

# Estimating historical mortality rates using crowd-sourced online genealogies

Monica Alexander, Statistical Sciences and Sociology, University of Toronto

# Background

- Historical mortality is important to understand
  - Relationship between industrialization/urbanization and health
  - Differences by geography, social class
- But data are limited, particularly before 1900
  - Civil registration systems generally did not exist
  - Rely on parish records, city records, approximations

17. In the next place, whereas many persons live in great fear and apprehension of some of the more formidable and notorious diseases following; I shall only set down how many died of each: that the respective numbers, being compared with the total 229,250, those persons may the better understand the hazard they are in.

Table of notorious diseases		Table of casualties	
<i>Apoplexy</i>	1,306	<i>Bleeding</i>	69
<i>Cut of the Stone</i>	38	<i>Burnt, and Scalded</i>	125
<i>Falling Sickness</i>	74	<i>Drowned</i>	829
<i>Dead in the streets</i>	243	<i>Excessive drinking</i>	2
<i>Gowt</i>	134	<i>Frighted</i>	22
<i>Head-Ache</i>	51	<i>Grief</i>	279
<i>Jaundice</i>	998	<i>Hanged themselves</i>	222
<i>Lethargy</i>	67	<i>Killed by several</i>	
<i>Leprosy</i>	6	<i>accidents</i>	1,021
<i>Lunatick</i>	158	<i>Murdered</i>	86
<i>Overlaid, and Starved</i>	529	<i>Poisoned</i>	14
<i>Palsy</i>	423	<i>Smothered</i>	26
<i>Rupture</i>	201	<i>Shot</i>	7
<i>Stone and Strangury,</i>	863	<i>Starved</i>	51
<i>Sciatica</i>	5	<i>Vomiting</i>	136
<i>Sodainly</i>	454		



# The emergence of online genealogies

- User-entered information on family trees
- Ascendant genealogies, ancestry is reconstructed retrospectively
- Social networking aspect



## Powerful Genealogy Tools to Help You Grow Your Tree



### Work Together

Add what you know, then invite your relatives to add the missing



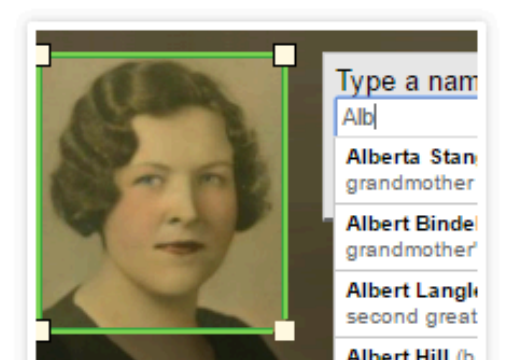
### Find Your Ancestors

Everyone's related. Geni users have already created over 265



### Connect to New Relatives

Our automatic tree matches let you discover cousins who are



### Stay Organized

Upload and store your family photos, videos, records, and

# Online genealogies as a demographic data source

- **Familinx:** 86 million individual records
- Demographic events: births, deaths, marriages
- Kinship ties: (known for 43 million individuals)
- Mostly in the Global North (85% of vital events occur in Europe or North America)
- Family ties not restricted by geographic boundaries
- But some clear issues (ascendants, selective remembering, selection of users, misreporting)



# This project

- Goal: Construct historical mortality rates and life expectancies for a group of countries between 1800-1900
- Developed a Bayesian model to estimate and correct for biases in mortality rates derived from Familinx
- Working paper: <https://www.demogr.mpg.de/papers/working/wp-2022-005.pdf>
- Code etc: <https://github.com/michael-chong/familinx-mort>

## Collaborators:



Michael Chong  
Statistics  
University of Toronto



Diego Alburez  
Kinequalities Group  
Max Planck Institute for  
Demographic Research



Emilio Zagheni  
Digital Demography Group  
Max Planck Institute for  
Demographic Research

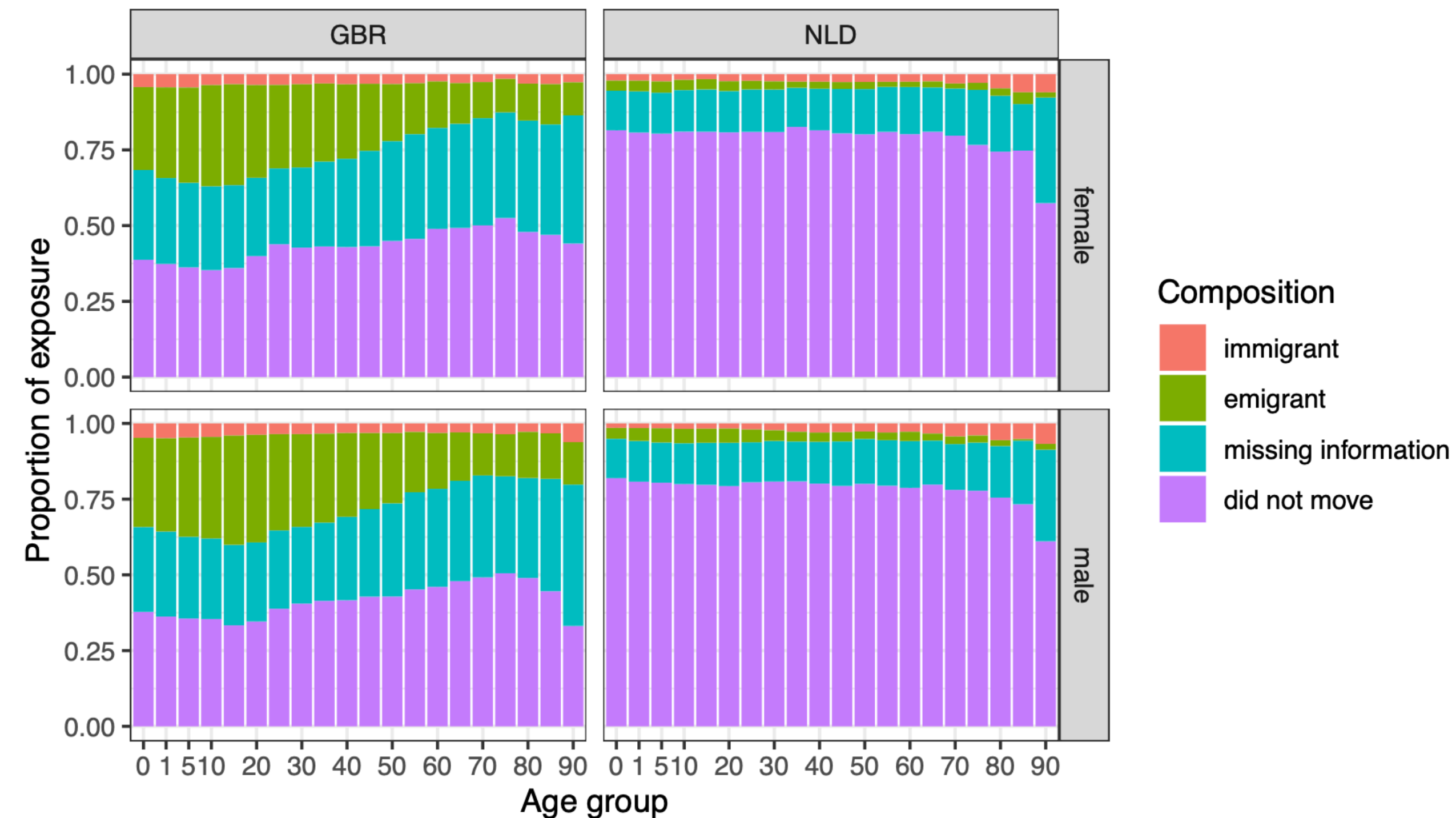
# Data

# Familinx overview

- Consider ten countries in the period 1800-1900: Belgium, Denmark, Finland, France, Netherlands, Norway, Sweden, Switzerland, UK, USA
- ~5.5 million individual records
- We tabulate deaths and exposure (person-years) by age group, time period, gender, and country
- Data issues:
  - Geographic names in free text (errors, non-English, historical names)
  - Some locations of birth/death missing
  - No direct information on the place of residence over the life course

# Constructing exposure counts from Familinx

- Exposures to death are divided among the countries in which they had vital events (birth, birth of child, death)
- Sometimes successive locations are missing
- In general, migrants contribute a small share of the exposure to death counts (although the UK is an exception)





# Gold-standard data

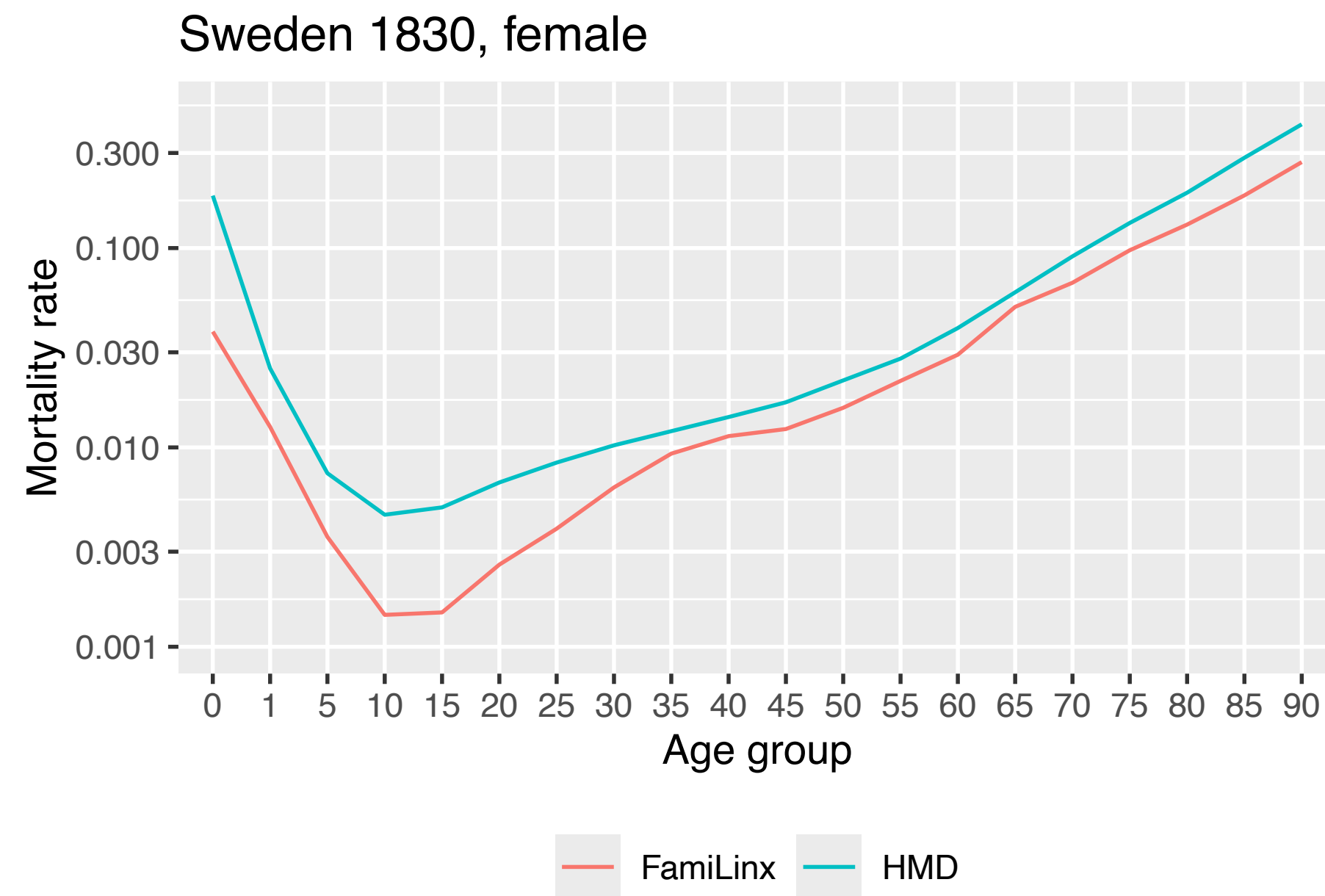
- Human Mortality Database: high-quality repository of harmonized mortality data
- Obtain death counts and exposure (person-years lived) by country, gender, age, and time period

Country	Earliest year available in Human Mortality Database
Sweden	1751
France	1816
Denmark	1835
Belgium	1841
Great Britain	1841
Norway	1846
Netherlands	1850
Switzerland	1876
Finland	1878

