Mortality Modelling with R

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Aims

Gain familiarity with use of the R packages **demography**, **StMoMo** and **lifecontingencies** to:

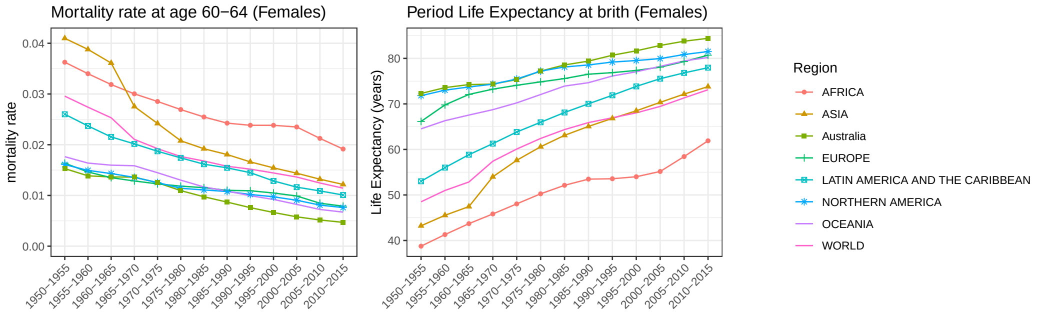
- Obtain mortality data from Human Mortality Database
- Fit stochastic mortality models (including Lee-Carter model)
- Compare goodness of fit of mortality models
- Forecast future mortality rates (deterministic and using Monte Carlo simulations)
- Compute demographic and actuarial quantities

Agenda

- Motivation
- Review of mortality modelling metodologies
- Mortality modelling with R
  - Downloading mortality data with **demography**
  - Fitting, comparing and projecting mortality model with **StMoMo**
  - Turning mortality projections into demographic calculations with **lifecontingencies**
- Conclusions and Summary
- Preview of recent **StMoMo** developments (if time permits!)

Motivation and Review of Mortality Modelling

Recent trends in mortality and life expectancy



Source: United Nations World Population Prospects 2017

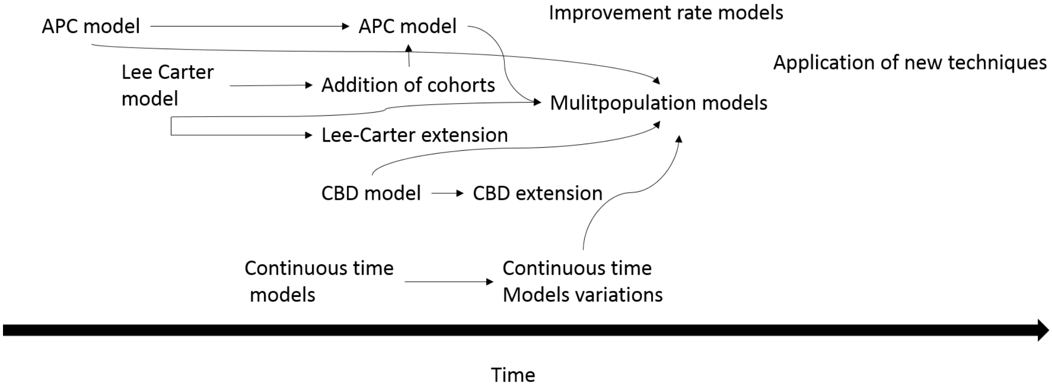
- Good-news!
- Important social and financial implications for governments, insurers, individuals.
- Need to model and project these trends

Mortality forecasting methodologies

A good overview of methodologies is given in the review papers by Booth and Tickle (2008), Wong-Fupuy and Haberman (2004), Pitacco (2004) and in the by Pitacco et al. (2009)

- Expert based
- Explanatory
  - Structural Modelling (Explanatory or Econometric).
  - Cause of death decomposition
- **Extrapolation**
  - Trend modelling

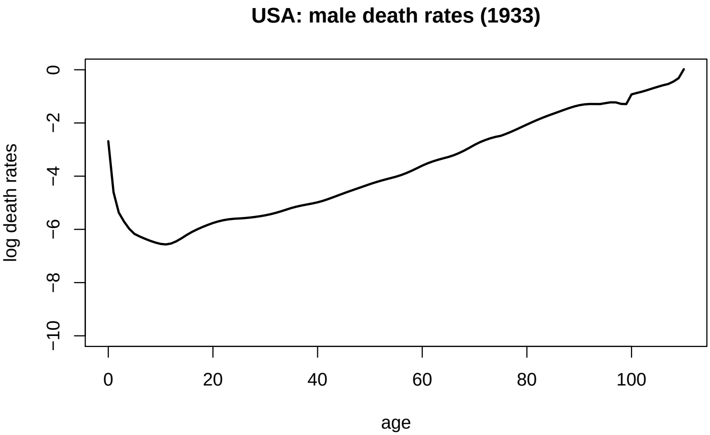
A timeline of "recent" mortality modelling methodologies



Advances in single population mortality modelling

- **Lee-Carter model** (Lee and Carter 1992)
  - Add more bilinear age-period components (Renshaw and Haberman 2003)
  - Add a cohort effect (Renshaw and Haberman 2006)
- Two factor **CBD model** (Cairns, Blake, and Dowd 2006)
  - Add cohort effect, quadratic age term (Cairns et al. 2009)
  - Combine with features of the Lee-Carter (Plat 2009)
- **Many more models** proposed in the literature (e.g. Aro and Pennanen (2011), O'Hare and Li (2012), Börger, Fleischer, and Kuksin (2013), Alai and Sherris (2014))

Lee-Carter model



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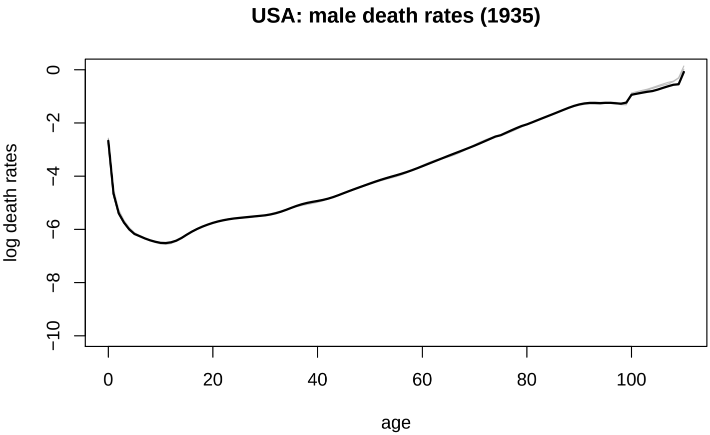

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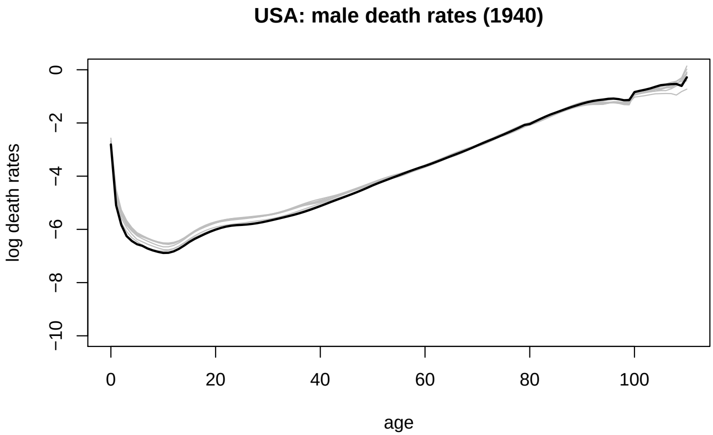

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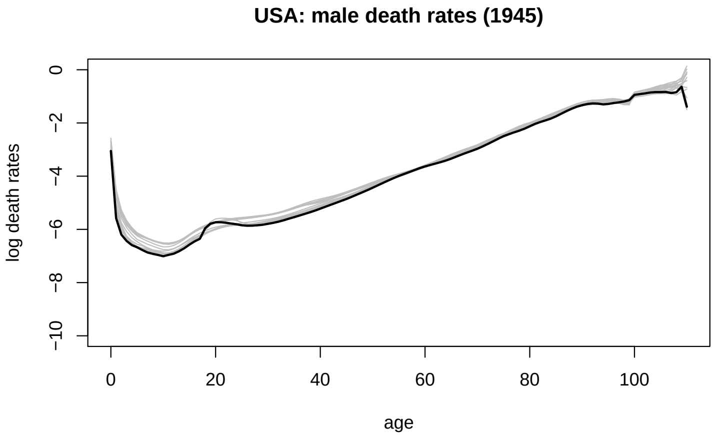

