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1. Data Sources

a. US male and female life expectancy, 1980-2018

Life expectancies for U.S. male and female populations in 1980, 1995, 2010, and 2018 were recorded from official life tables obtained from the National Center for Health Statistics (NCHS).

b. 18 Peer Countries' male and female life expectancy, 1980-2018

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

Criteria for inclusion in the peer country comparison group were: (1) high-income, (2) advanced democracy, and (3) data availability for 1980, 1995, 2010, and 2018 in the Human Mortality Database (HMD) 5 x 1 period life tables as well as data availability in the HMD-Short Term Mortality Fluctuations (STMF) reports of weekly deaths in 2020. (Direct sources were used for Germany, Israel, and New Zealand 2018 life tables, which were not available in the HMD.)

Period life tables (5-year age X 1-year period) for each peer country’s female population and male population for years 1980, 1995, 2010, and 2018 were saved separately from the Human Mortality Database (HMD). The average life expectancy at birth (e₀), the average age-specific probability of death (qₓ), and the average age-specific person-years lived by the deceased (aₓ) were also calculated for each year. From the average qₓ and average aₓ, we estimated peer composite life tables for 1980, 1995, 2010, and 2018.

c. 2018, 2019, and 2020 Death Counts in US Populations

Counts of death in the United States were obtained from the September 29, 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 15 age groups 0-14; 15-19; …; 80-84; and 85+ for years 2015-2021. We summed the weekly counts for years 2018, 2019, and 2020 separately for each age group for the U.S. male and female populations:

\[d_{x,t} = \sum_{i=1}^{52} d_{x,t_i} \text{ for } x = 0 - 14, 15 - 19, 20 - 24, ..., 75 - 79, 80 - 84, 85 +\]

d. 2018, 2019, and 2020 Population Counts in US Populations

Mid-year population estimates were obtained from the U.S. Census Bureau file, *2019 Population Estimates by Age, Sex, Race, and Hispanic Origin*. 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 *AH Excess Deaths by Sex, Age, and Race* files. 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. male population, in which the gray bars represent the 2015-2019 Census population estimates and the black bars indicate 2020 estimates:

Death counts in 2018, 2019, and 2020 by sex and by age in each country were obtained from the September 29, 2021 release of the Human Mortality Database - Short-term Mortality Fluctuations original input data in standardized format files.

The death counts for each country's male and female populations were recorded for the following age groups:

- **Austria:** 0-4, 5-9, …, 85-89, 90+
- **Belgium:** 0-4, 5-9, …, 85-89, 90+
- **Denmark:** 0-4, 5-9, …, 95-99, 100+
- **England & Wales:** 0-1, 1-14, 15-44, 45-64, 65-74, 75-84, 85+
- **Finland:** 0-4, 5-9, …, 85-89, 90+
- **France:** 0-4, 5-9, …, 90-94, 95+
- **Germany:** 0-29, 30-34, …, 90-94, 95+
- **Israel:** 0-19, 20-29, …, 70-79, 80+
- **Italy:** 0-4, 5-9, …, 85-89, 90+
- **Northern Ireland:** 0-4, 5-9, …, 85-89, 90+
- **Norway:** 0-4, 5-9, …, 95-99, 100+
- **Portugal:** 0-4, 5-9, …, 80-84, 85+
- **Scotland:** 0-4, 5-9, …, 85-89, 90+
- **Spain:** 0-4, 5-9, …, 85-89, 90+
- **Sweden:** 0-4, 5-9, …, 85-89, 90+
Switzerland: 0-4, 5-9, ..., 85-89, 90+
Taiwan: 0-4, 5-9, ..., 95-99, 100+

Death counts in the male and female populations of Canada, the Netherlands, and New Zealand, are made available at five collapsed age groups (i.e., 0-14, 15-64, 64-74, 75-84, 85+) that are the same as the age groups for the year-specific mortality rates published by the HMD-STMF. Therefore, we do not combine original death counts with population estimates for the Netherlands, New Zealand, and Canada, but instead simply use the mortality rates provided by the HMD-STMF for the five age groups 0-14, 15-64, 64-74, 75-84, 85+

f. 2018, 2019, and 2020 Population Counts in Peer Country Populations

Population counts in 2018, 2019, and 2020 by sex and by age in each country were obtained from each country's central statistical agency. The data sources are listed below.

Austria: Statistik Austria
Belgium: Statbel
Canada: Statistics Canada
Denmark: Statistics Denmark
Finland: Tilastokeskus
France: INSEE
Germany: Destatis
Israel: CBS
Italy: Istat
Netherlands: CBS
New Zealand: NZStat
Norway: Statistisk sentralbyrå
Portugal: Pordata
Spain: INE
Sweden: SCB
Switzerland: Schwizerische Eidgenossenschaft Confédération suisse
Taiwan: Monthly Bulletin of Interior Statistics
United Kingdom: Office for National Statistics

We aggregated population counts for each country's male and female population by age in order to match the reporting of each country's death counts by age in the HMDB-STMF data on page 4 above.
2. 2019 and 2020 Life Expectancy Estimates

a. US Populations

Age-specific death rates \( (m_x) \) for US male and female populations in 2017, 2018, 2019, and 2020 were calculated by merging estimates of age-specific counts of death (NCHS 2021) for ages 0-14, 15-19, ..., 80-84, 85+ with estimates of age-specific population counts (Census 2020) for ages 0-14, 15-19, ..., 80-84, 85+:

\[
m_{x_{2017}} = \frac{d_{x_{2017}}}{L_{x_{2017}}}
\]

\[
m_{x_{2018}} = \frac{d_{x_{2018}}}{L_{x_{2018}}}
\]

\[
m_{x_{2019}} = \frac{d_{x_{2019}}}{L_{x_{2019}}}
\]

\[
m_{x_{2020}} = \frac{d_{x_{2020}}}{L_{x_{2020}}}
\]

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 (Arias et al. 2019) and 2018 (Arias & Xu 2020) U.S. life tables to validate the accuracy of the data. We expect older-age \( m_x \) estimates in the NCHS-Census data to be lower than the older-age \( m_x \) in the official life tables. This is because the death counts in the NCHS-Census data are derived from the vital statistics data only whereas older-age \( m_x \) in the official life tables are estimated by "blending" vital statistics data with age-specific death rates in Medicare files (Anderson 1999; Arias 2010). Below, for example, are the 2018 male \( m_x \) for ages 60-64, ..., 80-84, 85+ from (1) the 2018 official life tables (derived from the vital statistics data combined with the Medicare data), (2) the 2018 official life tables using only the vital statistics data (obtained on 8/11/2021 via correspondence with Dr. Elizabeth Arias of NCHS), and (3) the NCHS-Census linked data described above:

| 2018 mx, US Male Population | Arias & Xu 2020 | NVSS Only | NCHS-Census |
|-----------------------------|-----------------|-----------|-------------|
| 65-69                       | 0.019           | 0.019     | 0.019       |
| 70-74                       | 0.027           | 0.027     | 0.027       |
| 75-79                       | 0.043           | 0.042     | 0.042       |
| 80-84                       | 0.071           | 0.068     | 0.068       |
| 85+                         | 0.167           | 0.145     | 0.144       |

The \( m_x \) estimates for the NVSS only data and the NCHS-Census data are nearly identical, demonstrating that the methods we use to calculate \( m_x \) using the NCHS weekly death counts and the Census Bureau's population estimates accurately estimate the \( m_x \) derived from the official
NVSS data. However, we see that the official Life Table estimates of $m_x$ are higher because the final estimates in the official Life Table use Medicare data to adjust older aged $m_x$.

Reported below are 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, separately by U.S. female and male populations, as well as the RRs between the estimated 2018 $m_x$ using the NCHS-Census linked data and the 2018 $m_x$ derived from Arias & Xu (2020). Also shown are the ratio of the 2018 and 2017 ratios and the absolute differences between the 2018 and 2017 ratios.

| Age | 2017 | 2018 | Ratio | Difference | 2017 | 2018 | Ratio | Difference |
|-----|------|------|-------|------------|------|------|-------|------------|
| 0   | 0.90 | 0.89 | 1.00  | -0.01      | 0.90 | 0.89 | 1.00  | -0.01      |
| 15  | 1.01 | 1.00 | 1.00  | 0.00       | 1.01 | 1.01 | 1.00  | 0.00       |
| 20  | 1.01 | 1.01 | 1.00  | 0.00       | 1.01 | 1.01 | 1.00  | 0.00       |
| 25  | 1.00 | 1.01 | 1.00  | 0.00       | 1.01 | 1.01 | 1.00  | 0.00       |
| 30  | 1.00 | 1.00 | 1.00  | 0.00       | 1.00 | 1.00 | 1.00  | 0.00       |
| 35  | 1.00 | 1.00 | 1.00  | 0.00       | 1.00 | 1.00 | 1.00  | 0.00       |
| 40  | 1.00 | 1.00 | 1.00  | 0.00       | 1.01 | 1.01 | 1.00  | 0.00       |
| 45  | 1.01 | 1.00 | 1.00  | 0.00       | 1.01 | 1.01 | 1.00  | 0.00       |
| 50  | 1.00 | 1.00 | 1.00  | 0.00       | 1.01 | 1.01 | 1.00  | 0.00       |
| 55  | 1.00 | 1.00 | 1.00  | 0.00       | 1.00 | 1.00 | 1.00  | 0.00       |
| 60  | 1.00 | 1.00 | 1.00  | 0.00       | 1.00 | 1.00 | 1.00  | 0.00       |
| 65  | 0.99 | 0.99 | 1.00  | 0.00       | 1.00 | 1.00 | 1.00  | 0.00       |
| 70  | 0.98 | 0.98 | 1.00  | 0.00       | 0.99 | 0.99 | 1.00  | 0.00       |
| 75  | 0.97 | 0.97 | 1.00  | 0.00       | 0.97 | 0.97 | 1.00  | 0.00       |
| 80  | 0.96 | 0.95 | 1.00  | 0.00       | 0.96 | 0.96 | 1.00  | 0.00       |
| 85  | 0.90 | 0.90 | 1.00  | 0.00       | 0.87 | 0.86 | 0.99  | -0.01      |

Although the estimated $m_x$ from the NCHS-Census linked data are quite close to the reported $m_x$ in Arias et al. 2019 and Arias and Xu 2020, the NCHS-Census $m_x$ 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). Also, as expected, the $m_x$ estimates are smaller for all older-age groups (65-69, ..., 80-84) because these estimates are derived only from vital statistics data while the official estimates use Medicare records to adjust $m_x$ upwards at older ages (Anderson 1999; Arias 2010).

Because concerns about bias in $m_x$ estimates are evident in both the 2017 and 2018 NCHS-Census linked data, we assume the 2019 and 2020 estimates are biased as well. Further, we assume that the degree of bias remains unchanged across 2017, 2018, 2019, and 2020 by age and sex. That is, we assume the degree of bias is consistent across the years, such that rate ratios in the estimated 2017, 2018, 2019, 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 supported in the table above, which shows the absolute differences between the rate ratios to be minimal (i.e., less than .005 at nearly all ages). The size of bias in $m_x$ estimates in the NCHS-Census data are consistent between 2017 and 2018. At all ages, 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 and we do not use the 2019 $m_x$ estimated in the NCHS-Census linked data to calculate 2019 U.S. life tables.

