio.

	Switzerland			Norway			Average	
Age	2017:2014 m _x	2017:2014 q _x	Ratio	2017:2014 m _x	2017:2014 q _x	Ratio	Ratio	q _x est - q
0	0.890	0.890	1.000	1.014	1.018	1.005	1.000	0.00
1-4	0.917	0.878	0.957	1.500	1.424	0.949	0.999	0.00
5-9	1.250	1.286	1.029	1.800	1.731	0.962	1.001	0.00
10-14	0.889	0.870	0.978	2.750	2.650	0.964	0.980	0.00
15-19	1.083	1.082	0.999	1.000	1.000	1.000	0.995	0.00
20-24	0.765	0.724	0.947	0.750	0.752	1.003	0.997	0.00
25-29	1.000	1.010	1.010	1.368	1.419	1.037	0.998	0.00
30-34	0.759	0.767	1.011	0.829	0.828	0.999	1.000	0.00
35-39	1.158	1.160	1.002	1.071	1.087	1.014	1.002	0.00
40-44	0.841	0.853	1.014	1.015	1.009	0.994	1.001	0.00
45-49	0.990	0.990	1.000	0.906	0.907	1.001	0.999	0.00
50-54	0.903	0.906	1.003	0.830	0.833	1.003	1.001	0.00
55-59	0.935	0.938	1.003	0.892	0.893	1.001	1.001	0.00
60-64	0.919	0.919	1.000	0.920	0.920	1.001	1.000	0.00
65-69	0.972	0.971	0.999	0.959	0.960	1.001	1.000	0.00
70-74	0.982	0.983	1.001	1.092	1.090	0.998	1.000	0.00
75-79	0.982	0.983	1.001	0.974	0.974	1.000	1.001	0.00
80-84	0.991	0.992	1.000	0.952	0.955	1.003	1.002	0.00
85-89	0.983	0.985	1.002	0.999	1.002	1.004	1.000	0.00
90-94	1.005	1.008	1.004	1.003	1.005	1.002	1.013	0.00
95-99	0.997	0.999	1.002	1.019	1.009	0.990	0.983	0.01
100-104	0.999	1.000	1.001	1.025	1.006	0.981	0.973	0.02
105-109	1.001	1.000	1.000	1.024	1.003	0.979	0.970	0.01
110+	1.001	1.000	0.999	1.020	1.000	0.980	0.970	0.00

Sizable differences between the estimated 2017 q_x and the actual 2017 q_x are observed only at ages 95-99, 100-104, and 105-109, which have little effect on life expectancy estimates. Indeed, the average difference between the estimated 2017 life expectancies using the estimated 2017 q_x and the actual 2017 life expectancies is -.0177 years. This exercise shows that combining each country's 2017 q_x with the countries' mortality rate ratios between 2020 and 2017 likely approximates each country's 2020 q_x .

To account for possible error in 2020 m_x reported in the STMF data, possible error in estimated mortality rate ratios between 2020 m_x and 2016/2017/2018 m_x , we simulated 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 average ax in the aggregate 2017 HMDB life tables. We report the 5th percentiles, medians, and 95th percentiles of life expectancies at birth, at age 25, and at age 65 for total peer populations and by sex.