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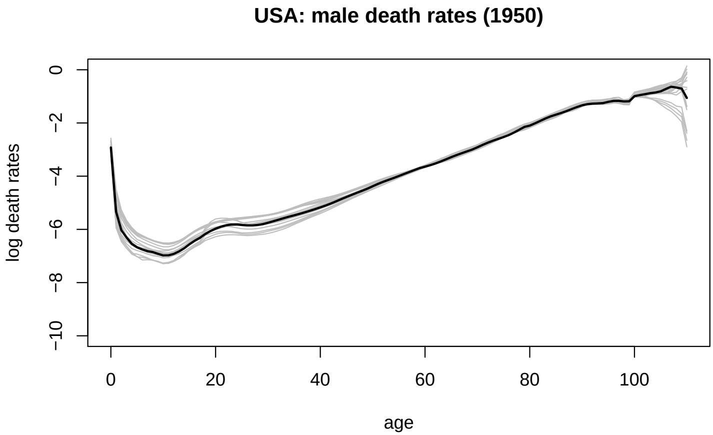

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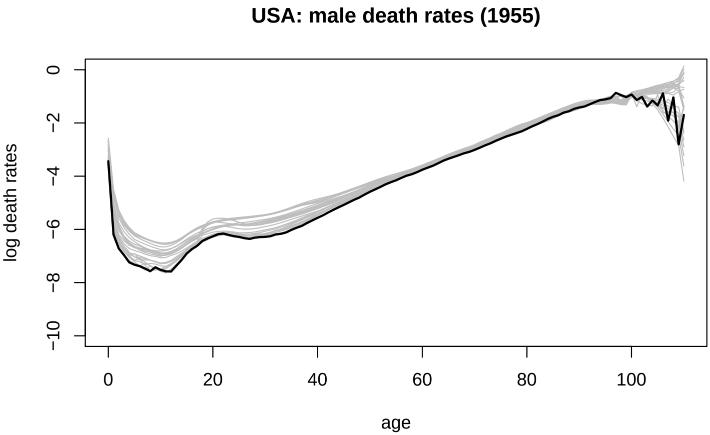

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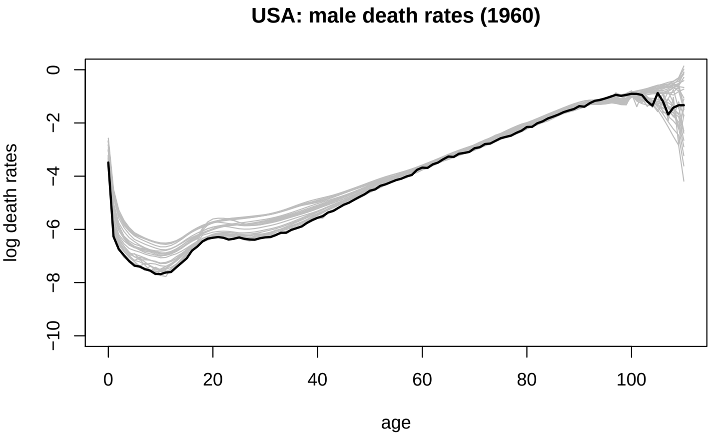

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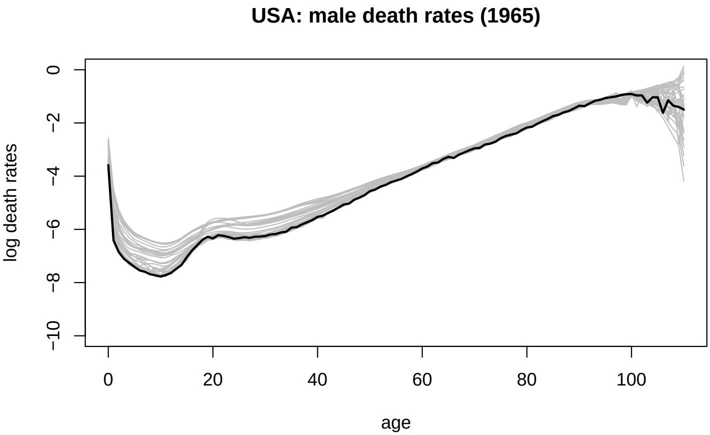

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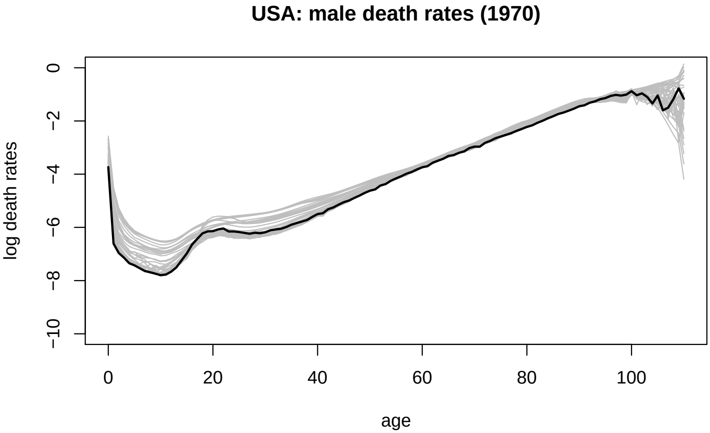

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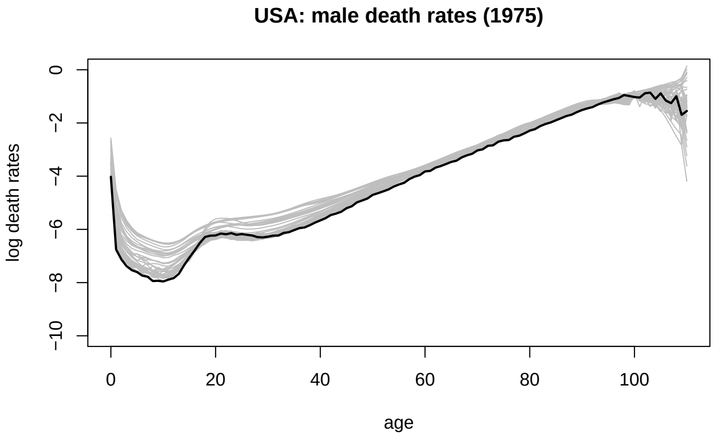

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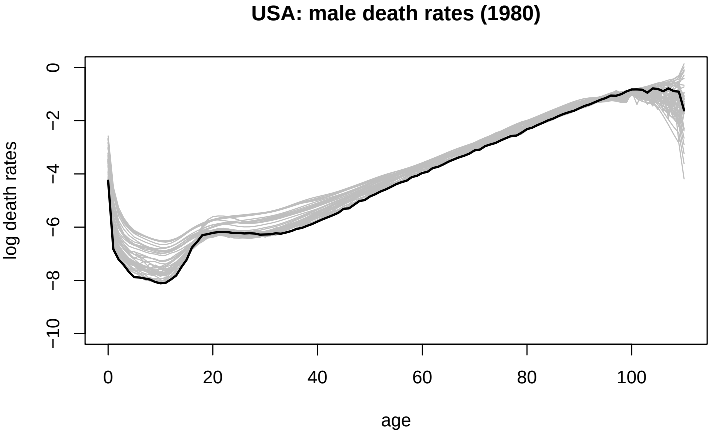

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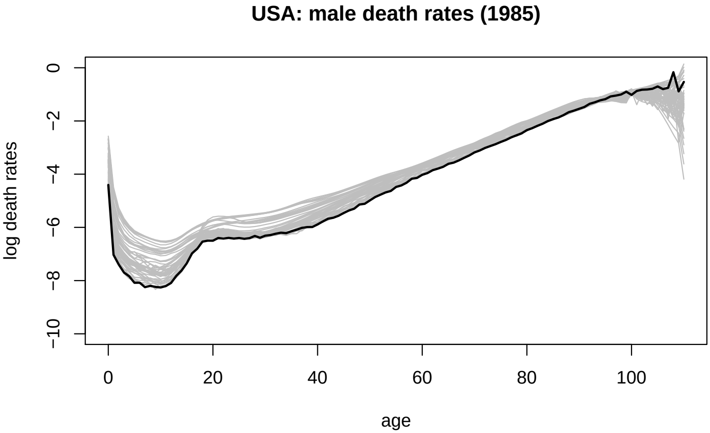

