

Estimating and modelling mortality rates in the absence of population denominators

Andrés M. Villegas and Munir Hiabu



AFRIC, Victorial Falls, Zimbabwe
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Agenda

- Motivation
- Calculating the (forward) mortality rate (the usual way – if population data is available)
- The reversed mortality rate
 - ▷ From reversed mortality rate to forward mortality rate
 - ▷ Modelling the reversed mortality rate
- Illustration using HMD data for England and Wales males
- Conclusion

Motivation

- Mortality rate (heuristic):

$$\frac{\# \text{ occurred deaths}}{\text{population size}}$$

- Problem: Denominator often poor quality or not known at all.
 - ▷ Developing countries
 - ▷ Subpopulations
 - ▷ Old ages

Motivation - Quality of population data is sometimes doubtful



Colombia's population was **overestimated by 5 million**: Instead of the projected 50 millions population expected in 2018 in the Census 2005 projections, the population in 2018 was 45.5 million

Calculating the mortality rate (the usual way – if population data is available)

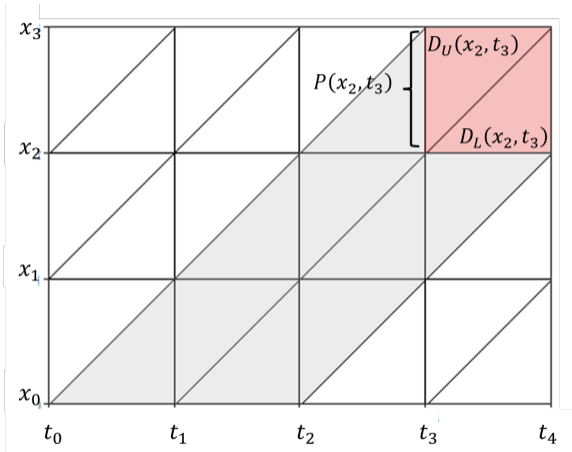
Calculating the mortality rate (the usual way – if population data is available)

We are interested in estimating the (forward) mortality rate

$$\mu(x|t) = \lim_{h \downarrow 0} h^{-1} \Pr\{\underbrace{X \in [x, x+h] | X \geq x, T - X = t - x}_{\text{Die in the next instant given survival to age } x}\}.$$

- X is age of death
- T is date (also called period) of death
- $C = T - X$ is cohort; known before death

Calculating the mortality rate – The Lexis diagram



$$D_U(x_j, t_k) = \sum_i I\{X_i \in [x_j, x_{j+1}), T_i - X_i \in [t_k - x_{j+1}, t_k - x_j)\}$$

$$D_L(x_j, t_k) = \sum_i I\{X_i \in [x_j, x_{j+1}), T_i - X_i \in [t_k - x_j, t_{k+1} - x_j)\}$$

$$P(x_j, t_k) = \sum_i I\{T_i > t_k, T_i - X_i \in [t_k - x_{j+1}, t_k - x_j)\}$$

Calculating the mortality rate (the usual way – if population data is available) – central mortality rate

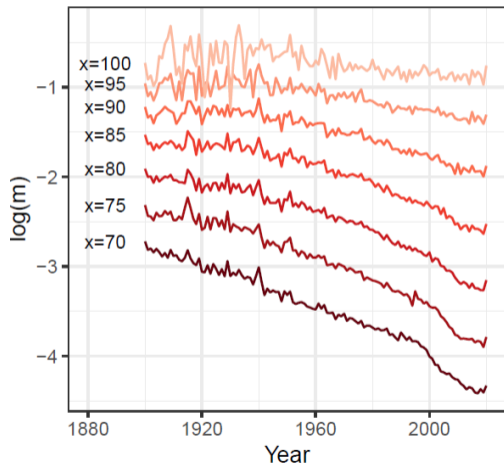
The central mortality rate is defined as

$$m(x_j|t_k) = \frac{D(x_j, t_k)}{E(x_j, t_k)} = \frac{D(x_j, t_k)}{\frac{1}{2}\{P(x_j, t_k) + P(x_j, t_{k+1})\} + \frac{1}{3}\{D_L(x_j, t_k) - D_U(x_j, t_k)\}}.$$