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

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4. Analytic Scripts

estimates

```
****** All US Pop ***********
*** 2020 NCHS Mortality Data, by Week ***
import delimited "/.../NCHS
Data/AH Excess Deaths by Sex Age and Race 3 7.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 == 2017 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 == 2017 gen country = "Belgium" save "/.../HMDB data/women/belgium paper1.dta", replace ****** **** Israel **** * * * * * * * * * * * * * * * * *

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import delimited "/.../HMDB data/women/Israel Women.txt",
         delimiter(space, collapse) varnames(1) encoding(ISO-8859-1)
         clear
         keep if
                    year == 2010
         gen country = "Israel"
         save "/.../HMDB data/women/israel paper1.dta", replace
         * Data from Central Bureau of Statistics, State of Israel 2017
16
         Life Table
         import excel "/.../HMDB data/Israel/Israel 2017.xlsx",
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19
         sheet("female") firstrow clear
20
         append using "/.../HMDB data/women/israel paper1.dta"
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         replace country = "Israel" if country == ""
         * USE Data Editor to change String Variable Coding of Age
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         * *(1 variable, 24 observations pasted into data editor)
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         * save "/.../HMDB data/women/israel paper1.dta", replace
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         save "/.../HMDB data/women/israel paper1.dta", replace
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         **** S Korea ****
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         import delimited "/.../HMDB data/women/Korea Women.txt",
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         delimiter(space, collapse) varnames(1) encoding(ISO-8859-1)
         clear
         keep if year == 2010 | year == 2017
         gen country = "S Korea"
         save "/.../HMDB data/women/korea paper1.dta", replace
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          * * * *
                Denmark ****
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import delimited "/.../HMDB data/women/Denmark Women.txt",
delimiter(space, collapse) varnames(1) encoding(ISO-8859-1)
clear
keep if
        year == 2010 | year == 2017
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
       year == 2010 | year == 2017
keep if
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
          year == 2010 | year == 2017
keep if
gen country = "France"
save "/.../HMDB data/women/france paper1.dta", replace
*****
**** Italy ****
*****
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             import delimited "/.../HMDB data/women/Italy Women.txt",
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delimiter(space, collapse) varnames(1) encoding(ISO-8859-1)
clear
keep if
         year == 2010 | year == 2017
gen country = "Italy"
save "/.../HMDB data/women/italy 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 == 2017
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
gen country = "New Zealand"
save "/.../HMDB data/women/nz paper1.dta", replace
* Data from Stats NZ, 2016-2018 Life Table
import excel "/.../HMDB data/New Zealand/NZ 2017.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
         year == 2010 | year == 2017
keep if
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 == 2017
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
```

```
year == 2010 | year == 2017
keep if
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 == 2017
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
         year == 2010 | year == 2017
keep if
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
        year == 2010 | year == 2017
keep if
```

```
gen country = "Switzerland"
        save "/.../HMDB data/women/swiss paper1.dta", replace
        *****
        **** United Kingdom ****
        ******
16
        import delimited "/.../HMDB data/women/England Wales Women.txt",
        delimiter(space, collapse) varnames(1) encoding(ISO-8859-1)
18
19
        clear
20
        keep if
                 year == 2010 | year == 2017
        gen country = "England & Wales"
        save "/.../HMDB data/women/england wales paper1.dta", replace
28
        import delimited "/.../HMDB data/women/Scotland Women.txt",
        delimiter(space, collapse) varnames(1) encoding(ISO-8859-1)
30
        clear
        keep if
                 year == 2010 | year == 2017
        gen country = "Scotland"
        save "/.../HMDB data/women/scotland paper1.dta", replace
38
40
        import delimited "/.../HMDB data/women/Northern/
        Ireland Women.txt", delimiter(space, collapse) varnames(1)
        encoding(ISO-8859-1) clear
        keep if
                 year == 2010 | year == 2017
        gen country = "Northern Ireland"
        save "/.../HMDB data/women/northern ireland paper1.dta", replace
50
52
53
        54
        **** Germany ****
        56
58
```

```
import delimited "/.../HMDB data/women/Germany Women.txt",
delimiter(space, collapse) varnames(1) encoding(ISO-8859-1)
clear
         year == 2010 | year == 2017
keep if
gen country = "Germany"
save "/.../HMDB data/women/germany paper1.dta", replace
************
* Append Peer Countries *
***************
* 18 Country Comparison Group
use "/.../HMDB data/women/germany paper1.dta", clear
append using "/.../HMDB data/women/swiss paper1.dta"
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/italy 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 "/.../peer18 paper1sep.dta", replace
* Variation in LE at Birth
```

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```
2
3
         set scheme s1manual
4
5
         kdensity ex if nage==1 & year==2010
6
         kdensity ex if nage==1 & year==2017
7
8
         sum ex if nage==1 & year==2010, detail
9
10
         sum ex if nage==1 & year==2017, detail
11
12
13
         * Individual LT Kept for Merging with STMF RR
14
15
         qen id = .
16
         replace id = 1 if country == "Austria"
17
         replace id = 2 if country == "Belgium"
18
19
         replace id = 3 if country == "Denmark"
20
         replace id = 4 if country == "Finland"
21
         replace id = 5 if country == "France"
22
         replace id = 6 if country == "Germany"
23
         replace id = 7 if country == "Israel"
24
         replace id = 8 if country == "Italy"
25
         replace id = 9 if country == "Netherlands"
26
27
         replace id = 10 if country == "New Zealand"
28
         replace id = 11 if country == "Norway"
29
         replace id = 12 if country == "Portugal"
30
         replace id = 13 if country == "Spain"
31
         replace id = 14 if country == "Sweden"
32
         replace id = 15 if country == "Switzerland"
33
         replace id = 16 if country == "Taiwan"
34
         replace id = 17 if country == "England & Wales"
35
36
         replace id = 18 if country == "Scotland"
37
         replace id = 19 if country == "Northern Ireland"
38
         replace id = 20 if country == "S Korea"
39
40
         sort id year
41
42
43
         save "/.../peer18 paper1 sepLT.dta", replace
44
45
         merge id using "/.../paper3 rr female.dta"
46
47
         sort id year nage
48
49
         drop 1x dx Lx Tx countrycode sex merge
50
51
52
         bysort nage: gen mx20 = mx*rr 0 if year == 2017
53
         bysort nage: replace mx20 = mx*rr 15 if nage >= 5 & nage < 15 &
54
         year == 2017
55
56
57
58
59
```

