

Incorporating Mortality Estimation into Population Reconstruction

April 10, 2021

Brief Introduction to Mortality Modelling

Let T be the time (number of years) to death of a newborn (i.e. aged 0), we have

$${}_tq_x = P(T \leq t + x | T > x),$$

i.e. the probability that the newborn will die *within* t years given that she has survived for x years, then

$${}_tp_x = 1 - {}_tq_x = P(T \geq t + x | T > x)$$

is the probability that an individual aged x will survive *at least* t years.

Brief Introduction to Mortality Modelling

Some common demographic measures:

- ▶ ${}_5q_0$: child mortality, i.e. probability of a newborn dying *within* 5 years, before reaching age 5
- ▶ ${}_{45}q_{15}$: adult mortality, i.e. probability of an individual aged 15 dying *within* 45 years, before reaching age 60

Force of Mortality vs Death Probabilities

Force of mortality is defined as:

$$\begin{aligned}\mu_{x+t} &= \lim_{\delta t \rightarrow 0} \frac{P(T \leq x+t+\delta t | T > x+t)}{\delta t}, \\ &= -\frac{1}{{}_tp_x} \frac{d}{{}_tp_x} {}_tp_x, \\ &= -\frac{d}{dt} \log {}_tp_x, \\ \implies {}_tq_x &= 1 - {}_tp_x = 1 - e^{-\int_0^t \mu_{x+s} ds}.\end{aligned}$$

Intuitively it can be thought as a measure of the instantaneous “death probability” at age $x+t$.

- ▶ the force of mortality is a *rate*, $\mu \in [0, \infty)$
- ▶ the death probability is a *probability*, $\in [0, 1]$

Central Mortality Rates

It is often impossible to model directly on μ .

A usual practice is to aggregate data into separate age groups (usually 1 year), with mortality measured by the *central mortality rates*:

$${}_1m_x = m_x = \frac{\int_0^1 E_{x+t} \mu_{x+t} dt}{\int_0^1 E_{x+t} dt} = \frac{\mathbb{E}({}_1d_x)}{{}_1E_x^C}$$

where ${}_1E_x^C$ and ${}_1d_x$ are the central exposures and number of deaths in age $[x, x + 1)$ in 1 year.

- ▶ Intuitively the central mortality rate can be viewed as the average force of mortality weighted by the corresponding exposures
- ▶ Most mortality modelling is done on m_x .

Conversion between μ_x , m_x and q_x

As mentioned before, the exact relationship between μ_x and q_x is ${}_tq_x = 1 - e^{-\int_0^t \mu_{x+s} ds}$, however, this requires integration over the age range. Often simplifying assumptions are made, two common ones are:

- 1) Constant force of mortality \rightarrow the force of mortality is constant within the age group

$$\implies q_x = 1 - e^{-\mu_{x+0.5}} \approx 1 - e^{-m_x}$$

- 2) Uniform distribution of deaths \rightarrow deaths are uniformly distributed over the age range

$$\implies q_x = \frac{m_x}{1+0.5m_x}$$

Mortality Models

Recall

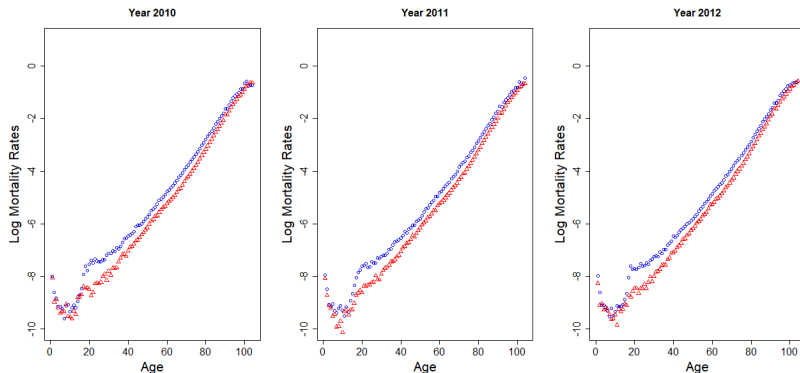
$$m_x = \frac{\mathbb{E}(d_x)}{E_x^C} \implies \mathbb{E}(d_x) = E_x^C m_x$$

