Demographic Forecasting

Lecture 4: the Lee-Carter method

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Course overview

- Lecture 1: direct extrapolation by (generalized) linear models
- Lecture 2: direct extrapolation by time-series methods
- Lecture 3: parametric approaches
- Lecture 4: the Lee-Carter method

Mortality forecasting

- Crucial for sustainability of pensions, insurances, elderly care; predicting population ageing and projecting populations; . . .
- Until the 1980s, the methods used to forecast mortality were **deterministic**, based on mathematical formulae or expert judgment
- Revived interest in recent years following the introduction of the Lee-Carter method in 1992
- One of the firstly introduced **stochastic** mortality models $\Rightarrow$ the model “revolutionized probabilistic mortality and population forecasting” (Raftery 2023)

The Lee-Carter method (1992)

- Proposed in 1992 to model and forecast US mortality
- After 30+ years, Lee-Carter (LC) still widely employed by variety of users: governments, private companies, international organizations, …
- The landmark model in mortality forecasting
- An **extrapolation** method:
  - model the mortality surface over age and time
  - extrapolate trends in the future, assuming that observed trends will continue
- Simplicity, robustness and objectivity have made the model so successful
- Nonetheless, some limitations of the model have stimulated several extensions over the years (see Basellini et al. (2023) for a recent comprehensive review)

The LC method

- A simple log-bilinear functional form for mortality rates $m_{x,t}$ at age x and time t

$$\ln(m_{x,t}) = \alpha_x + \beta_x \kappa_t + \epsilon_{x,t}$$

where:

  - α_x is the general shape of log-mortality at age x
  - β_x is the rate of mortality improvement at age x
  - κ_t is the general level of mortality at time t
  - $\epsilon_{x,t}$ is the error term with mean 0 and variance σ_ϵ^2, reflecting residual age-specific influences not captured by the model

- Modelling log-rates $\Rightarrow$ fitted and forecast rates constrained to be positive
- Log transformation partially counters heteroscedasticity of observed rates

The LC method: a schematic view

$$\ln(m_{x,t}) \simeq \alpha_x + \beta_x \kappa_t$$

$$\begin{pmatrix} \ln(m_{x_1,t_1}) & \ln(m_{x_1,t_2}) & \dots & \ln(m_{x_1,t_n}) \\ \ln(m_{x_2,t_1}) & \ln(m_{x_2,t_2}) & \dots & \ln(m_{x_2,t_n}) \\ \ln(m_{x_3,t_1}) & \ln(m_{x_3,t_2}) & \dots & \ln(m_{x_3,t_n}) \\ \vdots & \vdots & \ddots & \vdots \\ \ln(m_{x_m,t_1}) & \ln(m_{x_m,t_2}) & \dots & \ln(m_{x_m,t_n}) \end{pmatrix} \simeq$$

$$\begin{pmatrix} \alpha_{x_1} \\ \alpha_{x_2} \\ \alpha_{x_3} \\ \vdots \\ \alpha_{x_m} \end{pmatrix} + \begin{pmatrix} \beta_{x_1} \\ \beta_{x_2} \\ \beta_{x_3} \\ \vdots \\ \beta_{x_m} \end{pmatrix} \begin{pmatrix} \kappa_{t_1} & \kappa_{t_2} & \dots & \kappa_{t_n} \end{pmatrix}$$

$$\underbrace{n}_{\text{years}} \times \underbrace{m}_{\text{ages}} = \underbrace{mn}_{\text{cells}} \simeq \underbrace{m}_{\alpha_i} + \underbrace{m}_{\beta_i} + \underbrace{n}_{\kappa_j} - \underbrace{2}_{\text{constraints}} = \underbrace{2m+n-2}_{\text{parameters}}$$

The LC method

- The model is undetermined: if $\boldsymbol{\theta}_1 = [\boldsymbol{\alpha}, \boldsymbol{\beta}, \boldsymbol{\kappa}]$ is a solution, then for any scalar c:
  - $\boldsymbol{\theta}_2 = [\boldsymbol{\alpha} - \boldsymbol{\beta} c, \boldsymbol{\beta}, \boldsymbol{\kappa} + c]$ is also a solution
  - $\boldsymbol{\theta}_3 = [\boldsymbol{\alpha}, \boldsymbol{\beta} c, \boldsymbol{\kappa} / c]$ is also a solution
- Two constraints introduced to ensure model identification:

$$\sum_x \beta_x = 1 \qquad \text{and} \qquad \sum_t \kappa_t = 0$$

Model estimation

- The model is estimated by minimizing the residual sum of squares:

$$\sum_{x,t}\left(\ln(m_{x,t}) - \alpha_x - \beta_x\kappa_t\right)^2 \qquad (1)$$

- A singular value decomposition (SVD) is employed to minimize Equation 1 & derive an ordinary least squares (OLS) solution:
    - $\hat{\alpha}_x$ is the average of the observed $\ln(m_{x,t})$: $\hat{\alpha}_x = \frac{1}{n}\sum_{t=1}^{n}\ln(m_{x,t})$

Exercise

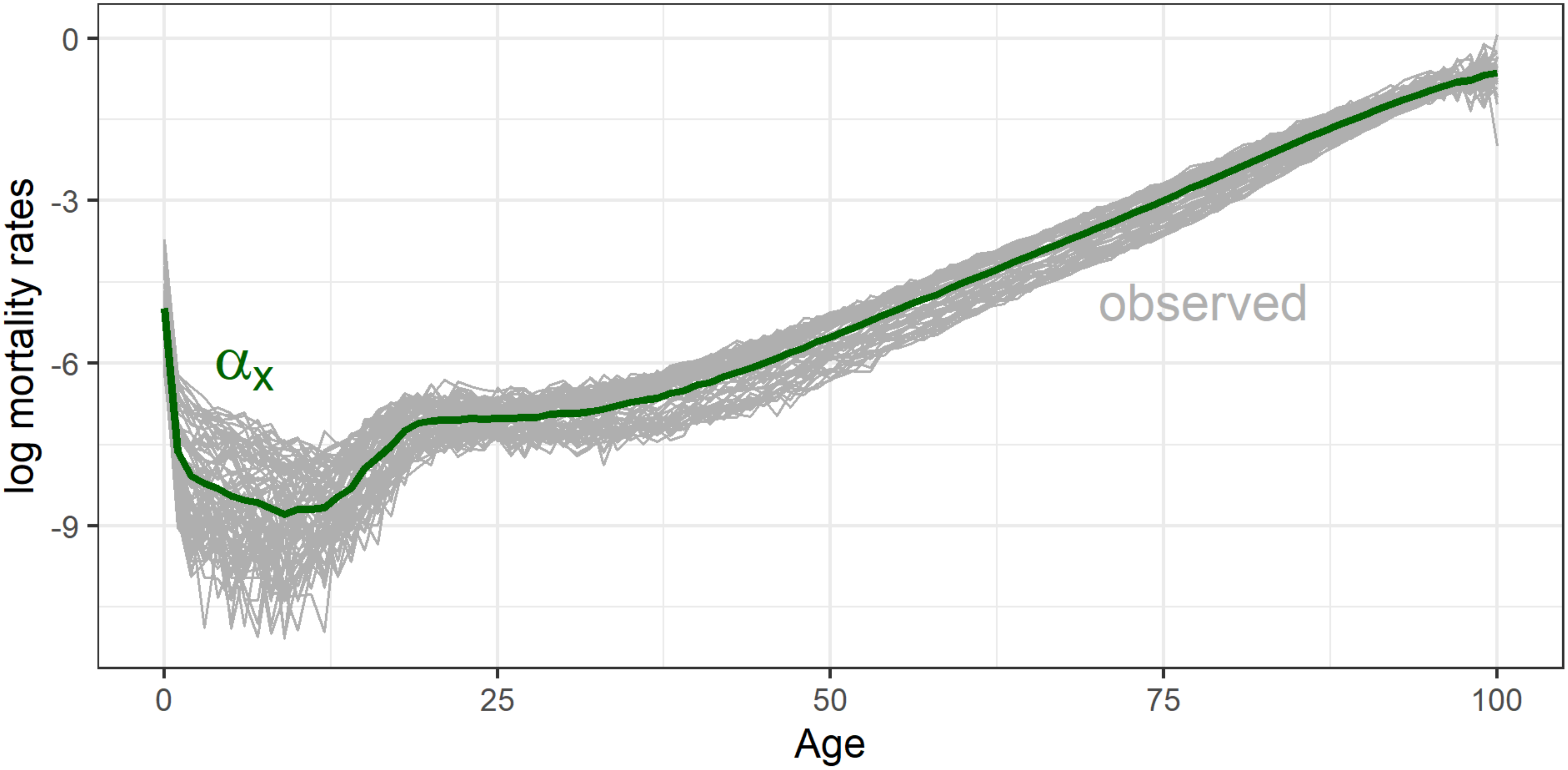
Exercise

Open your R session. Load the `MortSWE.Rdata` dataset, and consider only data from 1950 onward for males aged $0 \leq x \leq 100$. Derive the LC estimate of the $\alpha_x = \frac{1}{n} \sum_{t=1}^{n} \ln(m_{x,t})$ parameter

Hint: Replace the only cell with 0 deaths with a tiny number of deaths (e.g., 1), and compute again the matrix of log-mortality rates. This will be particularly helpful later on.

