

Estimating and modelling mortality rates in the absence of population denominators

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Agenda

Motivation

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

The reversed mortality rate

B From reversed mortality rate to forward mortality rate

B 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.

- B Developing countries
- B Subpopulations
- B 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)

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We are interested in estimating the (forward) mortality rate

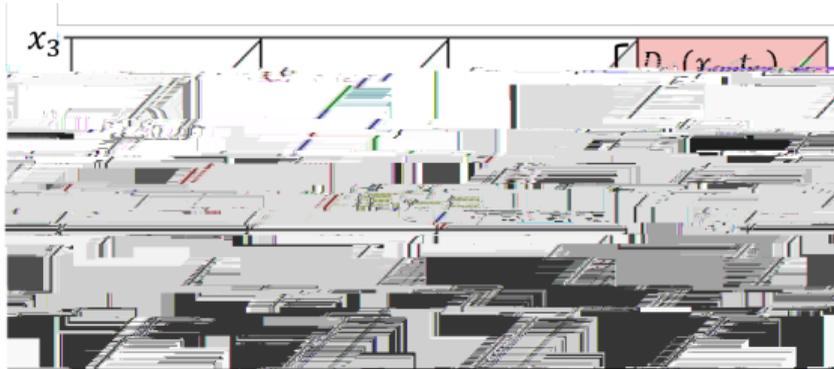
$$(x|t) = \lim_{h \rightarrow 0} \frac{1}{h} \Pr \left\{ \underbrace{X \in [x, x+h] \mid X \geq x, T = t}_{\text{Die in the next instant given survival to age } x} \right\}$$

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



$$D_U(x_j; t_k) = \sum_{i=0}^{\infty} \text{If } X_i \in [x_j; x_{j+1}); T_i \in [t_k; x_{j+1}; t_k; x_j) g$$

$$D_L(x_j; t_k) = \sum_{i=0}^j \text{If } X_i \in [x_j; x_{j+1}); T_i \in [t_k; x_j; t_{k+1}; x_j) g$$

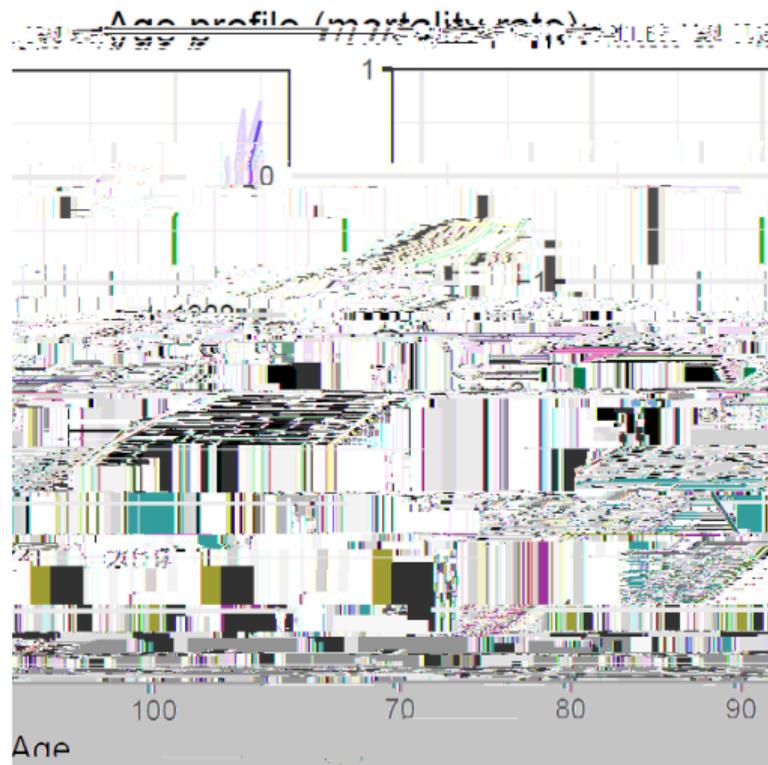
$$P(x_j; t_k) = \sum_{i=0}^j \text{If } T_i > t_k; T_i \in [t_k; x_{j+1}; t_k; x_j)$$

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

The central mortality rate is defined as

$$m(x_j; t_k) = \frac{D(x_j; t_k)}{E(x_j; t_k)} = \frac{D(x_j; t_k)}{\frac{1}{2}f P(x_j; t_k) + P(x_j; t_{k+1})g + \frac{1}{3}f D_L(x_j; t_k)}$$