```
2
3
         bysort nage: replace mx20 = mx*rr 65 if nage >= 15 & nage < 17 &
4
         year == 2017
5
         bysort nage: replace mx20 = mx*rr 75 if nage >= 17 & nage < 19 &
6
         year == 2017
7
         bysort nage: replace mx20 = mx*rr 85 if nage >= 19 & year ==
8
9
         2017
10
11
         bysort nage: gen qx20 = qx*rr 0 if year == 2017
12
         bysort nage: replace qx20 = qx*rr 15 if nage >= 5 & nage < 15 &
13
         year == 2017
14
         bysort nage: replace qx20 = qx*rr 65 if nage >= 15 & nage < 17 &
15
         year == 2017
16
         bysort nage: replace qx20 = qx*rr 75 if nage >= 17 & nage < 19 &
17
         year == 2017
18
19
         bysort nage: replace qx20 = qx*rr 85 if nage >= 19 & year ==
20
         2017
21
22
         save "/.../peer18 paper1 sepLT.dta", replace
23
24
         sort id year nage
25
26
27
         export excel using "/.../peer sepLT female.xls",
                                      , ce
28
         firstrow(variables) nolabel replace
29
30
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                                https://mc.manuscriptcentral.com/bmj
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```

```
c. Stata files estimating 2017 and 2020 death rates in peer country data.
*** Import HMDB Raw .txt Data ***
import delimited "/.../peer STMF/pooled stmf 2 14 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")
keep if year >= 2016
* 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 average of (2016,2017,2018)
* Compute Average of 2016/2017/2018
                                             4.02
tempfile a b c
sort countrycode
save `a'
keep if year >=2016 & year <= 2018
collapse (mean) r017=r0 r1517=r15 r6517=r65 r7517=r75 r8517=r85,
by (countrycode)
sort countrycode
save `b'
use `a', clear
sort countrycode
keep if year == 2020
```

```
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53
54
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56
57
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59
```

sort countrycode

save `c'

```
merge using `b'
drop _merge
* Data are now Country-specific ASDRs in 2020 and average ASDRs in
2016/2017/2018
* Estimate RR
* Take Average for peers
* Combine with the 2017 Peer Life Table to Estimate ASDRs for 2020
Life Table
gen rr 0 = r0/r017
gen rr_{15} = r15/r1517
gen rr 65 = r65/r6517
gen rr 75 = r75/r7517
gen rr 85 = r85/r8517
* 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
collapse (mean) rr 0=rr 0 rr 15=rr 15 rr 65=rr 65 rr 75=rr 75
rr85=rr 85
```

1	
2	
3	d. Python files simulating life tables. Norway female population as example.
4	, , , , , , , , , , , , , , , , , , , ,
5 6	
7	Peer 2020 Life Tables from 2017 qx*2020:2017RR and 2017 ax
8	
9	@author:
10	Watthol
11	
12	
13 14	#import packages
15	import random
16	
17	# importing in the qx and error and ax
18	nor_f = r"//nor_f.txt"
19	# change as needed for input files
20	
21 22	# read in the file
22	textFile = open(nor_f,'r')
24	text = textFile.readlines()
25	# split into different age categories
26	a0=text[1]
27	a1=text[2]
28 29	
30	a5=text[3]
31	a10=text[4]
32	a15=text[5]
33	a20=text[6]
34	
35	a25=text[7]
36 37	a30=text[8]
38	a35=text[9]
39	a40=text[10]
40	a45=text[11]
41	a50=text[12]
42	a55=text[13]
43 44	a60=text[14]
45	a65=text[15]
46	a70=text[16]
47	a75=text[17]
48	a80=text[18]
49	a85=text[19]
50	
51 52	a90=text[20]
53	a95=text[21]
54	a100=text[22]
55	a105=text[23]
56	a110=text[24]
57 59	
58 59	

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2	
3 4	
5	a0_sp = a0.split(",")
6	a1_sp = a1.split(",")
7	a5_sp = a5.split(",")
8	a10_sp = a10.split(",")
9	
10	a15_sp = a15.split(",")
11	a20_sp = a20.split(",")
12	a25_sp = a25.split(",")
13	a30_sp = a30.split(",")
14	a35_sp = a35.split(",")
15	a40_sp = a40.split(",")
16 17	a45_sp = a45.split(",")
17	a50_sp = a50.split(",")
19	
20	a55_sp = a55.split(",")
21	a60_sp = a60.split(",")
22	a65_sp = a65.split(",")
23	a70_sp = a70.split(",")
24	a75_sp = a75.split(",")
25	a80_sp = a80.split(",")
26	a85_sp = a85.split(",")
27 28	a90_sp = a90.split(",")
28 29	a95_sp = a95.split(",")
30	
31	a100_sp = a100.split(",")
32	a105_sp = a105.split(",")
33	a110_sp = a110.split(",")
34	
35	# qx
36	a0_qx = float(a0_sp[1])
37	a1_qx = float(a1_sp[1])
38 39	a5_qx = float(a5_sp[1])
39 40	a10_qx = float(a10_sp[1])
41	a15 $qx = float(a15 sp[1])$
42	
43	a20_qx = float(a20_sp[1])
44	a25_qx = float(a25_sp[1])
45	a30_qx = float(a30_sp[1])
46	a35_qx = float(a35_sp[1])
47	a40_qx = float(a40_sp[1])
48	a45_qx = float(a45_sp[1])
49 50	$a50_qx = float(a50_sp[1])$
50 51	$a55_qx = float(a55_sp[1])$
52	$a55_qx = float(a55_sp[1])$ $a60_qx = float(a60_sp[1])$
53	
54	$a65_qx = float(a65_sp[1])$
55	a70_qx = float(a70_sp[1])
56	a75_qx = float(a75_sp[1])
57	
58	