# Model

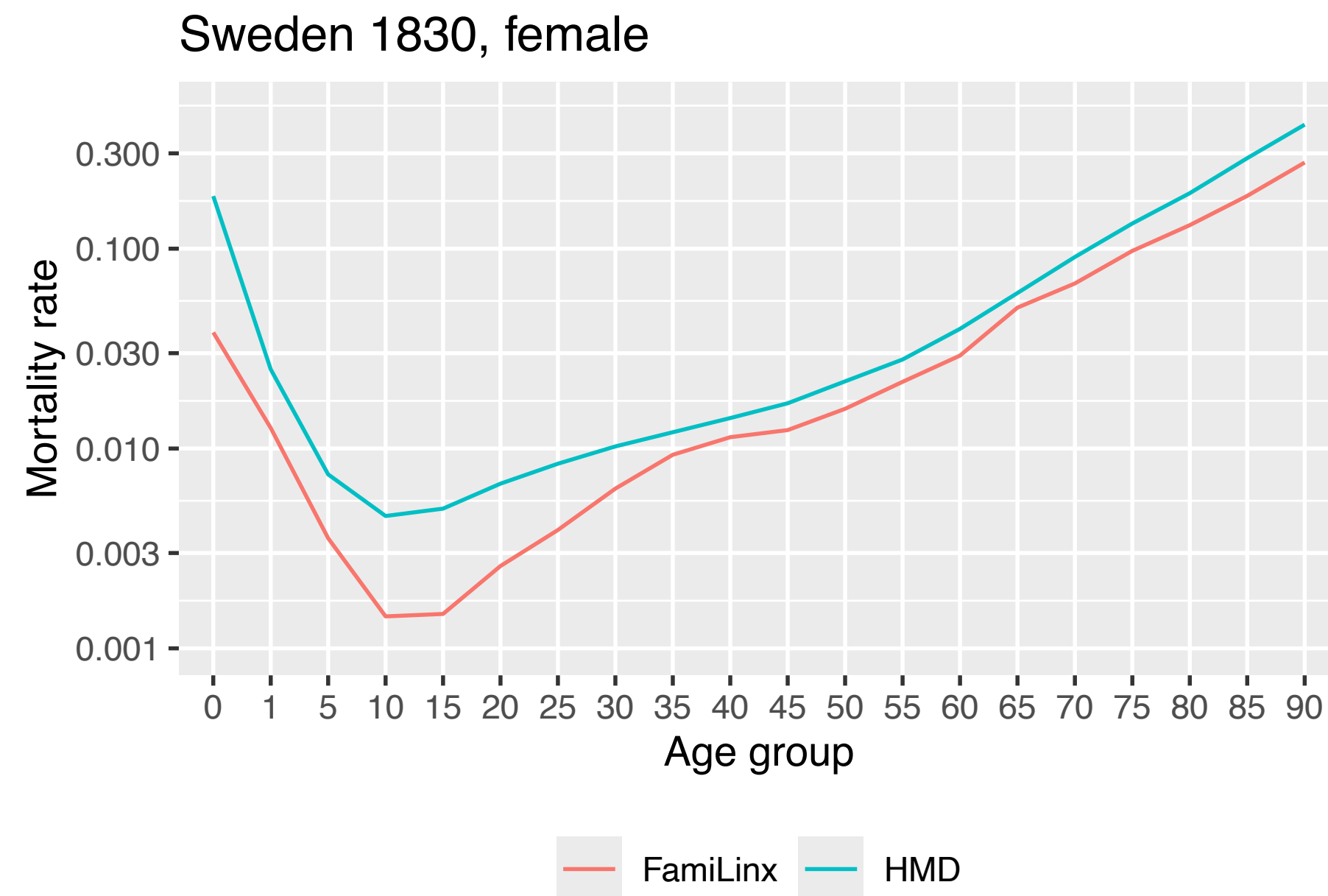
# Modeling goals

In some country-years we have both Familinx and HMD data



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In some country-years we have both Familinx and HMD data

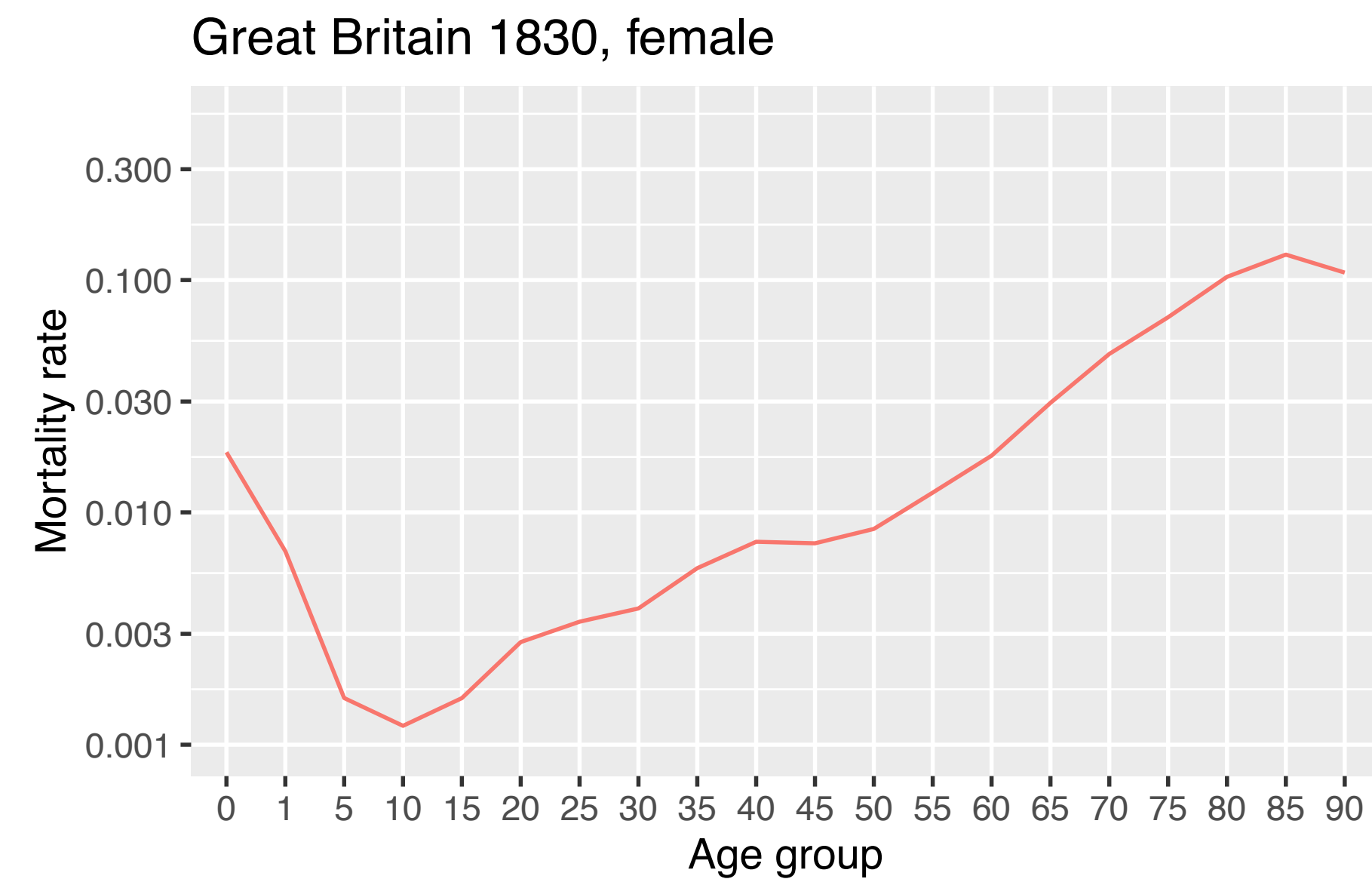
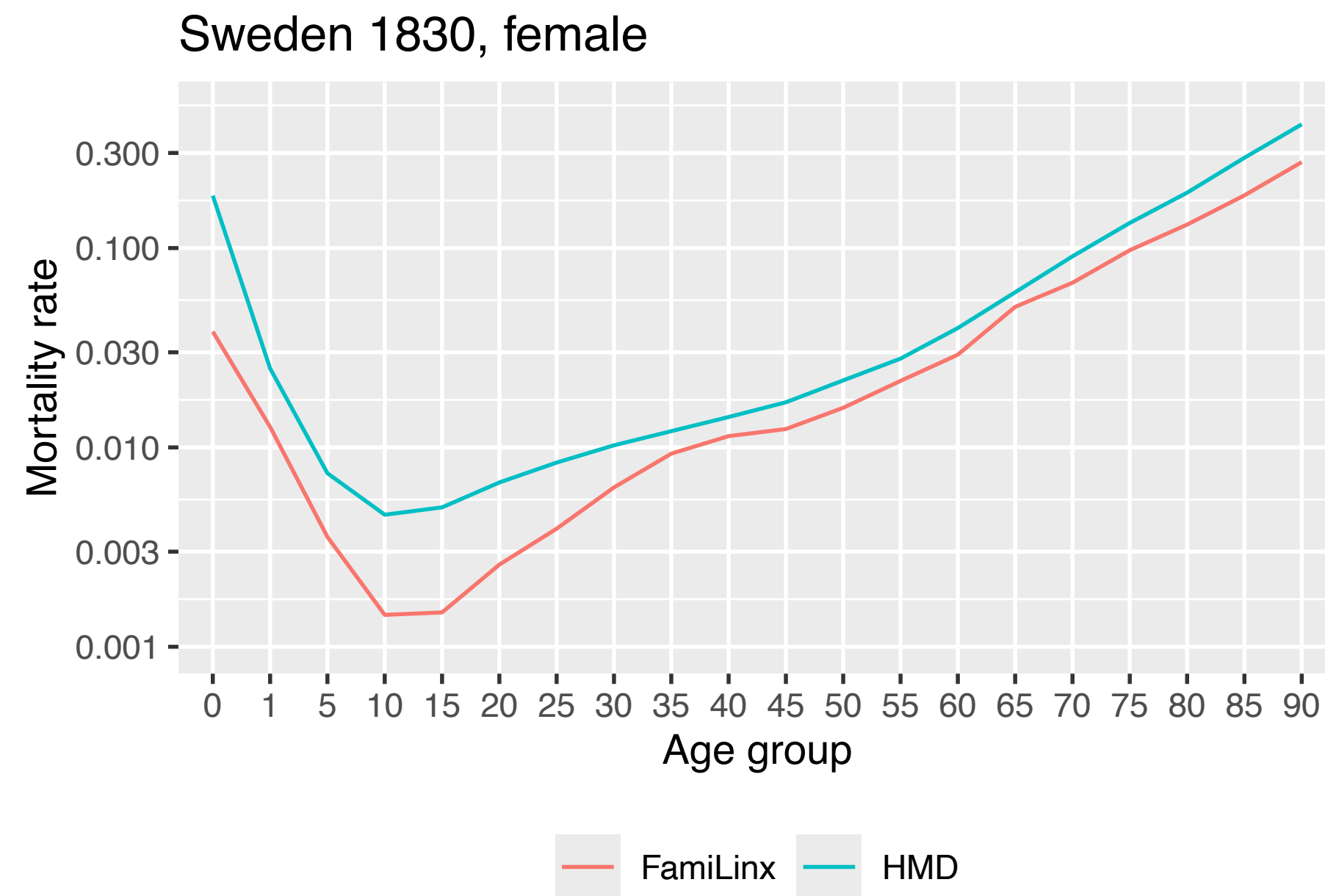


In these cases, could directly calculate a set of 'adjustment factors' by age for a particular country / year/ gender to adjust the familinx mortality data