Since d_x is a count variable, it is often modelled as Poisson distributions, i.e. $d_x \sim \text{Poisson}(E_x^C m_x)$. Alternatives include

- ▶ $d_x \sim \text{Binomial}(E_x^0, q_x)$, where E_x^0 is the initial exposures
- ▶ $\log(m_x) \sim N(\log(\hat{m}_x), \sigma)$, where \hat{m}_x is the crude mortality rates
- ▶ the Poisson distribution is often too restrictive as $\text{Var}(d_x) = \mathbb{E}(d_x)$, and over-dispersion usually presents in mortality data.
 - ↪ introduce an extra parameter of specific form to capture the excessive variance, one arrives at a Negative Binomial distribution, i.e. $d_x \sim \text{NegBinom}(E_x^C m_x, s)$

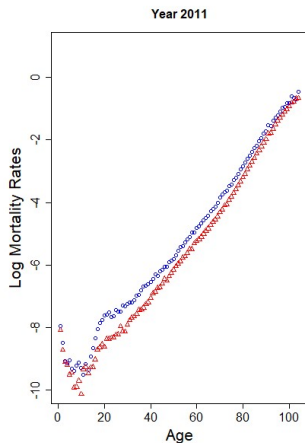
Mortality Models

Typical non-HIV infected mortality schedules, England and Wales
males and females ¹



¹Data obtained from the Office for National Statistics

Mortality Models



- ▶ male mortality (blue) is higher than female mortality (red) most of the time
- ▶ infant mortality is exceptionally high, followed by a sharp decrease into early teens
- ▶ humps can be observed at late teens to early adulthood, more prominent for males (accident hump / maternal hump)
- ▶ mortality increases steadily and relatively log-linearly after the mortality humps into older ages due to senescence

Mortality Models

One of the earliest attempts in mortality modelling dates back to 1825, the Gompertz law of mortality ([Gompertz, 1825](#)),

$$\log(m_x) = a + bx,$$

which is then modified to the Gompertz-Makeham law ([Makeham, 1860](#)) with the addition of an age invariant background mortality constant (age-unrelated deaths such as accidents)

$$m_x = A + BC^x$$

- ▶ relatively simple, with only few parameters
- ▶ provides adequate fit to mortality at older ages
- ▶ only applicable to older ages, due to the log-linearity assumption

Mortality Models

The mortality schedules often deviate from the log-linearity and level-off (mortality plateau) at the oldest ages (approx after 92, [Carriere, 1992](#)). [Perks \(1932\)](#), [Beard \(1959\)](#) and [Thatcher \(1999\)](#) proposed logistic models of the form

$$m_x = \frac{cz}{1+z} + \gamma$$

- ▶ at younger ages the logistic curve behaves similarly to a log-linear curve
- ▶ at the oldest ages provides a level-off to an asymptote
- ▶ again only applicable to older ages
- ▶ other attempts to capture the mortality plateau include [Coale and Kisker \(1990\)](#), [Lindbergson \(2001\)](#)

Mortality Models

Full age range models require relatively complicated forms due to the peculiar shape of mortality age patterns.

Several parametric models have been proposed which share a similar concept - decomposition of mortality into different stages: child mortality, young adult mortality and senescence, e.g. [Thiele \(1871\)](#), [Heligman and Pollard \(1980\)](#), [Siler \(1983\)](#) and [Carriere \(1992\)](#).

Some non-parameteric models have also been developed as well as a vast number of mortality models designed with focuses on projection, but I will not be discussing them here.

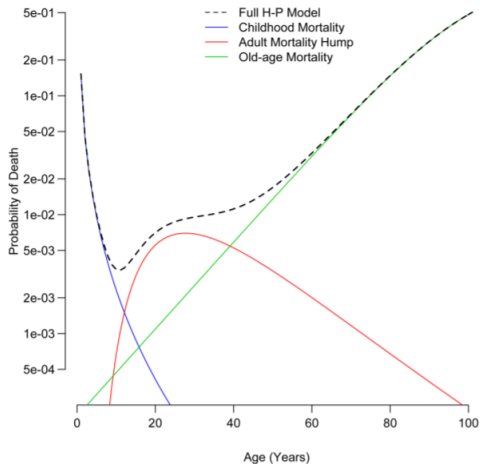
Mortality Models

Among them, the Heligman-Pollard model ([Heligman and Pollard, 1980](#)) is probably the most popular:

$$\frac{q_x}{1 - q_x} = A^{(x+B)^C} + De^{-E(\ln x - \ln F)^2} + GH^x,$$

- ▶ 8 interpretable parameters
- ▶ suitable for the whole age range
- ▶ some variants also proposed in [Heligman and Pollard \(1980\)](#)
- ▶ very high correlation among parameters during estimation, adding difficulties
- ▶ the high correlation also compromises the interpretability