60

1	
2	
2	
4	a80_qx = float(a80_sp[1])
5	a85_qx = float(a85_sp[1])
6	a90 qx = float(a90 sp[1])
7	$a95_qx = float(a95_sp[1])$
8	$a_{100_qx} = float(a_{100_sp[1]})$
9	
10	a105_qx = float(a105_sp[1])
11	a110_qx = float(a110_sp[1])
12	
13	# qx - lower bound
14	$a0_qxl = float(a0_sp[2])$
15	
16	a1_qxl = float(a1_sp[2])
17	a5_qxl = float(a5_sp[2])
18	a10_qxl = float(a10_sp[2])
19	a15_qxl = float(a15_sp[2])
20	a20_qxl = float(a20_sp[2])
21	a25_qxl = float(a25_sp[2])
22	
23	a30_qxl = float(a30_sp[2])
24	a35_qxl = float(a35_sp[2])
25	a40_qxl = float(a40_sp[2])
26 27	a45_qxl = float(a45_sp[2])
27 28	a50_qxl = float(a50_sp[2])
28 29	a55_qxl = float(a55_sp[2])
30	
31	a60_qxl = float(a60_sp[2])
32	a65_qxl = float(a65_sp[2])
33	a70_qxl = float(a70_sp[2])
34	a75_qxl = float(a75_sp[2])
35	a80 qxl = float(a80 sp[2])
36	a85_qxl = float(a85_sp[2])
37	
38	a90_qxl = float(a90_sp[2])
39	a95_qxl = float(a95_sp[2])
40	a100_qxl = float(a100_sp[2])
41	a105_qxl = float(a105_sp[2])
42	a110 qxl = float(a110 sp[2])
43	# qx - Upper bound
44	
45	a0_qxu = float(a0_sp[3])
46	a1_qxu = float(a1_sp[3])
47	a5_qxu = float(a5_sp[3])
48 40	a10_qxu = float(a10_sp[3])
49 50	a15 qxu = float(a15 sp[3])
50 51	$a20_qxu = float(a20_sp[3])$
52	
52	a25_qxu = float(a25_sp[3])
55	a30_qxu = float(a30_sp[3])
55	a35_qxu = float(a35_sp[3])
56	a40_qxu = float(a40_sp[3])
57	
58	
50	-

3	a45_qxu = float(a45_sp[3])
4 5	a50_qxu = float(a50_sp[3])
6	a55_qxu = float(a55_sp[3])
7	a60_qxu = float(a60_sp[3])
8	a65 qxu = float(a65 sp[3])
9	$a70_qxu = float(a70_sp[3])$
10	$a75_qxu = float(a75_sp[3])$
11	$ay_2(xu = float(ay_2)p[3])$ $a80_qxu = float(a80_sp[3])$
12 13	
13	a85_qxu = float(a85_sp[3])
15	$a90_qxu = float(a90_sp[3])$
16	a95_qxu = float(a95_sp[3])
17	a100_qxu = float(a100_sp[3])
18	a105_qxu = float(a105_sp[3])
19	a110_qxu = float(a110_sp[3])
20	
21 22	# ax
23	a0_ax = float(a0_sp[4])
24	a1_ax = float(a1_sp[4])
25	a5_ax = float(a5_sp[4])
26	$a_{10} a_{10} $
27	a15_ax = float(a15_sp[4])
28 29	
29 30	$a20_ax = float(a20_sp[4])$
31	a25_ax = float(a25_sp[4])
32	a30_ax = float(a30_sp[4])
33	a35_ax = float(a35_sp[4])
34	a40_ax = float(a40_sp[4])
35	a45_ax = float(a45_sp[4])
36 37	a50_ax = float(a50_sp[4])
37	a55_ax = float(a55_sp[4])
39	a60_ax = float(a60_sp[4])
40	a65_ax = float(a65_sp[4])
41	a70_ax = float(a70_sp[4])
42	a75_ax = float(a75_sp[4])
43 44	a80 ax = float(a80 sp[4])
44 45	a85_ax = float(a85_sp[4])
46	a90 ax = float(a90 sp[4])
47	a95_ax = float(a95_sp[4])
48	a100_ax = float(a100_sp[4])
49	$a100_ax = float(a100_sp[4])$ $a105_ax = float(a105_sp[4])$
50	
51 52	a110_ax = float(a110_sp[4])
52 53	
54	
55	
56	count = 0
F7	

a45 qxu = float(a45 sp[3])