# Modeling goals

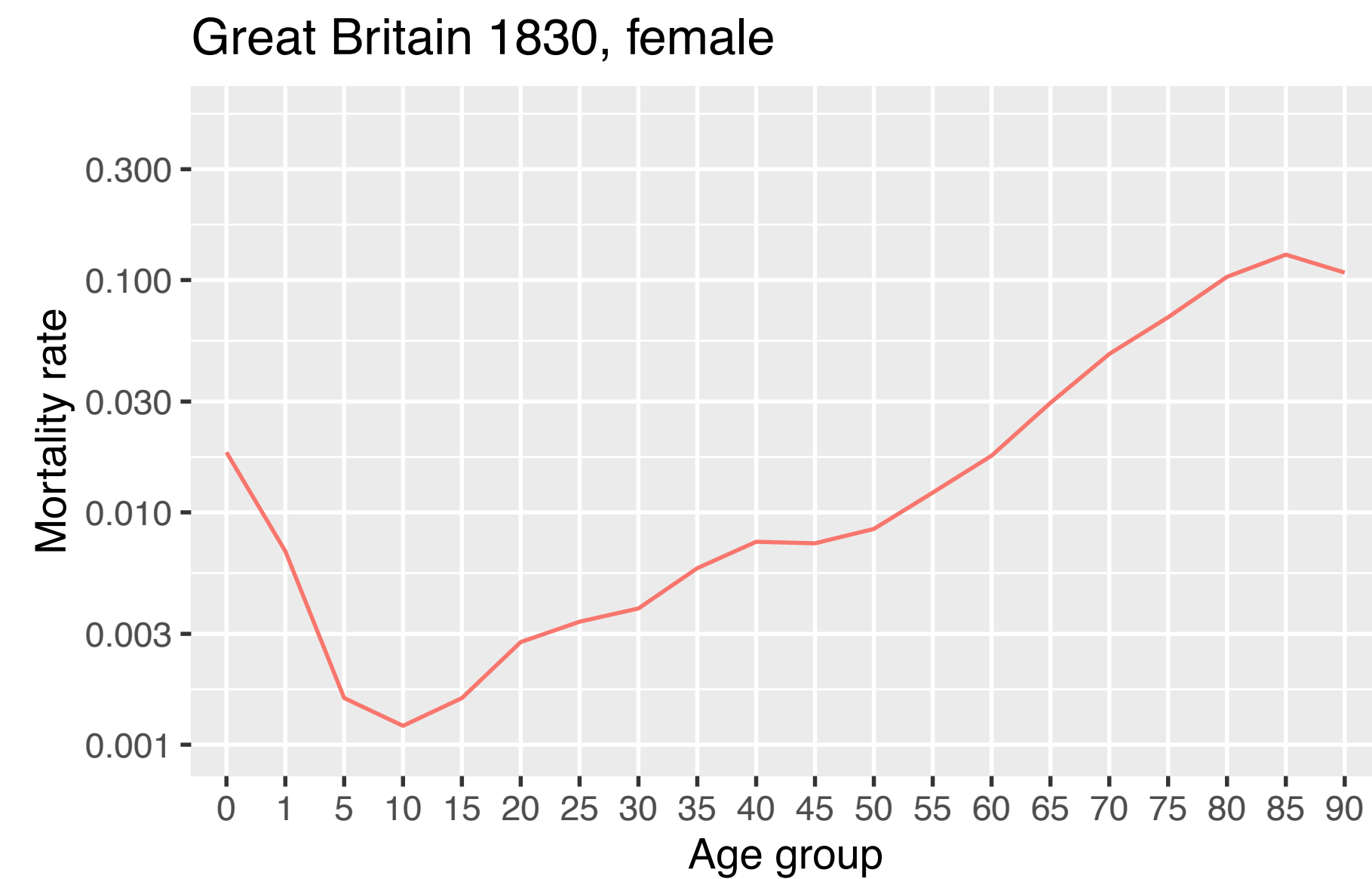
But for many country-years we only have Familinx



# Modeling goals

But for many country-years we only have Familinx

So need a model to estimate a set of adjustment factors



# Modeling goals

- Estimate age-specific mortality rates for each country and five-year periods between 1800 and 1900
- Account for
  - Characteristic shape of mortality over age
  - Biases in Familinx data share similarities across age/years/countries
  - Mortality rates tend to evolve smoothly over age and time (although sometimes don't)

# Notation

- Latent mortality rate for country  $c$ , gender  $g$ , time period  $t$ , age group  $x$ :  $\mu_{c,g,t,x}$
- Observed death and exposure counts from HMD:  $d_{c,g,t,x}^{(H)}, P_{c,g,t,x}^{(H)}$
- Observed death and exposure counts from Familinx:  $d_{c,g,t,x}^{(F)}, P_{c,g,t,x}^{(F)}$
- Adjustment factors for Familinx:  $\psi_{c,g,t,x}$



# Data models

- For HMD

$$d_{c,g,t,x}^{(H)} \mid \mu_{c,g,t,x}, \phi_x^{(H)} \sim \text{NegBinom} \left( \mu_{c,g,t,x} P_{c,g,t,x}^{(H)}, \phi_x^{(H)} \right)$$

- For Familinx

$$d_{c,g,t,x}^{(F)} \mid \mu_{c,g,t,x}, \phi_x^{(F)} \sim \text{NegBinom} \left( \mu_{c,g,t,x} \psi_{c,g,t,x} P_{c,g,t,x}^{(F)}, \phi_x^{(F)} \right)$$

# Data models

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$$d_{c,g,t,x}^{(F)} \mid \mu_{c,g,t,x}, \phi_x^{(F)} \sim \text{NegBinom} \left( \mu_{c,g,t,x} \psi_{c,g,t,x} P_{c,g,t,x}^{(F)}, \phi_x^{(F)} \right)$$

# Mortality model

# Mortality model (for $\mu_{c,g,t,x}$ )

$$d_{c,g,t,x}^{(F)} \mid \mu_{c,g,t,x}, \phi_x^{(F)} \sim \text{NegBinom} \left( \mu_{c,g,t,x} \psi_{c,g,t,x} P_{c,g,t,x}^{(F)}, \phi_x^{(F)} \right)$$

- Mortality rates over age are expected to conform to characteristic shapes ('J' shape)
- We incorporate this assumption by modelling the logged mortality rates as a linear combination of 'principal components', which are derived from gold-standard data (HMD)
- We also allow for historical mortality shocks by including a regularized error term



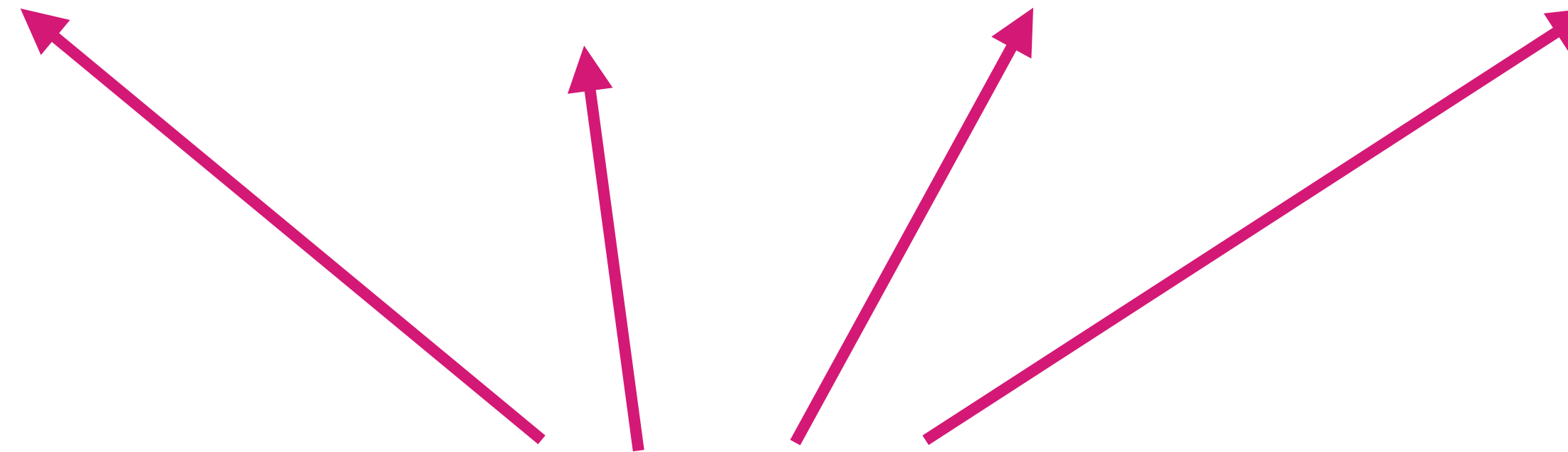
# Mortality model

$$\log \overrightarrow{\mu}_{c,g,t} = \eta_{1,c,g,t} \overrightarrow{v}_{g,1} + \eta_{2,c,g,t} \overrightarrow{v}_{g,2} + \eta_{3,c,g,t} \overrightarrow{v}_{g,3} + \eta_{4,c,g,t} \overrightarrow{v}_{g,4} + \overrightarrow{\varepsilon}_{c,g,t}$$

# Mortality model

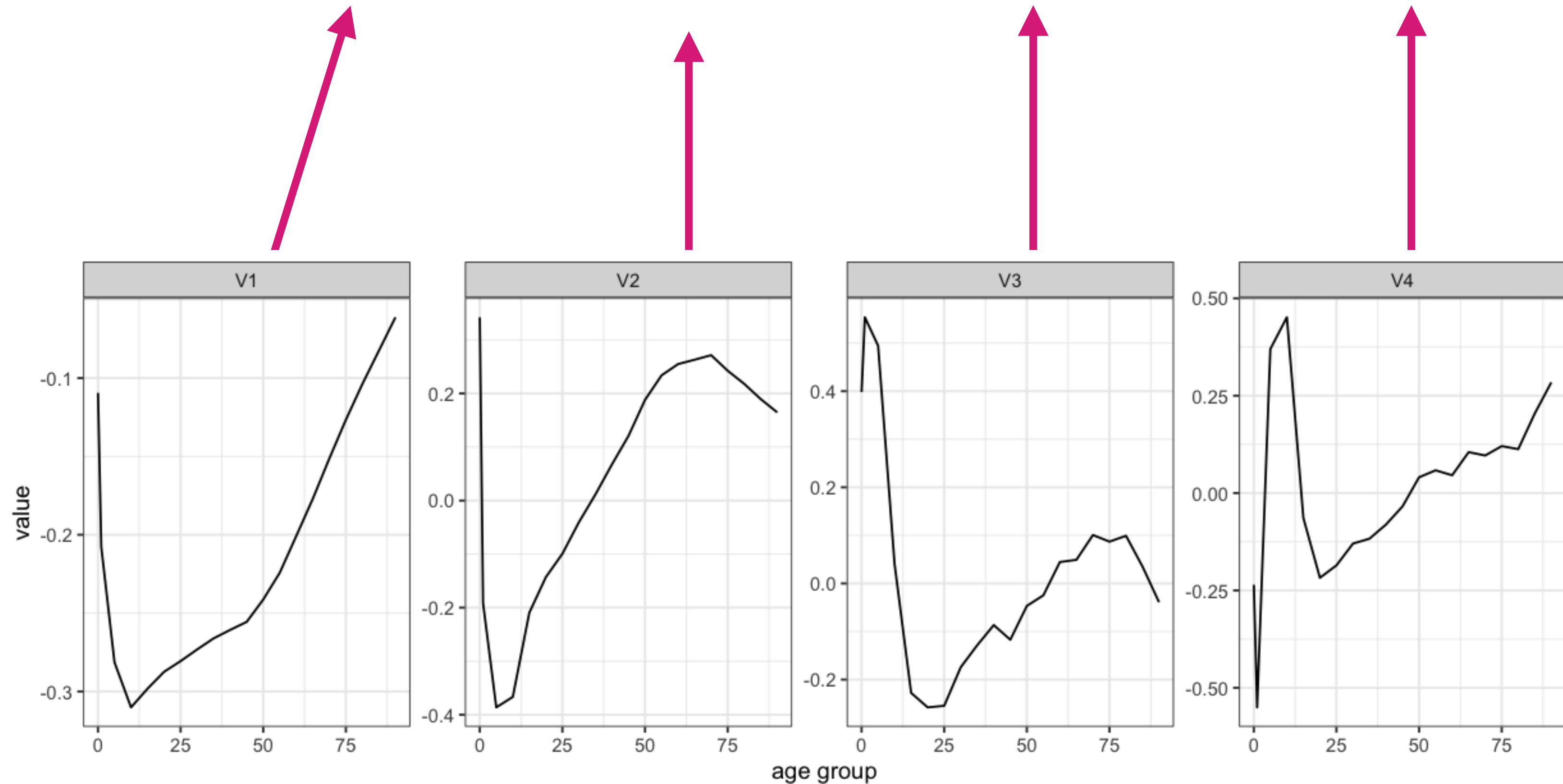
$$\log \vec{\mu}_{c,g,t} = \eta_{1,c,g,t} \vec{v}_{g,1} + \eta_{2,c,g,t} \vec{v}_{g,2} + \eta_{3,c,g,t} \vec{v}_{g,3} + \eta_{4,c,g,t} \vec{v}_{g,4} + \vec{\varepsilon}_{c,g,t}$$

Derived from SVD of  
HMD rates: first four  
right singular vectors



# Mortality model

$$\log \vec{\mu}_{c,g,t} = \eta_{1,c,g,t} \vec{v}_{g,1} + \eta_{2,c,g,t} \vec{v}_{g,2} + \eta_{3,c,g,t} \vec{v}_{g,3} + \eta_{4,c,g,t} \vec{v}_{g,4} + \vec{\varepsilon}_{c,g,t}$$