The central mortality rate (England and Wales males)



The reversed mortality rate

We aim to estimate

$${}^R m(x; t) = \lim_{h \rightarrow 0} \frac{1}{h} \Pr \left\{ \underbrace{X(t) = x \mid X(t-h) = x}_{\text{Die in the previous instant given dead by age } x} \right\} \quad C = \text{cg}$$

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

$$m^R(x; t_k) = \frac{D(x; t_k)}{E^R(x; t_k)}$$

The deaths counts $D(x; t_k)$ are the same as before

Now: How to calculate $E^R(x; t_k)$?

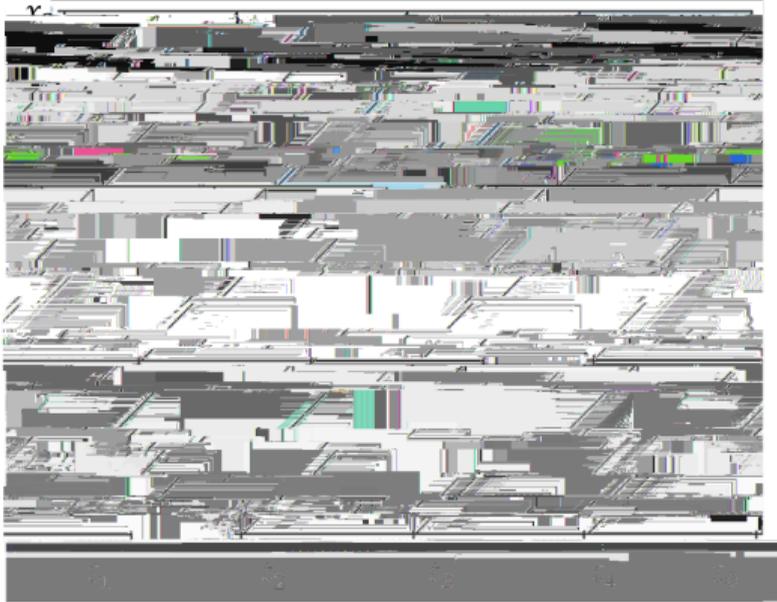
Exposed to risk (Under the assumption of closed population)

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.



$$\begin{aligned} e^R(x_j; t_k) = & \\ & \frac{1}{3} f D_U(x_j; t_k) + D_L(x_j; t_k) g \\ & + \frac{1}{3} X^j \sum_{l=0} D_L(x_{j-1}; t_{k-1}) + D_U(x_{j-1}; t_{k-1}) \\ & + \frac{2}{3} X^j \sum_{l=1} D_U(x_{j-1}; t_{k-1}) + D_L(x_{j-1}; t_{k-1}) \end{aligned}$$

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 ${}^R(X; T)$ for $(X; T)$ conditioned on the square $[x_j; x_j + 1) \quad [t_k; t_k + 1)$.