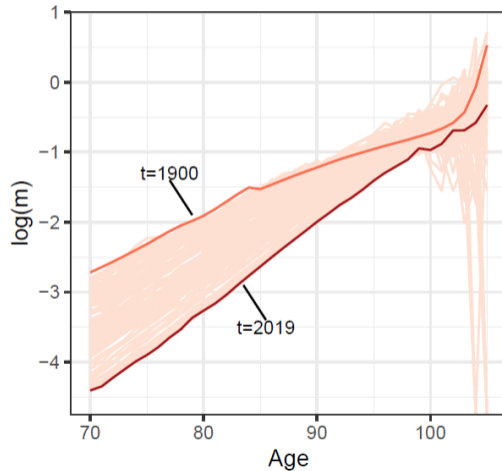
Under appropriate assumptions, $m(x_j|t_k)$ is an **unbiased estimator** of the expected value of $\mu(X|T)$ for (X, T) conditioned on the square $[x_j, x_j + 1) \times [t_k, t_k + 1)$.

The central mortality rate (England and Wales males)

Time trends (mortality rate)



Age profile (mortality rate)



Back to the original question:

Can we estimate the mortality rate without using information on the size of the population P ?

- Maybe.
- Let's look at the **reversed mortality** first.

The reversed mortality rate

We aim to estimate

$$\mu^R(x|t) = \lim_{h \downarrow 0} h^{-1} \Pr\{ \underbrace{X \in (x-h, x] | X \leq x, C = c}_{\text{Die in the previous instant given dead by age } x} \}.$$

The **reversed** central mortality rate is given as

$$m^R(x_j | t_k) = \frac{D(x_j, t_k)}{E^R(x_j, t_k)}.$$

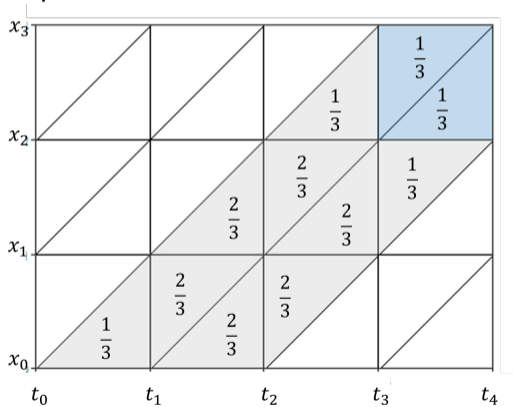
- The deaths counts $D(x_j, t_k)$ are the same as before
- Now: How to calculate $E^R(x_j, t_k)$?

Exposed to risk (Under the assumption of closed population)

- Forward rate: The number of people at risk of dying in next instant is the number of all future deaths. But this number is only known for extinct cohorts.
- Reversed rate: The number of people at risk of having died in the previous instant is the number of all people who have already died. **This number can be counted from death data.**

The reversed mortality rate – how to calculate $E^R(x_j, t_k)$

The figures below show the weights of the deaths when calculating the exposure.



$$\begin{aligned} \hat{E}^R(x_j, t_k) = & \frac{1}{3} \{D_U(x_j, t_k) + D_L(x_j, t_k)\} \\ & + \frac{1}{3} \sum_{l=0}^j D_L(x_{j-l}, t_{k-l-1}) + D_U(x_{j-l-1}, t_{k-l}) \\ & + \frac{2}{3} \sum_{l=1}^j D_U(x_{j-l}, t_{k-l}) + D_L(x_{j-l}, t_{k-l}) \end{aligned}$$

The reversed mortality rate

Under appropriate assumption,

$$m^R(x_j|t_k) = \frac{D(x_j, t_k)}{E^R(x_j, t_k)},$$

is an **unbiased estimator** of the expected value of $\mu^R(X|T)$ for (X, T) conditioned on the square $[x_j, x_j + 1) \times [t_k, t_k + 1)$.

Is the reversed mortality rate useful?