Mortality Models



Decomposition of the HP model ²

²Source: [Sharro et al. \(2013\)](#)

Mortality Models

Alternative to parametric mortality laws, several model life table systems have also been developed and widely used, such as the Coale-Demeny family (Coale and Demeny, 1966). Some organisations have also produced their own life table system, e.g. UN, GBD.

These systems often use a few summary indices such as the child mortality ${}_5q_0$, life expectancy at birth e_0 , adult mortality ${}_{45}q_{15}$ etc. to generate full mortality schedules.

Mortality Models

A more recent model life table system is developed by [Wilmoth et al. \(2012\)](#) which has 2 parameters, namely the Log Quadratic (LogQuad) model (still somehow parameteric I guess...):

$$\log(m_x) = a_x + b_x h + c_x h^2 + v_x k,$$

where a_x , b_x , c_x and v_x are constants derived from a set of life tables using SVD and h and k are the 2 effective parameters to vary. In addition, $h = \log({}_5q_0)$, therefore given a fixed level of child mortality, a full schedule can be generated.

Life Tables

ELT15 (Males)

| x | l_x | d_x | q_x | μ_x | $^o e_x$ |
|-----|---------|-------|----------|----------|----------|
| 0 | 100 000 | 814 | 0.008 14 | | 73.413 |
| 1 | 99 186 | 62 | 0.000 62 | 0.000 80 | 73.019 |
| 2 | 99 124 | 38 | 0.000 38 | 0.000 43 | 72.064 |
| 3 | 99 086 | 30 | 0.000 30 | 0.000 33 | 71.091 |
| 4 | 99 056 | 24 | 0.000 24 | 0.000 27 | 70.113 |
| 5 | 99 032 | 22 | 0.000 22 | 0.000 23 | 69.130 |
| 6 | 99 010 | 20 | 0.000 20 | 0.000 21 | 68.145 |
| 7 | 98 990 | 18 | 0.000 19 | 0.000 19 | 67.158 |
| 8 | 98 972 | 19 | 0.000 18 | 0.000 18 | 66.171 |
| 9 | 98 953 | 18 | 0.000 18 | 0.000 18 | 65.183 |
| 10 | 98 935 | 18 | 0.000 18 | 0.000 18 | 64.195 |
| 11 | 98 917 | 18 | 0.000 18 | 0.000 18 | 63.206 |
| 12 | 98 899 | 19 | 0.000 19 | 0.000 19 | 62.218 |
| 13 | 98 880 | 23 | 0.000 23 | 0.000 21 | 61.230 |
| 14 | 98 857 | 29 | 0.000 29 | 0.000 26 | 60.244 |

| x | ℓ_x | q_x | m_x | x | ℓ_x | q_x |
|-----|----------|----------|----------|-----|----------|----------|
| 0 | 100,000 | 0.004746 | 0.004766 | 58 | 92,261 | 0.006687 |
| 1 | 99,525 | 0.000306 | 0.000306 | 59 | 91,644 | 0.007299 |
| 2 | 99,495 | 0.000207 | 0.000207 | 60 | 90,975 | 0.008016 |
| 3 | 99,474 | 0.000147 | 0.000147 | 61 | 90,246 | 0.008773 |
| 4 | 99,460 | 0.000115 | 0.000115 | 62 | 89,454 | 0.009492 |
| 5 | 99,448 | 0.000099 | 0.000099 | 63 | 88,605 | 0.010259 |
| 6 | 99,438 | 0.000091 | 0.000091 | 64 | 87,696 | 0.011227 |
| 7 | 99,429 | 0.000088 | 0.000088 | 65 | 86,712 | 0.012404 |