One possible solution

One possible solution



Model estimation

- The model is estimated by minimizing the residual sum of squares:

$$\sum_{x,t}\Big(\ln(m_{x,t}) - \alpha_x - \beta_x \kappa_t\Big)^2 \qquad (2)$$

- A singular value decomposition (SVD) is employed to minimize Equation 2 & derive an ordinary least squares (OLS) solution:
  - $\hat{\alpha}_x$ is the average of the observed $\ln(m_{x,t})$: $\hat{\alpha}_x = \frac{1}{n}\sum_{t=1}^{n}\ln(m_{x,t})$
  - $\hat{\beta}_x$ and $\hat{\kappa}_t$ are the first left- and right-singular vectors of the SVD of the matrix $\ln(m_{x,t}) - \hat{\alpha}_x$, adjusted to comply with the two constraints $\sum_x \beta_x = 1 \qquad \text{and} \qquad \sum_t \kappa_t = 0$

Singular Value Decomposition

- An SVD of any $m \times n$ rectangular matrix $\boldsymbol{M}$ is a factorization of the form:

$$\boldsymbol{M} = \boldsymbol{U}\,\boldsymbol{\Sigma}\,\boldsymbol{V}'$$

  where

  - $\boldsymbol{U}$ is a $m \times m$ orthogonal matrix (left-singular vectors)
  - $\boldsymbol{V}$ is a $n \times m$ orthogonal matrix (right-singular vectors)
  - $\boldsymbol{\Sigma}$ is a $m \times m$ diagonal matrix with $\boldsymbol{s}_{ij} = 0$ if $i \neq j$ ($\boldsymbol{s}_{ii}$, singular values)

- In other words, we can decompose $\boldsymbol{M}$ as

$$\boldsymbol{M} = U_{,1}\,\boldsymbol{s}_{1,1}\,V_{,1}' + U_{,2}\,\boldsymbol{s}_{2,2}\,V_{,2}' + U_{,3}\,\boldsymbol{s}_{3,3}\,V_{,3}' + \ldots + U_{,m}\,\boldsymbol{s}_{m,m}\,V_{,m}'$$

- The first few singular values/vectors are more important in describing the information in $\boldsymbol{M}$

Exercise

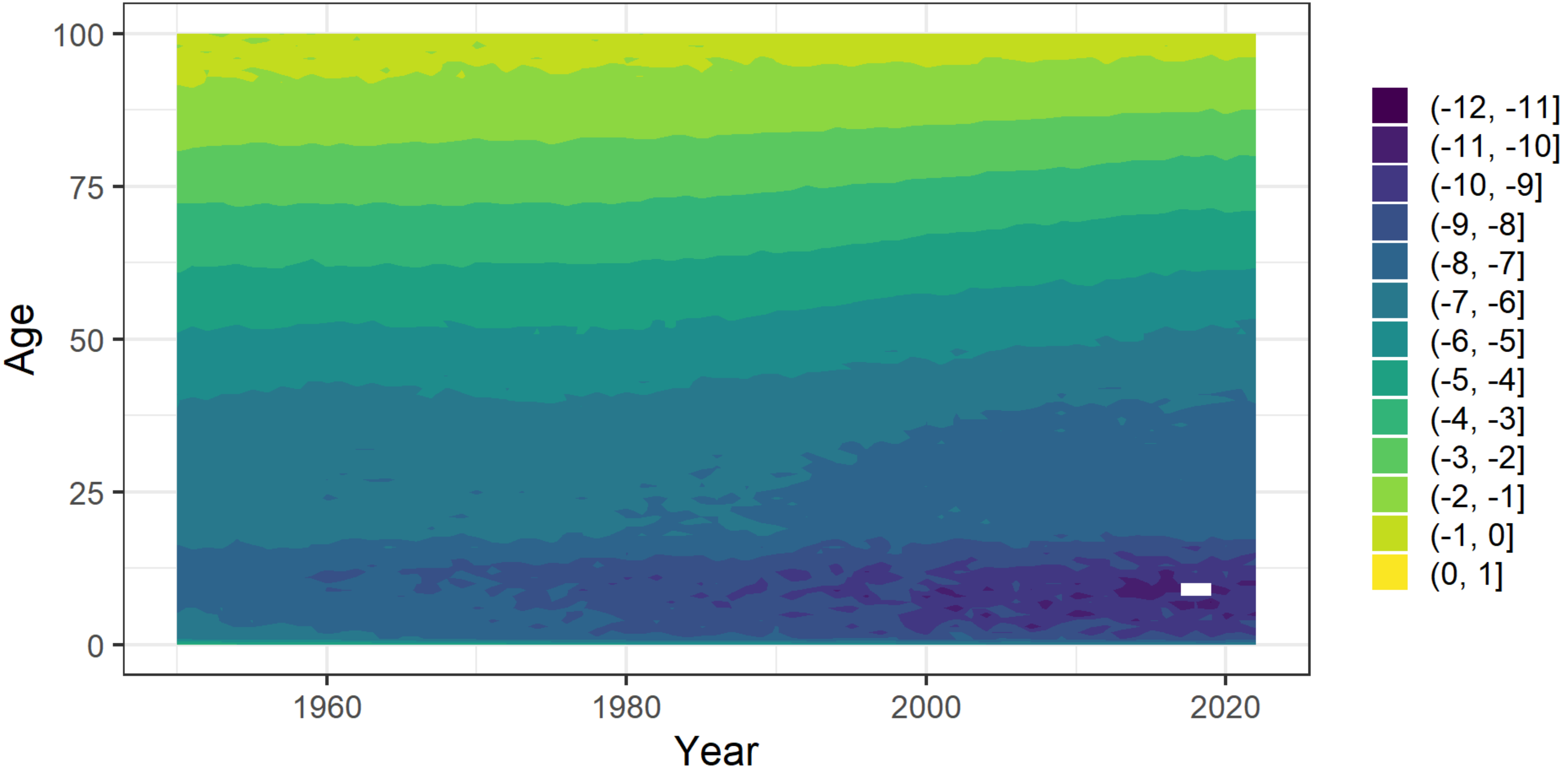
Exercise

Now perform a singular value decomposition of the matrix of “centered” mortality rates $\ln(m_{x,t}) - \hat{\alpha}_x$, and plot the first left- and right-singular vectors

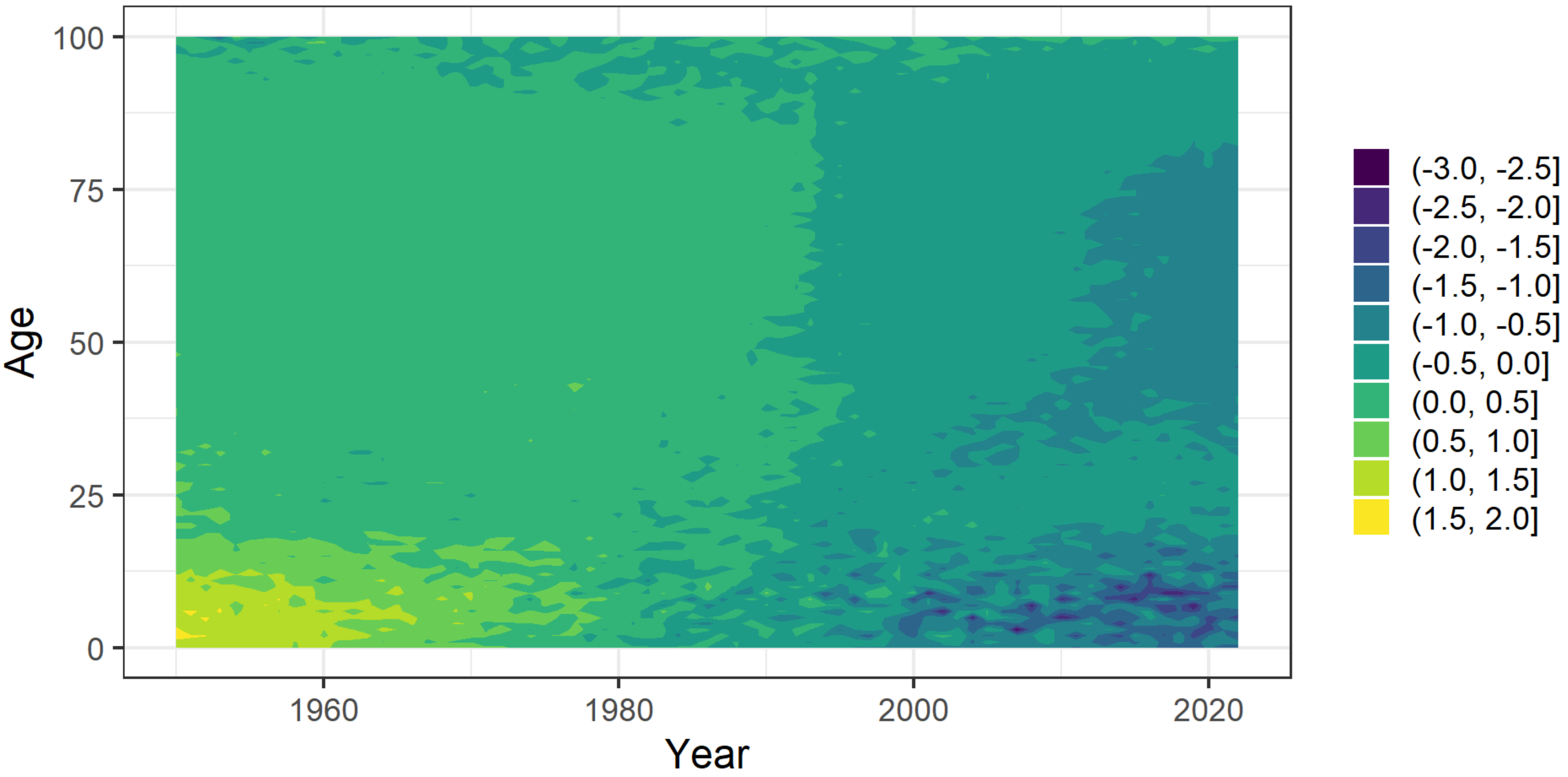
Hint: Use the command `svd(x=.,nu=1,nv=1)` to perform the SVD of your centred mortality rates matrix, and then extract the vectors `u` and `v` from the SVD object. Remember to use the modified log-rates matrix (which excludes infinite values).