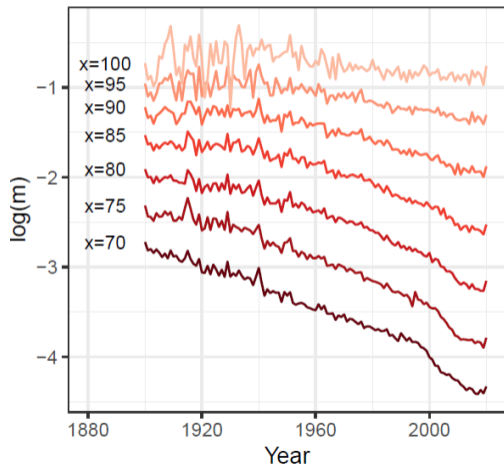
1. The reversed mortality rate can be interesting in **its own right**.
2. We can use the reversed mortality rate to **estimate the forward mortality rate**.
3. Modelling the reversed rate can give a **new perspective on mortality forecasting**.

Illustration using HMD data for England and Wales males

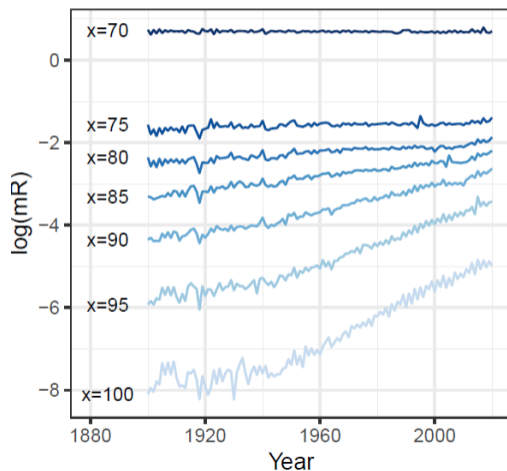
Reversed mortality rate can be interesting in its own right

Time trends

Time trends (mortality rate)



Time trends (reverse mortality rate)



Reversed mortality rate can be interesting in its own right

Age profile

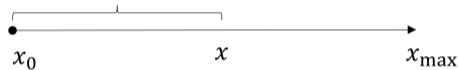


We can use the reversed mortality rate to estimate the forward mortality rate.

Relationship between reversed mortality rate and forward mortality rate

Forward time

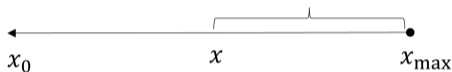
Survive to age x and die in the next instant



- $\mu(x) = \lim_{h \downarrow 0} h^{-1} \Pr\{X \in [x, x+h)\}$
- $f(x) = S(x)\mu(x)$
- $S(x) = e^{-\int_{x_0}^x \mu(v)dv}$

Reversed time

Be dead by age x and have died in the previous instant



- $\mu^R(x) = \lim_{h \downarrow 0} h^{-1} \Pr\{X \in (x-h, x]\}$
- $f(x) = F(x)\mu^R(x)$
- $F(x) = e^{-\int_x^{x_{\max}} \mu^R(v)dv}$

$$S(x)\mu(x) = F(x)\mu^R(x)$$

From reversed mortality rate to forward mortality rate

We have then

$$\mu(x|t) = \mu^R(x|t) \frac{e^{-\int_x^{x_{\max}} \mu^R(v|t-x+v)dv}}{1 - e^{-\int_x^{x_{\max}} \mu^R(v|t-x+v)dv}},$$

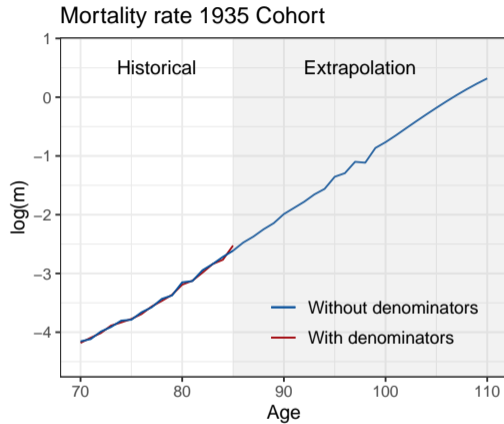
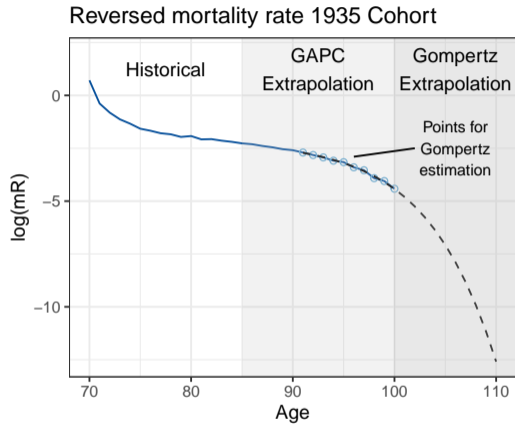
where