English Life Table 15 males ³

English Life Table 17 males ⁴

- ▶ information included may vary from tables to tables
- ▶ columns can be derived from each other

³Source: Formulae and Tables for The Institute and Faculty of Actuaries

⁴Source: [Dodd et al. \(2018\)](#)

Bayesian Population Reconstruction

Two main approaches:

- ▶ prospective reconstruction (“inverse projection”)
 - ↪ start with a “baseline population” at the initial time period and project and reconstruct the population forward with corresponding demographics rates
- ▶ retrospective reconstruction (“back projection”)
 - ↪ start with a final population at the terminal time period and propagate backwards in time
 - ↪ however, there was debates about the efficacy of this approach as it is *‘trying to “resurrect” members of the open ended age group and simultaneously estimate fertility, mortality and migration rates.’* (Wheldon et al., 2016)

Bayesian Population Reconstruction

I will be adopting the Bayesian population reconstruction framework by [Wheldon et al. \(2016\)](#)

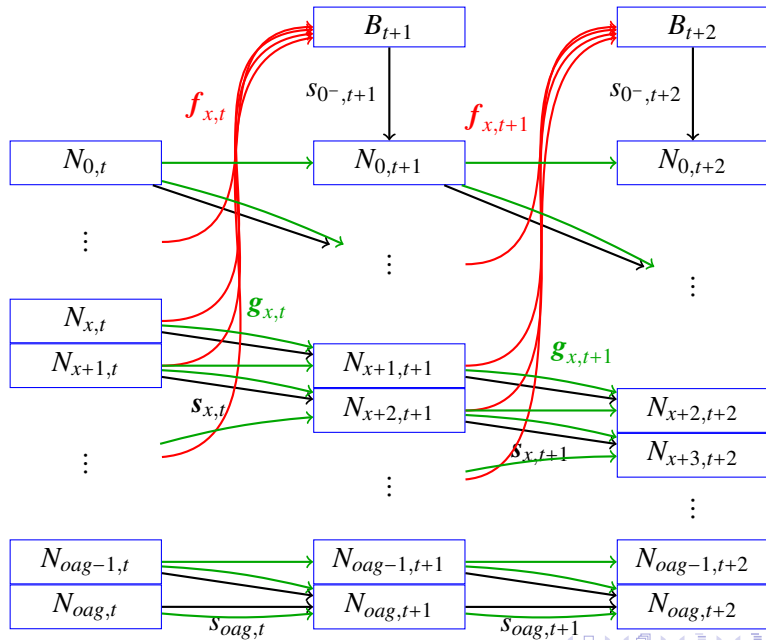
- ▶ prospective approach
- ▶ Bayesian approach, gives associated uncertainty ranges of the reconstructed population counts

The core of this framework is the cohort component method of population projection (CCMPP) which utilises the concept of the demographic balancing equation

$$\underbrace{N_{t+1}}_{\text{population at time } t+1} = \underbrace{N_t}_{\text{population at time } t} - \underbrace{D_t}_{\text{deaths in period } t} + \underbrace{B_t}_{\text{births in period } t} + \underbrace{G_t}_{\text{net migration in period } t}$$

- ▶ continuous process, need to discretise time steps
- ▶ population projected along the cohort direction

CCMPP



Bayesian Population Reconstruction

Require demographics rates (fertility rates, survival proportions, net migration proportions) to project the populations

$$N_{x,t_0}^* | \sigma_N^2 \sim \text{logNormal}(\log(N_{x,t_0}), \sigma_N^2)$$

$$f_{x,t}^* | \sigma_f^2 \sim \text{logNormal}(\log(f_{x,t}), \sigma_f^2) \quad \forall x \in [15, 50)$$

$$s_{x,t}^* | \sigma_s^2 \sim \text{logNormal}(\log(s_{x,t}), \sigma_s^2)$$

$$g_{x,t}^* | \sigma_g^2 \sim \text{AR1} : \text{AR1}(\rho_x, \rho_t, \sigma_g^2)$$

$$N_{x,t}^* | f_{x,t}^*, s_{x,t}^*, g_{x,t}^* = \text{CCMPP}(N_{x,t_0}^*, f_{x,t}^*, s_{x,t}^*, g_{x,t}^*, \text{srb}) \quad \forall t \neq t_0$$

$$N_{x,t} \sim \text{logNormal}(\log(N_{x,t}^*), \sigma_N^2) \quad \forall t \neq t_0$$

$$\sigma_N^2, \sigma_f^2, \sigma_s^2, \sigma_g^2, \rho_x, \rho_t \propto h(\cdot)$$