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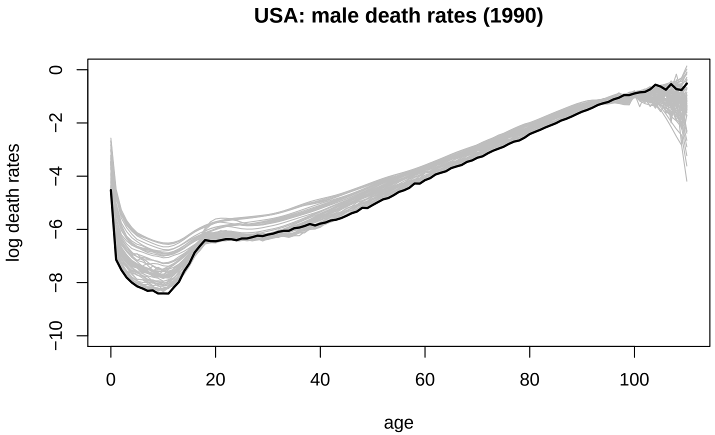

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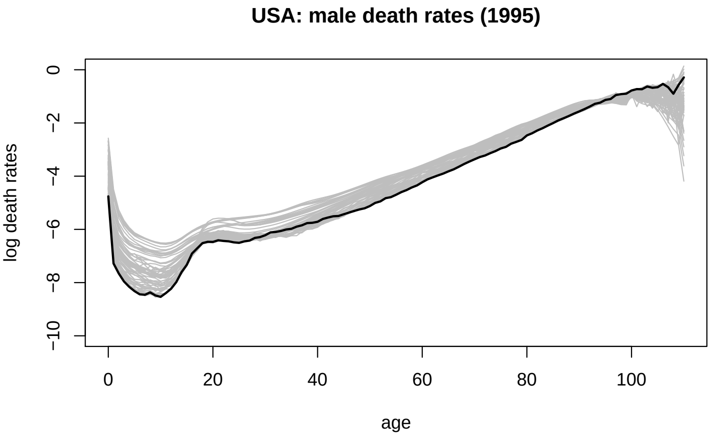

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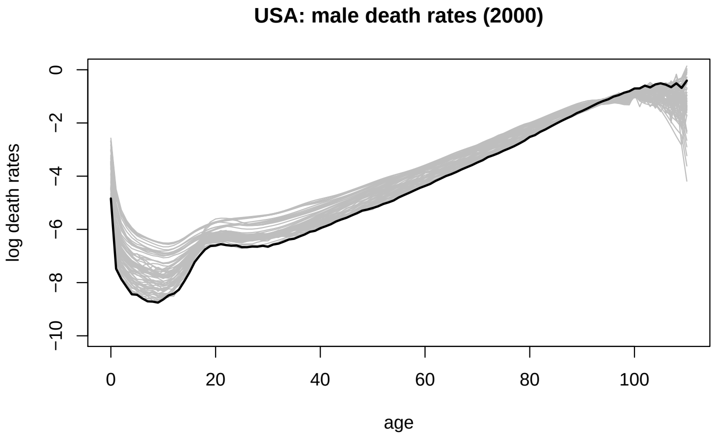

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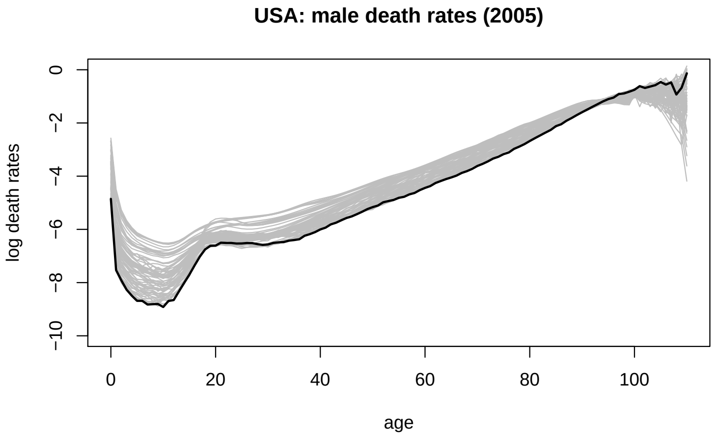

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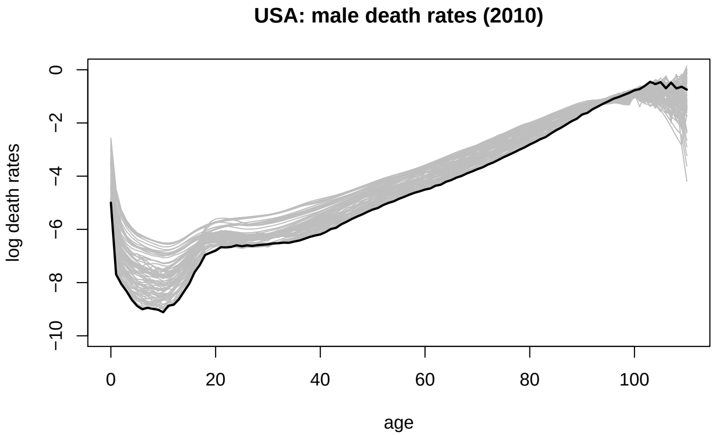

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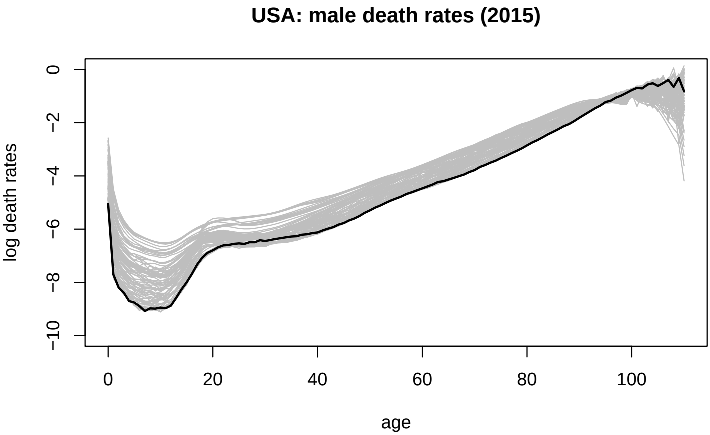

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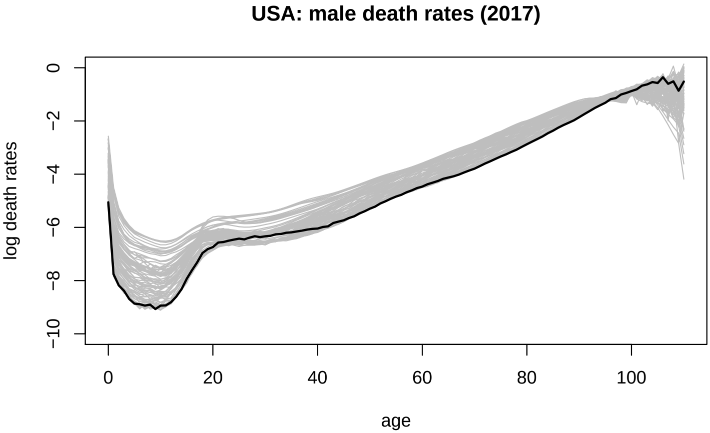