**2019 Life Expectancy for U.S. Populations**

We estimate the rate ratios (RRs) between the 2019 $m_x$ estimates in the NCHS-Census data and the 2018 $m_x$ estimates in the NCHS-Census data:

$$RR_{2019,\text{NCHS-Census}} = \frac{m_{x,2019,\text{NCHS-Census}}}{m_{x,2018,\text{NCHS-Census}}}$$

To estimate $m_{x,2019}$ that are used to generate 2019 U.S. life tables, we multiply the age-specific $RR_{2019,\text{NCHS-Census}}$ with the corresponding age-specific 2018 $m_x$ reported in the official 2018 US life tables from Arias and Xu (2020)\(^4\) for ages 0, 1-4, 5-9, ..., 95-99, 100+:

$$m_{x,2019} = m_{x,2018,\text{Official}} \times RR_{2019,\text{NCHS-Census}}$$

To generate 2019 life tables, we use the estimated $m_{x,2019}$ and the 2018 $a_x$ reported in the official 2018 life table\(^4\) to estimate $q_{x,2019}$ as:

$$q_{x,2019} = \frac{(m_{x,2019} \times n)}{(1 + [(1 - a_{x,2019}) \times m_{x,2019}])}$$

**Method Validation: Estimated 2019 U.S. Life expectancy vs. Reported 2019 Life Expectancy in Arias et al. 2021**

Official life tables for U.S. populations in 2019 have not yet been published by the National Center for Health statistics (NCHS), but Arias et al. (2021) and Kochanek et al. (2021) provide estimates of 2019 life expectancy to compare with the NCHS's provisional 2020 life tables reported by Arias et al. (2021). Full 2019 life tables are not provided, however, and 2019 life expectancy estimates are made available to one decimal place. Below, we compare 2019 life expectancy estimates reported in Arias et al. (2021) and Kochanek et al. (2021) with estimates derived from our method described above.

| Estimates of 2019 U.S. Life Expectancy at Birth | Predicted | NCHS |
|-----------------------------------------------|-----------|------|
| US Total                                      | 78.87     | 78.8 |
| US Female                                     | 81.41     | 81.4 |
| US Male                                       | 76.34     | 76.3 |
2020 Life Expectancy for U.S. Populations from Simulated 2020 Life Tables

We estimate the rate ratios (RRs) between the 2020 $m_x$ estimates in the NCHS-Census data and the 2018 $m_x$ estimates in the NCHS-Census data:

$$RR_{2020,NCHS-Census} = \frac{m_{x_{2020,NCHS-Census}}}{m_{x_{2018,NCHS-Census}}}$$

To estimate $m_{x_{2020}}$ that are then used to generate 2020 U.S. life tables, we multiply the age-specific $RR_{2020,NCHS-Census}$ with the corresponding age-specific 2018 $m_x$ reported in the official 2018 US life tables$^4$ for ages 0, 1-4, 5-9, ..., 95-99, 100+:

$$m_{x_{2020}} = m_{2018,Official} \times RR_{2020,NCHS-Census}$$

To estimate $q_{x_{2020}}$ for the 2020 U.S. life tables, we use the estimated $m_{x_{2020}}$ and the 2018 $a_x$ reported in the official U.S. life tables for 2018$^4$:

$$q_{x_{2020}} = \frac{(m_{x_{2020}} \times n)}{\left[1 + \left( (n - a_{x_{2018}}) \times m_{x_{2020}} \right) \right]}$$

where $n$ is the width of the age interval.

To account for possible error in 2020 provisional death counts, possible error in 2020 population estimates, and possible error in estimated mortality rate ratios between 2020 $m_x$ and 2018 $m_x$ in the NCHS-Census data, 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. We report the 5th percentiles, medians, and 95th percentiles of 2020 life expectancies at birth for the US male and female populations.
b. Peer Country Populations

2019 Life Expectancy Reported in Human Mortality Database 2019 Life Tables

2019 life expectancy for the total, male, and female populations of Austria, Denmark, Finland, Netherlands, Norway, Portugal, Sweden, and Taiwan are reported from the Human Mortality Database 5yr Age X 1yr period life tables. For example, below is the 2019 total life expectancy at birth reported for these countries from the HMDB 2019 life tables:

- Austria: 81.91
- Denmark: 81.43
- Finland: 81.91
- Netherlands: 82.05
- Norway: 82.96
- Portugal: 81.71
- Sweden: 83.06
- Taiwan: 80.58

2019 Life Expectancy from Estimated 2019 Life Tables

To estimate 2019 life tables for each peer country's male and female population, we first estimate age-specific death rates (m_x) for each country's male and female population in years 2018 and 2019. To do so, we merge estimates of age-specific death counts in the 9/29/2021 HMDB-STMF original input data in standardized format files with the age-specific counts of population provided by each country's central statistical agency:

\[ m_{x,2018} = \frac{d_{x,2018,STMF}}{L_{x,2018}} \]
\[ m_{x,2019} = \frac{d_{x,2019,STMF}}{L_{x,2019}} \]

Next, we estimate the 2019:2018 age-specific mortality rate ratios (RRs) for each country's total, male, and female populations using the estimated 2019 m_x and the estimated 2018 m_x:

\[ RR_{2019,STMF} = \frac{m_{x,2019}}{m_{x,2018}} \]

Third, to estimate \( m_{x,2019} \) used to generate 2019 life tables, we multiply the age-specific RR_{2019,STMF} with the corresponding age-specific 2018 m_x reported in the HMDB 2018 life table:

\[ m_{x,2019} = m_{2018,HMDB} * RR_{2019} \]

To generate 2019 life tables, we use the estimated \( m_{x,2019} \) and the 2018 a_x reported in the HMDB 2018 life table to estimate \( q_{x,2019} \) as:
\[ q_{x2019} = \left( m_{x2019} \ast n \right) / \left( 1 + \left[ (n - a_{x2018}) \ast m_{x2019} \right] \right) \]

where \( n \) is the width of the age interval. We use \( q_{x2019} \) and \( a_{x2018} \) to generate 2019 life tables for each country's total, male, and female populations.

HMDB Life Tables for Germany, Israel, and New Zealand are not available for 2018. For these countries, 2018 life tables were obtained from each country's central statistical agency: Germany, Israel, New Zealand.

**Method Validation: Estimated 2019 Life expectancy vs. HMDB Reported 2019 Life Expectancy**

| 2019 Life Expectancy at Birth | HMDB | Predicted | % Error |
|-------------------------------|------|-----------|---------|
| Austria                       | 81.91| 81.92     | 0.01    |
| Norway                        | 82.96| 83.02     | 0.07    |
| Portugal                      | 81.71| 81.66     | -0.06   |
| Taiwan                        | 80.58| 80.61     | 0.04    |

The 2019 life tables we generate for Austria, Denmark, Finland, the Netherlands, Norway, Portugal, Sweden, and Taiwan match very closely the 2019 life tables reported by the Human Mortality Database for these countries. For example, in the table above, we show that the life expectancy at birth estimated for Austria, Norway, Portugal, and Taiwan are within .1% the respective life expectancy reported in the HMDB.

**2020 Life Expectancy for Peer Populations from Simulated 2020 Life Tables**

We simulate 50,000 2020 life tables for each peer country's total population, male population, and female population. First, we estimate age-specific death rates (\( m_x \)) separately by country in years 2018 and 2020. To do so, we merge estimates of age-specific death counts in the 9/29/2021 HMDB-STMF original input data in standardized format files with the age-specific counts of population provided by each country's central statistical agency:

\[ m_{x2018} = \frac{d_{x2018,STMF}}{L_{x2018}} \]

\[ m_{x2020} = \frac{d_{x2020,STMF}}{L_{x2020}} \]

Next, we estimate the 2012:2018 age-specific mortality rate ratios (RRs) for each country's total, male, and female populations using the estimated 2020 \( m_x \) and the estimated 2018 \( m_x \):
Third, to estimate \( m_{2020} \) used to generate 2020 life tables, we multiply the age-specific RR\(_{2020,\text{STMF}}\) with the corresponding age-specific 2018 \( m_{x} \) reported in the HMDB 2018 life table:

\[
RR_{2020,\text{STMF}} = \frac{m_{x_{2020}}}{m_{x_{2018}}}
\]

To estimate \( q_{x_{2020}} \) for the 2020 life tables, we use the estimated \( m_{x_{2020}} \) and the 2018 \( a_{x} \) reported in the HMDB 2018 life table:

\[
q_{x_{2020}} = \frac{\left(m_{x_{2020}} \times n\right)}{\left(1 + \left(n - a_{x_{2018}}\right) \times m_{x_{2020}}\right)}
\]

where \( n \) is the width of the age interval.

To generate distributions of 2020 life tables for each country's total population, male population, and female population, we add 10% random uncertainty to \( q_{x_{2020}} \) and use Python version 3.9.1 to simulate 50,000 life tables for each country's population. We report the median (P\(_{50}\)) estimate for each life expectancy as well as the fifth (P\(_{5}\)) and ninety-fifth (P\(_{95}\)) percentiles as plausible ranges for 2020 life expectancies.

c. Composite Life Expectancy from Average of Peer \( q_{x} \) and \( a_{x} \)

In addition to generating life tables for each peer country's male and female population in 1980, 1995, 2010, 2019, and 2020, we also generate composite life tables for these years using the average \( q_{x} \) and average \( a_{x} \) among peer countries' male and female populations.

The composite life tables are generated in order to use Arriaga decomposition techniques to estimate how differences in age-specific death rates contribute to the differences between the U.S. male and female life expectancies and the composite male and female life expectancies in 1980, 1995, 2010, 2018, and 2020. That is, as opposed to using Arriaga decomposition to estimate age contributions to the male and female life expectancy differences between the U.S. and each peer country in all years (20 \( \times \) 2 \( \times \) 5 = 200 Arriaga decompositions) and then taking the average of these age contributions, we use Arriaga decomposition to estimate age contributions to the male and female life expectancy differences between the U.S. and the composite life tables derived from peer country averages of \( q_{x} \) and \( a_{x} \) (2 \( \times \) 5 = 10 Arriaga decompositions). Little information is lost by constructing this composite life table as opposed to taking the average from all possible Arriaga decompositions. Below is the average life expectancy among peer countries for all years contrasted with the life expectancy from the composite life table.
Male $e_0$ among peer countries by year: "Average" $e_0$ vs. "Composite" $e_0$

| Year | Avg. $e_0$ | Composite $e_0$ |
|------|------------|-----------------|
| 1980 | 70.8       | 70.7            |
| 1995 | 74.0       | 73.9            |
| 2010 | 78.3       | 78.2            |
| 2019 | 79.8       | 79.7            |
| 2020 | 79.2       | 79.1            |

Female $e_0$ among peer countries by year: "Average" $e_0$ vs. "Composite" $e_0$

| Year | Avg. $e_0$ | Composite $e_0$ |
|------|------------|-----------------|
| 1980 | 77.1       | 77.1            |
| 1995 | 80.0       | 79.9            |
| 2010 | 83.0       | 83.0            |
| 2019 | 84.2       | 84.2            |
| 2020 | 83.6       | 83.6            |

In all years, the average male and female life expectancy among peer countries is within .1 year of the male and female life expectancy estimated from the composite life table.
3. Sensitivity Analyses

a. Stability of life expectancy estimates across NCHS data release dates

Delays in processing death counts in the NCHS provisional data might generate bias in estimates of 2020 U.S. life expectancy. The substantive impact of these death undercounts on total U.S. life expectancy is likely to be small. Below, the estimated 2020 U.S. female and male life expectancy are shown across the data release dates for 2020 death counts. The estimates of 2020 life expectancy stabilized across the July, August, and September data as updates to the 2020 death counts had less and less effect on $m_x$. The stability across these most recent months suggest that changes in the future will likely be minimal.

| NCHS Data Release | Female | Male |
|-------------------|--------|------|
| 5_10              | 79.74  | 74.04|
| 6_13              | 79.72  | 74.02|
| 7_7               | 79.72  | 74.01|
| 8_1               | 79.72  | 74.01|
| 9_29              | 79.72  | 74.01|

b. Stability of life expectancy estimates across HMD-STMF data release dates

Delays in processing death counts in other countries' registries can also generate bias in estimates of 2020 life expectancy. However, most delays in registering deaths are only weeks or a few months in time, and the data from the HMD-STMF 9/29/2021 data release are likely close to complete. To illustrate, below are examples of some countries' statements on processing 2020 death records.

**Austria**

"...results for 2019 and 2020 are provisional. Data of the last three weeks of 2020 are estimated. Data for 2020 and 2021 are preliminary and can be modified continuously with each new update. Nevertheless, Statistics Austria estimates that the difference between preliminary and final is very small: between 90 and 95% of all deaths notifications is received within two weeks, and the rest are usually received four to five weeks after the death occurred." (emphasis added)

**Finland**

"2021 data are preliminary and the contain a two-week delay. Data on most recent week(s) are incomplete and they are revised and corrected in every weekly update" (emphasis added).

**France**
"Each monthly death file includes all the deaths in which INSEE becomes aware over the time. Because of delayed notifications, these files include also records of deaths occurred in earlier months and even years. That is, the monthly files of 2020, include numerous deaths occurred in previous months. Thus, 2010-2018 data can be considered final, data of the year 2019 may be still slightly incomplete. Data of 2020 and 2021 (especially the most recent weeks) should be considered as preliminary. Last available weeks in these data series may be incomplete."