One possible solution

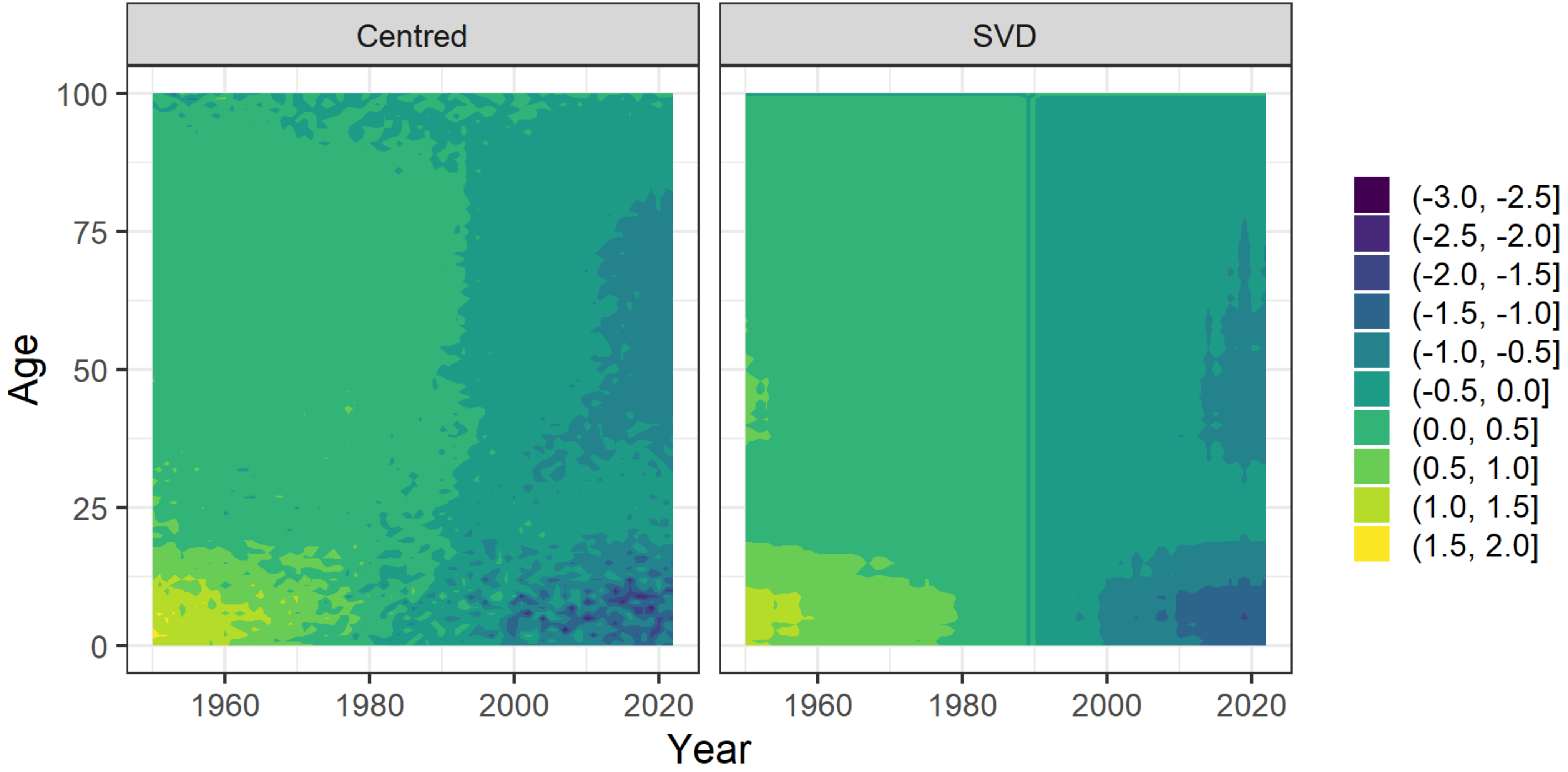
Log-mortality rates



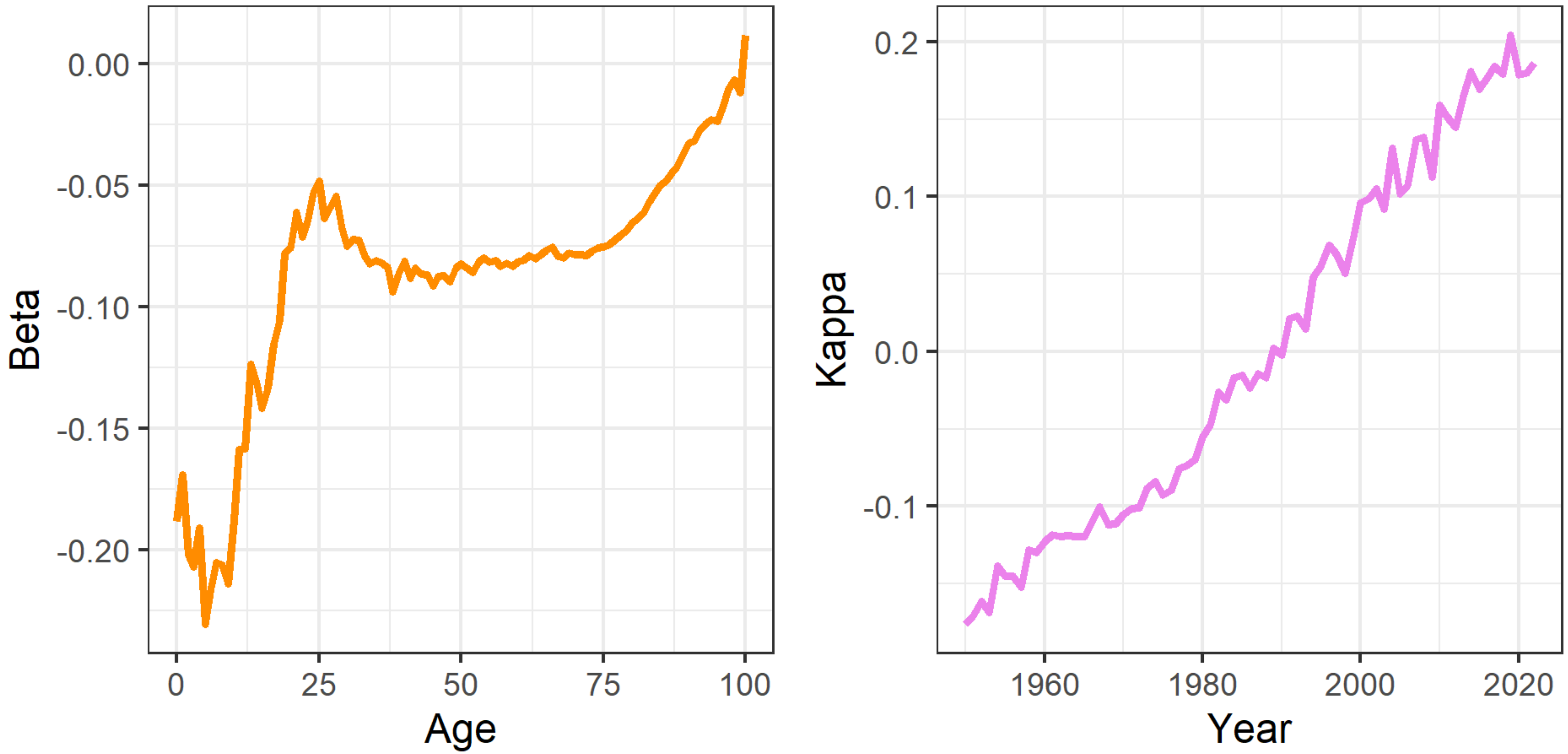
Centred log-mortality rates



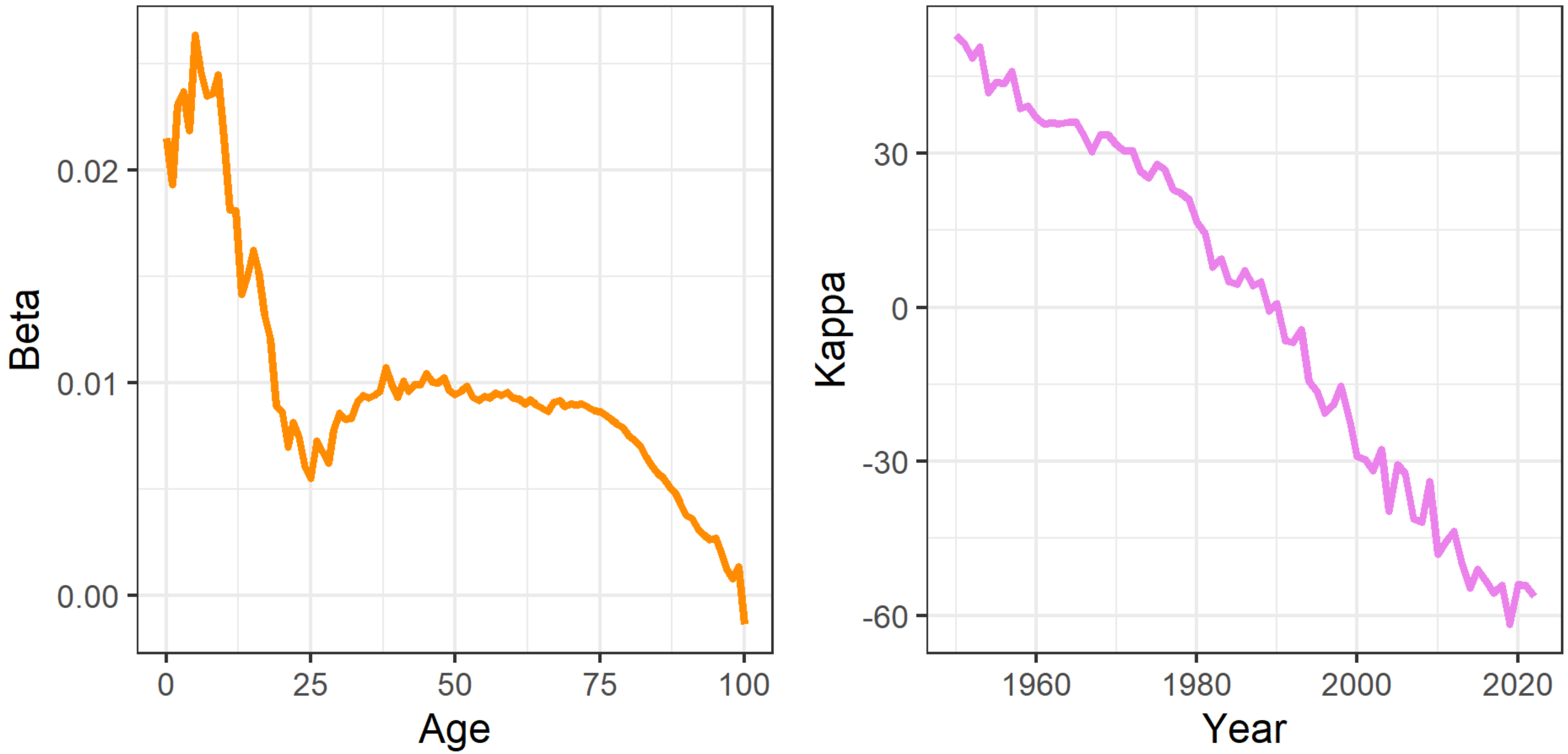
SVD approximation



$\hat{\beta}_x$ and $\hat{\kappa}_t$ from SVD



$\hat{\beta}_x$ and $\hat{\kappa}_t$ with constraints



Second step estimation of $\hat{\kappa}_t$

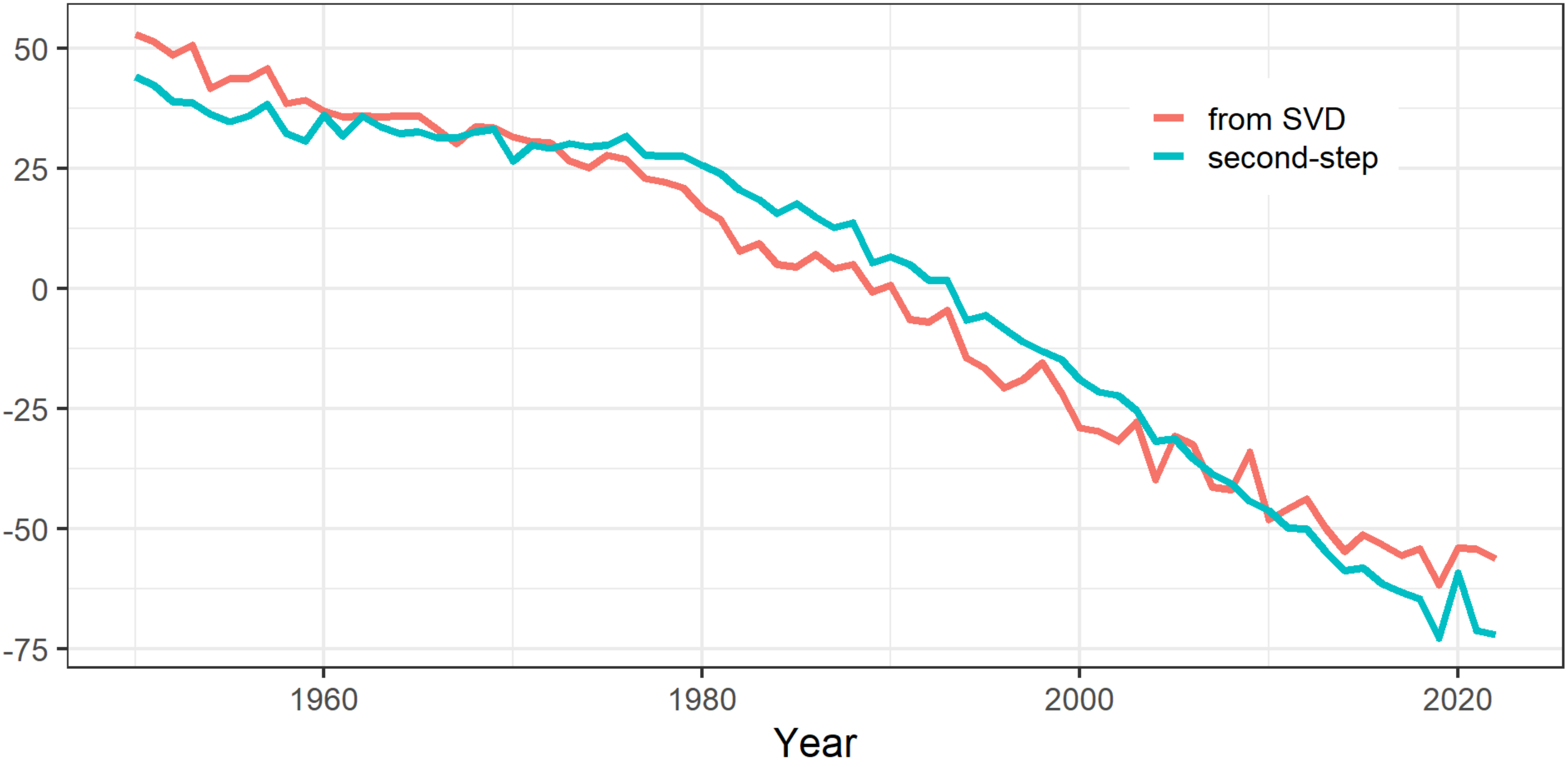
- In a second-step estimation, $\hat{\kappa}_t$ is adjusted so that the fitted deaths match the observed deaths in all years, i.e.

$$\sum_x \hat{y}_{x,t} = \sum_x y_{x,t} \quad \text{for all } t$$

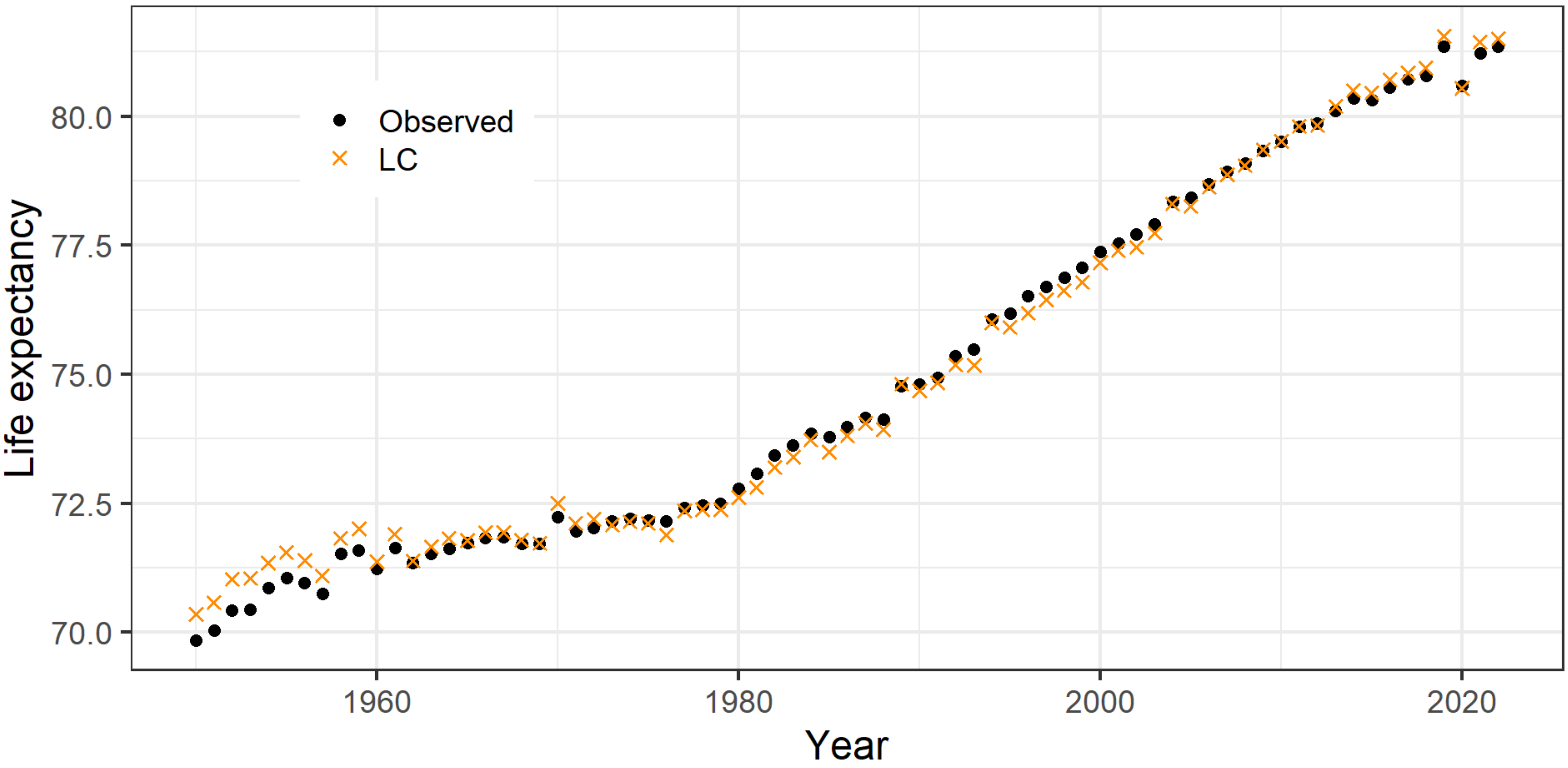
One possible solution

```
##---- step 3: adjust KAPPA -----
## function to compute difference between observed and fitted LC de
koptim <- function(par,alpha,beta,sum.dx,Exp){
  kappa <- par[1]
  lmx.lc <- alpha+beta*kappa
  z.lc <- exp(lmx.lc)*Exp
  sum.z.lc <- sum(z.lc)
  diff.lc <- abs(sum.dx-sum.z.lc)
  return(diff.lc)
}
## adjust Kappa every year
Kappa <- numeric(n)
for (i in 1:n){
  KappaSecStep <- optimize(f=koptim,interval=c(-100,100),alpha=Alph
  beta=Beta,sum.dx=sum(DEATHS[,i]),Exp=EXPOS[,i])
  Kappa[i] <- KappaSecStep$minimum
}
## plotting
plot(t,Kappa1,ylim=range(Kappa1,Kappa),t="l",lwd=2)
```

Second step estimation of $\hat{\kappa}_t$



Goodness-of-fit



Intermezzo : animated visualizations & shiny-app

In some instances, it can be useful to introduce dynamic plots, animations and flexible outputs in your presentations or documents:

- can grab the audience’s attention
- show time-series evolutions
- to describe your model
- sensitivity analysis of your results