Bayesian Population Reconstruction

Instead of using estimates of the survival proportions from other data source as priors, incorporate DHS data into population reconstruction

- ▶ DHS data supports estimation of mortality rates m_x , and most models are on m_x instead of survival proportions s_x
 - ↪ convert m_x to s_x
- ▶ DHS data limited age range (15 - 60), where as population reconstruction spans the full age range (0 - open age group)
 - ↪ utilise laws of mortality / model life tables, e.g. LogQuad, HP-8, Thiele

Conversion between m_x and s_x

s_x , the survivorship between age groups, are then calculated by $\frac{L_{x+1}}{L_x}$, where L_x denotes the exposures in the period at age $[x, x + 1)$. Under UDD, $L_x = l_x - \frac{1}{2}d_x$,

$$\begin{aligned} s_x^{\text{UDD}} &= \frac{0.5p_{x+0.5} + 0.5p_{x+1}}{1} \\ &= 1p_{x+0.5} \end{aligned}$$

Open Age Group Mortality Rate

Aggregating mortality rates of the last age groups into an open age group also needs attention.

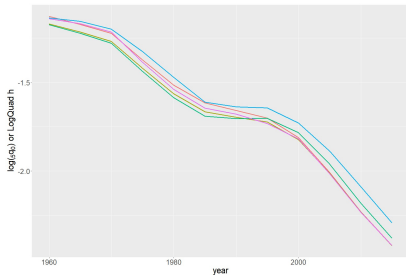
$$m_{oag} = \frac{\sum_{i \geq oag} w_i m_i}{\sum_{i \geq oag} w_i}$$

where, under UDD,

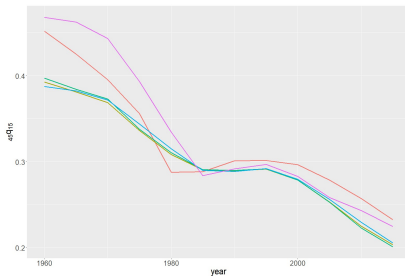
$$w_i = (1 - 0.5 q_i) \prod_{oag \leq j < i} p_j$$

LogQuad Model - Females

Using IGME child mortality estimates as priors for the LogQuad parameters

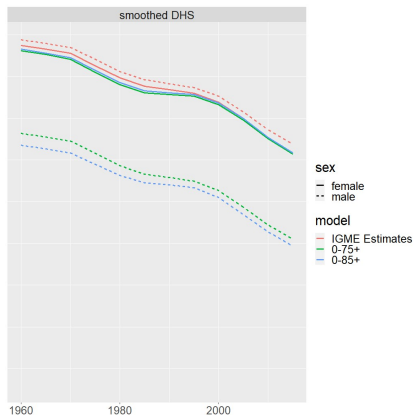


Estimated log child mortality.
IGME estimates in red.



Estimated 45q₁₅.WPP estimates in red.

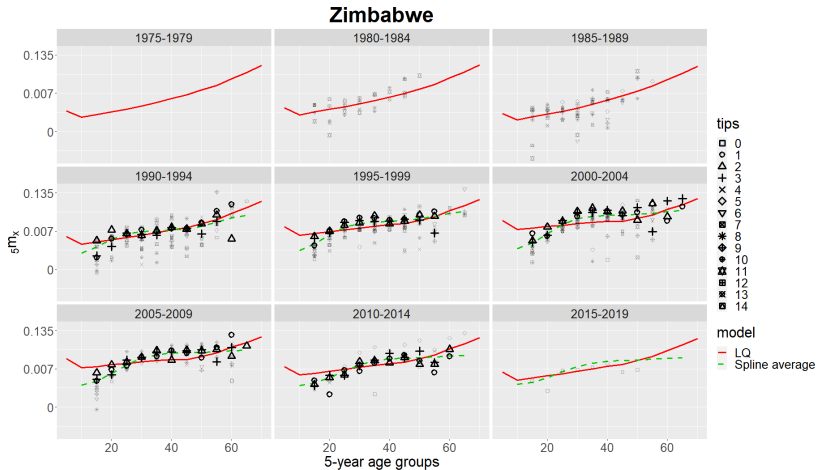
LogQuad Model - Joint Sex



Estimated log child mortality.
IGME estimates in red.