(emphasis added)

Germany

"Data for 2016-2019 are final. 2020 are provisional and may be revised and corrected as death notifications arrive with delay and are being included in the data series. Destatis estimates that around 80% of the deaths are notified after a week, around 90% after two and around 97% after a month." (emphasis added)

Italy

"2015-2019 data is, in principle, final. Nevertheless, this series has been revised by original source (Istituto Nazionale di Statistica, ISTAT) and corrected, affecting further excess mortality analysis. 2020 data is preliminary and its being updated regularly by the original sources and this may affect particularly data on most recent weeks." (emphasis added)

Republic of Korea

"According to KOSIS, 98% of deaths were registered within two months in 2019. 2010-2019 data are final. 2020 are provisional and therefore are subject to revisions. Last available weeks in 2020 may be incomplete due to delays in data processing and notification." (emphasis added)

Sweden

"data for 2020 and 2021 are preliminary and therefore it is being revised an corrected every week. Data for last available week(s) may be incomplete [sic]" (emphasis added)

Because 2020 life expectancies are estimated using death counts from records that are seven months after the last week of 2020, bias in 2020 death counts are likely minimal.

The table below shows estimates of 2020 female life expectancy across data release dates for the HMD-STMF original input data for Austria, Denmark, Italy, and France. Much like the stability in the estimates of 2020 U.S. life expectancies, we see no substantive changes in the life expectancy estimates across the May, June, and July data. While these 2020 provisional data may be subject to changes in the future, the substantive impact of these changes on the final 2020 life expectancy estimates will likely be minimal.
d. 2018 male and female life expectancy in Italy predicted from 2018 & 2016 HMD-STMF Italy data and 2016 HMD 5 x 1 male and female Italy life table.

To test the validity of our analytic approach to generating 2020 life tables for peer countries' populations, we replicate the approach to generate the 2018 HMD Italy 5 x 1 male and female life tables by using (a) the $m_x$ and $a_x$ in the 2016 HMD Italy 5 x 1 male and female life tables and (b) the 2018:2016 mortality rate ratios estimated in the HMD-STMF original source data combined with the 2016 and 2018 Italy male and female population estimates provided by Istat. The table below contrasts the 2018 Italy male and female life expectancy at birth, age 25, age 65,
and age 85 in the 2018 HMD Italy 5 x 1 life tables with the corresponding figures estimated from our analytic approach. The differences are negligible, showing that our analytic approach accurately estimates year-specific life expectancy for male and female populations in Italy.

|         | Female | Male |
|---------|--------|------|
|         | 2018 HMDB 2018 Est. | 2018 HMDB 2018 Est. |
| e₀      | 85.28  85.28 | 80.95  80.96 |
| e₂₅     | 60.67  60.68 | 56.51  56.52 |
| e₆₅     | 22.49  22.49 | 19.35  19.36 |
| e₈₅     | 7.16   7.16  | 5.96   5.95  |

e. Bias in NCHS 2020 Provisional Life Tables

Arias et al. (2021) published 2020 Provisional Life Tables suggesting a U.S. female life expectancy decline between 2019 and 2020 of 1.17 years (81.34 - 80.18) and a U.S. male life expectancy decline of 1.17 years (76.34 - 75.17). The 2019-2020 changes in U.S. female and male life expectancy estimated from our analytic approach, -1.23 years and -2.32 years, respectively, are considerably larger. The declines reported by Arias et al. (2021) fall well outside the P₅-P₉₅ range of our estimates, indicating that the large discrepancies between our estimates and those in the 2020 Provisional Life Table are not arising from chance random error:

|        | 2019 | 2020 | Change |
|--------|------|------|--------|
| Female |      |      |        |
| Provisional | 81.41 | 80.18 | -1.23  |
| Ours   | 81.41 | 79.72 | -1.69  |

|        | 2019 | 2020 | Change |
|--------|------|------|--------|
| Male   |      |      |        |
| Provisional | 76.34 | 74.49 | -1.85  |
| Ours   | 76.34 | 74.01 | -2.33  |

Note: Life expectancies in 2019 and in 2020, "Provisional", are obtained from Arias et al. (2021), and 2020, "Ours", from estimates reported in Table 1 of the manuscript.

If one were to trust the NCHS 2020 Provisional Life Tables, our estimates appear to be severely biased. Specifically, our estimated declines in U.S. male life expectancy are 26% larger than Arias et al.'s (2021): (-2.33--1.85)/-1.85 = .26; and our estimated declines in U.S. female life expectancy are 37% larger than Arias et al.'s (2021): (-1.69--1.23)/-1.23 = .37.

However, as we show below, there is strong evidence to indicate that the 2020 U.S. male and female life expectancies estimated from the NCHS 2020 Provisional Life Tables are too high (and, thus, the 2020 life expectancy declines too small). This is because the 2020 Provisional Life Tables are generated using death counts reported only from vital statistics (Arias et al. 2021). Without adjustments to older-age death rates from the Medicare files, the 2020 death rates
used to generate the 2020 Provisional Life Tables are downwardly biased at older ages. Evidence for this bias can be shown in three ways. First, by plotting the 2020:2018 $m_x$ ratios across older age groups (i.e., ages 60-64, ..., 80-84, 85+). Second, by comparing the 2020 $e_85$ implied in the 2020 Provisional Life Tables with the 2018 $e_85$. And third, by calculating the U.S. male and female 2020:2018 $m_{85+}$ ratios by race/ethnicity.

$2020:2018 \, m_x, \text{ ratios ages 60-64, ..., 85+}$

Source: 2018 $m_x$ from Arias & Xu (2020), Table 2 and Table 3; 2020 $m_x$ from Arias et al. (2021) 2020 Provisional Life Tables, Table I-2 and Table I-3.

From Table I-2 and Table I-3 in Arias et al.'s (2021) technical report, we calculated 2020 $m_x$ for the U.S. male and female population at ages 60-64, ..., 80-84, and 85+. We also calculated 2018 $m_x$ for these same age groups using the 2018 official life tables from Arias and Xu (2020), Table 2 and Table 3. The rate ratios (RR) between the 2020 $m_x$ and the 2018 $m_x$ are plotted in the figures above. The RRs appear to decline steadily across older ages. Moreover, for the U.S. male population, the 2020 mortality rate at ages 85 and above are suggested to have been lower than the 2018 mortality rates. As such, the mortality rates in the 2020 Provisional Life Tables suggest an implausible reality that the COVID-19 pandemic actually lowered mortality rates for U.S. men over the age of 85.

The age declines in the 2020:2018 $m_x$ ratios themselves are also implausible. Indeed, they are in contrast to the RRs observed in other populations that were significantly affected by the COVID-19 pandemic. For example, the figure below plots the RRs between the 2020 $m_x$ and the 2018 $m_x$ in the male and female populations of Austria, Belgium, England & Wales, France, Italy, Spain, and Switzerland. The average RRs are also highlighted to visualize the age patterns of the 2020:2018 RRs in these populations.
The RRs between 2020 and 2018 in these seven countries' male and female populations suggest that the mortality consequences of the COVID-19 pandemic are stable across older ages. No systematic declines in the 2020:2018 RRs are observed in any of the male or female populations. Further, the data for all of these countries except England & Wales are top-coded at age 90 (as opposed to age 85 in the US data), providing more accurate estimates of the 2020 mₜ for ages above 85. The age-declines in the 2020:2018 mₜ ratios suggested in Arias et al.’s (2021) 2020 Provisional Life Tables are at odds with the stable 2020:2018 mₜ ratios observed in these countries' male and female populations.

Further, the age-declines in the 2020:2018 U.S. RRs suggested by Arias et al. (2021) are also at odds with our estimates using the NCHS-Census data:

Note: gray shaded area indicates range of estimates between P₅ and P₉₅ from 50,000 simulations

Our estimates of the 2020:2018 RRs among the US female and male populations are consistent with the stable age patterns observed in the seven European countries' populations above. For example, among the U.S. male population, we estimate the 2020:2018 RRs for age groups 70-74, 75-79, 80-84, and 85+ to be 1.18, 1.18, 1.17, 1.14; and the error bands around these estimates indicate nonsignificant differences in these estimates. In contrast, the 2020:2018 RRs implied in the NCHS 2020 Provisional Life Table for the US male population drop precipitously across age,
reflecting the bias in estimates arising from the undercount of deaths at older ages in vital statistics data. For age groups 70-74, 75-79, 80-84, and 85+, the NCHS 2020 Provisional Life Tables suggest the 2020:2018 RRs to be 1.14, 1.12, 1.09, and an implausible .96.

2020 e85

The 2020 Provisional Life Tables (Arias et al. 2021) assume that U.S. life expectancy at age 85 in 2020 was either no different than U.S. life expectancy at age 85 in 2018 (for the U.S. female population) or was actually greater than U.S. life expectancy at age 85 in 2018 (for the U.S. male population). Specifically, from Table I-2 and Table I-3, we calculate U.S. male e85 in 2020 to be $T_{85}/L_{85} = 194,276/31,331 = 6.20$ and we calculate U.S. female e85 in 2020 to be $T_{85}/L_{85} = 323,783/46,553 = 6.96$. From Table 2 and Table 3 in the 2018 official life tables (Arias & Xu 2020), we calculate U.S. male e85 in 2018 to be $T_{85}/L_{85} = 214,242/35,806 = 5.98$ and we calculate U.S. female e85 in 2020 to be $T_{85}/L_{85} = 348,510/49,763 = 7.00$.

From these figures, we see that the 2020 Provisional Life Tables suggest that the COVID-19 pandemic did not substantively affect survival among the oldest-old U.S. populations. In fact, U.S. men aged 85 and older were estimated to have had greater longevity (.22 years) during the COVID-19 pandemic than in 2018.

| e85 Source      | Total | Male | Female |
|-----------------|-------|------|--------|
| Official 2018 LT| 6.61  | 5.98 | 7.00   |
| Arias et al. 2021| 6.70 | 6.20 | 6.96   |
| Difference      | 0.09  | 0.22 | -0.04  |

2020:2018 m85+ by Race/ethnicity

Evidence for bias in the 2020 Provisional Life Tables' m85+ at older ages can be further seen in the estimates of 2020:2018 m85+ ratios for the U.S. male and female non-Hispanic Black, non-Hispanic white, and Hispanic populations. From Arias et al. (2021) Tables I-1 through I-12, we can calculate 2020 m85+ for U.S. populations by sex and race/ethnicity, and from Arias and Xu (2020) Tables 1-12, we can calculate 20218 m85+ for U.S. populations by sex and race/ethnicity.

The table below shows the 2020:2018 m85+ ratios assumed by the 2020 Provisional Life Tables
Relative to U.S. mortality rates in 2018, the 2020 Provisional Life Tables assume that the COVID-19 pandemic (1) lowered mortality rates among the total U.S. population aged 85 years and older by 1%, (2) elevated mortality rates among the U.S. Black and white female populations aged 85 years and older by only 4%, (3) did not elevate mortality rates among the U.S. Black and white male populations aged 85 years and older, and (4) lowered older-aged mortality rates among the U.S. female and male Hispanic populations by 7% and 8%, respectively. That is, the U.S. population with the greatest loss of life in 2020 was assumed to have 7%-8% lower mortality at older ages, which are known to be susceptible to COVID-19 mortality risk (Rossen et al. 2021).

It is not likely that U.S. life expectancy at age 85 was higher in 2020 than in 2018. It is not likely that mortality rates among the oldest-old Hispanic populations were lower in 2020 than in 2018. And it is not likely that the 2020:2018 $m_x$ ratios among U.S. populations declined across older age groups. Yet, all of these unlikelihods are assumed in the NCHS 2020 Provisional Life Tables. The 2020 Provisional Life Tables published by NCHS substantially underestimate mortality rates at older ages (i.e., 60+) and, consequently, that the estimated losses in 2020 life expectancy among all U.S. populations is likely severely biased.