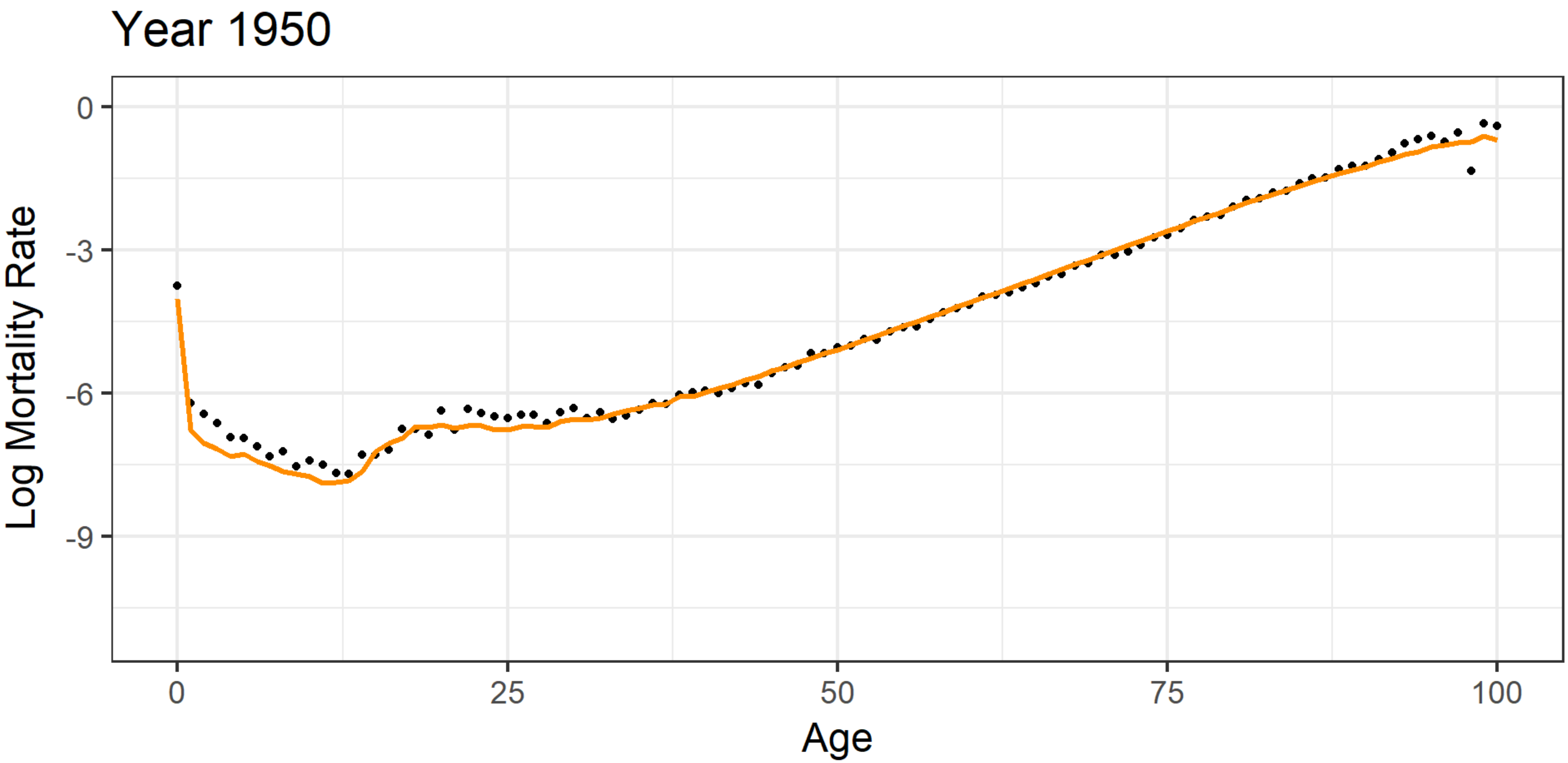
Animated images

- `\animategraphics` in Beamer (see LaTeX workshop)
- `gganimate` package in Quarto

Animation plots with gganimate

```r
## fitted log-mortality
Ones <- matrix(1,n)
ETAlc <- Alpha%*%t(Ones) + Beta%*%t(Kappa)
## basic plot
g <- my.df %>%
  mutate(logRates=case_when(
    is.infinite(logRates)~NA,
    TRUE~logRates),
    Fitted=c(ETAlc)) %>%
  ggplot(aes(x=Age,group=Year))+
  geom_point(aes(y=logRates))+
  geom_line(aes(y=Fitted),color="darkorange",linewidth=1.2)+
  scale_color_viridis_c() +
  theme_bw(base_size = 18) +
  labs(y= "Log Mortality Rate")
## animating with gganimate
library(gganimate)
gg <- g + transition_time(Year) +
  ggtitle("Year {frame_time}")
```

Goodness-of-fit



Shiny apps

- `shiny` is an `R` package that makes it easy to build interactive web apps straight from `R`
- keep them on webpages or embed them in R Markdown documents or Quarto presentations
- a user-friendly interface to interact with your `R` analysis and show your results (a nice example from DOI: 10.1215/00703370-9637380)
- it is composed by
  - an `UI` (user interface), where you can create the inputs for your and decide the outputs to display
  - a `server`, where you assemble the outputs from your given inputs
  - the `shinyApp`, putting the two together
- to learn more, visit https://shiny.posit.co/ to get started, plenty of videos and written tutorials

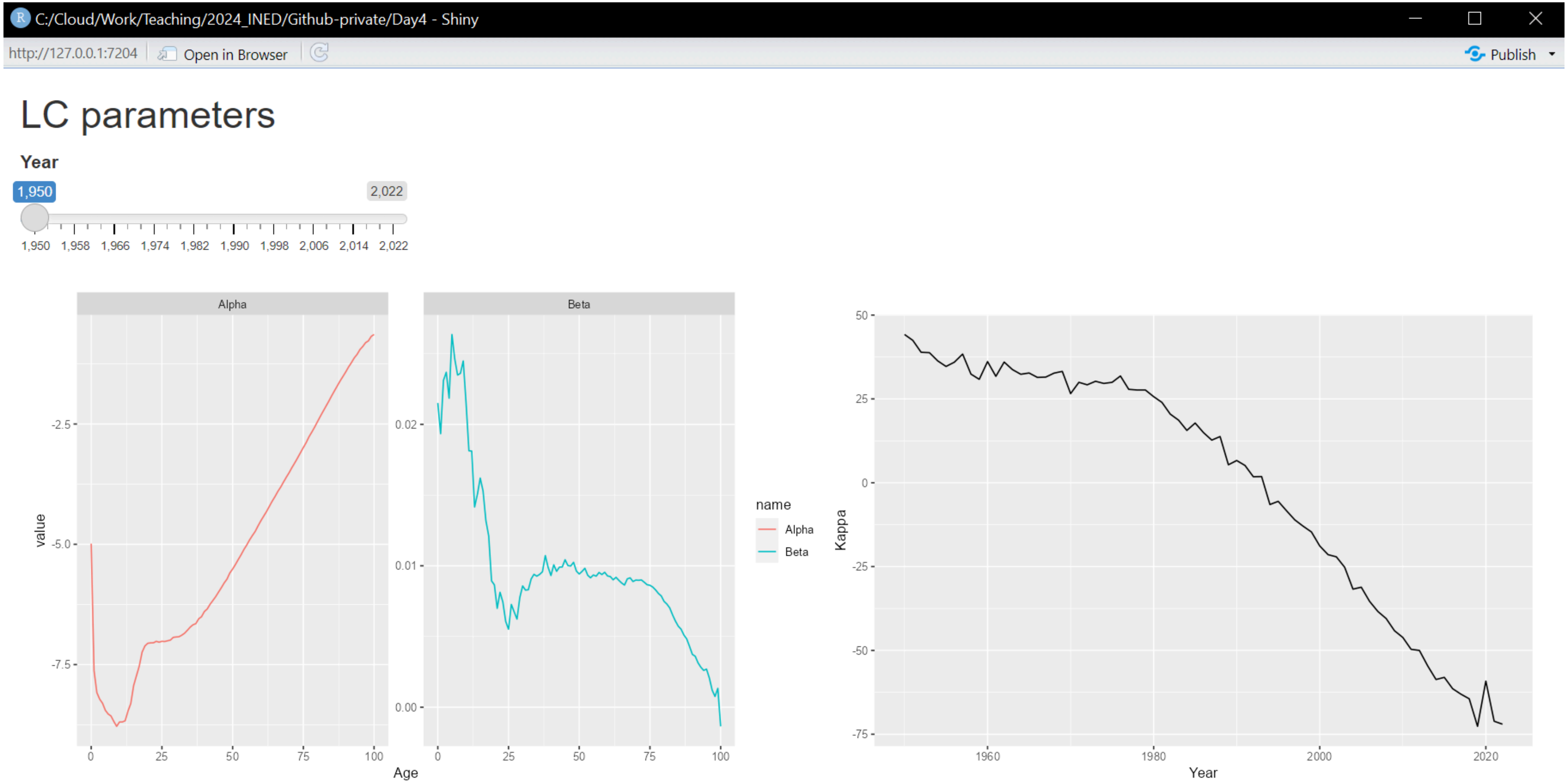
Shiny app: an example

```r
##---- SHINY APP EXAMPLE ----

## cleaning the workspace
rm(list=ls(all=TRUE))
## load useful packages
library(tidyverse)
library(patchwork)
library(shiny)
## loading data
setwd(dirname(rstudioapi::getActiveDocumentContext()$path))
load("data/MORTSWE.Rdata")
## subset
my.df <- MORT.SWE %>% filter(Sex=="Male", Age <= 100)

## build your user interface
ui <- fluidPage(
  ## title of your shiny
  titlePanel("LC parameters"),
  ## display a slider that returns input$year to pass to the server
```