# Mortality model

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Coefficients assumed to  
change smoothly over  
time

$$\eta_{j,c,g,t} = \theta_{j,c,g} + s_{j,c,g}(t)$$

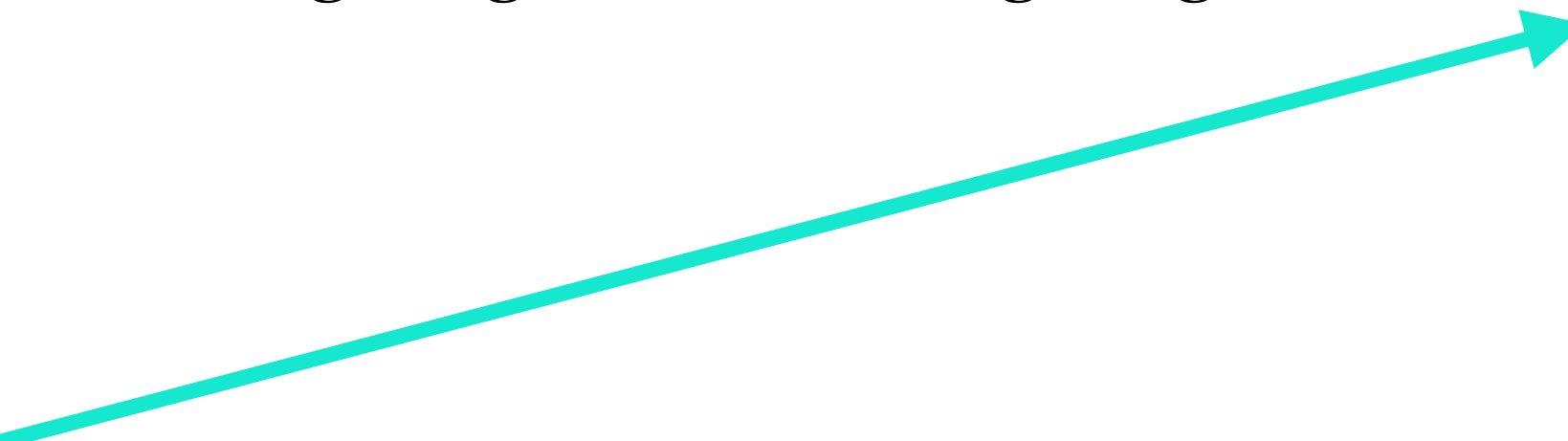
Cubic basis splines, second-  
order penalty



# Mortality model

$$\log \vec{\mu}_{c,g,t} = \eta_{1,c,g,t} \vec{v}_{g,1} + \eta_{2,c,g,t} \vec{v}_{g,2} + \eta_{3,c,g,t} \vec{v}_{g,3} + \eta_{4,c,g,t} \vec{v}_{g,4} + \vec{\varepsilon}_{c,g,t}$$

Error term, assume  
mostly close to zero  
unless detectable shock  
(e.g. war)



# Mortality model

$$\log \vec{\mu}_{c,g,t} = \eta_{1,c,g,t} \vec{v}_{g,1} + \eta_{2,c,g,t} \vec{v}_{g,2} + \eta_{3,c,g,t} \vec{v}_{g,3} + \eta_{4,c,g,t} \vec{v}_{g,4} + \vec{\varepsilon}_{c,g,t}$$

Regularized horseshoe  
prior:

$$\varepsilon_i \mid \tau, \lambda_i \sim N(0, \tau^2 \tilde{\lambda}_i^2)$$

$$\tilde{\lambda}_i^2 = \frac{d^2 \lambda_i^2}{d^2 + \tau^2 \lambda_i^2}$$

$$\tau \sim \text{Cauchy}(0, 0.01)$$

$$\lambda_i^2 \sim \text{Cauchy}(0, 1)$$

# Model for adjustment factors

# Adjustment factor

$$d_{c,g,t,x}^{(F)} \mid \mu_{c,g,t,x}, \phi_x^{(F)} \sim \text{NegBinom} \left( \mu_{c,g,t,x}, \boxed{\psi_{c,g,t,x}} \rho_{c,g,t,x}^{(F)}, \phi_x^{(F)} \right)$$

Goal: flexibly capture patterns in Familinx bias across age, time, gender, country

# Adjustment factor

$$d_{c,g,t,x}^{(F)} | \mu_{c,g,t,x}, \phi_x^{(F)} \sim \text{NegBinom} \left( \mu_{c,g,t,x}, \boxed{\psi_{c,g,t,x}} \rho_{c,g,t,x}^{(F)}, \phi_x^{(F)} \right)$$

Goal: flexibly capture patterns in Familinx bias across age, time, gender, country

$$\log \psi_{c,g,t,x} = \omega_c + \alpha_c I(x = 0) + \xi_c I(x < 20) + f_{c,g}(x, t)$$

# Adjustment factor

Goal: flexibly capture patterns in Familinx bias across age, time, gender, country

$$\log \psi_{c,g,t,x} = \omega_c + \alpha_c I(x = 0) + \xi_c I(x < 20) + f_{c,g}(x, t)$$



Country-specific intercept



# Adjustment factor

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$$\log \psi_{c,g,t,x} = \omega_c + \alpha_c I(x = 0) + \xi_c I(x < 20) + f_{c,g}(x, t)$$

Young age adjustments



# Adjustment factor

Goal: flexibly capture patterns in Familinx bias across age, time, gender, country

$$\log \psi_{c,g,t,x} = \omega_c + \alpha_c I(x = 0) + \xi_c I(x < 20) + f_{c,g}(x, t)$$

2D tensor product smoothing spline



# Adjustment factor

$$\log \psi_{c,g,t,x} = \omega_c + \alpha_c I(x = 0) + \xi_c I(x < 20) + f_{c,g}(x, t)$$

Has the form (for each  $c$  and  $g$ )

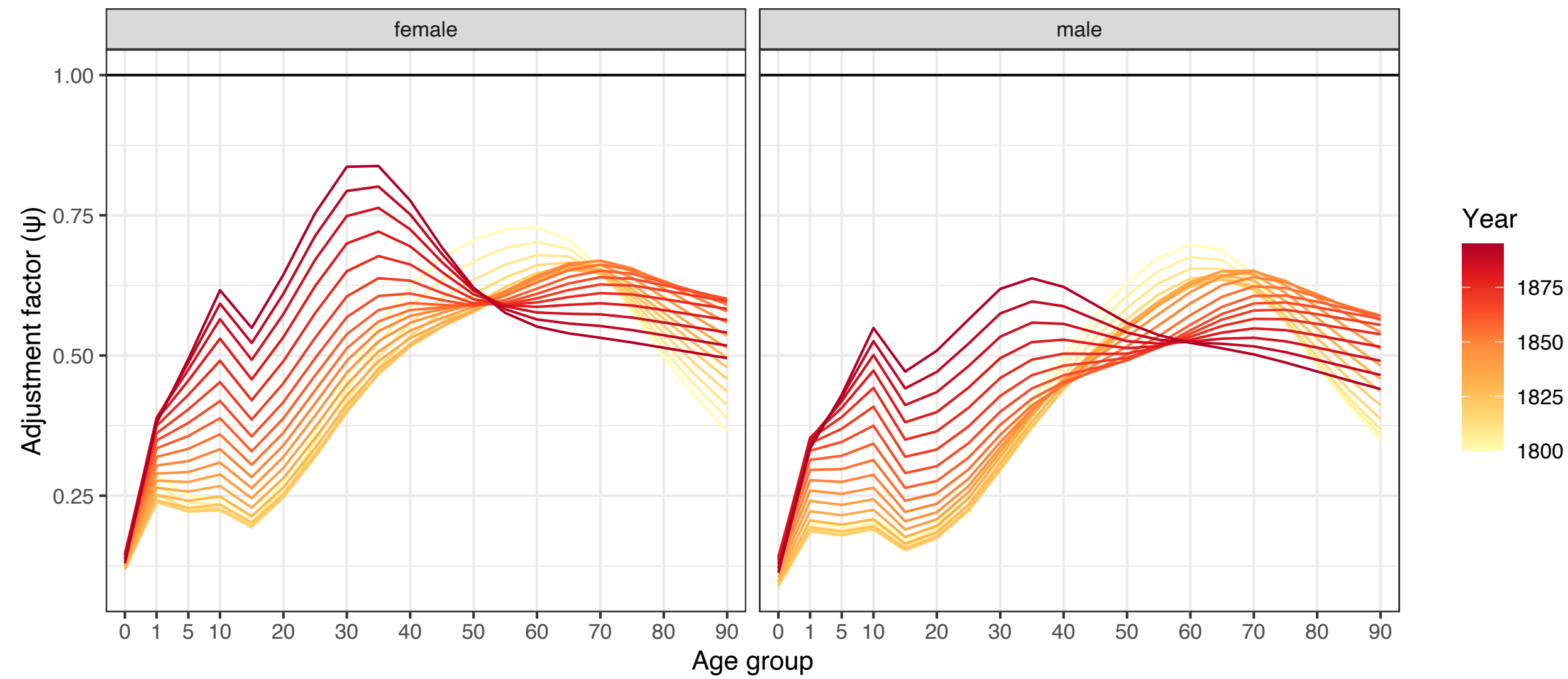
$$f(x, t) = \sum_{kj} \beta_{kj} h_j(t) g_k(x)$$

Coefficients (estimated hierarchically across countries)  
(second-order penalty on smoothness)

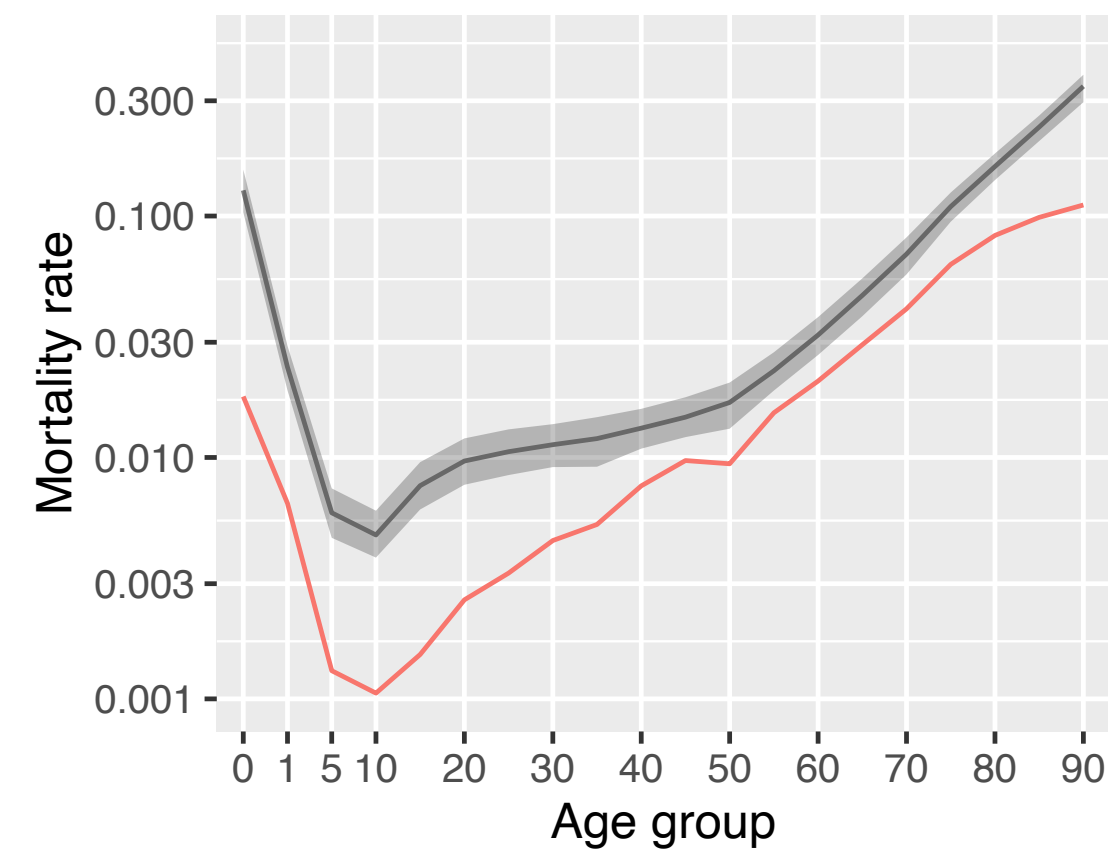
Cubic basis splines in  
age and time dimension