|                | 2020:2018 ratio |
|----------------|-----------------|
| Total          | 0.99            |
| Hispanic       | 0.94            |
| nH Black       | 1.03            |
| nH white       | 1.03            |
| Female         | 1.01            |
| Hispanic       | 0.93            |
| nH Black       | 1.04            |
| nH white       | 1.04            |
| Male           | 0.96            |
| Hispanic       | 0.92            |
| nH Black       | 1.00            |
| nH white       | 1.00            |
### 4. Estimates of 2019 and 2020 Female and Male Life Expectancy at Birth, by Country

|               | Female Life Expectancy at Birth | Male Life Expectancy at Birth |
|---------------|---------------------------------|------------------------------|
|               | 2019 | 2020 | 2020, LB | 2020, UB | 2019 | 2020 | 2020, LB | 2020, UB |
| Austria       | 84.20 | 83.52 | 83.37 | 83.67 | 79.54 | 78.73 | 78.57 | 78.89 |
| Belgium       | 84.02 | 82.96 | 82.81 | 83.11 | 79.60 | 78.44 | 78.28 | 78.60 |
| Canada        | 84.34 | 83.73 | 83.57 | 83.88 | 80.24 | 79.41 | 79.25 | 79.57 |
| Denmark       | 83.42 | 83.35 | 83.19 | 83.50 | 79.44 | 79.45 | 79.29 | 79.61 |
| England & Wales | 83.53 | 82.46 | 82.31 | 82.62 | 79.85 | 78.47 | 78.32 | 78.64 |
| Finland       | 84.53 | 84.57 | 84.42 | 84.72 | 79.22 | 79.05 | 78.89 | 79.21 |
| France        | 85.63 | 85.06 | 84.91 | 85.21 | 79.76 | 79.01 | 78.85 | 79.17 |
| Germany       | 83.67 | 83.35 | 83.20 | 83.50 | 78.94 | 78.48 | 78.32 | 78.64 |
| Israel        | 84.31 | 84.18 | 84.03 | 84.33 | 80.64 | 80.05 | 79.89 | 80.21 |
| Italy         | 85.40 | 84.43 | 84.28 | 84.58 | 81.14 | 79.83 | 79.67 | 79.99 |
| Netherlands   | 83.56 | 82.85 | 82.70 | 83.00 | 80.46 | 79.84 | 79.69 | 79.99 |
| New Zealand   | 83.56 | 84.09 | 83.96 | 84.23 | 80.00 | 80.65 | 80.50 | 80.80 |
| Northern Ireland | 82.74 | 81.85 | 81.70 | 82.01 | 79.02 | 78.05 | 77.89 | 78.21 |
| Norway        | 84.70 | 84.72 | 84.58 | 84.88 | 81.18 | 81.32 | 81.17 | 81.48 |
| Portugal      | 84.56 | 83.78 | 83.64 | 83.93 | 78.64 | 77.66 | 77.50 | 77.82 |
| Scotland      | 81.26 | 80.60 | 80.45 | 80.76 | 77.28 | 76.06 | 75.90 | 76.23 |
| Spain         | 86.21 | 84.88 | 84.73 | 85.02 | 80.83 | 79.40 | 79.24 | 79.56 |
| Sweden        | 84.73 | 84.12 | 83.98 | 84.27 | 81.35 | 80.41 | 80.26 | 80.57 |
| Switzerland   | 85.58 | 84.97 | 84.83 | 85.12 | 81.89 | 80.87 | 80.72 | 81.02 |
| Taiwan        | 83.78 | 84.26 | 84.11 | 84.42 | 77.53 | 78.07 | 77.90 | 78.25 |
| United States | 81.41 | 79.72 | 79.56 | 79.88 | 76.34 | 74.01 | 73.84 | 74.19 |

Note: "LB" indicates the value of the fifth percentile case from the 50,000 values and "UB" indicates the value of the ninety-fifth percentile case.
5. Analytic Scripts

a. Stata files merging death counts and population counts, US populations 2017, 2018, 2020.

********** All Male and All Female **********
*** 2020 NCHS Mortality Data, by Week ***

import delimited "../../NCHS Data/AH_Excess_Deaths_by_Sex__Age__and_Race_8_1.csv",
encoding(ISO-8859-1)

drop footnote geography
drop numberaboveaverageweighted percentaboveaverageweighted
numberaboveaverageunweighted percentaboveaverageunweighted
drop timeperiod analysisdate weekending

keep if mmwryear == 2020
keep if raceethnicity == "All Race/Ethnicity Groups"
drop covid19weighted covid19unweighted averagenumberofdeathsweighted
averagenumberofdeathsunweighted

encode sex, gen(female)
encode agegroup, gen(age)
drop if female == 1
replace female = 1 if female == 2
replace female = 0 if female == 3

label define femalel 0 "male" 1 "female"
label values female femalel
drop if age == 17 | age == 18

*** Sum Deaths for Entire 2020 by Age for Men and Women ***
sort female age
collapse (sum) mort = deathsunweighted, by(female age)
save "../../NCHS Data/total sex_age specific death counts_2020.dta", replace

****** Import 2020 Pop Estimates ******
* Linear Trend Approximations from Age-specific Populations 2015-2019
* All US Men and Women, 0-14, 15-19, … , 80-84, 85+

import excel "../../Pop Estimates_2015_2019/sex_pop_age.xlsx", sheet("2020 pop") firstrow

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

merge using "../../NCHS Data/total sex_age specific death counts_2020.dta"
drop _merge

gen mx = mort/pop

save "../../NCHS Data/total sex_2020 mx.dta", replace
b. Stata files creating age-specific 2018 and 2020 death counts in peer country HMD-STMF original input data.

*** Import HMD Raw .txt Data ***

***************
*** Austria ***
***************

import delimited "/Users.../STMFinput_7_26/AUTstmf.csv", encoding(ISO-8859-1) clear

keep year week sex age deaths

keep if year == 2018 | year == 2020

drop if age == "TOT"
drop if age == "UNK"
destring age, gen(age5)
drop age
rename age5 age

* Estimate Yearly Age-specific Death Count - Sum across the 52 weeks

sort sex year age
collapse (sum) deaths, by(sex year age)

gen nage = .
replace nage = 1 if age ==0
replace nage = 2 if age ==5
replace nage = 3 if age ==10
replace nage = 4 if age ==15
replace nage = 5 if age ==20
replace nage = 6 if age ==25
replace nage = 7 if age ==30
replace nage = 8 if age ==35
replace nage = 9 if age ==40
replace nage = 10 if age ==45
replace nage = 11 if age ==50
replace nage = 12 if age ==55
replace nage = 13 if age ==60
replace nage = 14 if age ==65
replace nage = 15 if age ==70
replace nage = 16 if age ==75
replace nage = 17 if age ==80
replace nage = 18 if age ==85
replace nage = 19 if age ==90

gen country = "Austria"

sort year sex nage

save "/Users.../STMFinput_7_26/austria_1820 deaths.dta", replace

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

import delimited "/Users.../STMFinput_7_26/BELstmf.csv", encoding(ISO-8859-1) clear
keep year week sex age deaths

keep if year == 2018 | year == 2020

drop if age == "TOT"
drop if age == "UNK"
destring age, gen(age5)
rename age5 age

* Estimate Yearly Age-specific Death Count - Sum across the 52 weeks

sort sex year age
collapse (sum) deaths, by(sex year age)

gen nage = .
replace nage = 1 if age == 0
replace nage = 2 if age == 5
replace nage = 3 if age == 10
replace nage = 4 if age == 15
replace nage = 5 if age == 20
replace nage = 6 if age == 25
replace nage = 7 if age == 30
replace nage = 8 if age == 35
replace nage = 9 if age == 40
replace nage = 10 if age == 45
replace nage = 11 if age == 50
replace nage = 12 if age == 55
replace nage = 13 if age == 60
replace nage = 14 if age == 65
replace nage = 15 if age == 70
replace nage = 16 if age == 75
replace nage = 17 if age == 80
replace nage = 18 if age == 85
replace nage = 19 if age == 90

gen country = "Belgium"
sort year sex nage
save "/Users/.../STMInput_7_26/belgium_1820 deaths.dta", replace

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

import delimited "/Users/.../STMInput_7_26/DNKstmf.csv", encoding(ISO-8859-1) clear
keep year week sex age deaths
keep if year == 2018 | year == 2020
drop if age == "TOT"
drop if age == "UNK"
destring age, gen(age5)
rename age5 age
rename age5 age

* Estimate Yearly Age-specific Death Count - Sum across the 52 weeks

sort sex year age

collapse (sum) deaths, by(sex year age)

gen nage = .
replace nage = 1 if age ==0
replace nage = 2 if age ==5
replace nage = 3 if age ==10
replace nage = 4 if age ==15
replace nage = 5 if age ==20
replace nage = 6 if age ==25
replace nage = 7 if age ==30
replace nage = 8 if age ==35
replace nage = 9 if age ==40
replace nage = 10 if age ==45
replace nage = 11 if age ==50
replace nage = 12 if age ==55
replace nage = 13 if age ==60
replace nage = 14 if age ==65
replace nage = 15 if age ==70
replace nage = 16 if age ==75
replace nage = 17 if age ==80
replace nage = 18 if age ==85
replace nage = 19 if age ==90
replace nage = 20 if age ==95
replace nage = 21 if age ==100

gen country = "Denmark"
sort year sex nage

save "/Users.../STMInput_7_26/denmark_1820 deaths.dta", replace

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

import delimited "/Users.../STMInput_7_26/FINstmf.csv", encoding(ISO-8859-1) clear
keep year week sex age deaths
keep if year == 2018 | year == 2020
drop if age == "TOT"
drop if age == "UNK"
destring age, gen(age5)
drop age
rename age5 age

* Estimate Yearly Age-specific Death Count - Sum across the 52 weeks

sort sex year age

collapse (sum) deaths, by(sex year age)

gen nage = .
replace nage = 1 if age ==0
replace nage = 2 if age == 5
replace nage = 3 if age == 10
replace nage = 4 if age == 15
replace nage = 5 if age == 20
replace nage = 6 if age == 25
replace nage = 7 if age == 30
replace nage = 8 if age == 35
replace nage = 9 if age == 40
replace nage = 10 if age == 45
replace nage = 11 if age == 50
replace nage = 12 if age == 55
replace nage = 13 if age == 60
replace nage = 14 if age == 65
replace nage = 15 if age == 70
replace nage = 16 if age == 75
replace nage = 17 if age == 80
replace nage = 18 if age == 85
replace nage = 19 if age == 90

gen country = "Finland"

sort year sex nage

save "/Users.../STMFinput_7_26/finland_1820 deaths.dta", replace

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

import delimited "/Users.../STMFinput_7_26/FRATNPstmf.csv", encoding(ISO-8859-1) clear

keep year week sex age deaths

keep if year == 2018 | year == 2020

drop if age == "TOT"
drop if age == "UNK"

destring age, gen(age5)
drop age
rename age5 age

* Estimate Yearly Age-specific Death Count - Sum across the 52 weeks

sort sex year age
collapse (sum) deaths, by(sex year age)

gen agen = age
replace agen = 0 if age == 1

sort year sex agen
collapse (sum) deaths, by(year sex agen)
rename agen age

gen nage =.
replace nage = 1 if age == 0
replace nage = 2 if age == 5
replace nage = 3 if age == 10
replace nage = 4 if age == 15
replace nage = 5 if age == 20
replace nage = 6 if age == 25
replace nage = 7 if age == 30
replace nage = 8 if age == 35
replace nage = 9 if age == 40
replace nage = 10 if age == 45
replace nage = 11 if age == 50
replace nage = 12 if age == 55
replace nage = 13 if age == 60
replace nage = 14 if age == 65
replace nage = 15 if age == 70
replace nage = 16 if age == 75
replace nage = 17 if age == 80
replace nage = 18 if age == 85
replace nage = 19 if age == 90
replace nage = 20 if age == 95

gen country = "France"

sort year sex nage

save "/Users.../STMInput_7_26/france_1820 deaths.dta", replace

***************
*** Germany ***
***************

import delimited "/Users.../STMInput_7_26/DEUTNPstmf.csv", encoding(ISO-8859-1) clear

keep year week sex age deaths
keep if year == 2018 | year == 2020
drop if age == "TOT"
drop if age == "UNK"
destring age, gen(age5)
drop age
rename age5 age

* Estimate Yearly Age-specific Death Count - Sum across the 52 weeks

sort sex year age
collapse (sum) deaths, by(sex year age)

gen nage = .
replace nage = 1 if age == 0
replace nage = 2 if age == 30
replace nage = 3 if age == 35
replace nage = 4 if age == 40
replace nage = 5 if age == 45
replace nage = 6 if age == 50
replace nage = 7 if age == 55
replace nage = 8 if age == 60
replace nage = 9 if age == 65
replace nage = 10 if age == 70
replace nage = 11 if age == 75
replace nage = 12 if age == 80
replace nage = 13 if age == 85
replace nage = 14 if age == 90

replace nage = 15 if age == 95

gen country = "Germany"

sort year sex nage

save "/Users.../STMInput_7_26/germany_1820 deaths.dta", replace

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

import delimited "/Users.../STMInput_7_26/ISRstmf.csv", encoding(ISO-8859-1) clear

keep year week sex age deaths

keep if year == 2018 | year == 2020

drop if age == "TOT"
drop if age == "UNK"
destring age, gen(age5)
drop age
rename age5 age

* Estimate Yearly Age-specific Death Count - Sum across the 52 weeks

sort sex year age

collapse (sum) deaths, by(sex year age)

gen nage = .
replace nage = 1 if age == 0
replace nage = 2 if age == 20
replace nage = 3 if age == 30
replace nage = 4 if age == 40
replace nage = 5 if age == 50
replace nage = 6 if age == 60
replace nage = 7 if age == 70
replace nage = 8 if age == 80

gen country = "Israel"

sort year sex nage

save "/Users.../STMInput_7_26/israel_1820 deaths.dta", replace

****************
*** Italy ***
****************

import delimited "/Users.../STMInput_7_26/ITAstmf.csv", encoding(ISO-8859-1) clear

keep year week sex age deaths

keep if year == 2018 | year == 2020

drop if age == "TOT"
drop if age == "UNK"
destring age, gen(age5)
drop age
rename age5 age