- ▶ Estimated male child mortality is much lower than the IGME estimates
- ▶ LogQuad developed for countries without HIV
- ▶ HIV-hump in mortality in adult ages (age range with DHS data) affects estimated child mortality due to the in-flexibility of the LogQuad model for HIV-infected populations

LogQuad Model - Zimbabwe



LQ obviously not meant for naive implementation in high-HIV countries, but this illustrates the LQ fit in this context

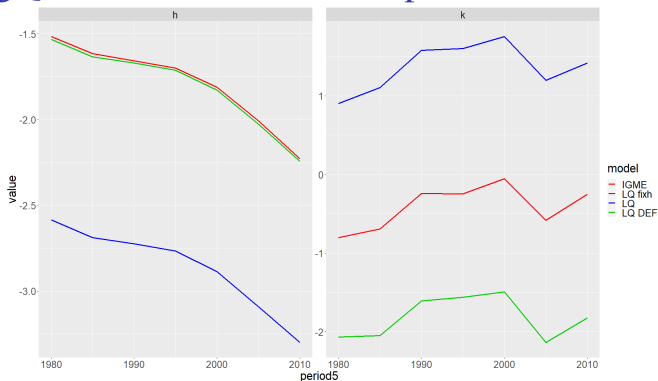
LogQuad Model + DEF Hump from the HP-8 Model

Recall the HP-8 Model decomposes the age pattern into 3 stages

$$\frac{q_x}{1 - q_x} = A^{(x+B)^C} + De^{-E(\ln x - \ln F)^2} + GH^x,$$

Attempted to extract the middle hump and add it on top of the LQ model and fit only to the DHS data, still using IGME estimates as priors.

LogQuad Model + DEF Hump from the HP-8



- ▶ LQ+DEF allows the estimated child mortality to be more consistent for males (green and red)
- ▶ difficult to converge for females and gives insensible results, possibly due to the less prominent hump in Burkina Faso as well as the correlation between the DEF and the LQ k

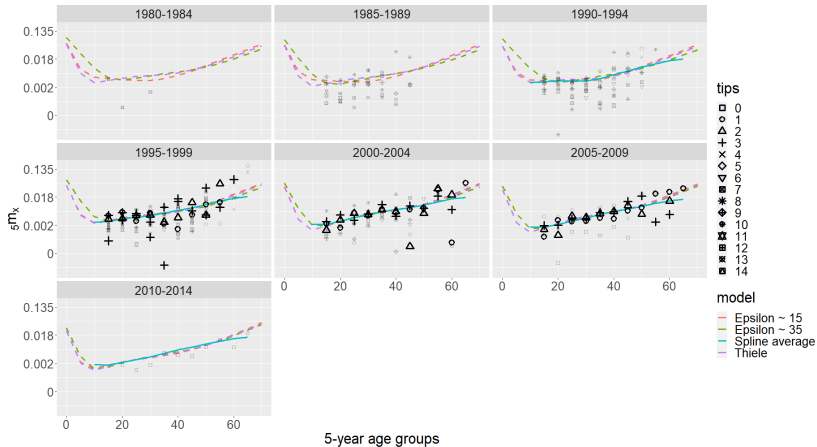
Thiele

$$m(x) = \underbrace{\varphi e^{-\psi x}}_{\text{negative exponential}} + \underbrace{\lambda e^{-\delta(x-\epsilon)^2}}_{\text{normal}} + \underbrace{Ae^{Bx}}_{\text{Gompertz}} \quad \varphi, \psi, \lambda, \delta, \epsilon > 0$$