# Illustrative Results

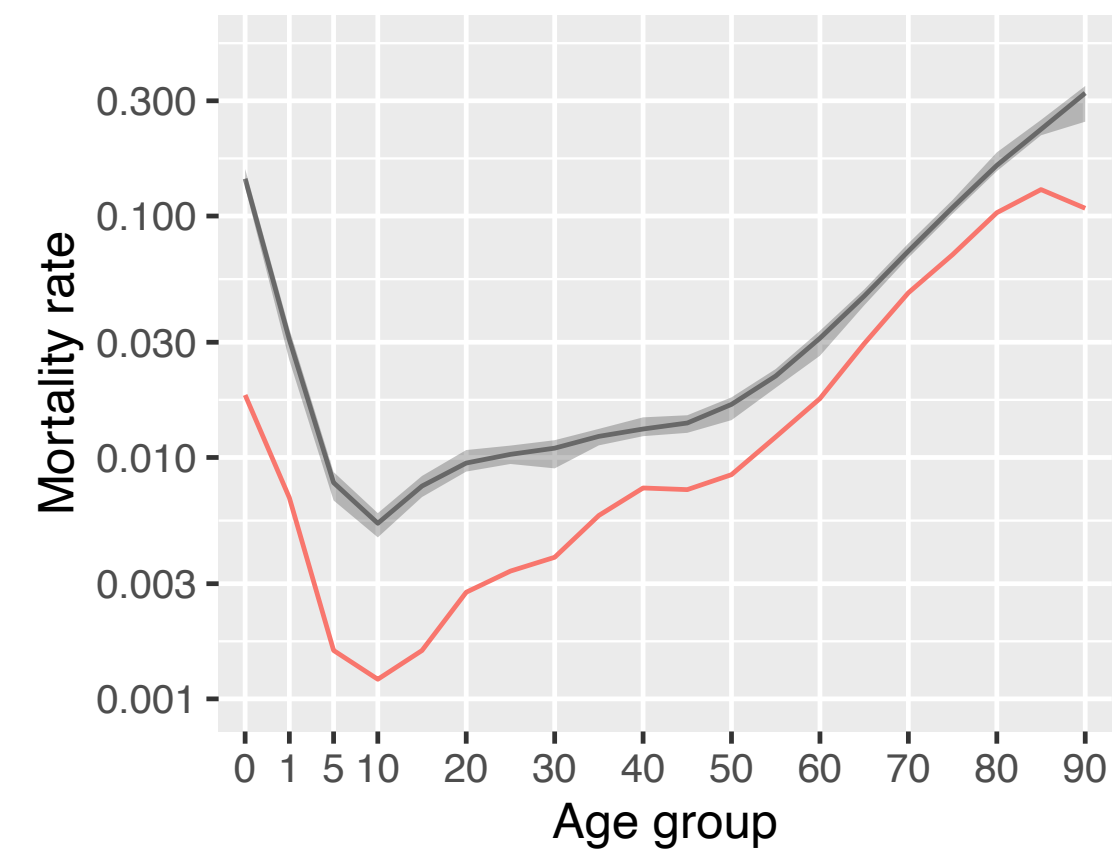
# Great Britain



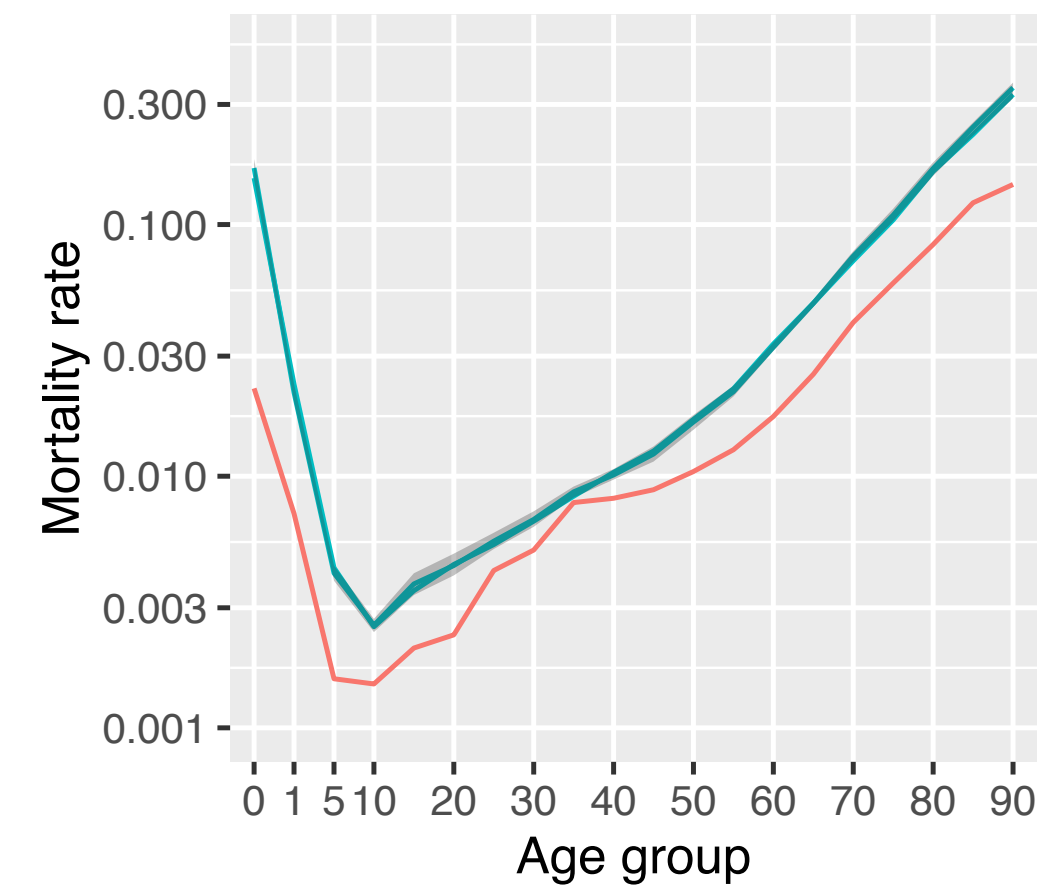
Great Britain 1805, female



1830

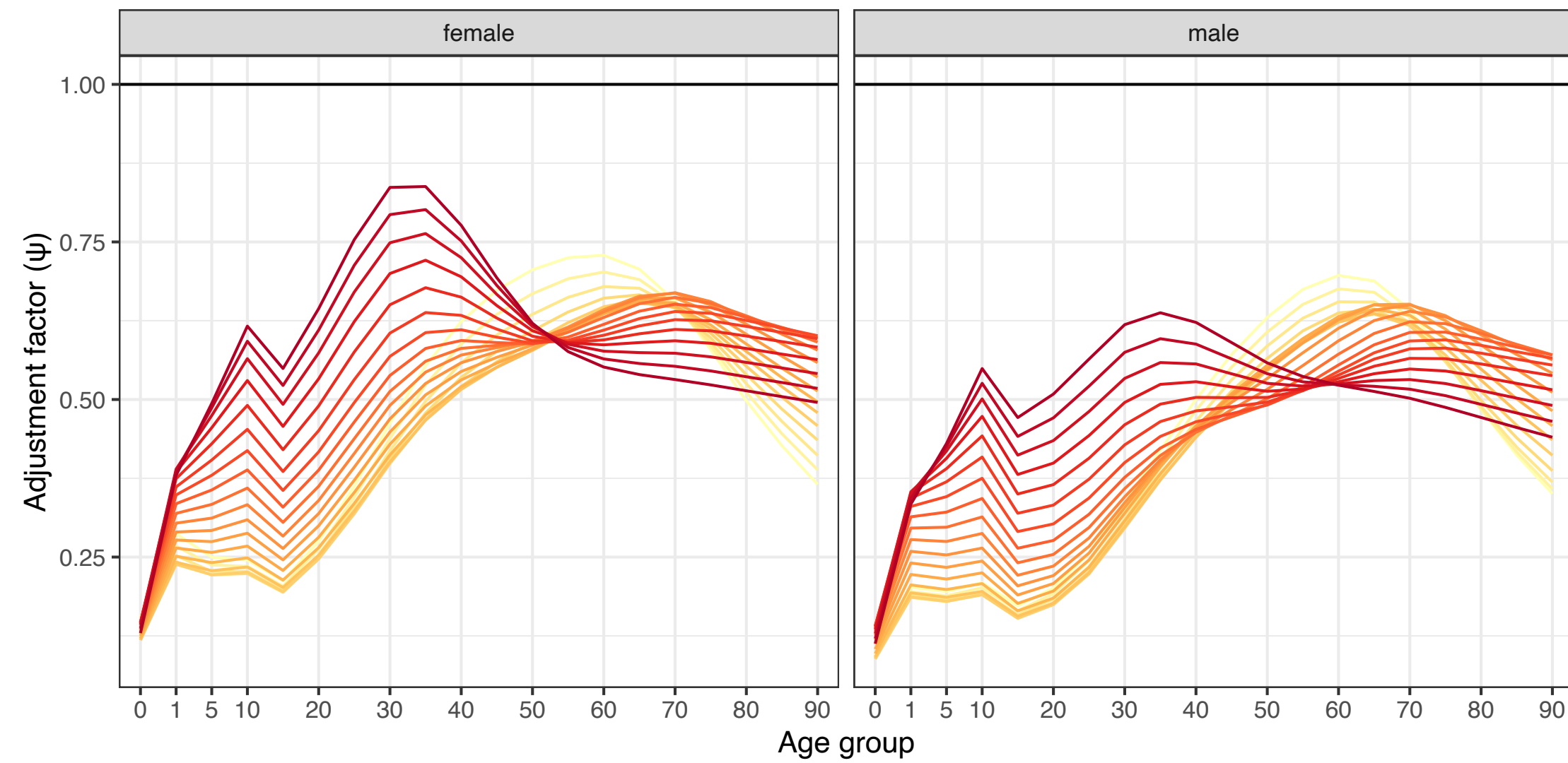


1895

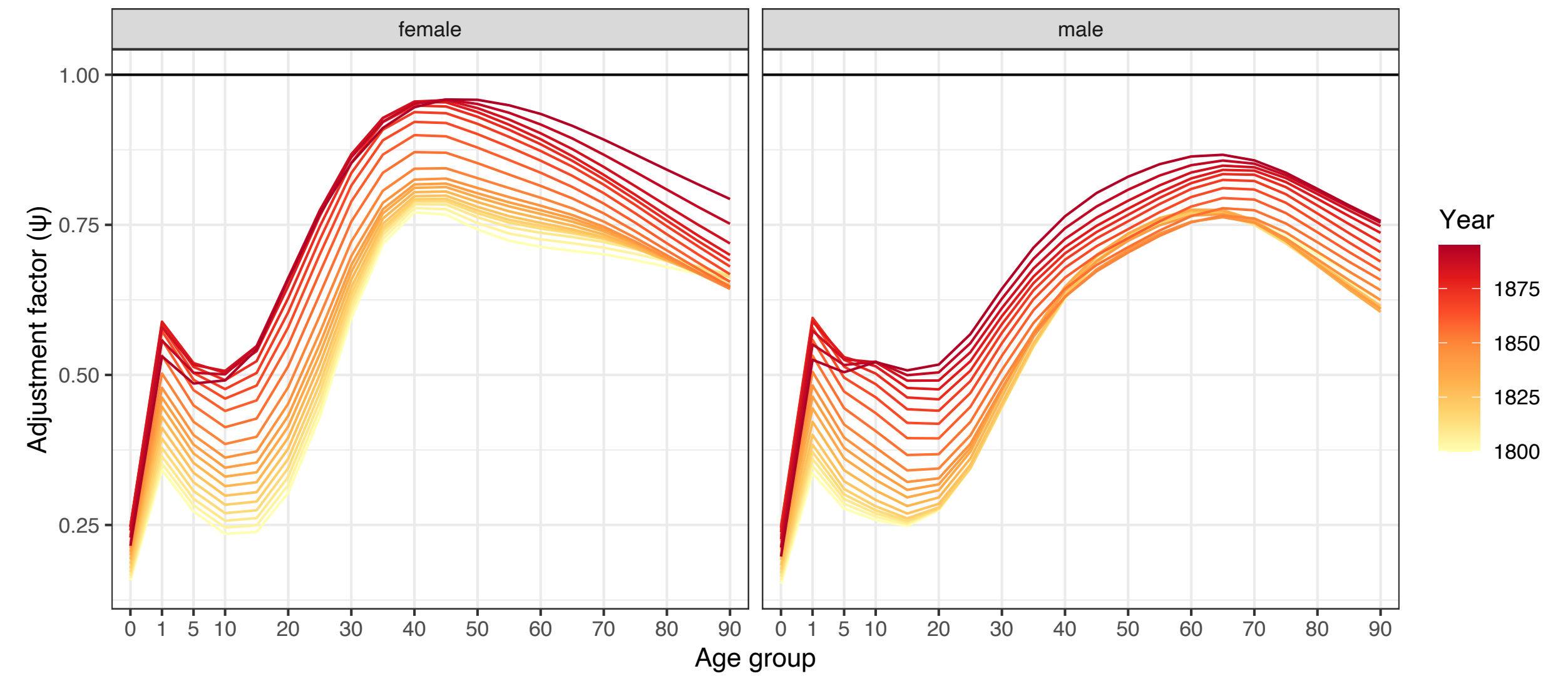


FamiLinx  
HMD

