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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

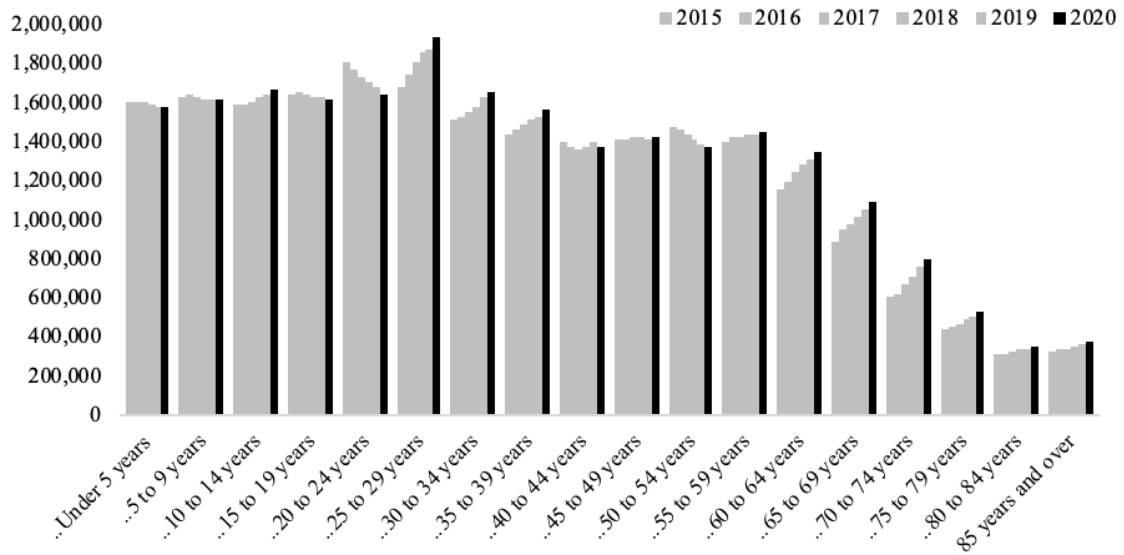
To calculate 2020 life tables for each U.S. population, we estimated 2020 age-specific death rates (m_x) for each U.S. population using (1) official life tables for 2018[9] (2) estimates of age-specific death counts among US populations in 2017, 2018 and 2020[8,9,13] and (3) estimates of age-specific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

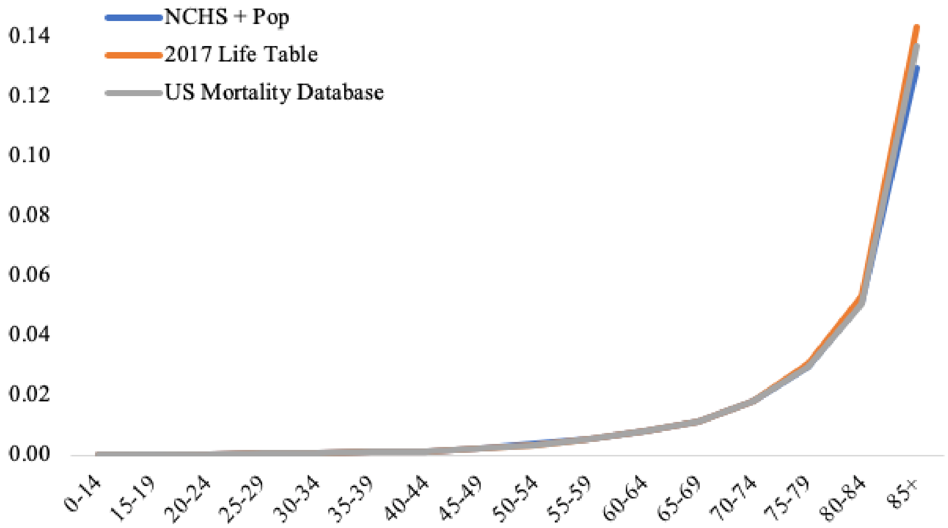
Mid-year population estimates were obtained from the U.S. Census Bureau file, *2019 Population Estimates by Age, Sex, Race, and Hispanic Origin*.[13] Tables *NC-EST2019-ASR5H* and *NC-EST2019-ASR6H* provide estimated annual counts of mid-year populations for ages 0-4; 5-9; …; 80-84; 85+ years for 2015-2019. 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+a105_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+a110_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
```

5. Comparing diverse populations

The United States is racially and ethnically diverse, with massive health disparities in historically marginalized groups. Such diversity may not exist in other countries. Comparisons between the life expectancy of the U.S. Black and Latinx populations to the average outcome of peer countries produces some asymmetry, because their outcomes are not being compared to the corresponding marginalized racial/ethnic populations within those countries. A complex cultural analysis across peer countries to determine comparable ethnic groups is beyond the scope of this paper. To our knowledge no metric has yet been widely accepted for international comparisons of ethnic diversity. The OECD Disparity Index[16] is an attempt at making such comparisons. We note that countries with a higher Diversity Index experienced a smaller decrease in life expectancy than did the United States (see Table below). We also note that our results, stratified by race-ethnicity, show that *even white Americans* experienced a larger decrease in life expectancy between 2018 and 2020 than did peer countries, including those whose populations are overwhelmingly white.

Table. OECD Diversity Index Based on Country of Birth, 2015

Low		**Moderately low**		**Moderately high**		**High**	
Poland	0.1	Portugal	1.3	Latvia	2.3	Ireland	3.1
Slovakia	0.2	Italy	1.8	United Kingdom	2.6	Sweden	3.2
Mexico	0.3	Slovenia	1.9	Norway	2.7	Austria	3.5
Chile	0.7	Netherlands	2.1	United States	2.8	Canada	4.5
Czech Republic	0.7	Denmark	2.1	Estonia	2.8	Switzerland	5.3
Hungary	0.8	France	2.2	Germany	2.8	Australia	5.5
Greece	1.2	Spain	2.2	Belgium	2.9	Israel	6.5
Finland	1.2						

From: OECD (2020), *All Hands In? Making Diversity Work for All*, OECD Publishing, Paris, 2020. https://doi.org/10.1787/efb14583-en.

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