$$\frac{e^{-\int_x^{x_{\max}} \mu^R(v|t-x+v)dv}}{1 - e^{-\int_x^{x_{\max}} \mu^R(v|t-x+v)dv}} = \frac{\text{Probability of dying before } x}{\text{Probability of dying after } x}$$

Problem: The integral runs over **unobserved ages for non-extinct cohorts**.

Solution: **Extrapolate the reversed mortality rate** to complete data for non-extinct cohort

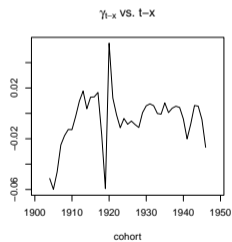
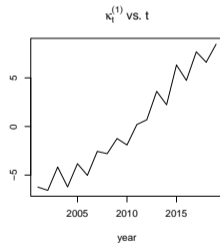
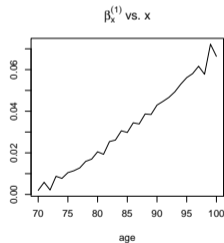
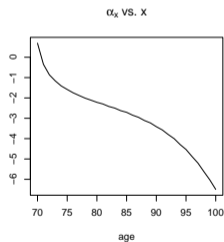
From reversed mortality rate to forward mortality rate



$$q^R(x_l) = \frac{2m^R(x_l)}{2 + m^R(x_l)}, \quad m^F(x_j) = m^R(x_j) \frac{\prod_{l=j}^J \{1 - q^R(x_l)\}}{1 - \prod_{l=j}^J \{1 - q^R(x_l)\}}$$

Lee-Carter + Cohorts in Reverse

$$\log m^R(x|t) = \alpha_x + \beta_x^{(1)} \kappa_t^{(1)} + \gamma_{t-x}$$



Gompertz model in Reverse

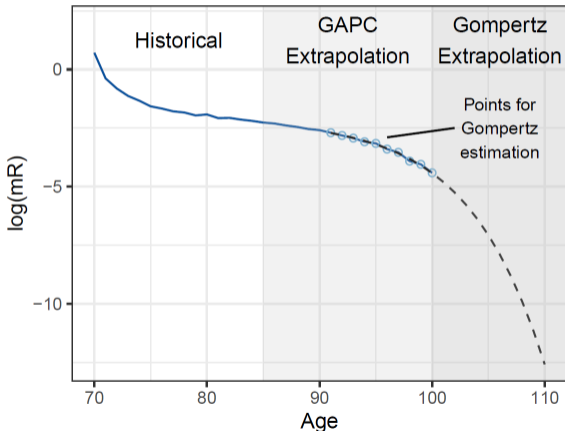
- Gompertz law

$$\mu(x) = e^{a+bx}$$

- Reversed Gompertz law

$$\mu^R(x) = e^{a+bx} \frac{\exp\left[-\frac{e^a}{b}(e^{bx} - 1)\right]}{1 - \exp\left[-\frac{e^a}{b}(e^{bx} - 1)\right]}$$