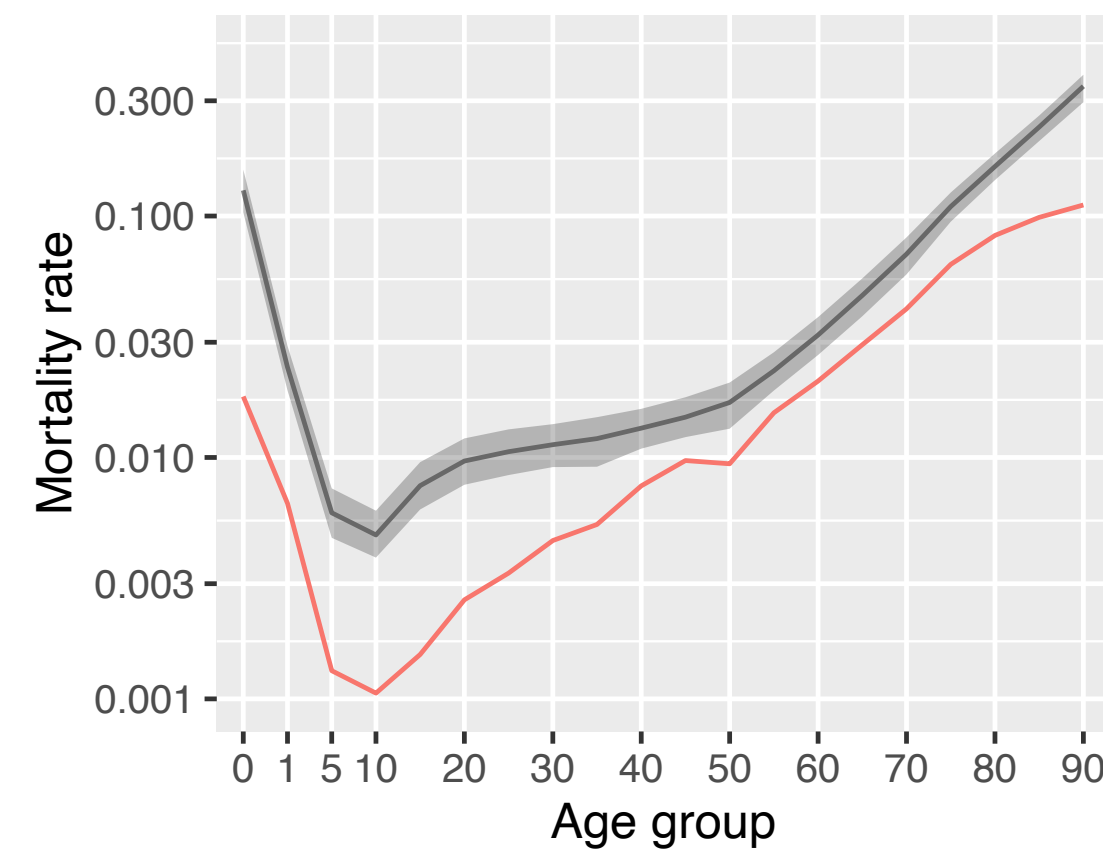
# Great Britain



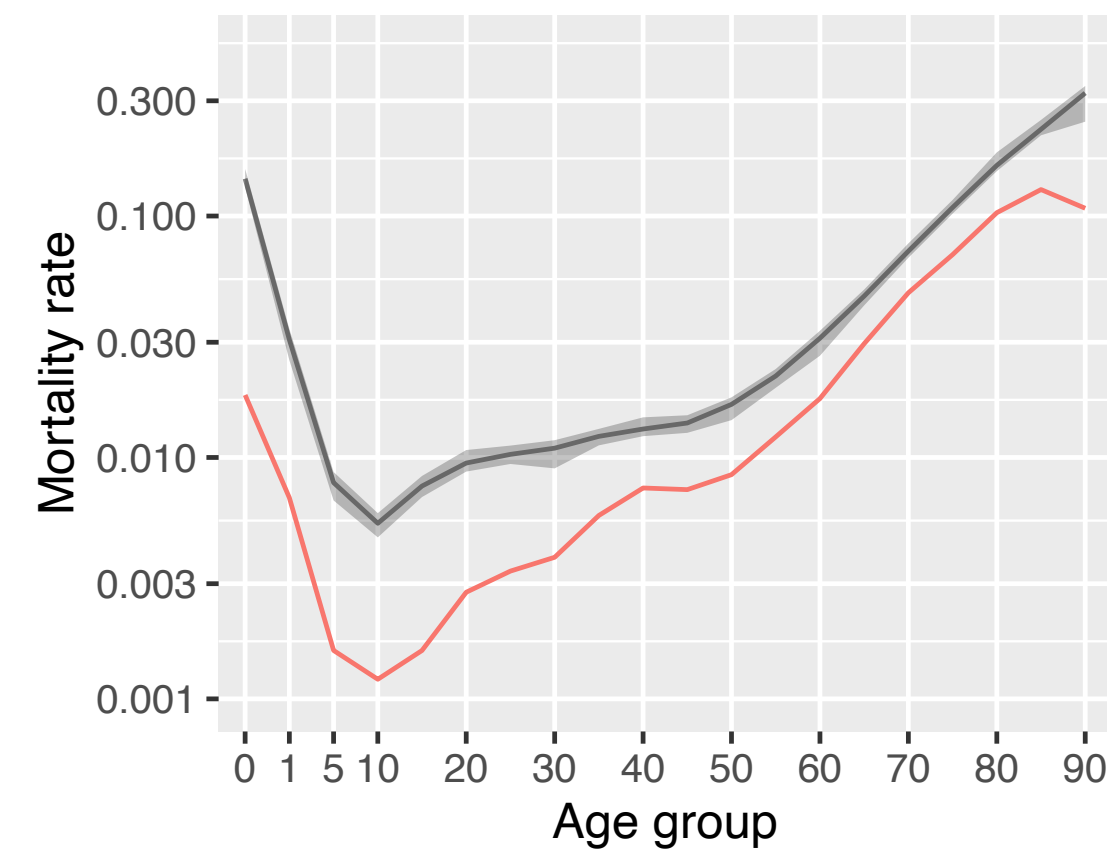
# Sweden



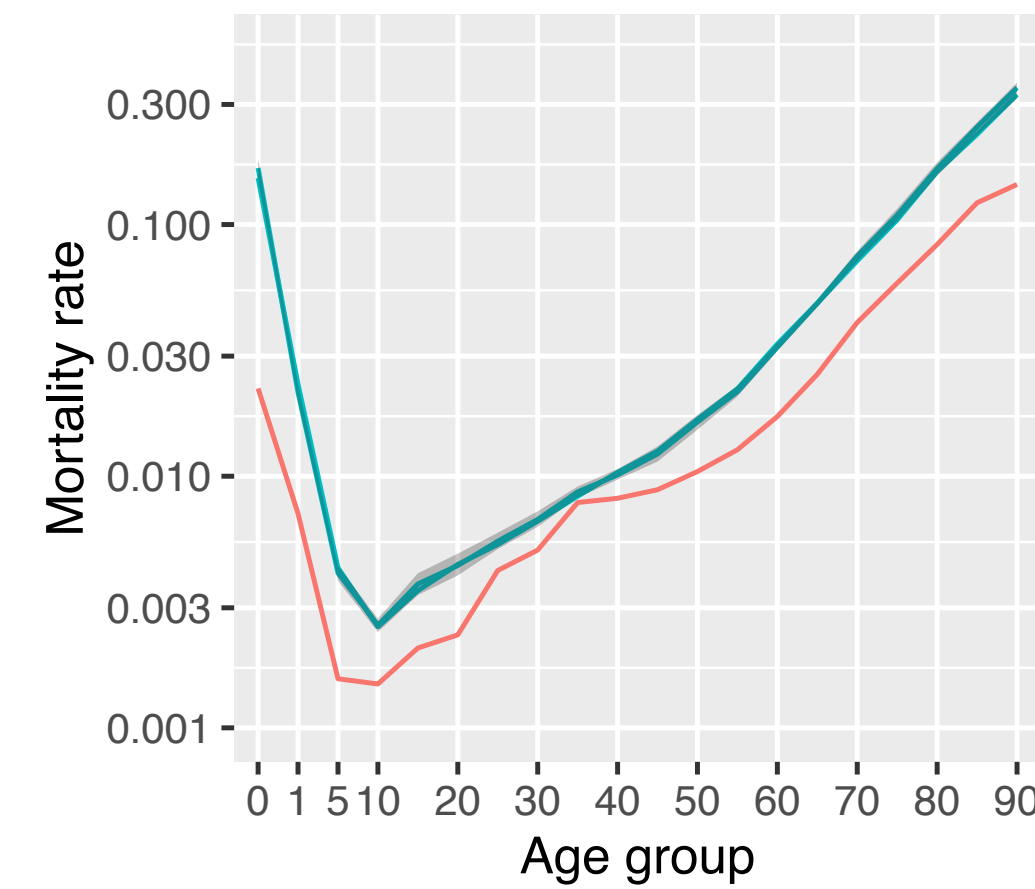
Great Britain 1805, female



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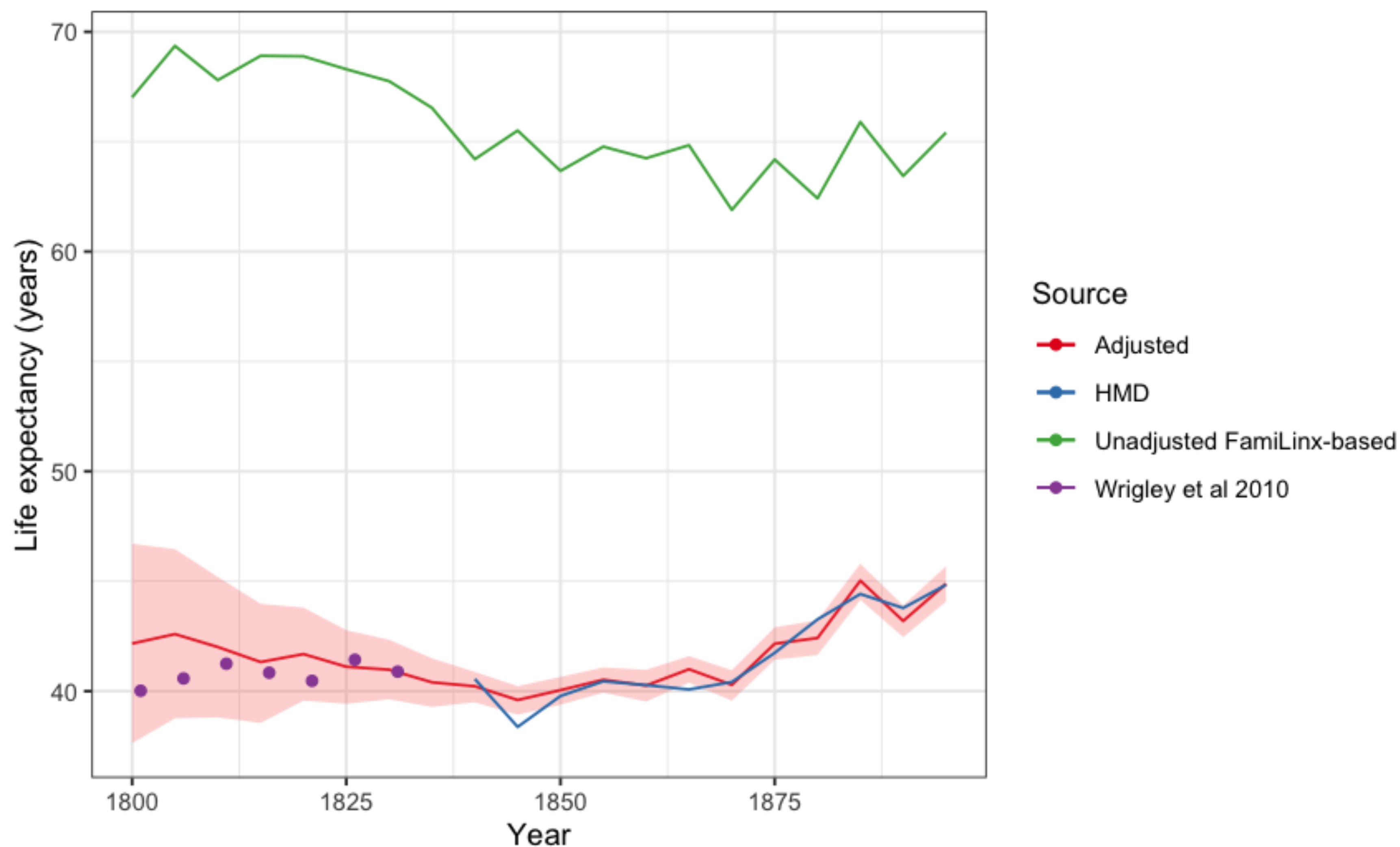
1895