* Estimate Yearly Age-specific Death Count - Sum across the 52 weeks

sort sex year age
collapse (sum) deaths, by(sex year age)
gen agen = age
replace agen = 0 if agen == 1
replace agen = 90 if agen >90
collapse (sum) deaths, by(sex year agen)
rename agen age
gen nage = .
replace nage = 1 if age ==0
replace nage = 2 if age ==5
replace nage = 3 if age ==10
replace nage = 4 if age ==15
replace nage = 5 if age ==20
replace nage = 6 if age ==25
replace nage = 7 if age ==30
replace nage = 8 if age ==35
replace nage = 9 if age ==40
replace nage = 10 if age ==45
replace nage = 11 if age ==50
replace nage = 12 if age ==55
replace nage = 13 if age ==60
replace nage = 14 if age ==65
replace nage = 15 if age ==70
replace nage = 16 if age ==75
replace nage = 17 if age ==80
replace nage = 18 if age ==85
replace nage = 19 if age ==90
gen country = "Italy"
sort year sex nage
save "/Users.../STMInput_7_26/italy_1820 deaths.dta", replace

*****************************************************************************
* Korea: Use STMF Rates *
*****************************************************************************

*****************************************************************************
* Netherlands: Use STMF Rates *
*****************************************************************************

*****************************************************************************
* New Zealand: Use STMF Rates *
*****************************************************************************

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

import delimited "/Users.../STMInput_7_26/NORstmf.csv", encoding(ISO-8859-1) clear
keep year week sex age deaths

keep if year == 2018 | year == 2020

drop if age == "TOT"
drop if age == "UNK"

destring age, gen(age5)
drop age
rename age5 age

* Estimate Yearly Age-specific Death Count - Sum across the 52 weeks

sort sex year age
collapse (sum) deaths, by(sex year age)
gen nage = .
replace nage = 1 if age ==0
replace nage = 2 if age ==5
replace nage = 3 if age ==10
replace nage = 4 if age ==15
replace nage = 5 if age ==20
replace nage = 6 if age ==25
replace nage = 7 if age ==30
replace nage = 8 if age ==35
replace nage = 9 if age ==40
replace nage = 10 if age ==45
replace nage = 11 if age ==50
replace nage = 12 if age ==55
replace nage = 13 if age ==60
replace nage = 14 if age ==65
replace nage = 15 if age ==70
replace nage = 16 if age ==75
replace nage = 17 if age ==80
replace nage = 18 if age ==85
replace nage = 19 if age ==90
replace nage = 20 if age ==95
replace nage = 21 if age ==100
gen country = "Norway"

sort year sex nage

save "/[Users]/STMInput_7_26/norway_1820 deaths.dta", replace

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

import delimited "/[Users]/STMInput_7_26/PRTstmf.csv", encoding(ISO-8859-1) clear

keep year week sex age deaths

keep if year == 2018 | year == 2020

drop if age == "TOT"
drop if age == "UNK"

destring age, gen(age5)
drop age
rename age5 age

* Estimate Yearly Age-specific Death Count - Sum across the 52 weeks

sort sex year age
collapse (sum) deaths, by(sex year age)

gen agen = age
replace agen = 85 if age == 90
collapse (sum) deaths, by(sex year agen)
rename agen age

gen nage = .
replace nage = 1 if age ==0
replace nage = 2 if age ==5
replace nage = 3 if age ==10
replace nage = 4 if age ==15
replace nage = 5 if age ==20
replace nage = 6 if age ==25
replace nage = 7 if age ==30
replace nage = 8 if age ==35
replace nage = 9 if age ==40
replace nage = 10 if age ==45
replace nage = 11 if age ==50
replace nage = 12 if age ==55
replace nage = 13 if age ==60
replace nage = 14 if age ==65
replace nage = 15 if age ==70
replace nage = 16 if age ==75
replace nage = 17 if age ==80
replace nage = 18 if age ==85

gen country = "Portugal"
sort year sex nage

save "/Users.../STMFinput_7_26/portugal_1820 deaths.dta", replace

*************
*** Spain ***
*************

import delimited "/Users.../STMFinput_7_26/ESPstmf.csv", encoding(ISO-8859-1) clear

keep year week sex age deaths

keep if year == 2018 | year == 2020
drop if age == "TOT"
drop if age == "UNK"
destring age, gen(age5)
drop age
rename age5 age

* Estimate Yearly Age-specific Death Count - Sum across the 52 weeks

sort sex year age
collapse (sum) deaths, by(sex year age)

gen nage = .
replace nage = 1 if age ==0
replace nage = 2 if age ==5
replace nage = 3 if age ==10
replace nage = 4 if age ==15
replace nage = 5 if age ==20
replace nage = 6 if age ==25
replace nage = 7 if age ==30
replace nage = 8 if age ==35
replace nage = 9 if age ==40
replace nage = 10 if age ==45
replace nage = 11 if age ==50
replace nage = 12 if age ==55
replace nage = 13 if age ==60
replace nage = 14 if age ==65
replace nage = 15 if age ==70
replace nage = 16 if age ==75
replace nage = 17 if age ==80
replace nage = 18 if age ==85
replace nage = 19 if age ==90

replace nage = 16 if age ==75
replace nage = 17 if age ==80
replace nage = 18 if age ==85
replace nage = 19 if age ==90

gen country = "Spain"

sort year sex nage

save "/Users.../STMFinput_7_26/spain_1820 deaths.dta", replace

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

import delimited "/Users.../STMFinput_7_26/SWEstmf.csv", encoding(ISO-8859-1) clear

keep year week sex age deaths

keep if year == 2018 | year == 2020

drop if age == "TOT"
drop if age == "UNK"

destring age = "TOT"
drop age
rename age5 age

* Estimate Yearly Age-specific Death Count - Sum across the 52 weeks

sort sex year age

collapse (sum) deaths, by(sex year age)

gen nage = .
replace nage = 1 if age ==0
replace nage = 2 if age ==5
replace nage = 3 if age ==10
replace nage = 4 if age ==15
replace nage = 5 if age ==20
replace nage = 6 if age ==25
replace nage = 7 if age ==30
replace nage = 8 if age ==35
replace nage = 9 if age ==40
replace nage = 10 if age ==45
replace nage = 11 if age ==50
replace nage = 12 if age ==55
replace nage = 13 if age ==60
replace nage = 14 if age ==65
replace nage = 15 if age ==70
replace nage = 16 if age ==75
replace nage = 17 if age ==80
replace nage = 18 if age ==85
replace nage = 19 if age ==90

gen country = "Sweden"

sort year sex nage

save "/Users.../STMFinput_7_26/sweden_1820 deaths.dta", replace

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

import delimited "/Users.../STMFinput_7_26/CHEstmf.csv", encoding(ISO-8859-1) clear

keep if year == 2018 | year == 2020

destring age, gen(age5)
drop age
rename age5 age

* Estimate Yearly Age-specific Death Count - Sum across the 52 weeks

sort sex year age
collapse (sum) deaths, by(sex year age)

gen nage = .
replace nage = 1 if age ==0
replace nage = 2 if age ==5
replace nage = 3 if age ==10
replace nage = 4 if age ==15
replace nage = 5 if age ==20
replace nage = 6 if age ==25
replace nage = 7 if age ==30
replace nage = 8 if age ==35
replace nage = 9 if age ==40
replace nage = 10 if age ==45
replace nage = 11 if age ==50
replace nage = 12 if age ==55
replace nage = 13 if age ==60
replace nage = 14 if age ==65
replace nage = 15 if age ==70
replace nage = 16 if age ==75
replace nage = 17 if age ==80
replace nage = 18 if age ==85
replace nage = 19 if age ==90

gen country = "Switzerland"
sort year sex nage
save "./STMFindput_7_26/switzerland_1820 deaths.dta", replace

**************
*** Taiwan ***
**************

import delimited "./STMFindput_7_26/TWNstmf.csv", encoding(ISO-8859-1) clear
keep year week sex age deaths
keep if year == 2018 | year == 2020
drop if age == "TOT"
drop if age == "UNK"
destring age, gen(age5)
drop age
rename age5 age

* Estimate Yearly Age-specific Death Count - Sum across the 52 weeks
sort sex year age
collapse (sum) deaths, by(sex year age)
gen nage = .
replace nage = 1 if age == 0
replace nage = 2 if age == 5
replace nage = 3 if age == 10
replace nage = 4 if age == 15
replace nage = 5 if age == 20
replace nage = 6 if age == 25
replace nage = 7 if age == 30
replace nage = 8 if age == 35
replace nage = 9 if age == 40
replace nage = 10 if age == 45
replace nage = 11 if age == 50
replace nage = 12 if age == 55
replace nage = 13 if age == 60
replace nage = 14 if age == 65
replace nage = 15 if age == 70
replace nage = 16 if age == 75
replace nage = 17 if age == 80
replace nage = 18 if age == 85
replace nage = 19 if age == 90
replace nage = 20 if age == 95
replace nage = 21 if age == 100
gen country = "Taiwan"
sort year sex nage
save "./STMFindput_7_26/taiwan_1820 deaths.dta", replace

***** United Kingdom: Northern Ireland, Scotland, England + Wales *****
import delimited "~/Users.../STMinput_7_26/GBR_NIRstmf.csv", encoding(ISO-8859-1)
clear
keep year week sex age deaths
keep if year == 2018 | year == 2020
drop if age == "TOT"
drop if age == "UNK"
destring age, gen(age5)
drop age
rename age5 age
* Estimate Yearly Age-specific Death Count - Sum across the 52 weeks
sort sex year age
collapse (sum) deaths, by(sex year age)
gen agen = age
replace agen = 0 if agen == 1
collapse (sum) deaths, by(sex year agen)
rename agen age

gen nage = .
replace nage = 1 if age ==0
replace nage = 2 if age ==5
replace nage = 3 if age ==10
replace nage = 4 if age ==15
replace nage = 5 if age ==20
replace nage = 6 if age ==25
replace nage = 7 if age ==30
replace nage = 8 if age ==35
replace nage = 9 if age ==40
replace nage = 10 if age ==45
replace nage = 11 if age ==50
replace nage = 12 if age ==55
replace nage = 13 if age ==60
replace nage = 14 if age ==65
replace nage = 15 if age ==70
replace nage = 16 if age ==75
replace nage = 17 if age ==80
replace nage = 18 if age ==85
replace nage = 19 if age ==90

gen country = "Northern Ireland"
sort year sex nage
save "~/Users.../STMinput_7_26/northern ireland_1820 deaths.dta", replace

***************
*** Scotland ***
***************
import delimited "/Users/STMInput_7_26/GBR_SCOfstmf.csv", encoding(ISO-8859-1)
clear

keep year week sex age deaths
keep if year == 2018 | year == 2020
drop if age == "TOT"
drop if age == "UNK"
destring age, gen(age5)
drop age
rename age5 age

* Estimate Yearly Age-specific Death Count - Sum across the 52 weeks
sort sex year age
collapse (sum) deaths, by(sex year age)
gen agen = age
replace agen = 0 if agen == 1
replace agen = 90 if agen == 95
collapse (sum) deaths, by(sex year agen)
rename agen age
gen nage = .
replace nage = 1 if age == 0
replace nage = 2 if age == 5
replace nage = 3 if age == 10
replace nage = 4 if age == 15
replace nage = 5 if age == 20
replace nage = 6 if age == 25
replace nage = 7 if age == 30
replace nage = 8 if age == 35
replace nage = 9 if age == 40
replace nage = 10 if age == 45
replace nage = 11 if age == 50
replace nage = 12 if age == 55
replace nage = 13 if age == 60
replace nage = 14 if age == 65
replace nage = 15 if age == 70
replace nage = 16 if age == 75
replace nage = 17 if age == 80
replace nage = 18 if age == 85
replace nage = 19 if age == 90
gen country = "Scotland"
sort year sex nage
save "/Users/STMInput_7_26/scotland_1820 deaths.dta", replace