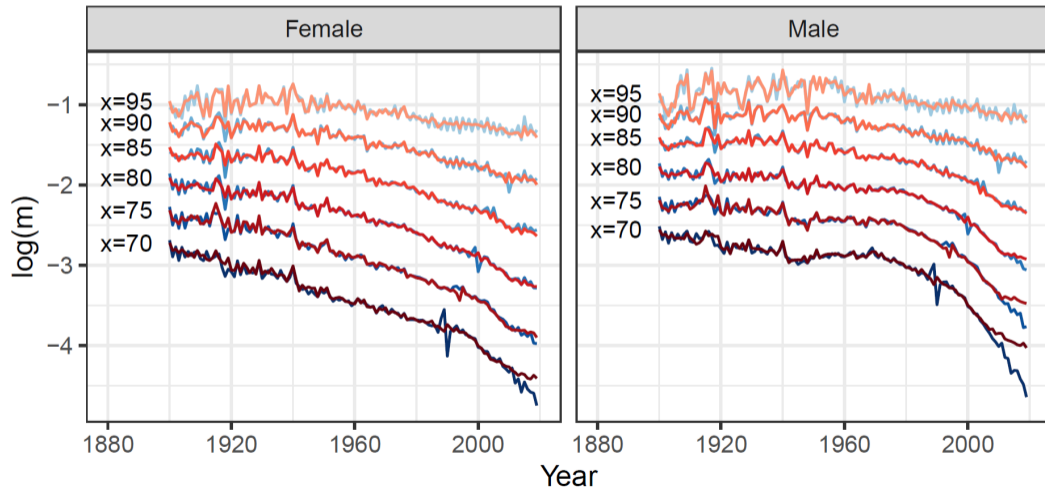
Reversed mortality rate 1935 Cohort



How does the traditional central mortality rate $m(x_j, t_k)$ which uses population data, compare to $m^F(x_j, t_k)$ which only uses death counts?

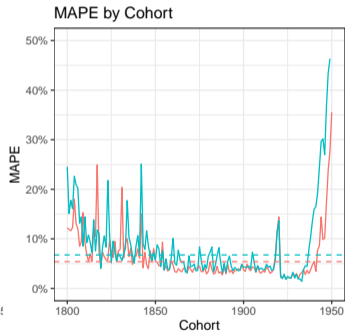
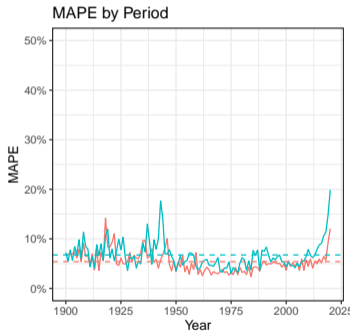
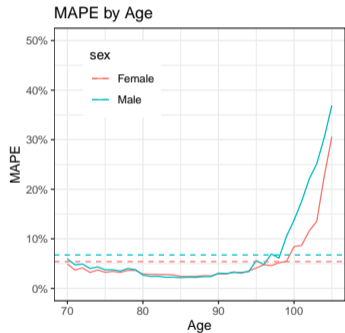
Mortality rates - England and Wales