1	
2	
3	while count < 50000: #5000: #50000
4	
5	
6	a0_rand_qx = random.uniform(a0_qxl,a0_qxu)
7	a1_rand_qx = random.uniform(a1_qxl,a1_qxu)
8	a5_rand_qx = random.uniform(a5_qxl,a5_qxu)
9	a10 rand qx = random.uniform(a10 qxl,a10 qxu)
10	a15 rand $qx = random.uniform(a15 qxl,a15 qxu)$
11	
12	a20_rand_qx = random.uniform(a20_qxl,a20_qxu)
13	a25_rand_qx = random.uniform(a25_qxl,a25_qxu)
14	a30_rand_qx = random.uniform(a30_qxl,a30_qxu)
15	a35 rand qx = random.uniform(a35 qxl,a35 qxu)
16 17	a40 rand gx = random.uniform(a40 gxl,a40 gxu)
18 19	a45_rand_qx = random.uniform(a45_qxl,a45_qxu)
20	a50_rand_qx = random.uniform(a50_qxl,a50_qxu)
20	a55_rand_qx = random.uniform(a55_qxl,a55_qxu)
22	a60_rand_qx = random.uniform(a60_qxl,a60_qxu)
23	a65 rand gx = random.uniform(a65 gxl,a65 gxu)
24	a70 rand $qx = random.uniform(a70 qxl,a70 qxu)$
25	
26	a75_rand_qx = random.uniform(a75_qxl,a75_qxu)
27	a80_rand_qx = random.uniform(a80_qxl,a80_qxu)
28	a85_rand_qx = random.uniform(a85_qxl,a85_qxu)
29	a90 rand qx = random.uniform(a90 qxl,a90 qxu)
30	a95_rand_qx = random.uniform(a95_qxl,a95_qxu)
31	a100 rand qx = random.uniform(a100 qxl,a100 qxu)
32	
33	a105_rand_qx = random.uniform(a105_qxl,a105_qxu)
34	a110_rand_qx = 1
35	
36	# without randomization
37	# a0_rand_qx = a0_qx
38	
39	# a1_rand_qx = a1_qx
40	# a5_rand_qx = a5_qx
41	# a10_rand_qx = a10_qx 🥒
42	# a15_rand_qx = a15_qx
43	# a20_rand_qx = a20_qx
44 45	# $a25_rand_qx = a25_qx$
45 46	
46 47	# a30_rand_qx = a30_qx
47 48	# a35_rand_qx = a35_qx
48 49	# a40_rand_qx = a40_qx
50	# a45_rand_qx = a45_qx
51	# a50 rand $qx = a50 qx$
52	# a55_rand qx = a55_qx
53	
54	# a60_rand_qx = a60_qx
55	# a65_rand_qx = a65_qx
56	# a70_rand_qx = a70_qx
57	
58	

59

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1

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 qxa105 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

ι

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

1	
1	
2	
3	# calculate survivors
4	a95_lx=(a90_lx-a90_dx)
5	
6	a95_sx = a95_lx/radix
7	
8	# calculate the number of deaths age95
9	a95 dx = a95 rand qx*a95 lx
10	
11	# calculate survivors
12	a100_lx=(a95_lx-a95_dx)
13	a100 sx = a100 $lx/radix$
14	
15	# calculate the number of deaths age100
16	
17	a100_dx = a100_rand_qx*a100_lx
18	# calculate survivors
19	a105 lx=(a100 lx-a100 dx)
20	a105_sx = a105_lx/radix
21	
22	
23	# calculate the number of deaths age105
24	a105 dx = a105 rand qx*a105 lx
25	# calculate survivors
26	
27	a110_lx=(a105_lx-a105_dx)
28	a110_sx = a110_lx/radix
29	
30	# calculate the number of deaths age110
31	a110 dx = a110 rand qx*a110 lx
32	# No Survivors - top-coded
33	
34	
35	#calculate Lx
36	a0_Lx = (a1_lx*1)+(a0_dx*a0_ax)
37	a1 Lx = $(a5 lx^{*}4)$ + $(a1 dx^{*}a1 ax)$
38	a5 Lx = (a10 lx*5)+(a5 dx*a5 ax)
39	
40	a10_Lx = (a15_lx*5)+(a10_dx*a10_ax)
41	a15_Lx = (a20_lx*5)+(a15_dx*a15_ax)
42	a20 Lx = (a25 lx*5)+(a20 dx*a20 ax)
43	a25 Lx = (a30 lx*5)+(a25 dx*a25 ax)
44	
45	a30_Lx = (a35_lx*5)+(a30_dx*a30_ax)
46	a35_Lx = (a40_lx*5)+(a35_dx*a35_ax)
47	a40_Lx = (a45_lx*5)+(a40_dx*a40_ax)
48	a45 Lx = (a50 lx*5)+(a45 dx*a45 ax)
49	$a50 Lx = (a55 Lx^{+}5) + (a50 dx^{+}a50 ax)$
50	
51	$a55_Lx = (a60_lx*5)+(a55_dx*a55_ax)$
52	a60_Lx = (a65_lx*5)+(a60_dx*a60_ax)
53	a65_Lx = (a70_lx*5)+(a65_dx*a65_ax)
54	a70 Lx = (a75 lx*5)+(a70 dx*a70 ax)
55	a75 Lx = (a80 lx*5)+(a75 dx*a75 ax)
56 57	$a_{J} = a_{a_{J}} = a_{a_{J}$