Shiny app: an example



C:/Cloud/Work/Teaching/2024_INED/Github-private/Day4 - Shiny

http://127.0.0.1:7204

LC parameters

Year: 1,950 – 2,022

Forecasting with LC

- Forecasting "made simple": choose an appropriate time-series model for $\hat{\kappa}_t$ and extrapolate it
- The forecast $\hat{\kappa}_{T+h}$ allows one to derive the entire age-pattern of mortality at time $T+h$:

$$\ln(\hat{m}_{x,T+h}) = \hat{\alpha}_x + \hat{\beta}_x \hat{\kappa}_{T+h}$$

- LC suggest a random walk model (i.e. ARIMA(0,1,0)) with drift: $\kappa_t = \kappa_{t-1} + c + e_t$ where c is a constant (drift) and e_t the error term (purely random process)
- For this time-series model: $\hat{\kappa}_{T+h|T} = \hat{\kappa}_T + c\,h$
- Simulated future trajectories of $\hat{\kappa}_{T+h}$ to construct prediction intervals for $\hat{m}_{x,T+h}$ and other summary measures (e.g., $\hat{e}_{0,T+h}$)
- (Coale and Guo (1989) adjustment for forecast rates at ages 85+)

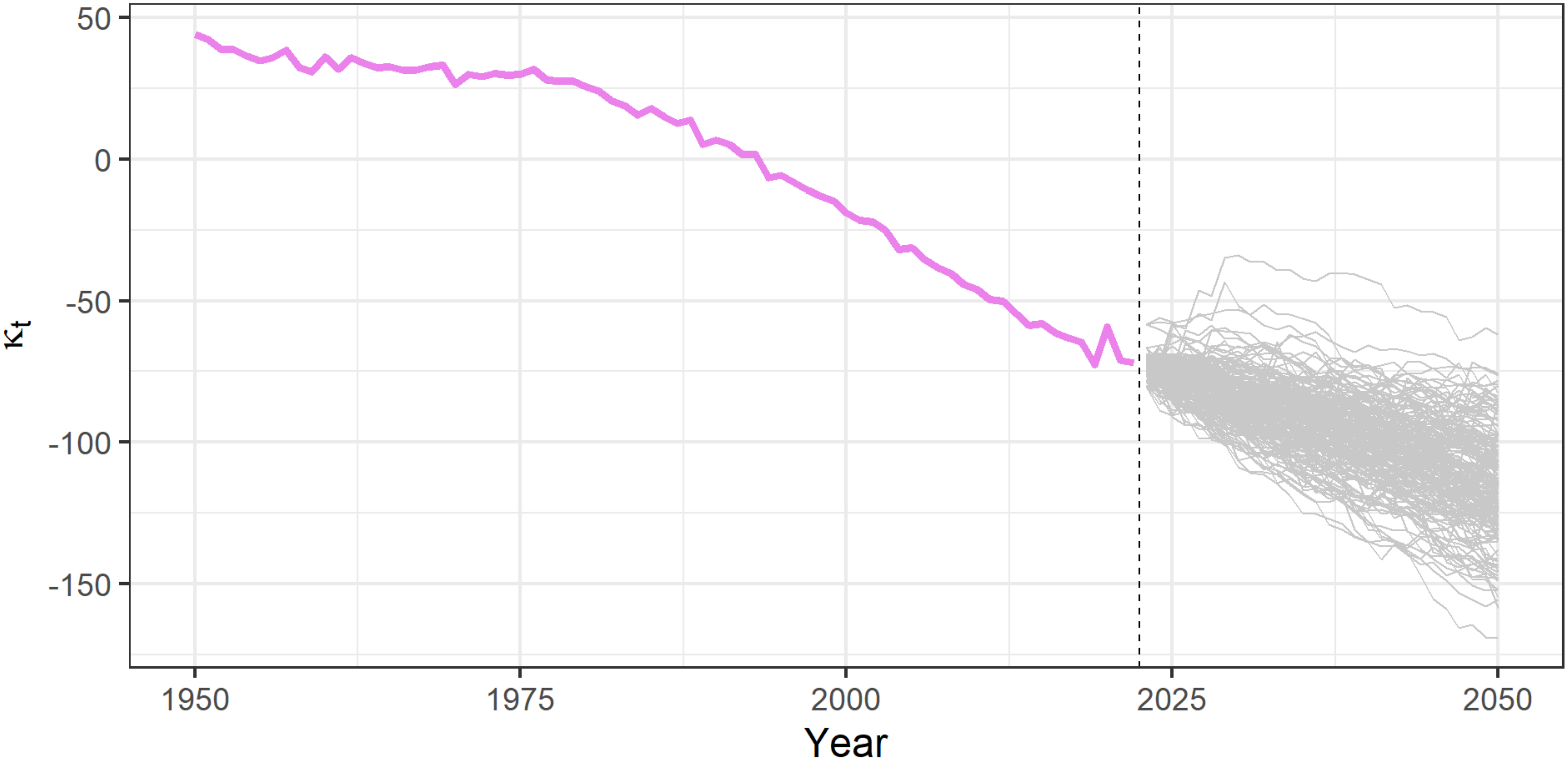
Forecasting with LC: a schematic view

$$\ln(m_{x,t}) \simeq \alpha_x + \beta_x \kappa_t \qquad \ln(m_{x,T+h}) \simeq \alpha_x + \beta_x \kappa_{t_F}$$

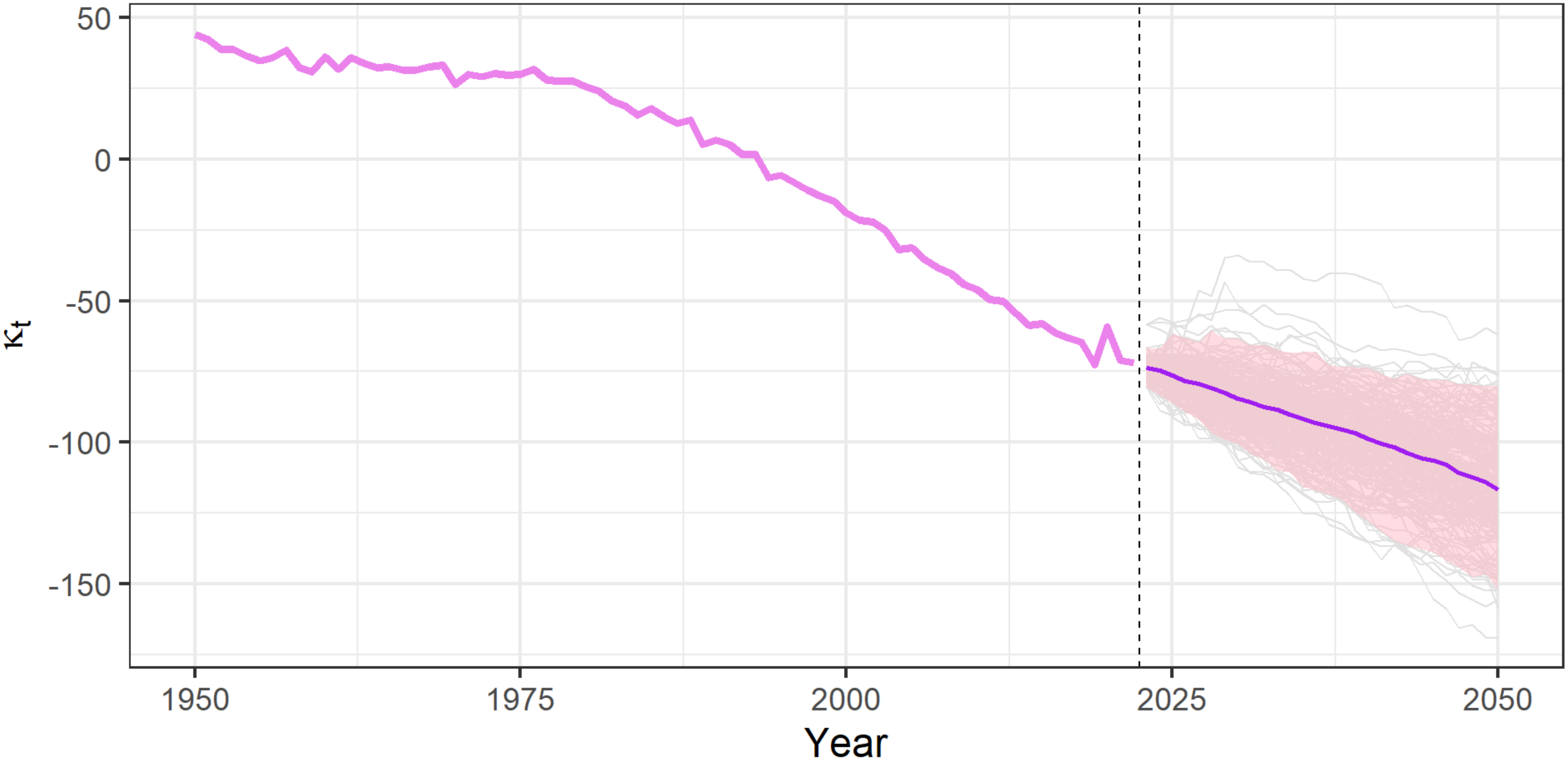
$$\begin{pmatrix} \ln(m_{x_1,t_1}) & \ln(m_{x_1,t_2}) & \dots & \ln(m_{x_1,T}) & \ln(m_{x_1,T+1}) & \dots & \ln(m_{x_1,T+h}) \\ \ln(m_{x_2,t_1}) & \ln(m_{x_2,t_2}) & \dots & \ln(m_{x_2,T}) & \ln(m_{x_2,T+1}) & \dots & \ln(m_{x_2,T+h}) \\ \ln(m_{x_3,t_1}) & \ln(m_{x_3,t_2}) & \dots & \ln(m_{x_3,T}) & \ln(m_{x_3,T+1}) & \dots & \ln(m_{x_3,T+h}) \\ \vdots & \vdots & \ddots & \vdots & \vdots & \ddots & \vdots \\ \ln(m_{x_m,t_1}) & \ln(m_{x_m,t_2}) & \dots & \ln(m_{x_m,T}) & \ln(m_{x_m,T+1}) & \dots & \ln(m_{x_m,T+h}) \end{pmatrix} \simeq$$

$$\begin{pmatrix} \alpha_{x_1} \\ \alpha_{x_2} \\ \alpha_{x_3} \\ \vdots \\ \alpha_{x_m} \end{pmatrix} + \begin{pmatrix} \beta_{x_1} \\ \beta_{x_2} \\ \beta_{x_3} \\ \vdots \\ \beta_{x_m} \end{pmatrix} \begin{pmatrix} \kappa_{t_1} & \kappa_{t_2} & \dots & \kappa_T & \kappa_{T+1} & \dots & \kappa_{T+h} \end{pmatrix}$$