Mortality rate



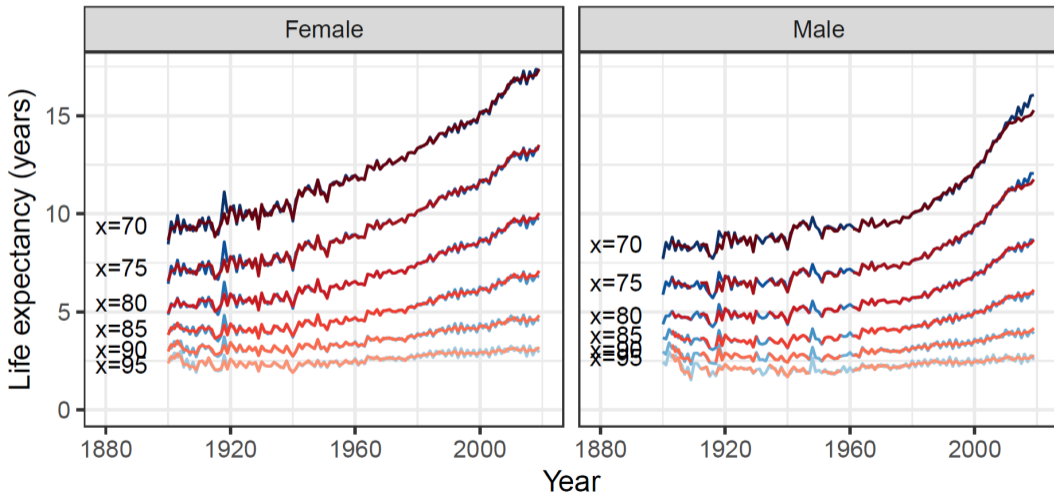
Mortality rates - England and Wales

Mean Absolute Percentage Error



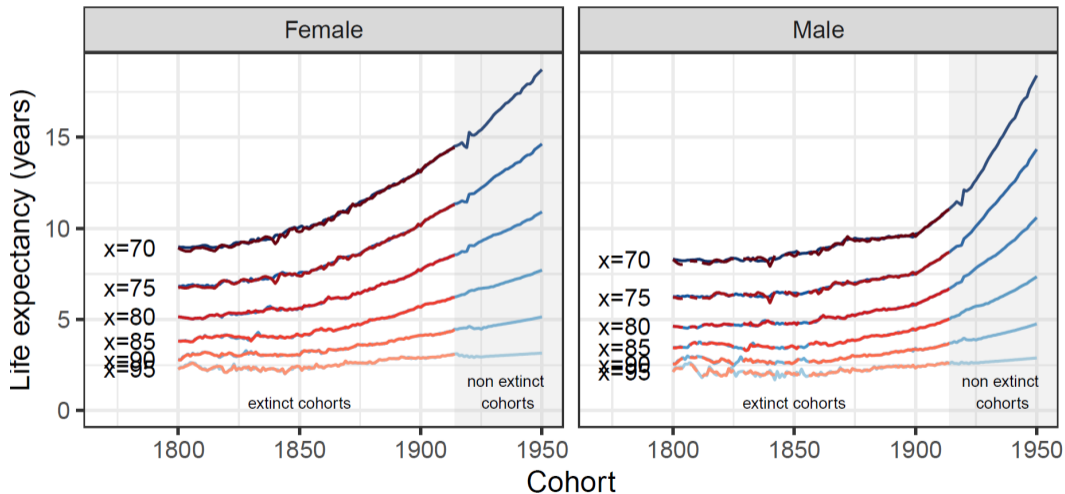
Period Life Expectancy - England and Wales

Period life expectancy



Cohort Life Expectancy - England and Wales

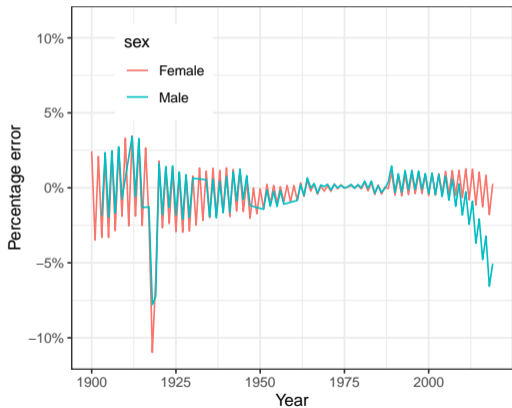
Cohort life expectancy



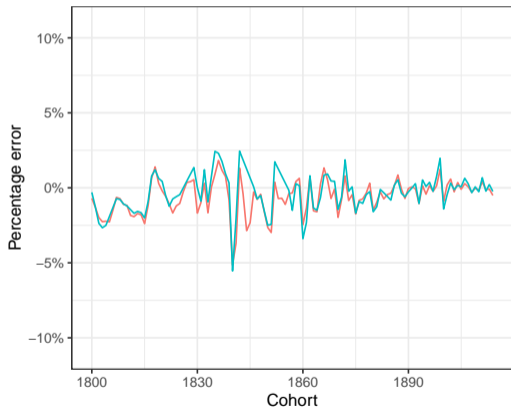
Life Expectancy - England and Wales

Percentage Error

Period Life Expectancy at age 70



Cohort Life Expectancy at age 70



Conclusion

- The actual size of the population of interest, if available at all, can often be poor quality
- Propose a way to estimate mortality rates by using death counts only
- The propose approach is reasonably accurate
 - ▷ Good fit of rates along both period and cohort
 - ▷ Good estimates and projections of life expectancies
- Useful new perspective for projection of mortality at older ages
 - ▷ Explore out-of-sample forecast accuracy
 - ▷ Check consistency of projections using population sizes
 - ▷ Add diversity of projections → model ensembles

Thank you!

a.villegas@unsw.edu.au