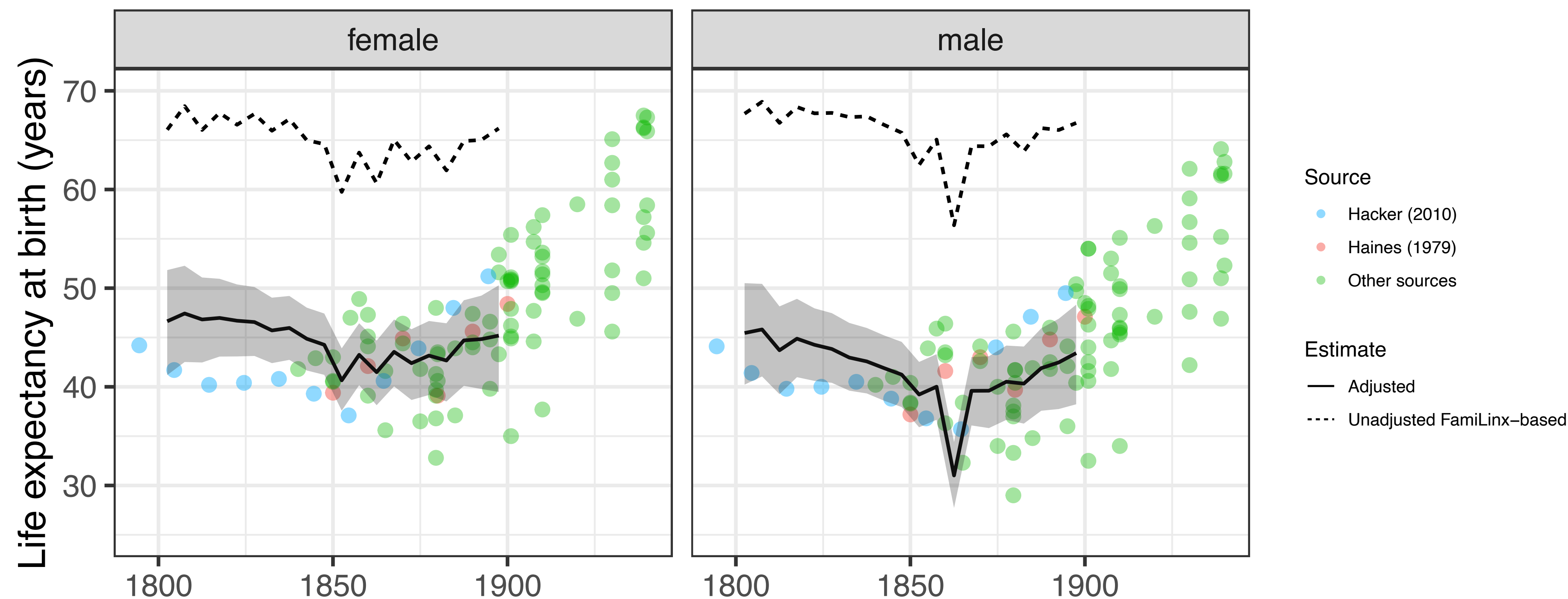
FamiLinx  
HMD



# Life expectancy in Great Britain

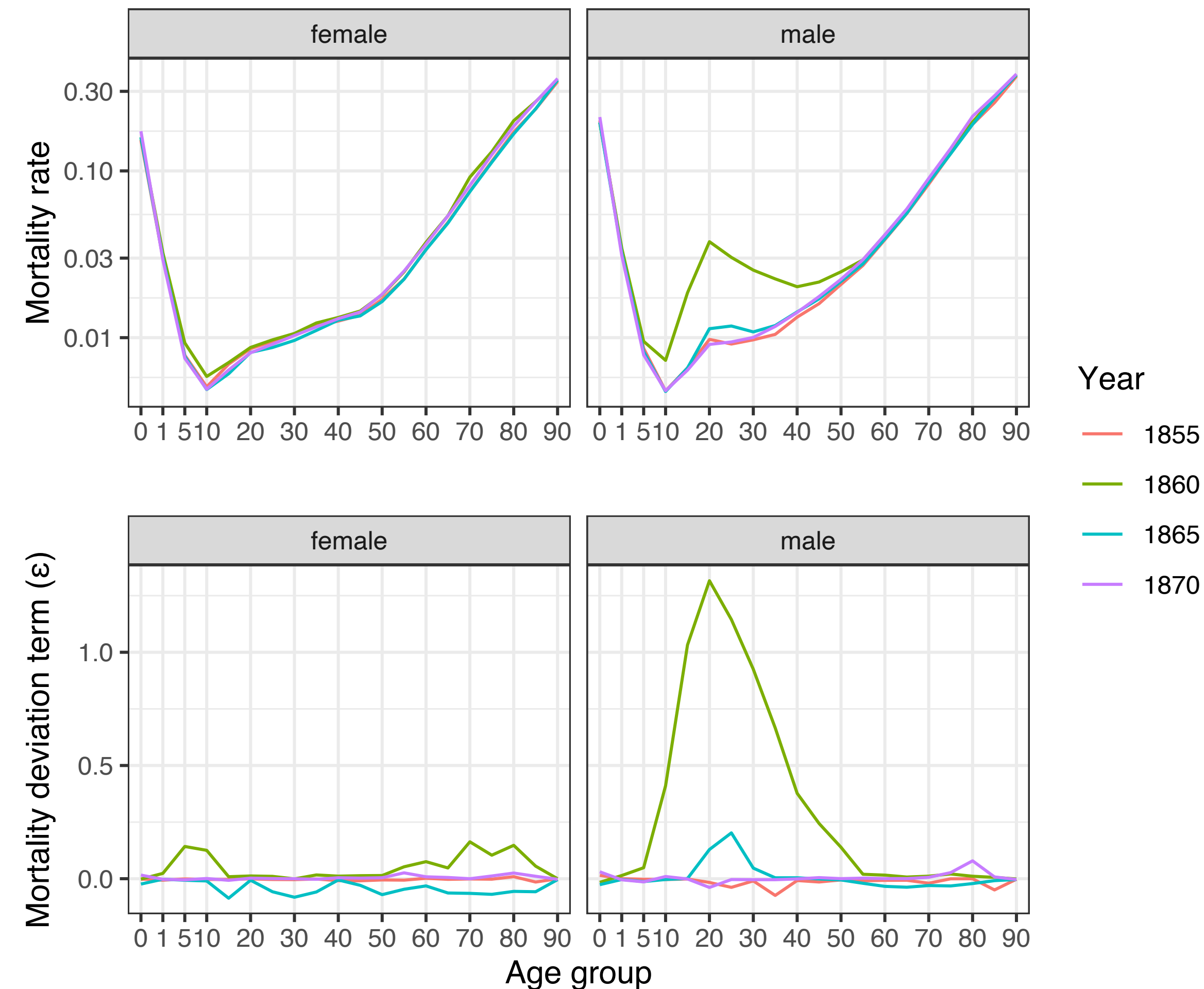


# US life expectancy



# Impact of regularized error term

Estimates for the United States in the Civil War years (1861-1865)



Systematic mortality rate variation is constrained to only vary in PC directions, and variation is smoothed over time

Leftover variation can be absorbed by the sparse  $\varepsilon$  terms

# Summary

- Online genealogies offer a new potential source for historical demography
  - Not just mortality! fertility, kin structures
- Data are biased because of both how genealogies are reported but also because of quality, representativeness
- Bayesian model centered on estimating and predicting a set of adjustment factors, which are useful in their own right
- Future work will investigate generative models of genealogical construction

# Thanks!

[monica.alexander@utoronto.ca](mailto:monica.alexander@utoronto.ca)

[monicaalexander.com](https://monicaalexander.com)