***********************
*** England & Wales ***
***********************
import delimited "/Users/STMInput_7_26/GBRENWstmf.csv", encoding(ISO-8859-1)
clear
keep year week sex age deaths
keep if year == 2018 | year == 2020
drop if age == "TOT"
drop if age == "UNK"
destring age, gen(age5)
drop age
rename age5 age
* Estimate Yearly Age-specific Death Count - Sum across the 52 weeks, but 2018 and 2020 have different age profiles
collapse (sum) deaths, by(sex year age)
    gen age20 = .
    replace age20 = age if year == 2018
    replace age20 = 0 if age == 1 & year == 2018
    replace age20 = 0 if age < 15 & year == 2020
    replace age20 = 15 if age >= 15 & age < 45 & year == 2020
    replace age20 = 45 if age >= 45 & age < 65 & year == 2020
    replace age20 = 65 if age >= 65 & age < 75 & year == 2020
    replace age20 = 75 if age >= 75 & age < 85 & year == 2020
    replace age20 = 85 if age >= 85 & year == 2020
sort sex year age20
    collapse (sum) deaths, by(sex year age20)
    rename age20 age
    gen nage = .
    replace nage = 1 if age == 0
    replace nage = 2 if age == 15
    replace nage = 3 if age == 45
    replace nage = 4 if age == 65
    replace nage = 5 if age == 75
    replace nage = 6 if age == 85
    gen country = "England & Wales"
sort year sex nage
save "/Users.../STMInput_7_26/england_wales_1820 deaths.dta", replace
c. Stata files loading age-specific death rates in 2018 and 2020 for Canada, New Zealand, and the Netherlands in the HMD-STMF data.

```stata
import delimited "/Users.../HMD data/peer_STMF/pooled_stmf_7_26_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"
keep if inlist(country,"CAN","NZL_NP","KOR","NLD")
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
sum rr_0 rr_15 rr_65 rr_75 rr_85

**** Save File to Merge with Appended HMD Life Tables ****
```
save "./HMD data/peer_STMF/suppl_2018rr_total.dta", replace

****** Separately by Sex ******

import delimited "./HMD data/peer_STMF/pooled_stmf_7_26_21.csv", encoding(ISO-8859-1) clear

drop split splitsex forecast rtotal dtotal d85p d75_74 d65_64 d15_64 d0_14
drop if sex == "f"
keep if inlist(country,"CAN","NZL_NP","KOR","NLD")
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 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
sum rr_0 rr_15 rr_65 rr_75 rr_85

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

save "/Users/.../HMD data/peer_STMF/suppl_2018rr_f.dta", replace

******
* Men *
******

import delimited "/Users/.../HMD data/peer_STMF/pooled_stmf_7_26_21.csv", encoding(ISO-8859-1) clear

drop split splitsex forecast rtotal dtotal d85p d75_84 d65_74 d5_64 d0_14
drop if sex == "m"
keep if inlist(country,"CAN","NZL_NP","KOR","NLD")
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 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

sum rr_0 rr_15 rr_65 rr_75 rr_85

**** Save File to Merge with Appended HMD Life Tables ****
save "/Users/.../HMD data/peer_STMF/suppl_2018rr_m.dta", replace

d. Stata files merging age-specific 2018 and 2020 death counts with population counts for peer countries.

*** Merge Population 2018 and 2020 with Death Counts from STMF Original Source ***

************
*** Austria ***
************
import excel "/Users/.../Peer Pop Estimates_2018_2020/pop input/aut_pop.xlsx",
sheet("Sheet1") firstrow clear
sort year sex nage
merge year sex nage using "/Users/.../STMFinput_7_26/austria_1820 deaths.dta"
gen mx = (deaths/pop)*100000
drop _merge
* Mx Rate Ratio b/w 2020 and 2018

tempfile a b c
sort country
save `a'
keep if year == 2018
collapse (mean) mx_18=mx, by(sex nage)
save `b'
use `a', clear
sort sex nage
keep if year == 2020
sort sex nage
save `c'
merge using `b'

drop _merge

* Estimate RR

gen rr = mx/mx_18

save "/Users/.../HMD data/peer_STMF/2020_2018 rate ratios_original source data/austria.dta", replace

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

import excel "/Users/.../Peer Pop Estimates_2018_2020/pop input/bel_pop.xlsx", sheet("Sheet1") firstrow clear

sort year sex nage
merge year sex nage using "/Users/.../STMFinput_7_26/belgium_1820 deaths.dta"

gen mx = (deaths/pop)*100000

drop _merge

* Mx Rate Ratio b/w 2020 and 2018

tempfile a b c

sort country
save `a'
keep if year == 2018

collapse (mean) mx_18=mx, by(sex nage)

save `b'

use `a', clear

sort sex nage

keep if year == 2020

sort sex nage

save `c'

merge using `b'

drop _merge

* Estimate RR

gen rr = mx/mx_18
save "/Users/.../HMD data/peer_STMF/2020_2018 rate ratios_original source
data/belgium.dta", replace

******************************************************************************
*** Canada: Use STMF rates ***
******************************************************************************

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

import excel "/Users/.../Peer Pop Estimates_2018_2020/pop input/den_pop.xlsx", sheet("Sheet1") firstrow clear
sort year sex nage
merge year sex nage using "/Users/.../STMFinput_7_26/denmark_1820 deaths.dta"
gen mx = (deaths/pop)*100000
drop _merge
* Mx Rate Ratio b/w 2020 and 2018
tempfile a b c
sort country
save `a'
keep if year == 2018
collapse (mean) mx_18=mx, by(sex nage)
save `b'
use `a', clear
sort sex nage

keep if year == 2020
sort sex nage
save `c'
merge using `b'
drop _merge
* Estimate RR
gen rr = mx/mx_18
save "/Users/.../HMD data/peer_STMF/2020_2018 rate ratios_original source
data/denmark.dta", replace
import excel "/Users/.../Peer Pop Estimates_2018_2020/pop input/fin_pop.xlsx", sheet("Sheet1") firstrow clear

sort year sex nage
merge year sex nage using "/Users/.../STMFinput_7_26/finland_1820 deaths.dta"

gen mx = (deaths/pop)*100000

drop _merge

* Mx Rate Ratio b/w 2020 and 2018
tempfile a b c

sort country
save `a'
keep if year == 2018
collapse (mean) mx_18=mx, by(sex nage)
save `b'
use `a', clear

sort sex nage
keep if year == 2020
sort sex nage
save `c'
merge using `b'

drop _merge

* Estimate RR
gen rr = mx/mx_18
save "/Users/.../HMD data/peer_STMF/2020_2018 rate ratios_original source data/finland.dta", replace

import excel "/Users/.../Peer Pop Estimates_2018_2020/pop input/fra_pop.xlsx", sheet("Sheet1") firstrow clear

sort year sex nage
merge year sex nage using "~/Users/.../STMFinput_7_26/france_1820 deaths.dta"
gen mx = (deaths/pop)*100000
drop _merge
* Mx Rate Ratio b/w 2020 and 2018
tempfile a b c
sort country
save `a'
keep if year == 2018
collapse (mean) mx_18=mx, by(sex nage)
save `b'
use `a', clear
sort sex nage
keep if year == 2020
sort sex nage
save `c'
merge using `b'
drop _merge
* Estimate RR
gen rr = mx/mx_18
save "/Users/.../HMD data/peer_STMF/2020_2018 rate ratios_original source
data/france.dta", replace

***************
*** Germany ***
***************
import excel "~/Users/.../Peer Pop Estimates_2018_2020/pop input/ger_pop.xlsx", sheet("Sheet1") firstrow clear
sort year sex nage
merge year sex nage using "~/Users/.../STMFinput_7_26/germany_1820 deaths.dta"
gen mx = (deaths/pop)*100000
drop _merge
* Mx Rate Ratio b/w 2020 and 2018
tempfile a b c

sort country
save `a'
keep if year == 2018
collapse (mean) mx_18=mx, by(sex nage)
save `b'
use `a', clear
sort sex nage
keep if year == 2020
sort sex nage
save `c'
merge using `b'
drop _merge
* Estimate RR
gen rr = mx/mx_18
save "/Users/.../HMD data/peer_STMF/2020_2018 rate ratios_original source data/germany.dta", replace

**************
*** Israel ***
**************
import excel "/Users/.../Peer Pop Estimates_2018_2020/pop input/isr_pop.xlsx", sheet("Sheet1") firstrow clear
sort year sex nage
merge year sex nage using "/Users/.../STMFinput_7_26/israel_1820 deaths.dta"
gen mx = (deaths/pop)*100000
drop _merge
* Mx Rate Ratio b/w 2020 and 2018
tempfile a b c
sort country
save `a'
keep if year == 2018
collapse (mean) mx_18=mx, by(sex nage)
save `b'
use `a', clear
sort sex nage
keep if year == 2020
sort sex nage
save `c'
merge using `b'
drop _merge

* Estimate RR
gen rr = mx/mx_18
save "/Users/.../HMD data/peer_STMF/2020_2018 rate ratios_original source data/israel.dta", replace

*************
*** Italy ***
*************

import excel "/Users/.../Peer Pop Estimates_2018_2020/pop input/ita_pop.xlsx",
sheet("Sheet1") firstrow clear
sort year sex nage
merge year sex nage using "/Users/.../STMFinput_7_26/italy_1820 deaths.dta"
gen mx = (deaths/pop)*100000
drop _merge

* Mx Rate Ratio b/w 2020 and 2018
tempfile a b c
sort country
save `a'
keep if year == 2018
collapse (mean) mx_18=mx, by(sex nage)
save `b'
use `a', clear
sort sex nage
keep if year == 2020
sort sex nage  
save `c'  
merge using `b'  

drop _merge  

* Estimate RR  
gen rr = mx/mx_18  
save "/Users/.../HMD data/peer_STMF/2020_2018 rate ratios_original source data/italy.dta", replace  

*************************  
* Korea: Use STMF Rates *  
*************************  

******************************  
* Netherlands: Use STMF Rates *  
******************************  

******************************  
* New Zealand: Use STMF Rates *  
******************************  

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

import excel "/Users/.../Peer Pop Estimates_2018_2020/pop input/nor_pop.xlsx", sheet("Sheet1") firstrow clear  
sort year sex nage  
merge year sex nage using "/Users/.../STMFinput_7_26/norway_1820 deaths.dta"  
gen mx = (deaths/pop)*100000  
drop _merge  

* Mx Rate Ratio b/w 2020 and 2018  
tempfile a b c  
sort country  
save `a'  
keep if year == 2018  
collapse (mean) mx_18=mx, by(sex nage)  
save `b'  
use `a', clear  
sort sex nage
keep if year == 2020
sort sex nage
save `c'
merge using `b'
drop _merge

* Estimate RR
gen rr = mx/mx_18
save "/Users/.../HMD data/peer_STMF/2020_2018 rate ratios_original source data/norway.dta", replace

****************
*** Portugal ***
****************
import excel "/Users/.../Peer Pop Estimates_2018_2020/pop input/por_pop.xlsx", sheet("Sheet1") firstrow clear
sort year sex nage
merge year sex nage using "/Users/.../STMFinput_7_26/portugal_1820 deaths.dta"
gen mx = (deaths/pop)*100000
drop _merge
* Mx Rate Ratio b/w 2020 and 2018
tempfile a b c
sort country
save `a'
keep if year == 2018
collapse (mean) mx_18=mx, by(sex nage)
save `b'
use `a', clear
sort sex nage

keep if year == 2020
sort sex nage
save `c'
merge using `b'
drop _merge

* Estimate RR

gen rr = mx/mx_18

save "~/Users/.../HMD data/peer_STMF/2020_2018 rate ratios_original source data/portugal.dta", replace

*************
*** Spain ***
*************

import excel "~/Users/.../Peer Pop Estimates_2018_2020/pop input/esp_pop.xlsx", sheet("Sheet1") firstrow clear

sort year sex nage
merge year sex nage using "~/Users/.../STMFinput_7_26/spain_1820 deaths.dta"

generate mx = (deaths/pop)*100000

drop _merge

* Mx Rate Ratio b/w 2020 and 2018

tempfile a b c

sort country

save `a'

keep if year == 2018

collapse (mean) mx_18=mx, by(sex nage)

save `b'

use `a', clear

sort sex nage

keep if year == 2020

sort sex nage

save `c'

merge using `b'


drop _merge

* Estimate RR

gen rr = mx/mx_18

save "~/Users/.../HMD data/peer_STMF/2020_2018 rate ratios_original source data/spain.dta", replace
import excel "./Peer Pop Estimates_2018_2020/pop input/swe_pop.xlsx", sheet("Sheet1") firstrow clear

sort year sex nage

merge year sex nage using "./STMFinput_7_26/sweden_1820 deaths.dta"

gen mx = (deaths/pop)*100000

drop _merge

* Mx Rate Ratio b/w 2020 and 2018

tempfile a b c

sort country
save `a'

keep if year == 2018

collapse (mean) mx_18=mx, by(sex nage)

save `b'

use `a', clear

sort sex nage

keep if year == 2020

sort sex nage

save `c'

merge using `b'

drop _merge

* Estimate RR

gen rr = mx/mx_18

save "./HMD data/peer_STMF/2020_2018 rate ratios_original source data/sweden.dta", replace

import excel "./Peer Pop Estimates_2018_2020/pop input/swz_pop.xlsx", sheet("Sheet1") firstrow clear

sort year sex nage
merge year sex nage using "/Users/.../STMInput_7_26/switzerland_1820 deaths.dta"

gen mx = (deaths/pop)*100000

drop _merge

* Mx Rate Ratio b/w 2020 and 2018

tempfile a b c

sort country

save `a'

keep if year == 2018

collapse (mean) mx_18=mx, by(sex nage)

save `b'

use `a', clear

sort sex nage

keep if year == 2020

sort sex nage

save `c'

merge using `b'

drop _merge

* Estimate RR

gen rr = mx/mx_18

save "/Users/.../HMD data/peer_STMF/2020_2018 rate ratios_original source
data/switzerland.dta", replace