- 00 1			
	(a85_lx*5)+(a80_dx*a80_ax)		
	(a90_lx*5)+(a85_dx*a85_ax) (a95_lx*5)+(a90_dx*a90_ax)		
_	$(a95_1x^5)+(a90_dx^a90_ax)$ $(a100_lx^5)+(a95_dx^a95_ax)$		
	= (a105 x*5) + (a100 dx*a100 a)		
_	$= (a105_1x 5)+(a105_0x a100_a)$ = (a110_1x*5)+(a105_0x*a105_a)		
	= (a110_dx*a110_ax)		
####			
# calcula	te Tx		
a0 Tx =			
_	Lx+a5_Lx+a10_Lx+a15_Lx+a20_L	x+a25_Lx+a30_Lx+a35_Lx+a40_L	x+a45_Lx+a50_Lx
a55_Lx+a6	0_Lx+a65_Lx+a70_Lx+a75_Lx+a80	0_Lx+a85_Lx+a90_Lx+a95_Lx+a1	.00_Lx+a105_Lx+a
10_Lx			
a1_Tx =			
a1_Lx+a5_	Lx+a10_Lx+a15_Lx+a20_Lx+a25_I	Lx+a30_Lx+a35_Lx+a40_Lx+a45_	_Lx+a50_Lx+a55_L
+a60_Lx+a	65_Lx+a70_Lx+a75_Lx+a80_Lx+a8	85_Lx+a90_Lx+a95_Lx+a100_Lx+	a105_Lx+a110_Lx
a5_Tx =			
	_Lx+a15_Lx+a20_Lx+a25_Lx+a30_		
_	a70_Lx+a75_Lx+a80_Lx+a85_Lx+a	390_Lx+a95_Lx+a100_Lx+a105_L	.x+a110_Lx
a10_Tx =			
_	5_Lx+a20_Lx+a25_Lx+a30_Lx+a3		
Lx+a70_Lx- a15_Tx =	+a75_Lx+a80_Lx+a85_Lx+a90_Lx+ :	+a95_Lx+a100_Lx+a105_Lx+a110	Lx
a15_Lx+a2	0_Lx+a25_Lx+a30_Lx+a35_Lx+a4(0_Lx+a45_Lx+a50_Lx+a55_Lx+a6	0_Lx+a65_Lx+a70
_	+a80_Lx+a85_Lx+a90_Lx+a95_Lx+	+a100_Lx+a105_Lx+a110_Lx	
a20_Tx =			
—	5_Lx+a30_Lx+a35_Lx+a40_Lx+a4		5_Lx+a70_Lx+a75
Lx+a80_Lx- a25_Tx =	+a85_Lx+a90_Lx+a95_Lx+a100_L	x+a105_Lx+a110_Lx	
a25_Lx+a3	0_Lx+a35_Lx+a40_Lx+a45_Lx+a50	0_Lx+a55_Lx+a60_Lx+a65_Lx+a7	0_Lx+a75_Lx+a80
Lx+a85_Lx·	+a90_Lx+a95_Lx+a100_Lx+a105_	Lx+a110_Lx	
a30_Tx =			
_	5_Lx+a40_Lx+a45_Lx+a50_Lx+a5!		5_Lx+a80_Lx+a85
Lx+a90_Lx- a35 Tx =	+a95_Lx+a100_Lx+a105_Lx+a110_ :	_Lx	
_	0_Lx+a45_Lx+a50_Lx+a55_Lx+a60	0_Lx+a65_Lx+a70_Lx+a75_Lx+a8	0_Lx+a85_Lx+a90
_	 +a100_Lx+a105_Lx+a110_Lx	_ _	
a40_Lx+a4	5_Lx+a50_Lx+a55_Lx+a60_Lx+a6!	5_Lx+a70_Lx+a75_Lx+a80_Lx+a8	5_Lx+a90_Lx+a95
Lx+a100_L a45 Tx =	k+a105_Lx+a110_Lx		
_	0_Lx+a55_Lx+a60_Lx+a65_Lx+a7(0_Lx+a75_Lx+a80_Lx+a85_Lx+a9	0_Lx+a95_Lx+a10
—	 Lx+a110_Lx	_	
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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 gx =
(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 \text{ gx} = (a85 \text{ dx} + a90 \text{ dx} + a95 \text{ dx})/a85 \text{ 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
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a80 ex = a80 Tx/a80 lxa85 ex = a85 Tx/a85 lxa90 ex = a90 Tx/a90 lx a95 ex = a95 Tx/a95 lxa100 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 else: tot_file_name = r"/.../nor_f_ex.txt"