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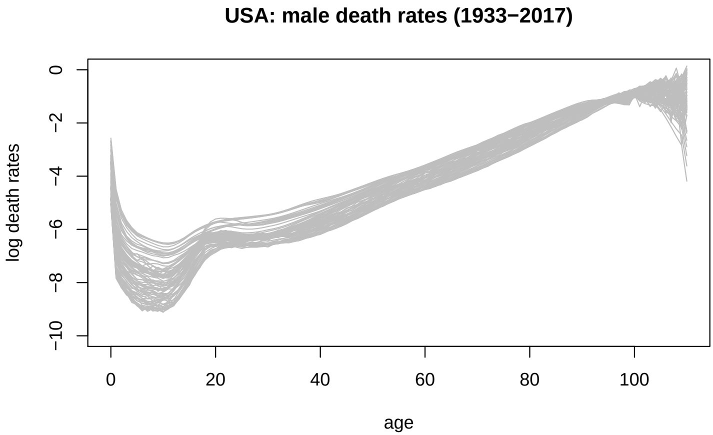
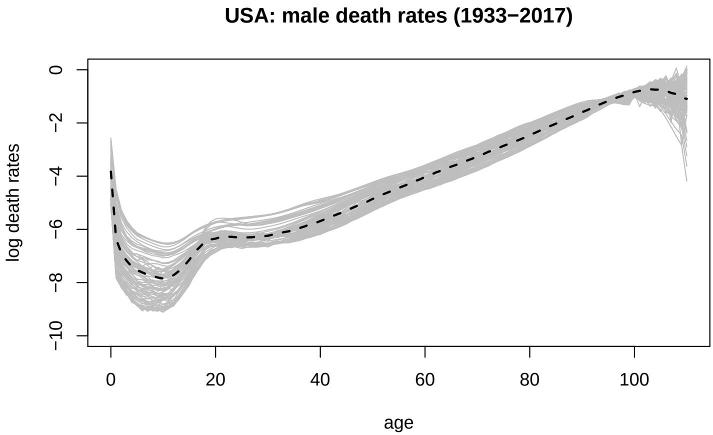


$$\log \mu_{xt} \quad =$$

Lee-Carter model



$$\log \mu_{xt} = \alpha_x$$

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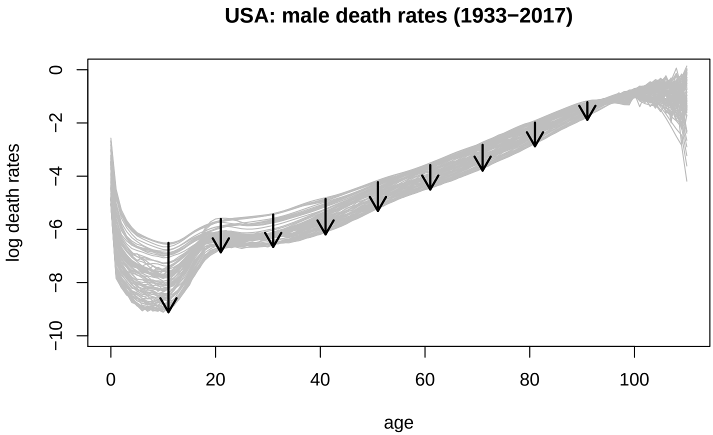
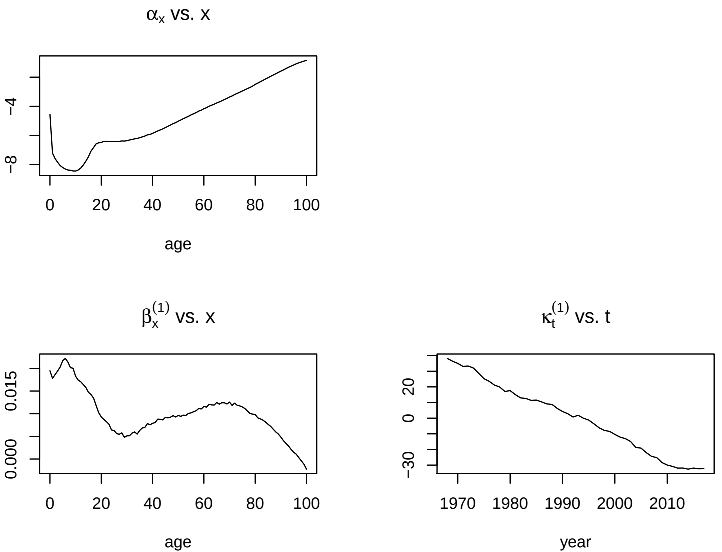


$$\log \mu_{xt} \quad = \quad \alpha_x \quad + \qquad\qquad \kappa_t$$

Lee-Carter model

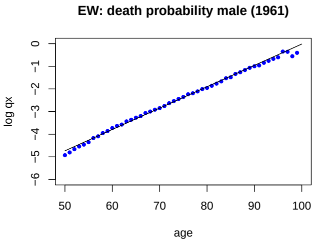
$$\log \mu_{xt} = \alpha_x + \beta_x \kappa_t$$

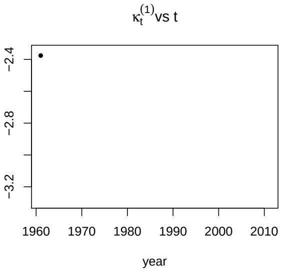
Lee-Carter model

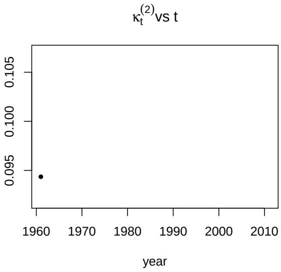


Cairns-Blake-Dowd model

$$\text{logit } q_{xt} = \kappa_t^{(1)} + (x - \bar{x})\kappa_t^{(2)}$$







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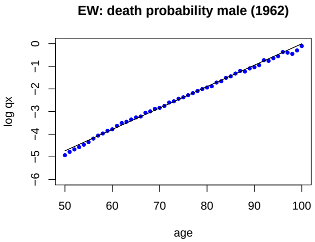

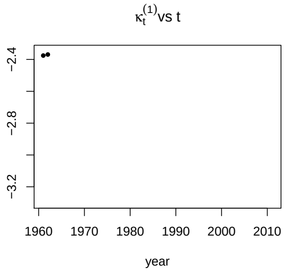

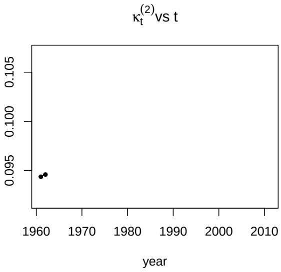

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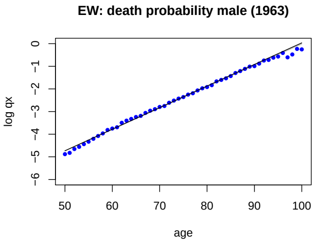

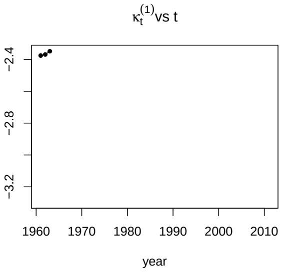

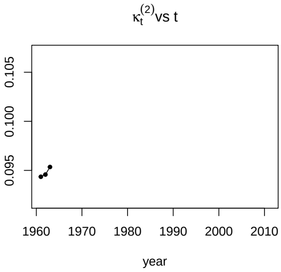

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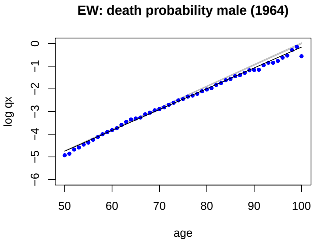

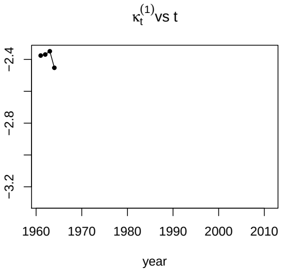

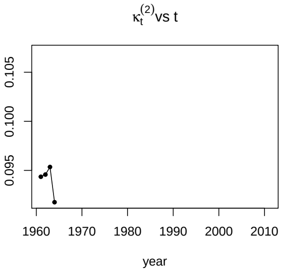

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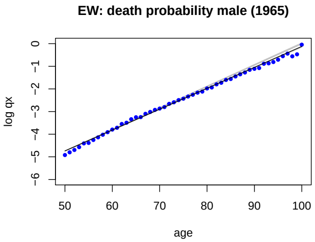