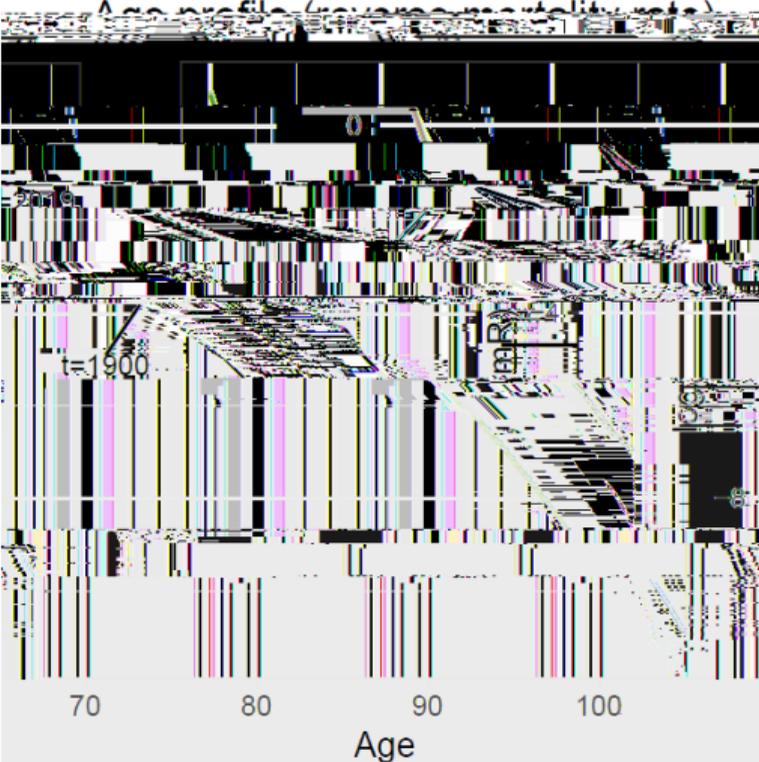
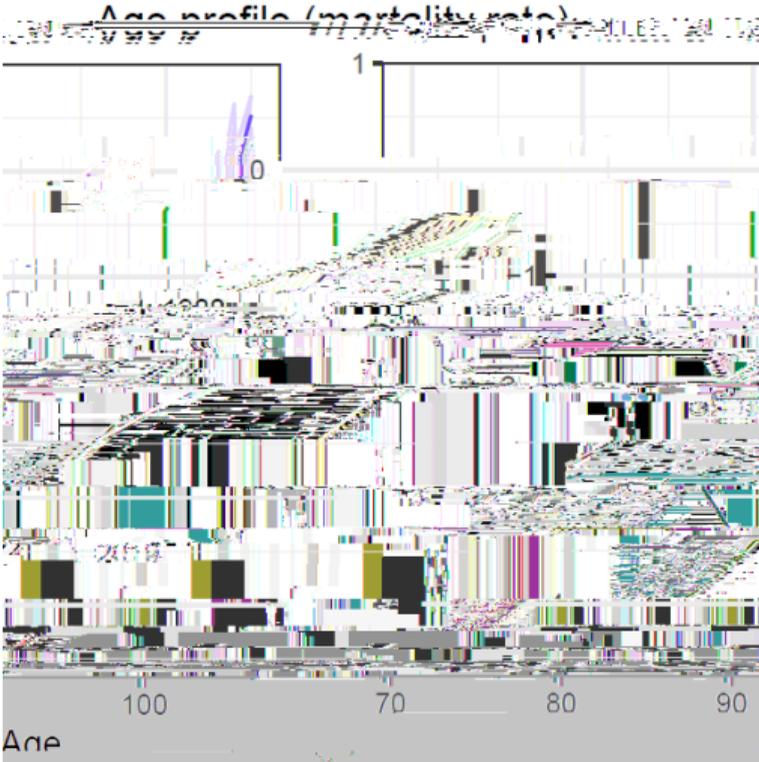
Is the reversed mortality rate useful?

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**.

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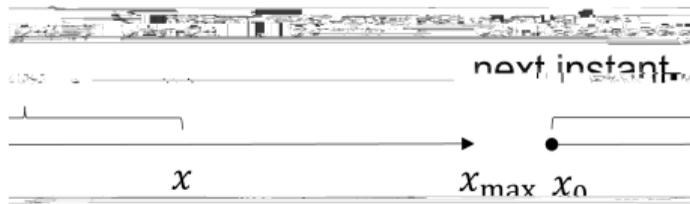
Age profile



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

Relationship between reversed mortality rate and forward mortality rate

Forward time



$$f(x) = \lim_{h \neq 0} \frac{1}{h} \Pr\{X \in [x; x+h) | X \geq x\}$$

$$f(x) = S(x) \mu(x)$$

$$S(x) = e^{-\int_0^x \mu(t) dt}$$

From reversed mortality rate to forward mortality rate

We have then

$${}_xq_{jt} = {}_xR(xjt) \frac{e^{-\int_x^{x_{\max}} \mu(v|jt, x+v) dv}}{1 - e^{-\int_x^{x_{\max}} \mu(v|jt, x+v) dv}};$$