**************
*** Taiwan ***
**************

import excel "/Users/.../Peer Pop Estimates_2018_2020/pop input/twn_pop.xlsx",
sheet("Sheet1") firstrow clear

sort year sex nage

merge year sex nage using "/Users/.../STMInput_7_26/taiwan_1820 deaths.dta"

gen mx = (deaths/pop)*100000

drop _merge

* Mx Rate Ratio b/w 2020 and 2018

tempfile a b c
sort country
save `a'
keep if year == 2018
collapse (mean) mx_18=mx, by(sex nage)
save `b'
use `a', clear
sort sex nage
keep if year == 2020
sort sex nage
save `c'
merge using `b'
drop _merge

* Estimate RR
gen rr = mx/mx_18
save "/Users/.../HMD data/peer_STMF/2020_2018 rate ratios_original source
data/taiwan.dta", replace

***** United Kingdom: Northern Ireland, Scotland, England + Wales *****

************************
*** Northern Ireland ***
************************
import excel "/Users/.../Peer Pop Estimates_2018_2020/pop input/nir_pop.xlsx",
sheet("Sheet1") firstrow clear
sort year sex nage
merge year sex nage using "/Users/.../STMFinput_7_26/northern ireland_1820 deaths.dta"
gen mx = (deaths/pop)*100000
drop _merge

* Mx Rate Ratio b/w 2020 and 2018
tempfile a b c
sort country
save `a'
keep if year == 2018
collapse (mean) mx_18=mx, by(sex nage)
save `b'
use `a', clear
sort sex nage
keep if year == 2020
sort sex nage
save `c'
merge using `b'
drop _merge

* Estimate RR
gen rr = mx/mx_18
replace rr = 1 if rr == 0
drop F G
save "'/Users/.../HMD data/peer_STMF/2020_2018 rate ratios_original source data/northern ireland.dta"", replace

***************
*** Scotland ***
***************
import excel "'/Users/.../Peer Pop Estimates_2018_2020/pop input/scot_pop.xlsx", sheet("Sheet1") firstrow clear
drop F G
sort year sex nage
merge year sex nage using "'/Users/.../STMFinput_7_26/scotland_1820 deaths.dta"
gen mx = (deaths/pop)*100000
don _merge
* Mx Rate Ratio b/w 2020 and 2018
tempfile a b c
sort country
save `a'
keep if year == 2018
collapse (mean) mx_18=mx, by(sex nage)
save `b'
use `a', clear
sort sex nage
keep if year == 2020
sort sex nage
save `c'
merge using `b'
drop _merge

* Estimate RR
gen rr = mx/mx_18
save "/Users/.../HMD data/peer_STMF/2020_2018 rate ratios_original source data/scotland.dta", replace

***********************
*** England & Wales ***
***********************
import excel "/Users/.../Peer Pop Estimates_2018_2020/pop input/eng_w_pop.xlsx", sheet("Sheet1") firstrow clear
sort year sex nage
merge year sex nage using "/Users/.../STMFinput_7_26/england_wales_1820 deaths.dta"
gen mx = (deaths/pop)*100000
drop _merge
* Mx Rate Ratio b/w 2020 and 2018
tempfile a b c
sort country
save `a'
keep if year == 2018
collapse (mean) mx_18=mx, by(sex nage)
save `b'
use `a', clear
sort sex nage
keep if year == 2020
sort sex nage

save `c'

merge using `b'

drop _merge

* Estimate RR

gen rr = mx/mx_18

save "/Users/.../HMD data/peer_STMF/2020_2018 rate ratios_original source data/england_wales.dta", replace
e. Python files simulating life tables, Norway’s female population as an example.

```python
# -*- coding: utf-8 -*-

Created August 1

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])
```python
# 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:
    # Random qx by age
    # make this uniform
    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

### calculate life table variables
radix = 1000000.000000

# calculate the number of deaths age0
a0_dx = a0_rand_qx*radix
# calculate survivors
a0_lx=radix
a0_sx=a0_lx/radix
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)
# 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
\[
\begin{align*}
a_{75\_dx} &= a_{75\_rand\_qx} a_{75\_lx} \\
\text{# calculate survivors} \\
a_{80\_lx} &= a_{75\_lx} - a_{75\_dx} \\
a_{80\_sx} &= a_{80\_lx} / \text{radix} \\
\text{# calculate the number of deaths age80} \\
a_{80\_dx} &= a_{80\_rand\_qx} a_{80\_lx} \\
\text{# calculate survivors} \\
a_{85\_lx} &= a_{80\_lx} - a_{80\_dx} \\
a_{85\_sx} &= a_{85\_lx} / \text{radix} \\
\text{# calculate the number of deaths age85} \\
a_{85\_dx} &= a_{85\_rand\_qx} a_{85\_lx} \\
\text{# calculate survivors} \\
a_{90\_lx} &= a_{85\_lx} - a_{85\_dx} \\
a_{90\_sx} &= a_{90\_lx} / \text{radix} \\
\text{# calculate the number of deaths age90} \\
a_{90\_dx} &= a_{90\_rand\_qx} a_{90\_lx} \\
\text{# calculate survivors} \\
a_{95\_lx} &= a_{90\_lx} - a_{90\_dx} \\
a_{95\_sx} &= a_{95\_lx} / \text{radix} \\
\text{# calculate the number of deaths age95} \\
a_{95\_dx} &= a_{95\_rand\_qx} a_{95\_lx} \\
\text{# calculate survivors} \\
a_{100\_lx} &= a_{95\_lx} - a_{95\_dx} \\
a_{100\_sx} &= a_{100\_lx} / \text{radix} \\
\text{# calculate the number of deaths age100} \\
a_{100\_dx} &= a_{100\_rand\_qx} a_{100\_lx} \\
\text{# calculate survivors} \\
a_{105\_lx} &= a_{100\_lx} - a_{100\_dx} \\
a_{105\_sx} &= a_{105\_lx} / \text{radix} \\
\text{# calculate the number of deaths age105} \\
a_{105\_dx} &= a_{105\_rand\_qx} a_{105\_lx} \\
\text{# calculate survivors} \\
a_{110\_lx} &= a_{105\_lx} - a_{105\_dx} \\
a_{110\_sx} &= a_{110\_lx} / \text{radix} \\
\text{# calculate the number of deaths age110} \\
a_{110\_dx} &= a_{110\_rand\_qx} a_{110\_lx} \\
\text{# No Survivors - top-coded} \\
\text{# calculate Lx} \\
a_{0\_Lx} &= (a_{1\_lx} \times 1) + (a_{0\_dx} \times a_{0\_ax}) \\
a_{1\_Lx} &= (a_{5\_lx} \times 4) + (a_{1\_dx} \times a_{1\_ax}) \\
a_{5\_Lx} &= (a_{10\_lx} \times 5) + (a_{5\_dx} \times a_{5\_ax}) \\
a_{10\_Lx} &= (a_{15\_lx} \times 5) + (a_{10\_dx} \times a_{10\_ax}) \\
a_{15\_Lx} &= (a_{20\_lx} \times 5) + (a_{15\_dx} \times a_{15\_ax}) \\
a_{20\_Lx} &= (a_{25\_lx} \times 5) + (a_{20\_dx} \times a_{20\_ax}) \\
a_{25\_Lx} &= (a_{30\_lx} \times 5) + (a_{25\_dx} \times a_{25\_ax}) \\
a_{30\_Lx} &= (a_{35\_lx} \times 5) + (a_{30\_dx} \times a_{30\_ax}) \\
a_{35\_Lx} &= (a_{40\_lx} \times 5) + (a_{35\_dx} \times a_{35\_ax}) \\
a_{40\_Lx} &= (a_{45\_lx} \times 5) + (a_{40\_dx} \times a_{40\_ax}) \\
a_{45\_Lx} &= (a_{50\_lx} \times 5) + (a_{45\_dx} \times a_{45\_ax}) \\
a_{50\_Lx} &= (a_{55\_lx} \times 5) + (a_{50\_dx} \times a_{50\_ax}) \\
a_{55\_Lx} &= (a_{60\_lx} \times 5) + (a_{55\_dx} \times a_{55\_ax}) \\
a_{60\_Lx} &= (a_{65\_lx} \times 5) + (a_{60\_dx} \times a_{60\_ax}) \\
a_{65\_Lx} &= (a_{70\_lx} \times 5) + (a_{65\_dx} \times a_{65\_ax}) \\
a_{70\_Lx} &= (a_{75\_lx} \times 5) + (a_{70\_dx} \times a_{70\_ax}) \\
a_{75\_Lx} &= (a_{80\_lx} \times 5) + (a_{75\_dx} \times a_{75\_ax})
\end{align*}
\]
```plaintext
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+a10_Lx+a1_Lx+a5_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
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_Lx+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, 85-94
```
\[ a_{1564 \text{ qx}} = \frac{(a_{15 \text{ dx}} + a_{20 \text{ dx}} + a_{25 \text{ dx}} + a_{30 \text{ dx}} + a_{35 \text{ dx}} + a_{40 \text{ dx}} + a_{45 \text{ dx}} + a_{50 \text{ dx}} + a_{55 \text{ dx}} + a_{60 \text{ dx}})}{a_{15 \text{ lx}}} \]
\[ a_{6584 \text{ qx}} = \frac{(a_{65 \text{ dx}} + a_{70 \text{ dx}} + a_{75 \text{ dx}} + a_{80 \text{ dx}})}{a_{65 \text{ lx}}} \]
\[ a_{8594 \text{ qx}} = \frac{(a_{85 \text{ dx}} + a_{90 \text{ dx}})}{a_{85 \text{ lx}}} \]

### estimate life expectancy

# calculate \( e_x \)
\[ a_{0 \text{ ex}} = \frac{a_{0 \text{ Tx}}}{\text{radix}} \]
\[ a_{1 \text{ ex}} = \frac{a_{1 \text{ Tx}}}{a_{1 \text{ lx}}} \]
\[ a_{5 \text{ ex}} = \frac{a_{5 \text{ Tx}}}{a_{5 \text{ lx}}} \]
\[ a_{10 \text{ ex}} = \frac{a_{10 \text{ Tx}}}{a_{10 \text{ lx}}} \]
\[ a_{15 \text{ ex}} = \frac{a_{15 \text{ Tx}}}{a_{15 \text{ lx}}} \]
\[ a_{20 \text{ ex}} = \frac{a_{20 \text{ Tx}}}{a_{20 \text{ lx}}} \]
\[ a_{25 \text{ ex}} = \frac{a_{25 \text{ Tx}}}{a_{25 \text{ lx}}} \]
\[ a_{30 \text{ ex}} = \frac{a_{30 \text{ Tx}}}{a_{30 \text{ lx}}} \]
\[ a_{35 \text{ ex}} = \frac{a_{35 \text{ Tx}}}{a_{35 \text{ lx}}} \]
\[ a_{40 \text{ ex}} = \frac{a_{40 \text{ Tx}}}{a_{40 \text{ lx}}} \]
\[ a_{45 \text{ ex}} = \frac{a_{45 \text{ Tx}}}{a_{45 \text{ lx}}} \]
\[ a_{50 \text{ ex}} = \frac{a_{50 \text{ Tx}}}{a_{50 \text{ lx}}} \]
\[ a_{55 \text{ ex}} = \frac{a_{55 \text{ Tx}}}{a_{55 \text{ lx}}} \]
\[ a_{60 \text{ ex}} = \frac{a_{60 \text{ Tx}}}{a_{60 \text{ lx}}} \]
\[ a_{65 \text{ ex}} = \frac{a_{65 \text{ Tx}}}{a_{65 \text{ lx}}} \]
\[ a_{70 \text{ ex}} = \frac{a_{70 \text{ Tx}}}{a_{70 \text{ lx}}} \]
\[ a_{75 \text{ ex}} = \frac{a_{75 \text{ Tx}}}{a_{75 \text{ lx}}} \]
\[ a_{80 \text{ ex}} = \frac{a_{80 \text{ Tx}}}{a_{80 \text{ lx}}} \]
\[ a_{85 \text{ ex}} = \frac{a_{85 \text{ Tx}}}{a_{85 \text{ lx}}} \]
\[ a_{90 \text{ ex}} = \frac{a_{90 \text{ Tx}}}{a_{90 \text{ lx}}} \]
\[ a_{95 \text{ ex}} = \frac{a_{95 \text{ Tx}}}{a_{95 \text{ lx}}} \]
\[ a_{100 \text{ ex}} = \frac{a_{100 \text{ Tx}}}{a_{100 \text{ lx}}} \]
\[ a_{105 \text{ ex}} = \frac{a_{105 \text{ Tx}}}{a_{105 \text{ lx}}} \]
\[ a_{110 \text{ ex}} = \frac{a_{110 \text{ Tx}}}{a_{110 \text{ lx}}} \]