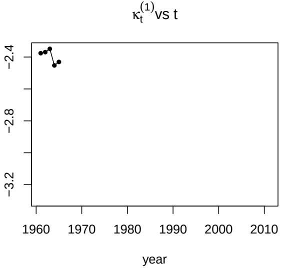

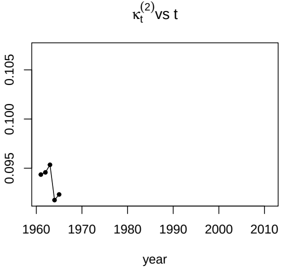

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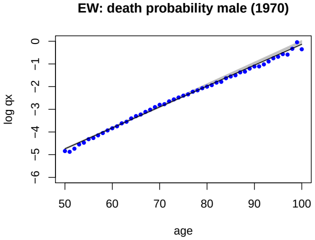

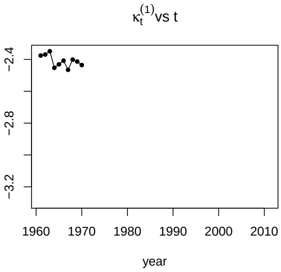

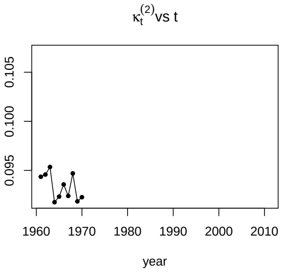

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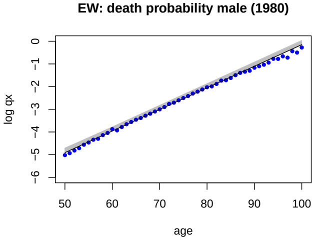

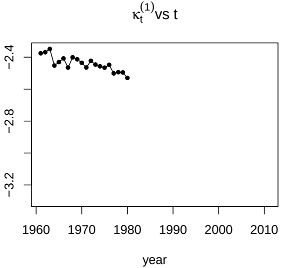

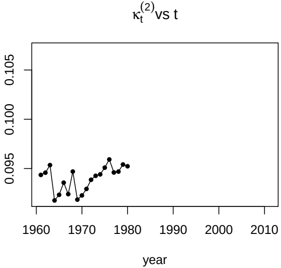

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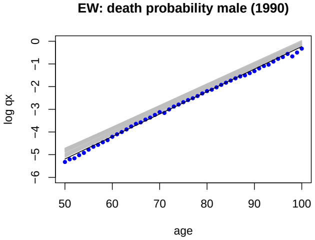

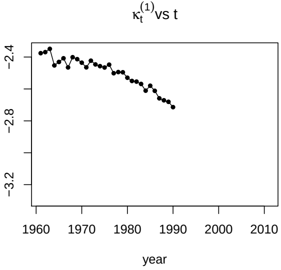

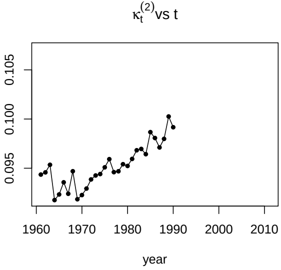

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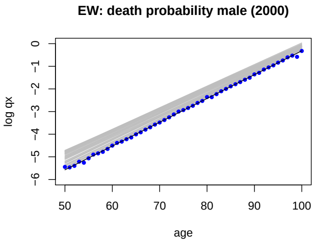

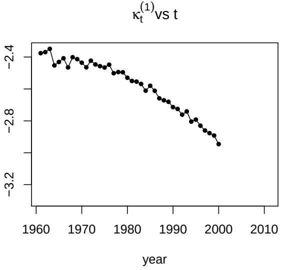

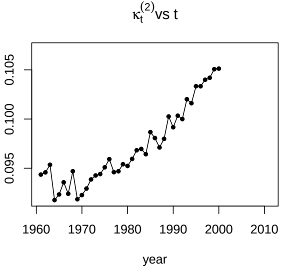

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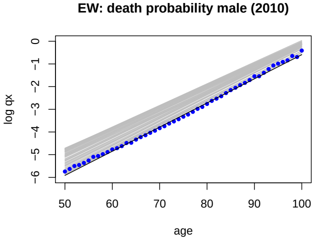
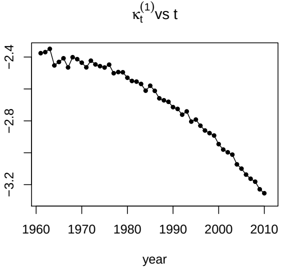
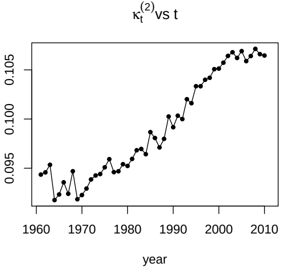






Other Stochastic Mortality Models

Name	Form	Parameters
LC	$\alpha_x + \beta_x^{(1)}\kappa_t^{(1)}$	$2n_a + n_y$
LC2	$\alpha_x + \beta_x^{(1)}\kappa_t^{(1)} + \beta_x^{(2)}\kappa_t^{(2)}$	$3n_a + 2n_y$
RH	$\alpha_x + \beta_x^{(1)}\kappa_t^{(1)} + \beta_x^{(0)}\gamma_c$	$3n_a + n_y + n_c$
APC	$\alpha_x + \kappa_t^{(1)} + \gamma_c$	$n_a + n_y + n_c$
CBD	$\kappa_t^{(1)} + (x - \bar{x})\kappa_t^{(2)}$	$2n_y$
M7	$\kappa_t^{(1)} + (x - \bar{x})\kappa_t^{(2)} + ((x - \bar{x})^2 - \sigma_x^2)\kappa_t^{(3)} + \gamma_c$	$3n_y + n_c$
sPLAT	$\alpha_x + \kappa_t^{(1)} + (\bar{x} - x)\kappa_t^{(2)} + \gamma_c$	$n_a + 2n_y + n_c$
cPLAT	$\alpha_x + \kappa_t^{(1)} + (\bar{x} - x)\kappa_t^{(2)} + (\bar{x} - x)^+\kappa_t^{(3)} + \gamma_c$	$n_a + 3n_y + n_c$

Generalised Age-Period-Cohort stochastic mortality models

Recent research has proposed a unifying framework discrete stochastic mortality models

- General Age-Period-Cohort model structure (Hunt and Blake 2015)
- Generalised (non-)linear model (Currie 2014)
- R Implementation of GAPC models (Villegas, Millossovich, and Kaishev 2018)

Generalised Age-Period-Cohort stochastic mortality models

1. Random Component:

$$D_{xt} \sim \text{Poisson}(E^c_{xt}\mu_{xt}) \quad \text{or} \quad D_{xt} \sim \text{Binomial}(E_{xt}, q_{xt})$$

2. Systematic Component:

$$\eta_{xt} \quad = \quad \alpha_x \quad + \quad \sum_{i=1}^{N} \beta_x^{(i)} \kappa_t^{(i)} \quad + \quad \beta_x^{(0)} \gamma_{t-x}$$

- Lee-Carter type $\rightsquigarrow \beta_x^{(i)}$, non-parametric
- CBD type $\rightsquigarrow \beta_x^{(i)} \equiv f^{(i)}(x)$, pre-specified parametric function

3. Link Function:

$$g\left(\mathbb{E}\left(\frac{D_{xt}}{E_{xt}}\right)\right) = \eta_{xt}$$

- log-Poisson: $\eta_{xt} = \log \mu_{xt}$
- logit-Binomial: $\eta_{xt} = \text{logit}\, q_{xt}$

Generalised Age-Period-Cohort stochastic mortality models

4. Set of parameter constraints:
   - Need parameters constraints to ensure identifiability
5. Forecasting and simulation
   - Period indexes: Multivariate random walk with drift

$$\boldsymbol{\kappa}_t = \boldsymbol{\delta} + \boldsymbol{\kappa}_{t-1} + \boldsymbol{\xi}_t^{\kappa}, \qquad \boldsymbol{\kappa}_t = \begin{pmatrix} \kappa_t^{(1)} \\ \vdots \\ \kappa_t^{(N)} \end{pmatrix}, \qquad \boldsymbol{\xi}_t^{\kappa} \sim N(\mathbf{0}, \Sigma),$$

   - Cohort effect: ARIMA(p, q, d) with drift

$$\Delta^d \gamma_c = \delta_0 + \phi_1 \Delta^d \gamma_{c-1} + \cdots + \phi_p \Delta^d \gamma_{c-p} + \epsilon_c + \delta_1 \epsilon_{c-1} + \cdots + \delta_q \epsilon_{c-q}$$