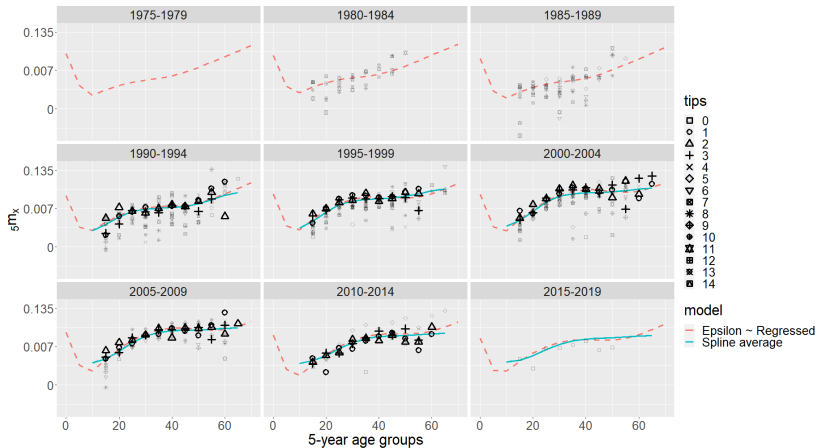
Used IGME estimates and LogQuad model to derive priors for the 7 parameters of Thiele

- ▶ consistent child mortality estimates with the IGME estimates
- ▶ sensible results
- ▶ converged quite stably for different countries (so far)

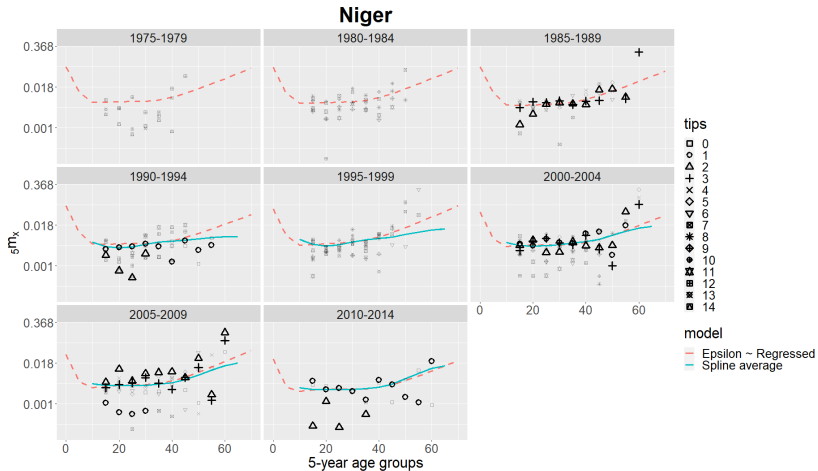
Burkina Faso



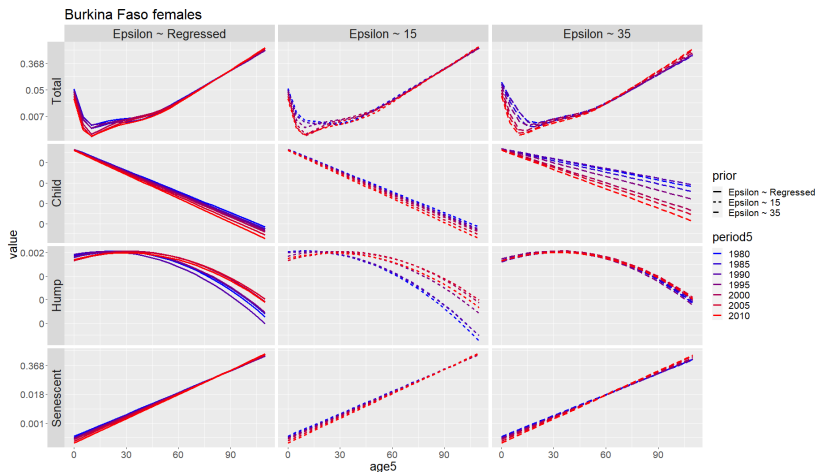
Zimbabwe



Adequate fit even to high HIV countries



Also in very low HIV countries



Thiele estimated m_x and decomposed

Next Steps

- ▶ So far, because of the issues encountered with the LogQuad model, took a step back and modelled only DHS data
- ▶ Incorporate Thiele model into population reconstruction
- ▶ Try to modify the hump component of the model such that it is on log-scale and compare fit
- ▶ Extend to other countries

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