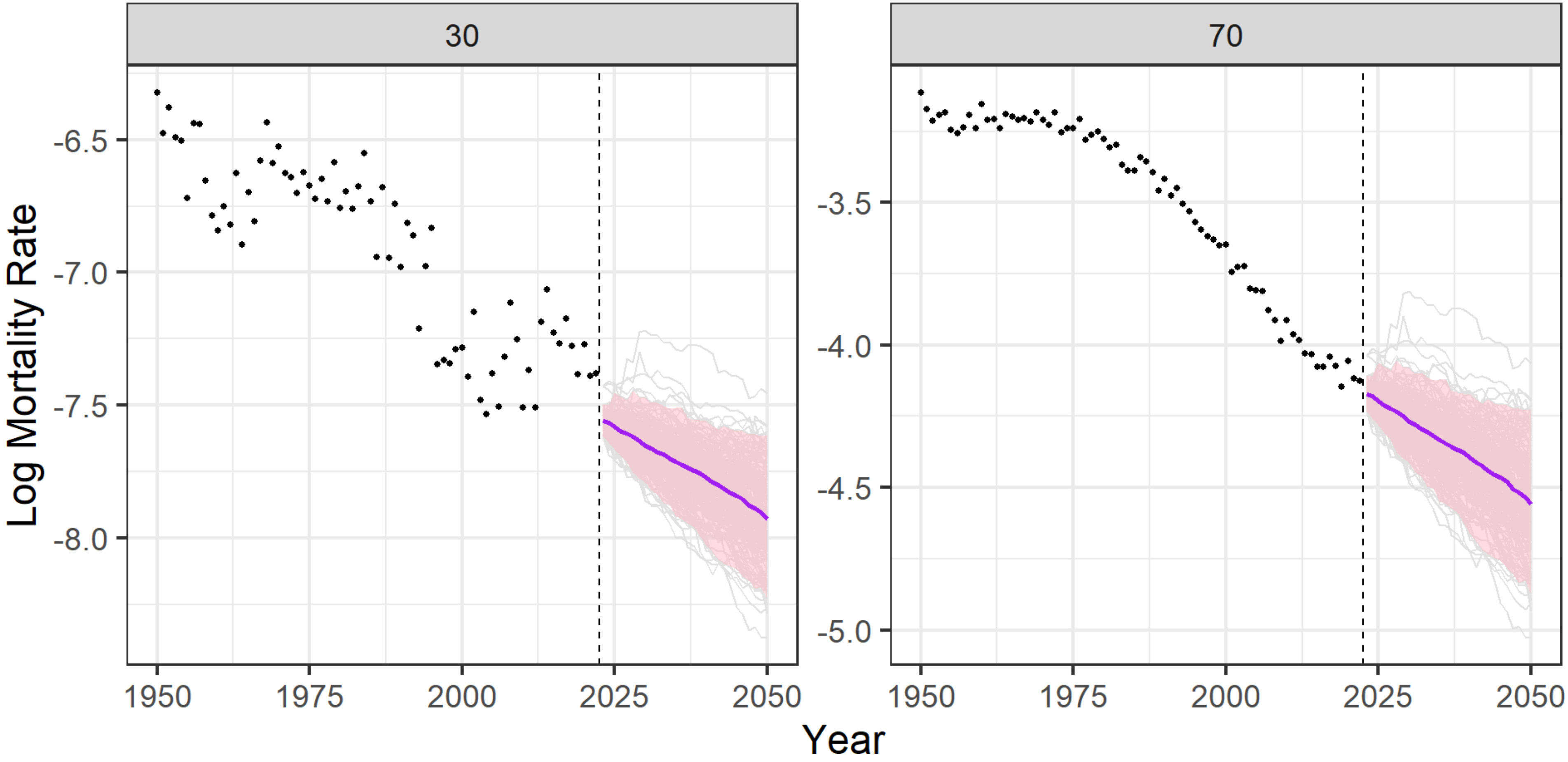
$\hat{\kappa}_t$ simulations



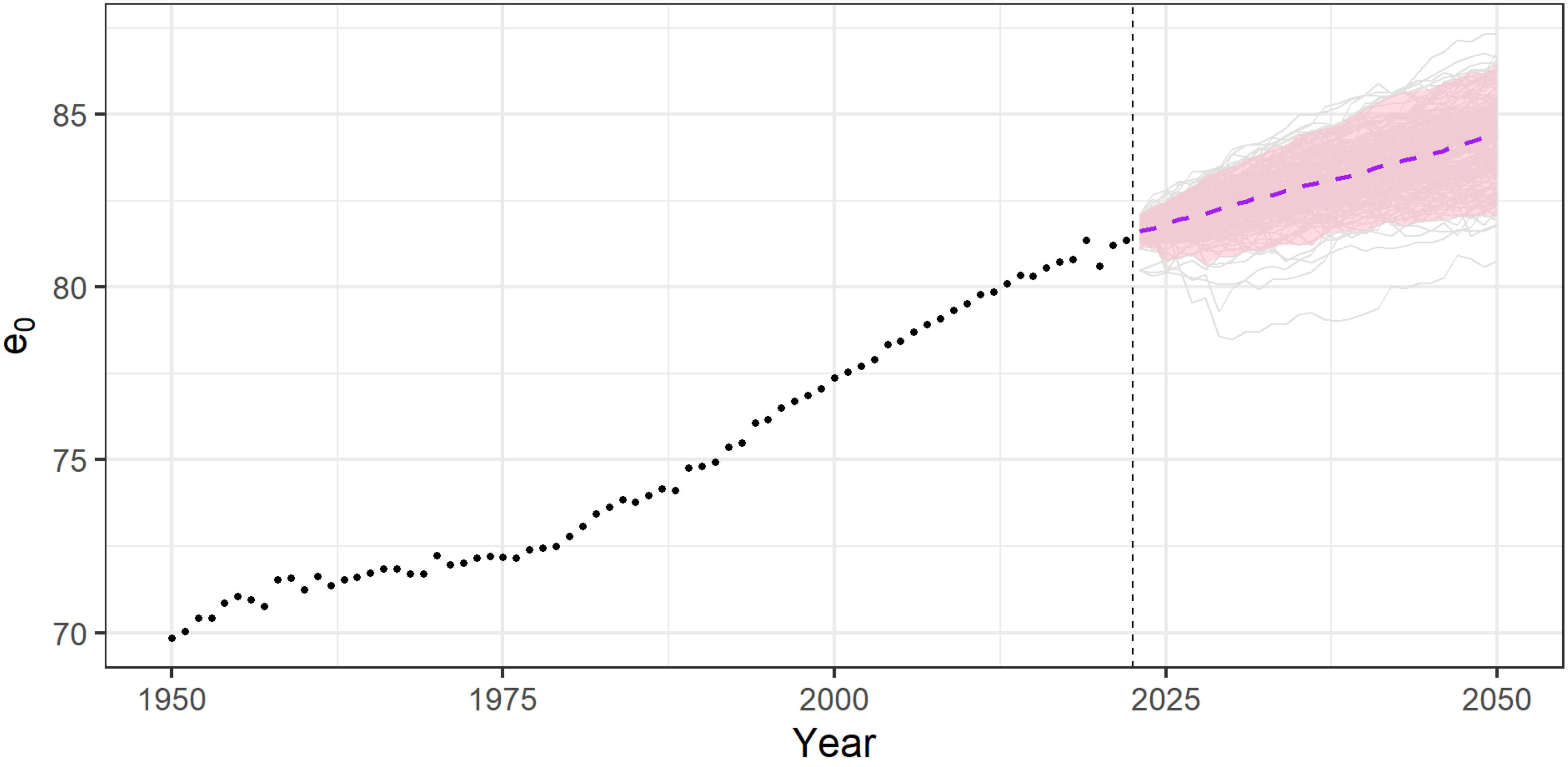
$\hat{\kappa}_t$ 95% PIs



From $\hat{\kappa}_t$ to $\ln(\hat{m}_{xt})$



From $\hat{\kappa}_t$ to $\hat{e}_0$



The LC model: a summary

- **Advantages**:
  - simple & powerful method: forecast rates derived by modeling single time index by standard time-series model
  - linear time index very often captures well historical decline in mortality
  - stochastic model $\Rightarrow$ probabilistic intervals
  - extrapolative approach, no expert opinions more accurate than previous methodologies
- **Disadvantages**:
  - jump-off bias
  - Normality assumption (from SVD)
  - jagged fitted and forecast age profile, lacking smoothness
  - fixed age-pattern of mortality decline
  - rigid structure
- Several extensions proposed to overcome some of these issues

Some LC extensions

- “jump-off” bias: use observed jump-off rates (Lee and Miller 2001)
- Normality assumption: Poisson LC (Brouhns et al. 2002)
- jagged fitted and forecast age profile, lacking smoothness: Smooth LC (Delwarde et al. 2007)
- fixed age-pattern of mortality decline: Li et al. (2013)
- rigid structure

Other LC extensions (single pop)

- Booth et al. (2002): adjusting κ_t to match the age-at-death distribution & determining optimal fitting period
- Renshaw and Haberman (2003): adding more than one principal components, i.e. $\ln(m_{x,t}) = \alpha_x + \sum_k \beta_x^k \kappa_t^k$
- Koissi et al. (2006): residual bootstrap to include parameter uncertainty in forecasts
- Renshaw and Haberman (2006): including cohort effects, i.e. $\ln(m_{x,t}) = \alpha_x + \beta_x^{(1)} \kappa_t + \beta_x^{(0)} \gamma_{t-x}$
- Hyndman and Ullah (2007): smooth underlying data (functional data) & additional principal components
- Camarda and Basellini (2021): smoothing, decomposing and forecasting the three components of mortality (childhood, early-adulthood and senescence), i.e. $m_{x,t} = \sum_k \exp\left(\alpha_x^k + \beta_x^k \kappa_t^k\right)$
- for a comprehensive review, see Basellini et al. (2023)