Mortality Modelling with R

Mortality modelling in R

- **Demography** (Hyndman 2014)
  - Download data from the Human Mortality Database
  - Lee-Carter model and several of its variants
- **ilc** (Butt, Haberman, and Shang 2014)
  - Lee-Carter with cohorts and Lee-Carter under a Poisson framework
- **Lifemetrics** (http://www.macs.hw.ac.uk/~andrewc/lifemetrics/)
  - CBD and extensions
  - Lee-Carter with cohorts and Lee-Carter under a Poisson framework
- **StMoMo** (Villegas, Millossovich, and Kaishev 2018)
  - Implements Generalised Age-Period-Cohort Models

Installation of R Packages

- To install the pacakges we use:

```r
install.packages("demography")
install.packages("StMoMo")
install.packages("lifecontingencies")
```

- To load within R:

```r
library(demography)
library(StMoMo)
library(lifecontingencies)
```

Downloading Data from the Human Mortality Database

- Human Mortality Database (http://www.mortality.org/) contains population mortality data for 39 countries under consistent data protocol and in consistent format
  - Very useful for cross-country comparisons
  - Need to register to obtain username and password
- Subregional versions available for:
  - USA (https://usa.mortality.org/)
  - Japan (http://www.ipss.go.jp/p-toukei/JMD/index-en.asp)
  - Australia (http://demography.cass.anu.edu.au/research/australian-human-mortality-database)
  - Canada (http://www.bdlc.umontreal.ca/CHMD/)
- For this example, we will use male USA data from 1950 to 2014

Australian Data from Human Mortality Database

```
library(demography)
USdata <- hmd.mx(country = "USA", username = "username",
                    password = "password")
```

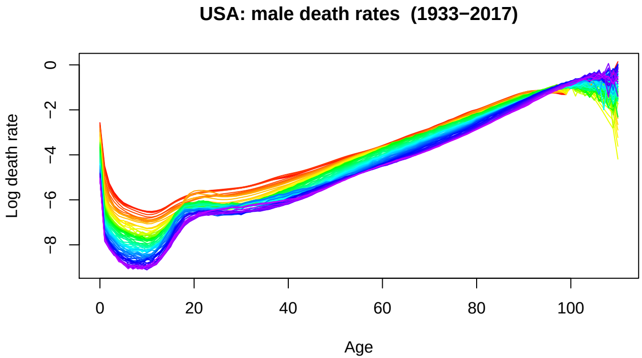
```
USdata
```

```
## Mortality data for AUS
##     Series: female male total
##     Years: 1921 - 2016
##     Ages:  0 - 110
```

USA Data from Human Mortality Database

```r
library(demography)
USdata <- hmd.mx(country = "USA", username = "username",
                 password = "password")
```

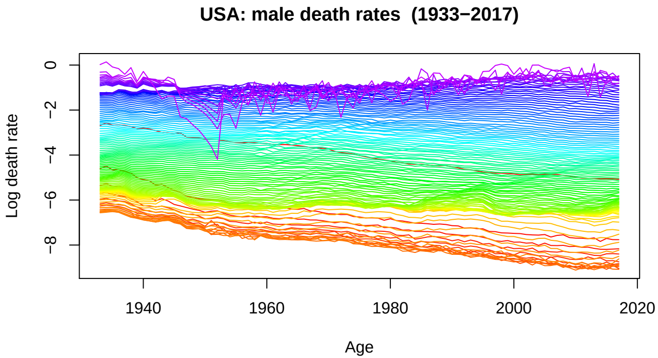
```r
plot(USdata, series = "male")
```



USA Data from Human Mortality Database

```r
library(demography)
USdata <- hmd.mx(country = "USA", username = "username",
                  password = "password")
```

```r
plot(USdata, series = "male", plot.type = "time")
```



StMoMo: **St**ochastic **Mo**rtality **Mo**delling

Who is MoMo?

StMoMo: Stochastic Mortality Modelling

Who is MoMo?

StMoMo: **St**ochastic **Mo**rtality **Mo**delling

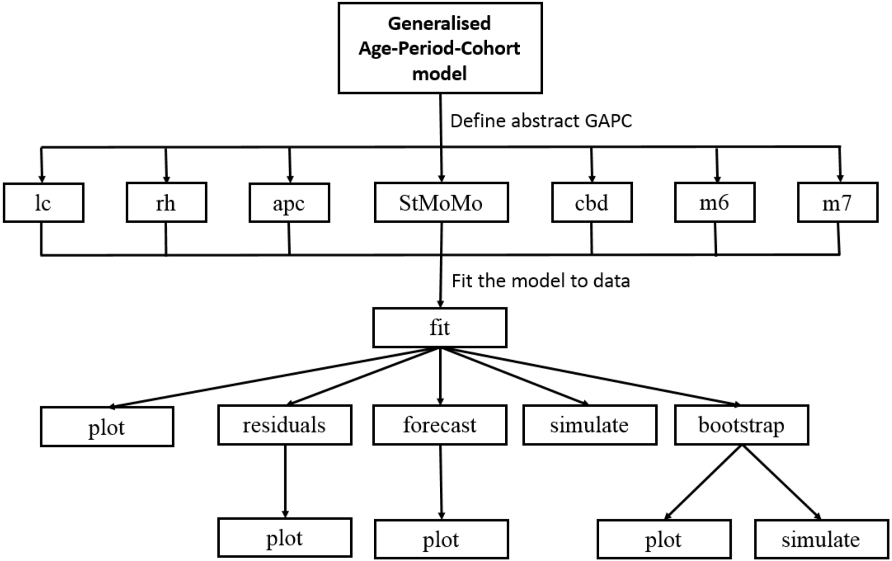
Who is MoMo?

Stochastic **Mo**rtality **Mo**delling

StMoMo: **St**ochastic **Mo**rtality **Mo**delling

Who is MoMo?

Overview of the structure of **StMoMo**



GAPC stochastic mortality models with **StMoMo**

Model	Predictor (η_{xt})
LC	$\alpha_x + \beta_x^{(1)}\kappa_t^{(1)}$
APC	$\alpha_x + \kappa_t^{(1)} + \gamma_{t-x}$
CBD	$\kappa_t^{(1)} + (x - \bar{x})\kappa_t^{(2)}$
M7	$\kappa_t^{(1)} + (x - \bar{x})\kappa_t^{(2)} + \left((x - \bar{x})^2 - \hat{\sigma}_x^2\right)\kappa_t^{(3)} + \gamma_{t-x}$

- For consistency, all under a log-Poisson setting:

$$D_{xt} \sim \mathrm{Poisson}(E_{xt}^c \mu_{xt})$$

$$\log \mu_{xt} = \eta_{xt}$$

Model definition: Predefined functions for common models

Model definition: Predefined functions for common models

```r
LC <- lc()
CBD <- cbd(link = "log")
APC <- apc()
M7 <- m7(link = "log")
```

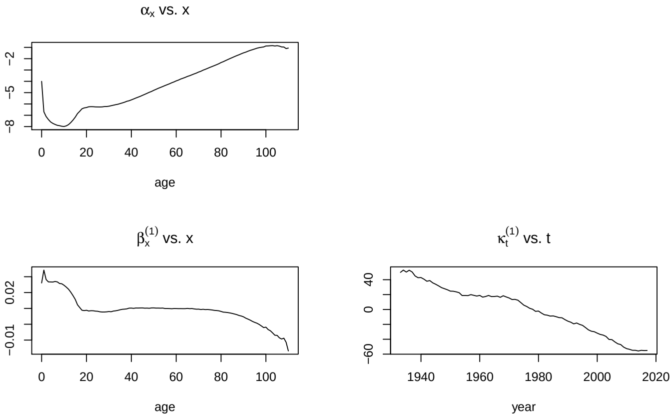
Model definition: Predefined functions for common models

```
LC <- lc()
CBD <- cbd(link = "log")
APC <- apc()
M7 <- m7(link = "log")
```

```
## Poisson model with predictor: log m[x,t] = a[x] + b1[x] k1[t]

## Poisson model with predictor: log m[x,t] = k1[t] + f2[x] k2[t]

## Poisson model with predictor: log m[x,t] = a[x] + k1[t] + g[t-x]

## Poisson model with predictor: log m[x,t] = k1[t] + f2[x] k2[t]
+ f3[x] k3[t] + g[t-x]
```