nor f filenm = r"/.../nor f gx.txt" opened file = open(nor f filenm, 'a')

if count==0:

a65 ex = a65 Tx/a65 lxa70 ex = a70 Tx/a70 lxa75 ex = a75 Tx/a75 lx

opened file.write('{0} {1} {2} {3}\n'.format("sim num","qx1564","qx6584","qx8599"))

opened file.write('{0} {1} {2} {3}\n'.format(count,a1564 qx,a6584 qx,a8599 qx))

save data

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))

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2 3	
4	tot_opened_file.write('{0} {1} {2} {3}\n'.format(count,"70",a70_sx,a70_ex))
5	tot_opened_file.write('{0} {1} {2} {3}\n'.format(count,"75",a75_sx,a75_ex))
6	tot_opened_file.write('{0} {1} {2} {3}\n'.format(count,"80",a80_sx,a80_ex))
7	tot_opened_file.write('{0} {1} {2} {3}\n'.format(count,"85",a85_sx,a85_ex))
8	tot_opened_file.write('{0} {1} {2} {3}\n'.format(count,"90",a90_sx,a90_ex))
9	tot opened file.write('{0} {1} {2} {3}\n'.format(count,"95",a95 sx,a95 ex))
10 11	tot_opened_file.write('{0} {1} {2} {3}\n'.format(count,"100",a100_sx,a100_ex))
12	tot_opened_file.write('{0} {1} {2} {3}\n'.format(count,"105",a105_sx,a105_ex))
13	tot_opened_file.write('{0} {1} {2} {3}\n'.format(count,"110",a110_sx,a110_ex))
14	
15	else:
16	tot opened file.write('{0} {1} {2} {3}\n'.format(count,"0",a0 sx,a0 ex))
17 18	tot opened file.write(' $\{0\}$ {1} {2} {3}\n'.format(count, '0', a0_s, a0_ex))
18	
20	tot_opened_file.write('{0} {1} {2} {3}\n'.format(count,"5",a5_sx,a5_ex))
21	tot_opened_file.write('{0} {1} {2} {3}\n'.format(count,"10",a10_sx,a10_ex))
22	tot_opened_file.write('{0} {1} {2} {3}\n'.format(count,"15",a15_sx,a15_ex))
23	tot_opened_file.write('{0} {1} {2} {3}\n'.format(count,"20",a20_sx,a20_ex))
24	tot_opened_file.write('{0} {1} {2} {3}\n'.format(count,"25",a25_sx,a25_ex))
25 26	tot_opened_file.write('{0} {1} {2} {3}\n'.format(count,"30",a30_sx,a30_ex))
27	tot_opened_file.write('{0} {1} {2} {3}\n'.format(count,"35",a35_sx,a35_ex))
28	tot_opened_file.write('{0} {1} {2} {3}\n'.format(count,"40",a40_sx,a40_ex))
29	tot_opened_file.write('{0} {1} {2} {3}\n'.format(count,"45",a45_sx,a45_ex))
30	tot_opened_file.write('{0} {1} {2} {3}\n'.format(count,"50",a50_sx,a50_ex))
31	tot_opened_file.write('{0} {1} {2} {3}\n'.format(count,"55",a55_sx,a55_ex))
32 33	tot_opened_file.write('{0} {1} {2} {3}\n'.format(count,"60",a60_sx,a60_ex))
34	tot_opened_file.write('{0} {1} {2} {3}\n'.format(count,"65",a65_sx,a65_ex))
35	tot_opened_file.write('{0} {1} {2} {3}\n'.format(count,"70",a70_sx,a70_ex))
36	tot_opened_file.write('{0} {1} {2} {3}\n'.format(count,"75",a75_sx,a75_ex))
37	tot_opened_file.write('{0} {1} {2} {3}\n'.format(count,"80",a80_sx,a80_ex))
38	tot opened file.write('{0} {1} {2} {3}\n'.format(count,"85",a85 sx,a85 ex))
39 40	tot opened file.write(' $\{0\}$ {1} {2} {3}\n'.format(count, '00', a90' sx, a90' ex))
41	tot_opened_file.write('{0} {1} {2} {3}\n'.format(count,'95",a95_sx,a95_ex))
42	$tot_opened_file.write('{0} {1} {2} {3} n'.format(count, '55, a55_sx, a55_ex))$
43	
44	tot_opened_file.write('{0} {1} {2} {3}\n'.format(count,"105",a105_sx,a105_ex))
45	tot_opened_file.write('{0} {1} {2} {3}\n'.format(count,"110",a110_sx,a110_ex))
46 47	
48	print(count)
49	count += 1 # This is the same as count = count + 1
50	
51	tot_opened_file.close()
52	opened_file.close()
53 54	print("simulation completed")
54 55	
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```
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
10
11
12
          * England, Female
13
14
          import delimited "/.../engw f ex.txt", delimiter(space) encoding(ISO-
15
          8859-1) clear
16
17
          gen country="England & Wales"
18
19
          keep if age==0 | age==25 | age==65
20
          drop sx
21
22
23
          save "/.../engw f.dta", replace
24
25
          * Spain, Female
26
27
28
          import delimited "/.../esp f ex.txt", delimiter(space) encoding(ISO-
29
          8859-1) clear
30
31
          gen country="Spain"
32
33
          keep if age==0 | age==25 | age==65
34
          drop sx
35
36
          save "/.../esp f.dta", replace
37
38
39
          * France, Female
40
41
          import delimited "/.../fra f ex.txt", delimiter(space) encoding(ISO-
42
          8859-1) clear
43
44
          gen country="France"
45
46
          keep if age==0 | age==25 | age==65
47
48
          drop sx
49
          save "/.../fra f.dta", replace
50
51
52
          * Germany, Female
53
54
55
          import delimited "/.../ger f ex.txt", delimiter(space) encoding(ISO-
56
          8859-1) clear
57
58
59
```