where

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

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

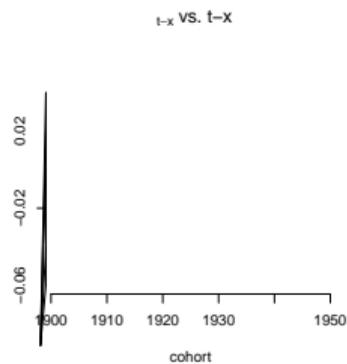
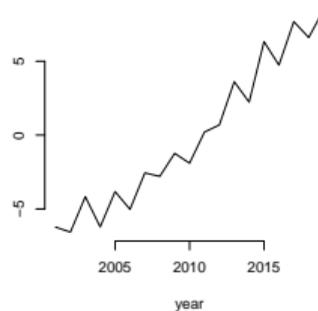
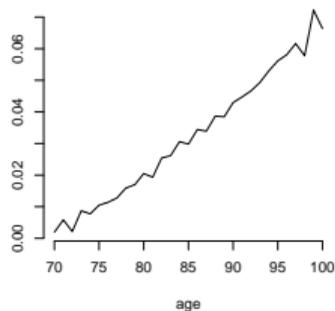
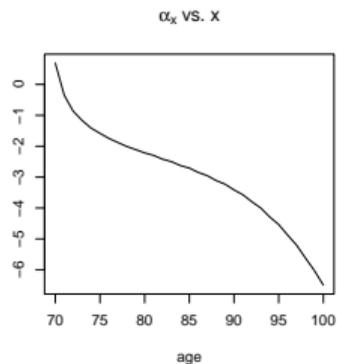
Solution: **Extrapolate the reversed mortality rate** to complete data for non-extinct cohort

From reversed mortality rate to forward mortality rate

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

Lee-Carter + Cohorts in Reverse

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



Gompertz model in Reverse

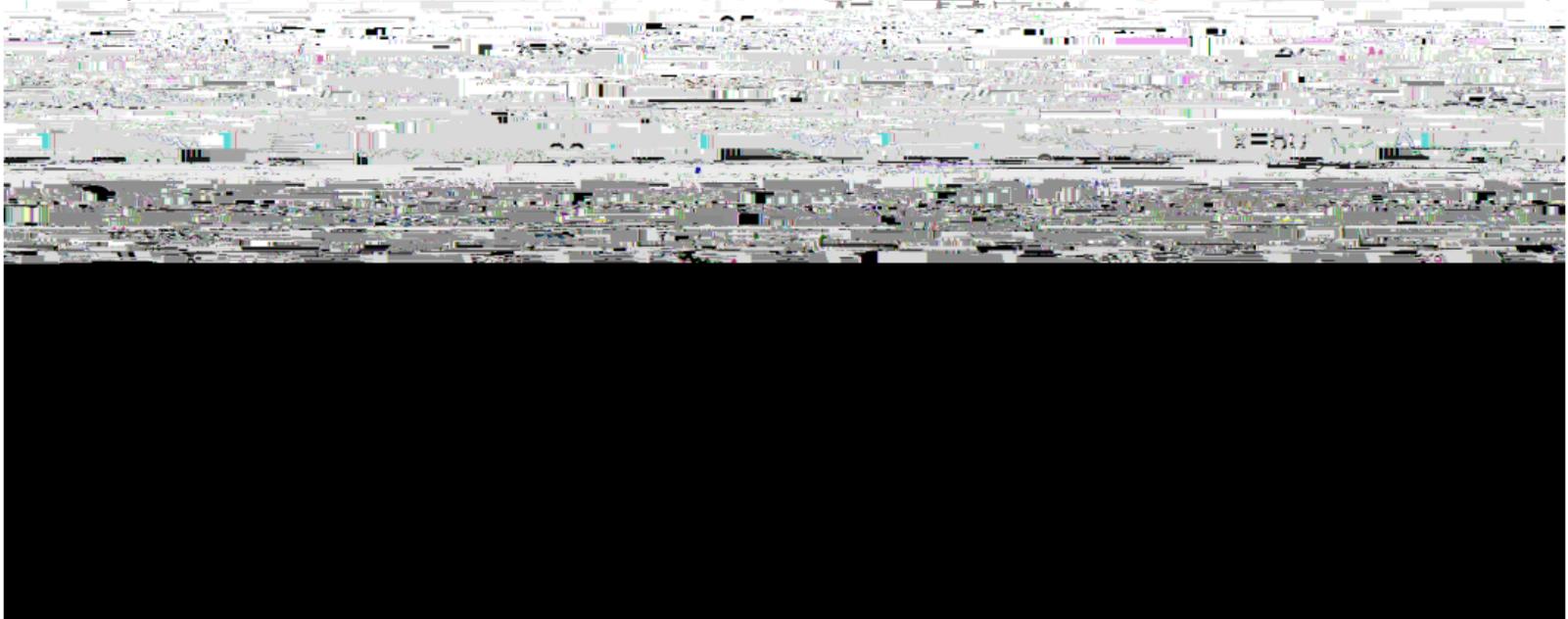
How does the traditional central mortality rate $m(x_j; t_k)$ which uses population data, compare to $m^F(x_j; t_k)$ which only uses death counts?