Model fitting: Lee-Carter Example

```r
USmale <- StMoMoData(USdata, series = "male")
LCfit <- fit(LC, data = USmale)
plot(LCfit)
```

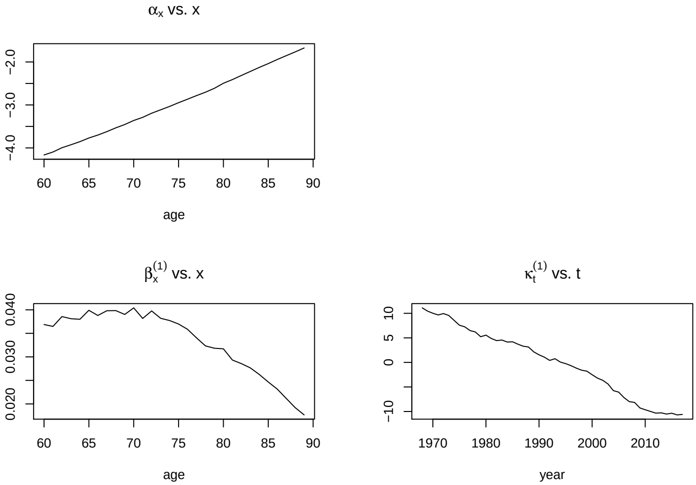


Model fitting: Concentrate on older ages

```r
#Ages for fitting
ages.fit <- 60:89
years.fit <- 1968:2017

#Fit all models
LCfit <- fit(LC, data=USmale, ages.fit=ages.fit,
             years.fit=years.fit)
CBDfit <- fit(CBD, data=USmale, ages.fit=ages.fit,
              years.fit=years.fit)
APCfit <- fit(APC, data=USmale, ages.fit=ages.fit,
              years.fit=years.fit)
M7fit <- fit(M7, data=USmale, ages.fit=ages.fit,
               years.fit=years.fit)
```

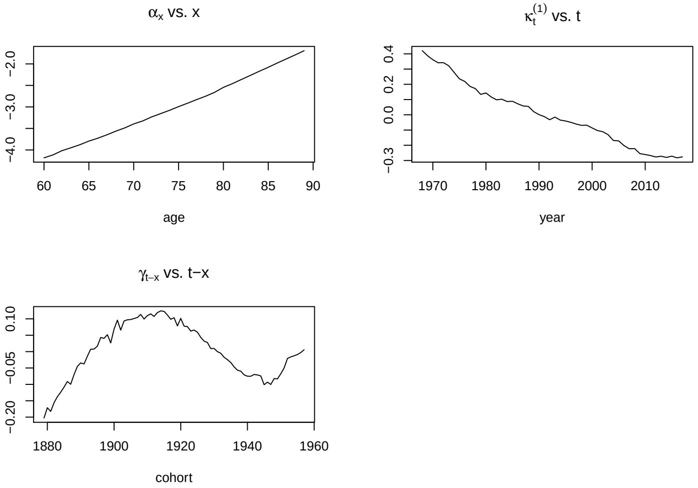
Parameter estimates – LC ($\log \mu_{xt} = \alpha_x + \beta_x^{(1)} \kappa_t^{(1)}$)

```r
plot(LCfit)
```



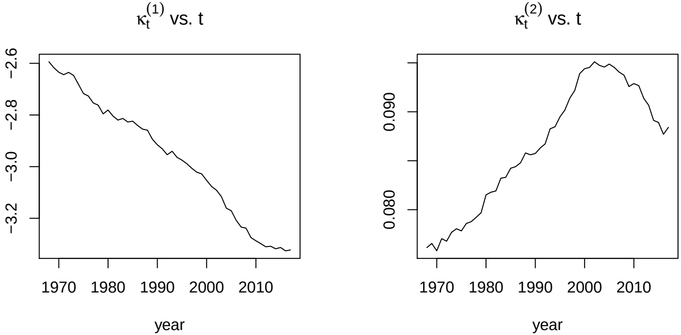
Parameter estimates – APC ($\log \mu_{xt} = \alpha_x + \kappa_t^{(1)} + \gamma_{t-x}$)

```r
plot(APCfit, parametricbx = FALSE)
```



Parameter estimates – CBD ($\log \mu_{xt} = \kappa_t^{(1)} + (x - \bar{x})\kappa_t^{(2)}$)

```r
plot(CBDfit, parametricbx = FALSE)
```



Goodness-of-fit: Deviance Residuals

$$r_{xt} = \operatorname{sign}(d_{xt} - \hat{d}_{xt})\sqrt{\frac{\operatorname{dev}(x,t)}{\hat{\phi}}}$$

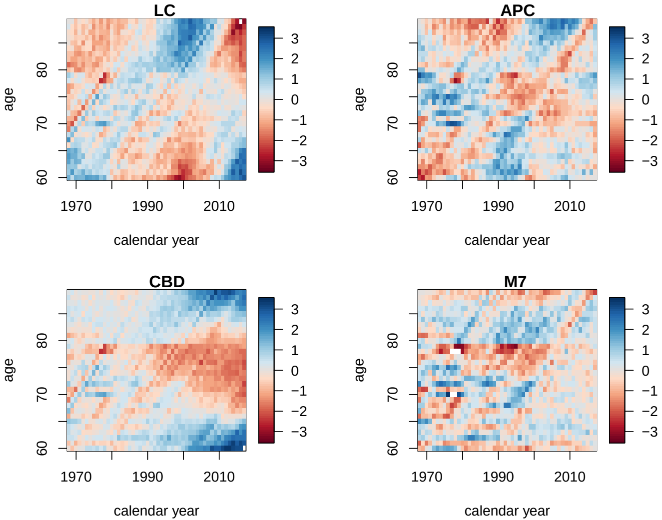
Goodness-of-fit: Deviance Residuals

$$r_{xt} = \mathrm{sign}(d_{xt} - \hat{d}_{xt})\sqrt{\frac{\mathrm{dev}(x,t)}{\hat{\phi}}}$$

```
#Compute residuals
LCres <- residuals(LCfit)
APCres <- residuals(APCfit)
CBDres <- residuals(CBDfit)
M7res <- residuals(M7fit)
```

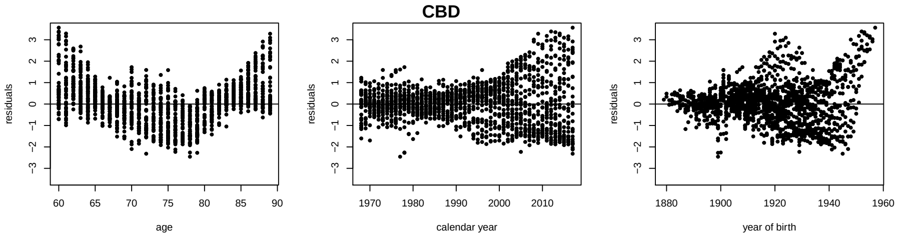
Goodness-of-fit: Residual heatmaps

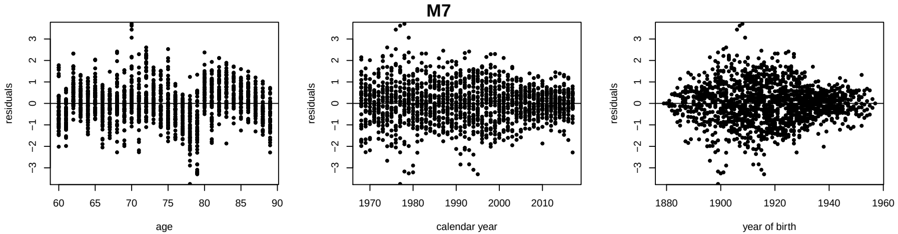
```
plot(LCres, type = "colourmap", reslim = c(-3.5, 3.5))
```



Goodness-of-fit: Residual scatterplots

```r
plot(CBDres, type = "scatter", reslim = c(-3.5, 3.5))
```





Goodness-of-fit vs Parsimony: AIC and BIC

$$AIC = -2\mathcal{L} + 2 \times \nu \qquad BIC = -2\mathcal{L} + \log K \times \nu$$