 MJAlexander

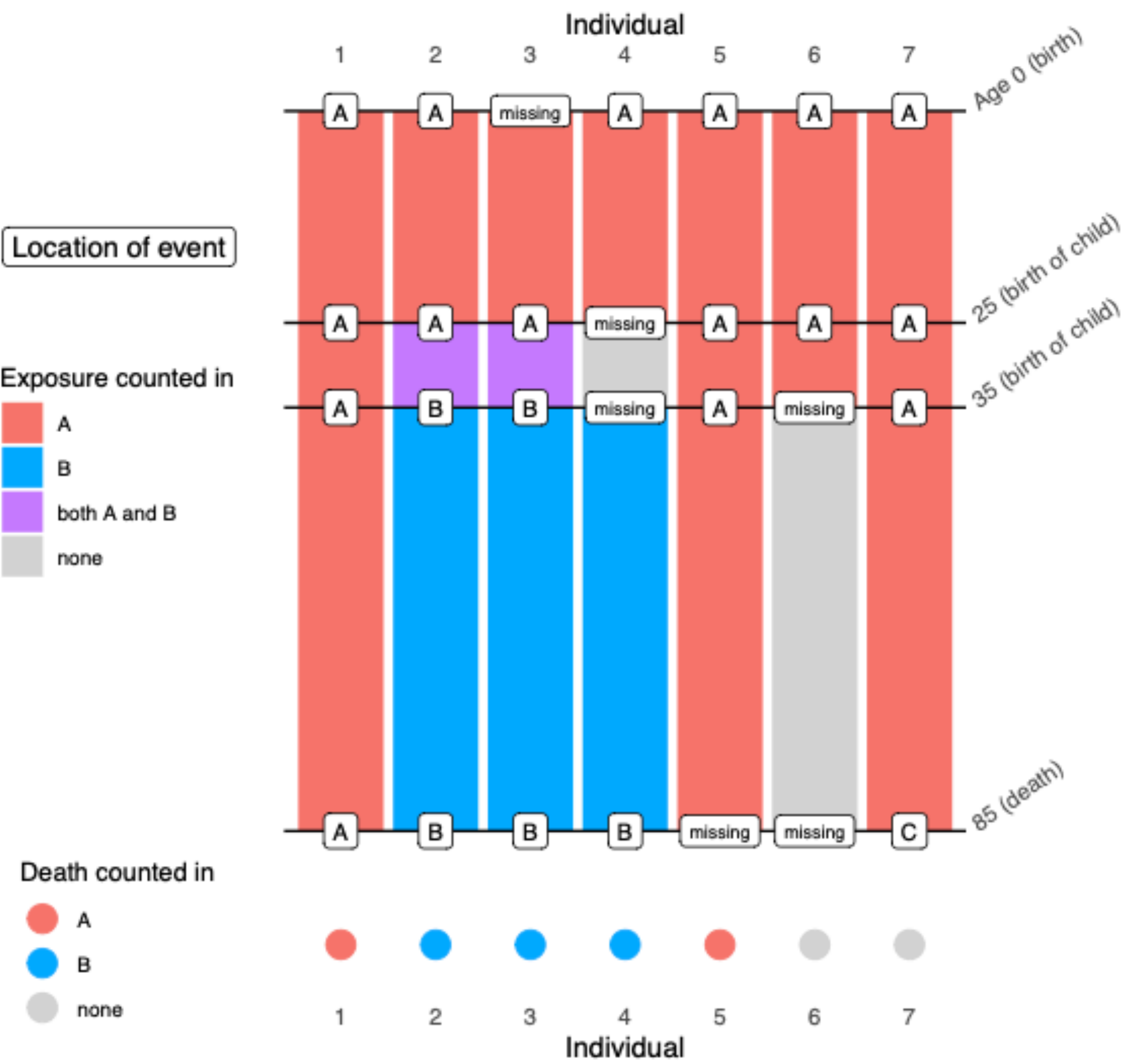


UNIVERSITY OF  
**TORONTO**

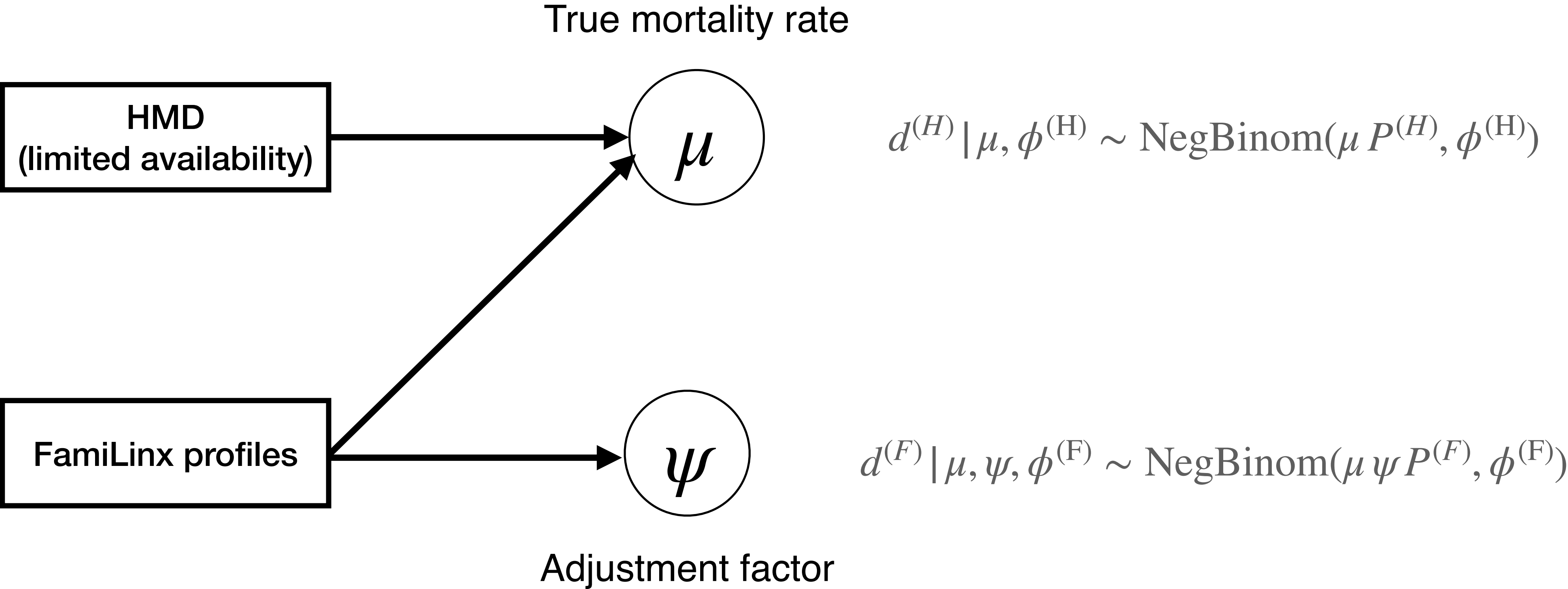
Extra



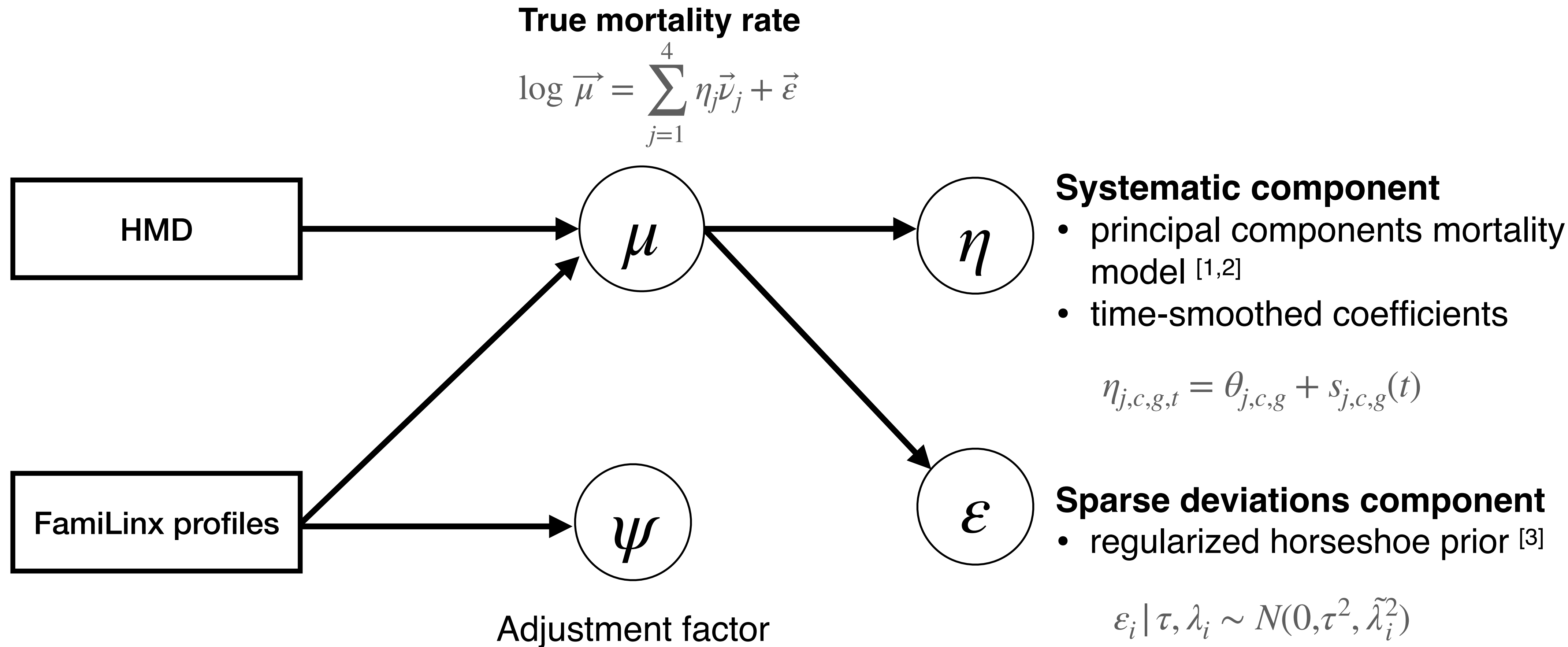
# Locations



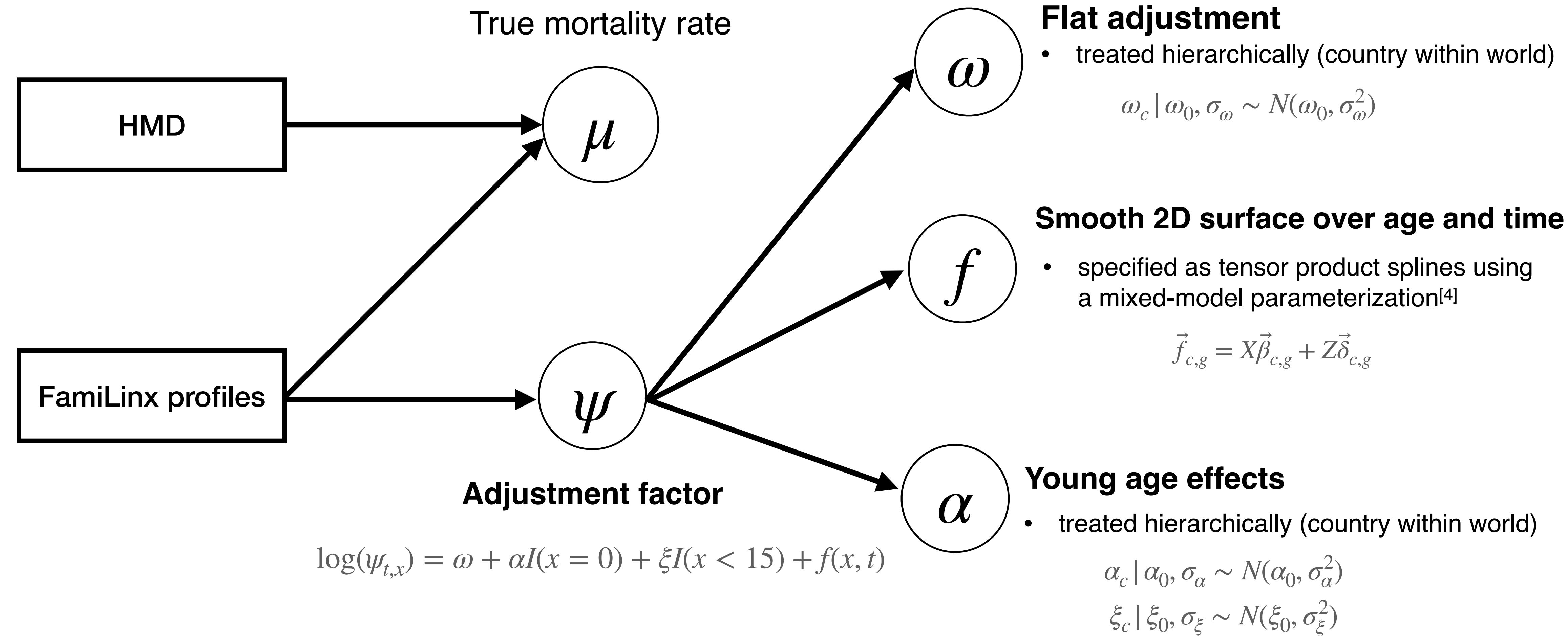
Our model compares FamiLinx-derived mortality to the Human Mortality Database (HMD)



# Mortality is assumed to (mostly) follow stable patterns of age-specific mortality



# The adjustment factors vary (mostly) smoothly over age and time



# More details on tensor smooth implementation

$$\text{Let } \vec{f} = \left[ f(x_1, t_1), \dots, f(x_N, t_N) \right]^T$$

$$\text{Reparameterize as } \vec{f}_{c,g} = X\vec{\beta}_{c,g} + Z\vec{\delta}_{c,g}$$

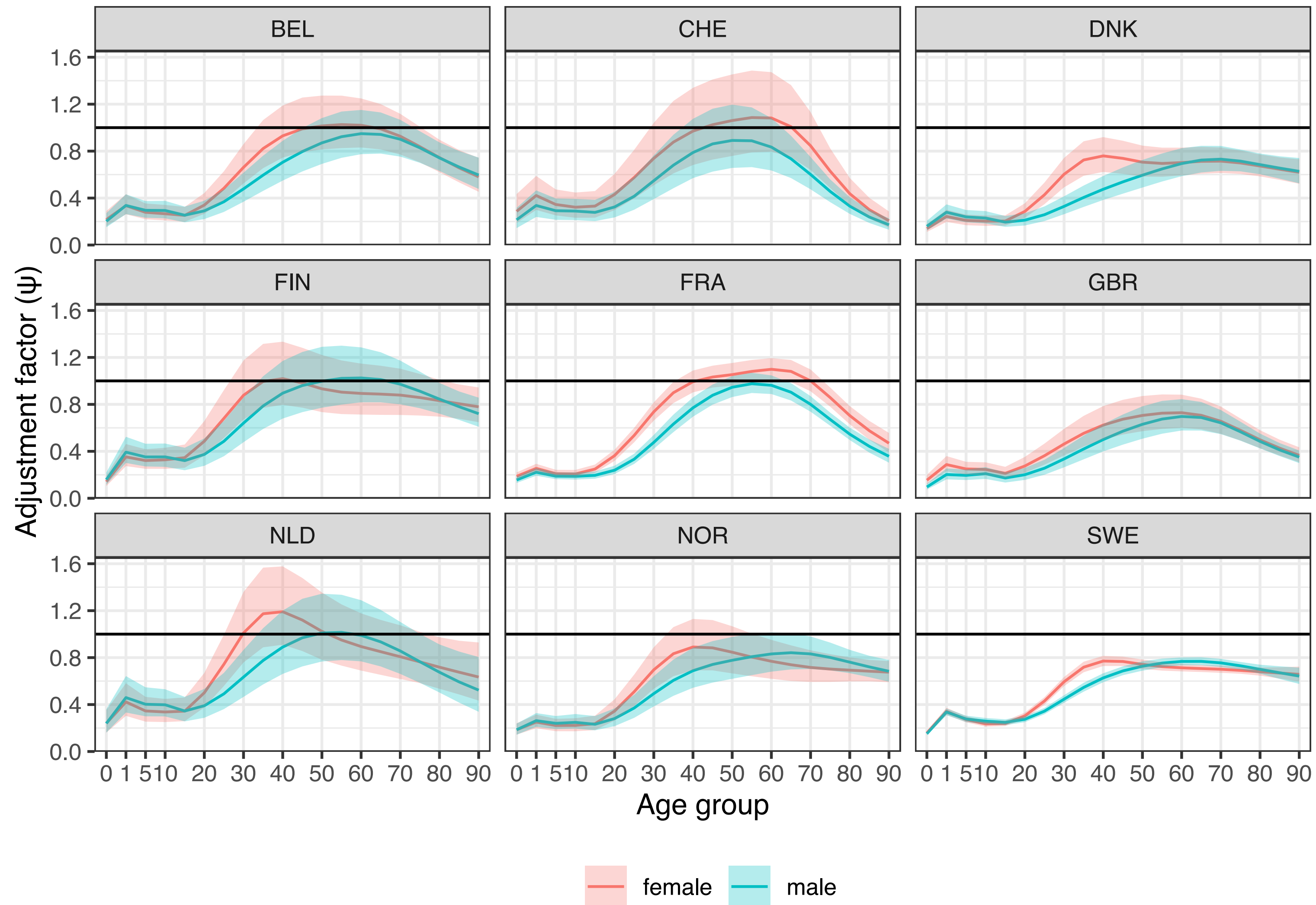
X represents unpenalized fixed effects, Z represents penalized components Using a typical 2nd derivative penalty, X contains the linear and constant functions. In the hierarchical Bayesian approach the fixed effect slopes are modelled

$$\vec{\beta}_{c,g} = \vec{\beta}_g + \vec{\gamma}_{c,g}$$

$$\text{with priors } \vec{\beta}_g \sim MVN(0, I_{2 \times 2}) \text{ and } \vec{\gamma}_{c,g} \mid \vec{\sigma}_\gamma \sim MVN\left(0, \text{diag}\left(\vec{\sigma}_\gamma^2\right)\right).$$

A similar approach is used for the random effects  $\delta$

# Adjustment factors in 1800



# Validation example