Mortality rates - England and Wales

Mortality rate

Female

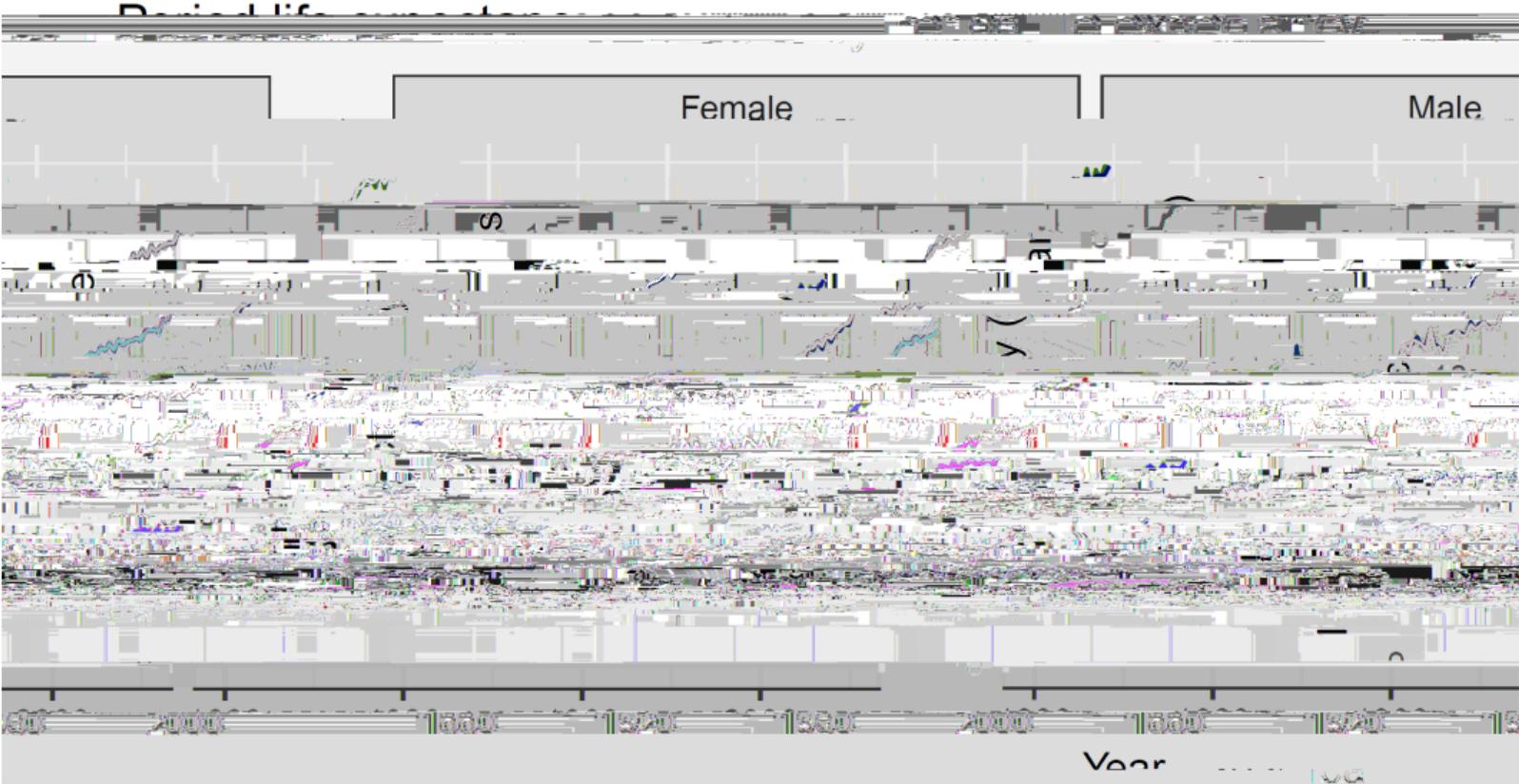
Male



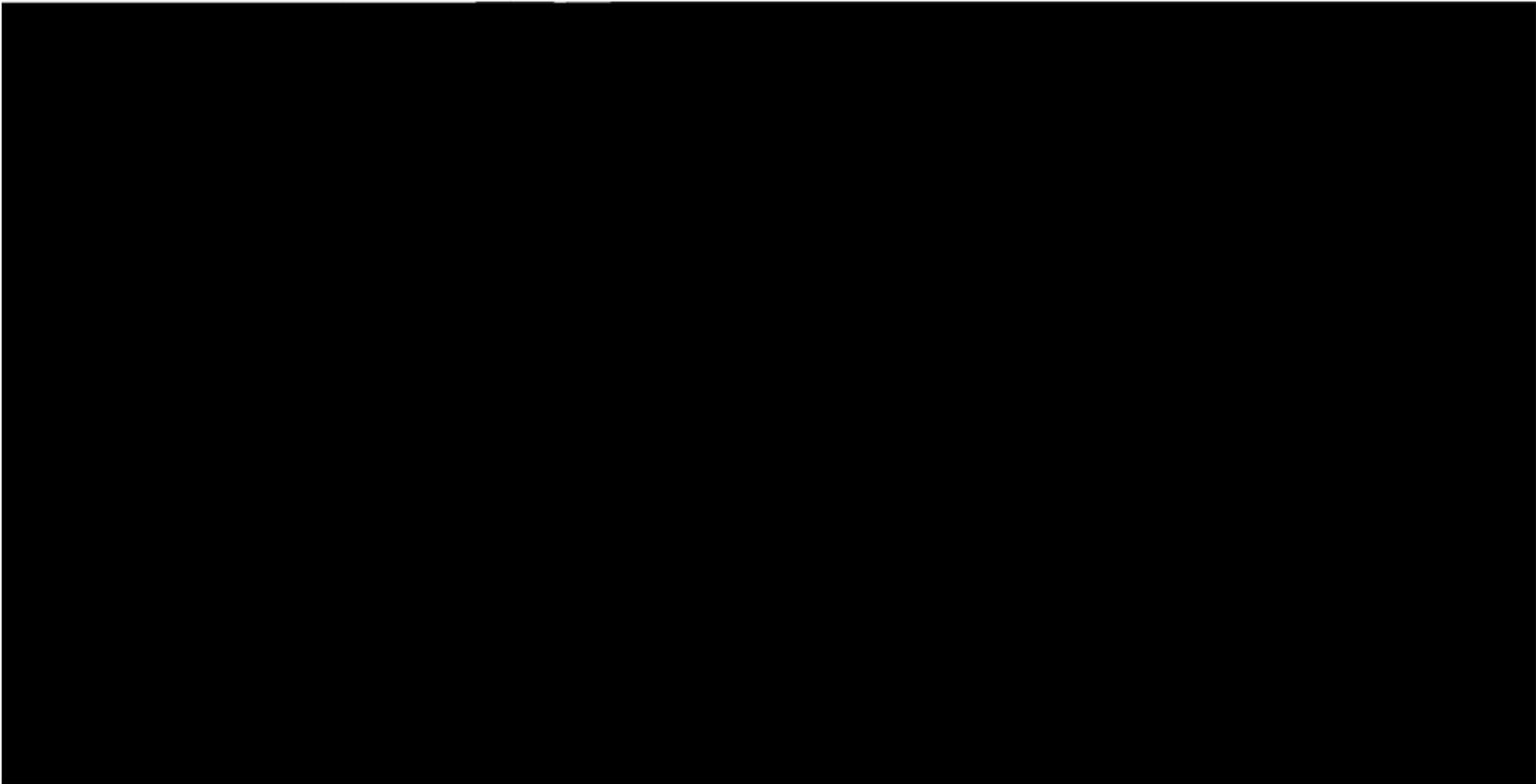
Mortality rates - England and Wales

Mean Absolute Percentage Error

Period Life Expectancy - England and Wales



Cohort Life Expectancy - England and Wales



Life Expectancy - England and Wales

Percentage Error



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

B Good t of rates along both period and cohort

B Good estimates and projections of life expectancies

Useful new perspective for projection of mortality at older ages

B Explore out-of-sample forecast accuracy

B Check consistency of projections using population sizes

B Add diversity of projections ~~§~~ model ensembles

Thank you!

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