Forecast evaluation

- How do we evaluate demographic forecasts?
- Option 1: wait until the future occurs (e.g., 2050) to find out
    - clearly not ideal :)
- Option 2: out-of-sample forecasting
    - from the observed time series $\boldsymbol{y} = [y_1, y_2, \ldots, y_{n-h}, \ldots y_T]$, suppose that you have observed only the first $n - h$ data points, forecast h years in the future and compare the forecasts with the withheld data points $y_{n-h+1}, \ldots y_T$
    - $\boldsymbol{y}$ can refer to any forecast measure (log-rates, rates, summary measures)

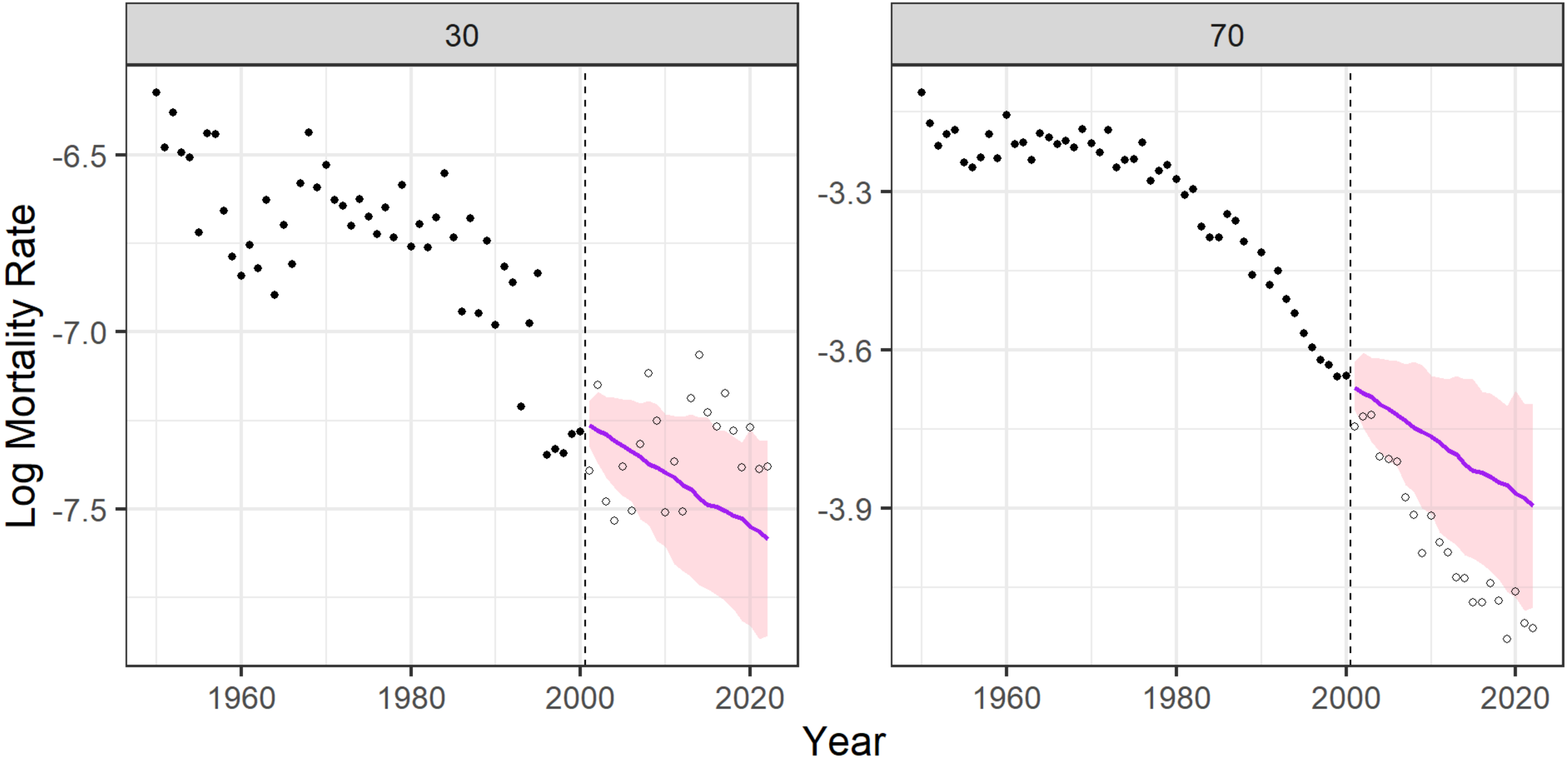
Point forecast accuracy

- Let $e_t = \hat{y}_t - y_t$ denote the forecast error, with $\hat{y}_t$ being the central forecast and y_t the withheld data point t
- Let $p_t = 100 e_t / y_t$ be the percentage error
- Compute one of the following measures of point forecast accuracy:
  - Mean Square Error (MSE) $= \frac{1}{h} \sum_{t=1}^{h} e_t^2$
  - Root MSE (RMSE) $= \sqrt{\text{MSE}}$
  - Mean Absolute Error (MAE) $= \frac{1}{h} \sum_{t=1}^{h} |e_t|$
  - Mean Absolute Percentage Error (MAPE) $= \frac{1}{h} \sum_{t=1}^{h} |p_t|$
- The smaller the error, the better

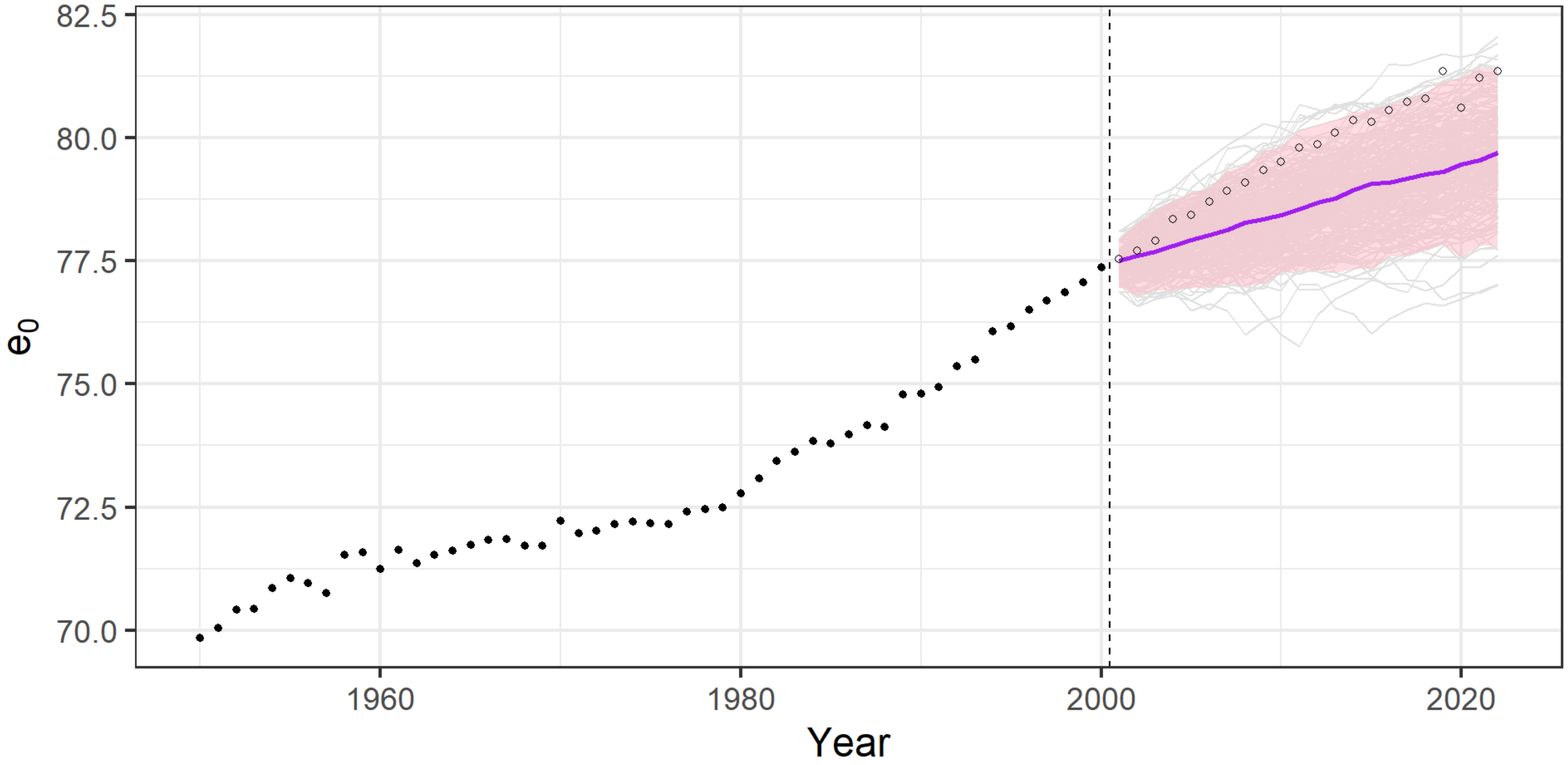
Interval forecast accuracy

- Compare withheld data points with the forecast α% prediction interval (PI):
  - Empirical Coverage Probability (ECP): proportion of observations falling into the PI
  - Coverage Probability Deviance (CPD) $= |\alpha - \mathrm{ECP}|$, with CPD $\in [0, \alpha]$
- The smaller the CPD, the better

LC forecast evaluation



LC forecast evaluation



Day 4 assignment

Assignment

8. Load the mortality data `MORTSWE.Rdata`, and focus on male mortality from 1950 to 2000 for ages $x \leq 100$. Fit and forecast mortality with the LC method, and produce forecasts up to 2022. Evaluate the forecast accuracy of the method by computing a point forecast accuracy measure of your choice on a single measure of interest (e.g. log-rates or e_o).

9. Consider again the setting of Exercise 8 (i.e. male mortality from 1950 to 2000 for ages $x \leq 100$). Compare the forecast accuracy of two different methods that we have seen during this course. Which model is more accurate?