```
2
3
4
          gen country="Germany"
5
6
          keep if age==0 | age==25 | age==65
7
          drop sx
8
9
          save "/.../ger f.dta", replace
10
11
12
          * Israel, Female
13
14
          import delimited "/.../isr f ex.txt", delimiter(space) encoding(ISO-
15
          8859-1) clear
16
17
          gen country="Israel"
18
19
          keep if age==0 | age==25 | age==65
20
          drop sx
21
22
23
          save "/.../isr f.dta", replace
24
25
          * Italy, Female
26
27
28
          import delimited "/.../ita f ex.txt", delimiter(space) encoding(ISO-
29
          8859-1) clear
30
31
          gen country="Italy"
32
33
          keep if age==0 | age==25 | age==65
34
          drop sx
35
36
          save "/.../ita f.dta", replace
37
38
39
          * S Korea, Female
40
41
          import delimited "/.../kor f ex.txt", delimiter(space) encoding(ISO-
42
          8859-1) clear
43
44
          gen country="Korea"
45
46
          keep if age==0 | age==25 | age==65
47
48
          drop sx
49
          save "/.../kor f.dta", replace
50
51
52
53
          * Northern Ireland, Female
54
55
          import delimited "/.../nir f ex.txt", delimiter(space) encoding(ISO-
56
          8859-1) clear
57
58
```

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```
2
3
4
          gen country="Northern Ireland"
5
6
          keep if age==0 | age==25 | age==65
7
          drop sx
8
9
          save "/.../nir f.dta", replace
10
11
12
          * Netherlands, Female
13
14
          import delimited "/.../nld f ex.txt", delimiter(space) encoding(ISO-
15
          8859-1) clear
16
17
          gen country="Netherlands"
18
19
          keep if age==0 | age==25 | age==65
20
          drop sx
21
22
23
          save "/.../nld f.dta", replace
24
25
          * Norway, Female
26
27
28
          import delimited "/.../nor f ex.txt", delimiter(space) encoding(ISO-
29
          8859-1) clear
30
31
          gen country="Norway"
32
33
          keep if age==0 | age==25 | age==65
34
          drop sx
35
36
          save "/.../nor f.dta", replace
37
38
39
          * Portugal, Female
40
41
          import delimited "/.../por f ex.txt", delimiter(space) encoding(ISO-
42
          8859-1) clear
43
44
          gen country="Portugal"
45
46
          keep if age==0 | age==25 | age==65
47
          drop sx
48
49
          save "/.../por f.dta", replace
50
51
52
          * Scotland, Female
53
54
55
          import delimited "/.../sco f ex.txt", delimiter(space) encoding(ISO-
56
          8859-1) clear
57
58
59
```

```
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 ***** Distributions of Sim LE at birth for 20 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 "/.../ger f.dta" append using "/.../isr f.dta" append using "/.../ita_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"

```
3
4
          append using "/.../nz f.dta"
5
6
          save "/.../female 2020ex sim.dta", replace
7
8
9
          tabstat ex if age==0, statistics( p5 p50 p95 ) by(country)
10
          tabstat ex if age==25, statistics( p5 p50 p95 ) by(country)
11
          tabstat ex if age==65, statistics( p5 p50 p95 ) by(country)
                      i.

* for a met.

i.d_ex25 = med.

i.d_ex55
12
13
14
          bysort country: egen med ex = median(ex) if age==0
15
          bysort country: egen med ex25 = median(ex) if age==25
16
          bysort country: egen med ex65 = median(ex) if age==65
17
          sum med ex med ex25 med ex65
18
19
20
21
22
23
24
25
26
27
28
29
30
31
32
33
34
35
36
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