# this outputs the probabilities of each estimate as a check

filenm = r"/.../nor_f_qx.txt"
opened_file = open(filenm, 'a')

if count==0:
    opened_file.write('{0} {1} {2}
{3}
'.format("sim_num","qx1564","qx6584","qx8594"))
else:
    opened_file.write('{0} {1} {2}
{3}
'.format(count,a1564_qx,a6584_qx,a8594_qx))

# save data

tot_file_name = r"/.../nor_f_ex.txt"
tot_opened_file = open(tot_file_name, 'a')

if count==0:
    tot_opened_file.write('{0} {1} {2} {3}
{4}
'.format("sim_num","age","sx","ex","count"))
tot_opened_file.write('{0} {1} {2} {3}
{4}
'.format(count,"0",a0_sx,a0_ex))
tot_opened_file.write('{0} {1} {2} {3}
{4}
'.format(count,"1",a1_sx,a1_ex))
tot_opened_file.write('{0} {1} {2} {3}
{4}
'.format(count,"5",a5_sx,a5_ex))
tot_opened_file.write('{0} {1} {2} {3}
{4}
'.format(count,"10",a10_sx,a10_ex))
tot_opened_file.write('{0} {1} {2} {3}
{4}
'.format(count,"15",a15_sx,a15_ex))
tot_opened_file.write('{0} {1} {2} {3}
{4}
'.format(count,"20",a20_sx,a20_ex))
print(count)
count += 1  # This is the same as count = count + 1

tot_opened_file.close()
opened_file.close()

print("simulation completed")
f. Stata files estimating median $e_x$, $P_5 e_x$, and $P_{95} e_x$ in life expectancy distributions from simulated life tables.

******************************************************************************
******************************************************************************
******************************************************************************
Append all Countries******************************************************************************
******************************************************************************
******************************************************************************

* Austria, Female
import delimited "/Users/.../aut_f_ex.txt", delimiter(space) varnames(1) encoding(ISO-8859-1) clear
gen country="Austria"
save "/Users/.../aut_f.dta", replace

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

gen country="Belgium"
save "/Users/.../bel_f.dta", replace

* Canada, Female
import delimited "/Users/.../can_f_ex.txt", delimiter(space) encoding(ISO-8859-1)
clear

gen country="Canada"
save "/Users/.../can_f.dta", replace

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

gen country="Denmark"
save "/Users/.../den_f.dta", replace

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

gen country="Finland"
save "/Users/.../fin_f.dta", replace

* Germany, Female
import delimited "/Users/.../ger_f_ex.txt", delimiter(space) encoding(ISO-8859-1)
clear

gen country="Germany"
save "/Users/.../ger_f.dta", replace

* England, Female
import delimited "/Users/.../eng_w_f_ex.txt", delimiter(space) encoding(ISO-8859-1)
clear

gen country="England & Wales"
save "/Users/.../eng_w_f.dta", replace

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

gen country="Spain"
save "/Users/.../esp_f.dta", replace

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

gen country="France"
save "/Users/.../fra_f.dta", replace

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

gen country="Israel"
save "/Users/.../isr_f.dta", replace

* Italy, Female
import delimited "/Users/.../ita_f_ex.txt", delimiter(space) encoding(ISO-8859-1)
clear

gen country="Italy"
save "/Users/.../ita_f.dta", replace

* Northern Ireland, Female
import delimited "/Users/.../nir_f_ex.txt", delimiter(space) encoding(ISO-8859-1)
clear

gen country="Northern Ireland"
save "/Users/.../nir_f.dta", replace

* Netherlands, Female
import delimited "/Users/.../nth_f_ex.txt", delimiter(space) encoding(ISO-8859-1)
clear

gen country="Netherlands"
save "/Users/.../nth_f.dta", replace

* Norway, Female
import delimited "~/nor_f_ex.txt", delimiter(space) encoding(ISO-8859-1)
clear
gen country="Norway"
save "~/nor_f.dta", replace

* Portugal, Female
import delimited "~/por_f_ex.txt", delimiter(space) encoding(ISO-8859-1)
clear
gen country="Portugal"
save "~/por_f.dta", replace

* Scotland, Female
import delimited "~/sco_f_ex.txt", delimiter(space) encoding(ISO-8859-1)
clear
gen country="Scotland"
save "~/sco_f.dta", replace

* Sweden, Female
import delimited "~/swe_f_ex.txt", delimiter(space) encoding(ISO-8859-1)
clear
gen country="Sweden"
save "~/swe_f.dta", replace

* Switzerland, Female
import delimited "~/swz_f_ex.txt", delimiter(space) encoding(ISO-8859-1)
clear
gen country="Switzerland"
save "~/swz_f.dta", replace

* Taiwan, Female
import delimited "~/twn_f_ex.txt", delimiter(space) encoding(ISO-8859-1)
clear
gen country="Taiwan"
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"
save "~/nz_f.dta", replace
use "~/aut_f.dta", clear
append using "~/bel_f.dta"
append using "/Users/.../can_f.dta"
append using "/Users/.../den_f.dta"
append using "/Users/.../fin_f.dta"
append using "/Users/.../ger_f.dta"
append using "/Users/.../eng_w_f.dta"
append using "/Users/.../esp_f.dta"
append using "/Users/.../fra_f.dta"
append using "/Users/.../isr_f.dta"
append using "/Users/.../ita_f.dta"
append using "/Users/.../nir_f.dta"
append using "/Users/.../nth_f.dta"
append using "/Users/.../nor_f.dta"
append using "/Users/.../por_f.dta"
append using "/Users/.../sco_f.dta"
append using "/Users/.../swe_f.dta"
append using "/Users/.../swz_f.dta"
append using "/Users/.../twn_f.dta"
append using "/Users/.../nz_f.dta"
save "/Users/.../Female_2020ex_sim.dta", replace

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

************************************
****** Probabilities of Death ******
************************************

* Austria, Female

import delimited "/Users/.../aut_f_qx.txt", delimiter(space) varnames(1) encoding(ISO-8859-1)clear
gen country="Austria"
save "/Users/.../aut_f_qx.dta", replace

* Belgium, Female

import delimited "/Users/.../bel_f_qx.txt", delimiter(space) encoding(ISO-8859-1)clear
gen country="Belgium"
save "/Users/.../bel_f_qx.dta", replace

* Canada, Female

import delimited "/Users/.../can_f_qx.txt", delimiter(space) encoding(ISO-8859-1)clear
gen country="Canada"
save "/Users/.../can_f_qx.dta", replace

* Denmark, Female

import delimited "/Users/.../den_f_qx.txt", delimiter(space) encoding(ISO-8859-1)clear
gen country="Denmark"
save "/Users/.../den_f_qx.dta", replace
* Finland, Female

import delimited "'/Users/.../fin_f_qx.txt', delimiter(space) encoding(ISO-8859-1)"
clear
gen country="Finland"
save "'/Users/.../fin_f_qx.dta', replace

* Germany, Female

import delimited "'/Users/.../ger_f_qx.txt', delimiter(space) encoding(ISO-8859-1)"
clear
gen country="Germany"
save "'/Users/.../ger_f_qx.dta', replace

* England, Female

import delimited "'/Users/.../eng_w_f_qx.txt', delimiter(space) encoding(ISO-8859-1)"
clear
gen country="England & Wales"
save "'/Users/.../eng_w_f_qx.dta', replace

* Spain, Female

import delimited "'/Users/.../esp_f_qx.txt', delimiter(space) encoding(ISO-8859-1)"
clear
gen country="Spain"
save "'/Users/.../esp_f_qx.dta', replace

* France, Female

import delimited "'/Users/.../fra_f_qx.txt', delimiter(space) encoding(ISO-8859-1)"
clear
gen country="France"
save "'/Users/.../fra_f_qx.dta', replace

* Israel, Female

import delimited "'/Users/.../isr_f_qx.txt', delimiter(space) encoding(ISO-8859-1)"
clear
gen country="Israel"
save "'/Users/.../isr_f_qx.dta', replace

* Italy, Female

import delimited "'/Users/.../ita_f_qx.txt', delimiter(space) encoding(ISO-8859-1)"
clear
gen country="Italy"
save "'/Users/.../ita_f_qx.dta', replace
* Northern Ireland, Female
import delimited "~/data/nir_f_qx.txt", delimiter(space) encoding(ISO-8859-1)
clear
gen country="Northern Ireland"
save "~/data/nir_f_qx.dta", replace

* Netherlands, Female
import delimited "~/data/nth_f_qx.txt", delimiter(space) encoding(ISO-8859-1)
clear
gen country="Netherlands"
save "~/data/nth_f_qx.dta", replace

* Norway, Female
import delimited "~/data/nor_f_qx.txt", delimiter(space) encoding(ISO-8859-1)
clear
gen country="Norway"
save "~/data/nor_f_qx.dta", replace

* Portugal, Female
import delimited "~/data/por_f_qx.txt", delimiter(space) encoding(ISO-8859-1)
clear
gen country="Portugal"
save "~/data/por_f_qx.dta", replace

* Scotland, Female
import delimited "~/data/sco_f_qx.txt", delimiter(space) encoding(ISO-8859-1)
clear
gen country="Scotland"
save "~/data/sco_f_qx.dta", replace

* Sweden, Female
import delimited "~/data/swe_f_qx.txt", delimiter(space) encoding(ISO-8859-1)
clear
gen country="Sweden"
save "~/data/swe_f_qx.dta", replace

* Switzerland, Female
import delimited "~/data/swz_f_qx.txt", delimiter(space) encoding(ISO-8859-1)
clear
gen country="Switzerland"
save "~/data/swz_f_qx.dta", replace
* Taiwan, Female
import delimited "~/twn_f_qx.txt", delimiter(space) encoding(ISO-8859-1) clear
   gen country="Taiwan"
save "~/twn_f_qx.dta", replace

* New Zealand, Female
import delimited "~/nz_f_qx.txt", delimiter(space) encoding(ISO-8859-1) clear
gen country="New Zealand"
save "~/nz_f_qx.dta", replace

**********************************************************
***************** Append all Countries *******************
***** Distributions of Sim qx for 18 peer countries *****
**********************************************************

use "~/aut_f_qx.dta", clear
append using "~/bel_f_qx.dta"
append using "~/can_f_qx.dta"
append using "~/den_f_qx.dta"
append using "~/fin_f_qx.dta"
append using "~/ger_f_qx.dta"
append using "~/eng_w_f_qx.dta"
append using "~/esp_f_qx.dta"
append using "~/fra_f_qx.dta"
append using "~/isr_f_qx.dta"
append using "~/ita_f_qx.dta"
append using "~/nir_f_qx.dta"
append using "~/nth_f_qx.dta"
append using "~/nor_f_qx.dta"
append using "~/por_f_qx.dta"
append using "~/sco_f_qx.dta"
append using "~/swe_f_qx.dta"
append using "~/swz_f_qx.dta"
append using "~/twn_f_qx.dta"
append using "~/nz_f_qx.dta"
save "~/Female_2020qx_sim.dta", replace

replace qx8594 = . if country == "New Zealand"
tabstat qx1564, statistics( p5 p50 p95 ) by(country)
tabstat qx6584, statistics( p5 p50 p95 ) by(country)
tabstat qx8594, statistics( p5 p50 p95 ) by(country)
bysort country: egen med_qx1564 = median(qx1564)
sum med_qx1564
bysort country: egen med_qx6584 = median(qx6584)
sum med_qx6584
bysort country: egen med_qx8594 = median(qx8594)
sum med_qx8594