Goodness-of-fit vs Parsimony: AIC and BIC

$$AIC = -2\mathcal{L} + 2 \times \nu \qquad BIC = -2\mathcal{L} + \log K \times \nu$$

```
#Compute residuals
AIC(CBDfit)
```

```
## [1] 74754.48
```

```
BIC(CBDfit)
```

```
## [1] 75285.8
```

Goodness-of-fit vs Parsimony: AIC and BIC

$$AIC = -2\mathcal{L} + 2 \times \nu \qquad BIC = -2\mathcal{L} + \log K \times \nu$$

```r
#Compute residuals
AIC(CBDfit)
```

```
## [1] 74754.48
```

```r
BIC(CBDfit)
```

```
## [1] 75285.8
```

Criterion	LC	APC	CBD	M7
AIC	56814	32063	74754	**27575**
BIC	57388	32892	75286	**28775**

Forecasting and simulation

- **Period indexes:** Multivariate random walk with drift

$$\boldsymbol{\kappa}_t = \boldsymbol{\delta} + \boldsymbol{\kappa}_{t-1} + \boldsymbol{\xi}^{\kappa}_t, \qquad \boldsymbol{\kappa}_t = \begin{pmatrix} \kappa^{(1)}_t \\ \vdots \\ \kappa^{(N)}_t \end{pmatrix}, \qquad \boldsymbol{\xi}^{\kappa}_t \sim N(\mathbf{0}, \Sigma),$$

- **Cohort effect:** ARIMA(p, q, d) with drift

$$\Delta^d \gamma_c = \delta_0 + \phi_1 \Delta^d \gamma_{c-1} + \cdots + \phi_p \Delta^d \gamma_{c-p} + \epsilon_c + \delta_1 \epsilon_{c-1} + \cdots + \delta_q \epsilon_{c-q}$$

Forecasting

Model	Model for γ_{t-x}
APC	ARIMA$(1, 1, 0)$ with zero mean
M7	ARIMA$(0, 0, 0)$ with zero mean

Forecasting

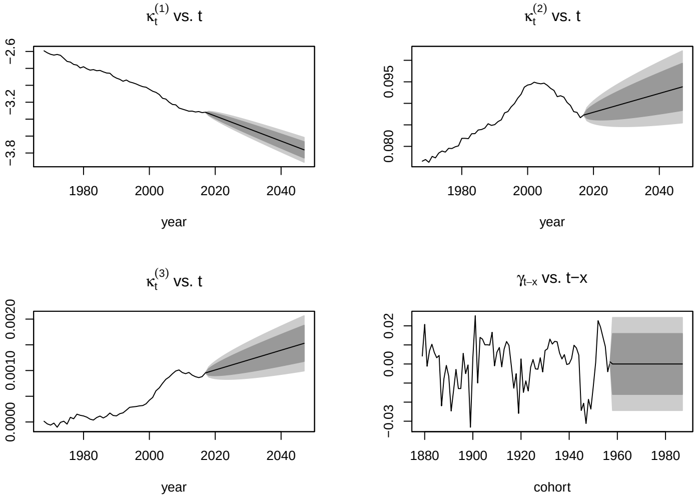
Model	Model for γ_{t-x}
APC	ARIMA$(1, 1, 0)$ with zero mean
M7	ARIMA$(0, 0, 0)$ with zero mean

30-year ahead ($h = 30$) central projections: period indexes, cohort index, and death rates probabilities:

```
LCfor <- forecast(LCfit, h=30)
APCfor <- forecast(APCfit, h=30, gc.order = c(1,1,0),
                   gc.include.constant = FALSE)
CBDfor <- forecast(CBDfit, h=30)
M7for <- forecast(M7fit, h=30, gc.order = c(0,0,0),
                  gc.include.constant = FALSE)
```

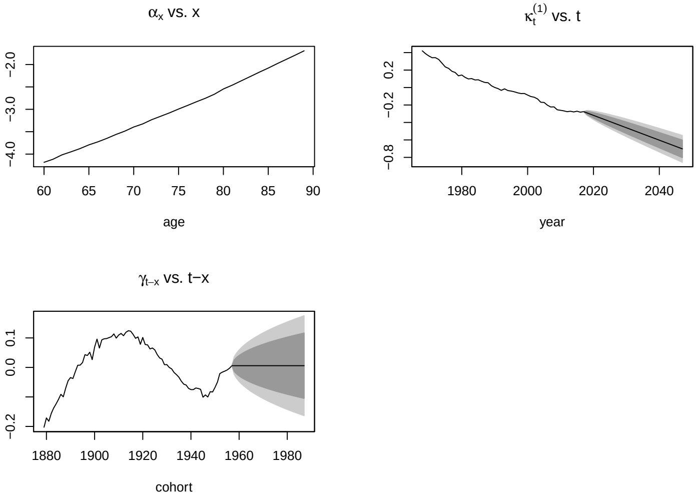
Forecasted period and cohort indexes

```r
plot(M7for, parametricbx = FALSE)
```



Forecasted period and cohort indexes

```r
plot(APCfor, parametricbx = FALSE)
```

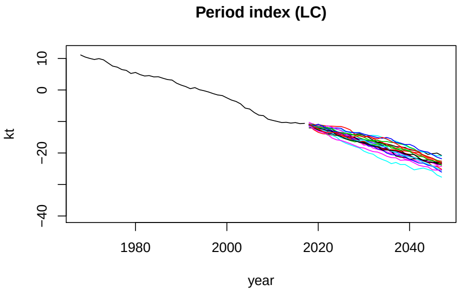


Simulation

```
LCsim <- simulate(LCfit, nsim=1000, h=30)
APCsim <- simulate(APCfit, nsim=1000, h=30,
                   gc.order = c(1,1,0),
                   gc.include.constant = FALSE)
CBDsim <- simulate(CBDfit, nsim=1000, h=30)
M7sim <- simulate(M7fit, nsim=1000, h=30,
                  gc.order = c(0,0,0),
                  gc.include.constant = FALSE)
```

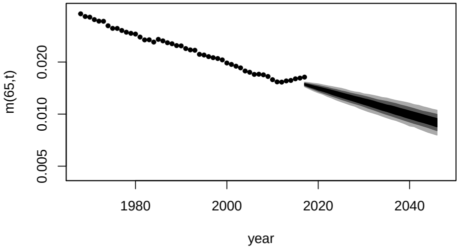
Simulation

```
#Plot period index trajectories for the LC model
plot(LCfit$years, LCfit$kt[1,], type="l", xlim=c(1968,2047),
     ylim=c(-40,12), xlab="year", ylab="kt",
     main="Period index (LC)")
matlines(LCsim$kt.s$years, LCsim$kt.s$sim[1,,1:20], type="l",
         lty=1)
```

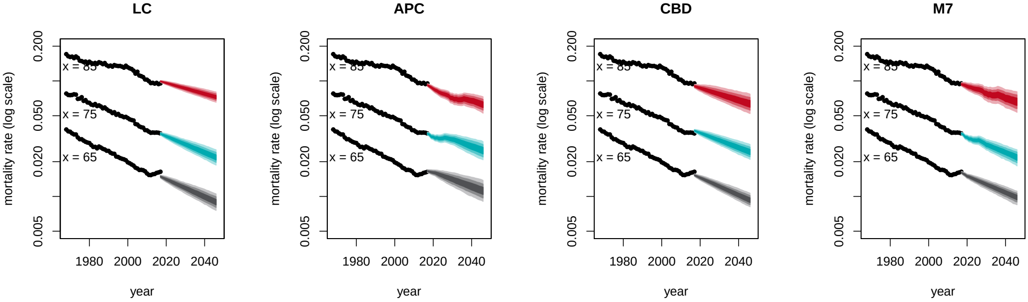


Fancharts

```
library(fanplot)
mxt <- LCfit$Dxt/LCfit$Ext
plot(LCfit$years, mxt["65",], pch=20, xlim=c(1968,2047),
     ylim=c(0.0045,0.04), log="y", xlab="year", ylab="m(65,t)")
fan(t(LCsim$rates["65",,]), start=2017, probs=c(50,75,90,97.5),
  n.fan=4, ln=NULL, fan.col=colorRampPalette(c("black","white")))
```



Fancharts



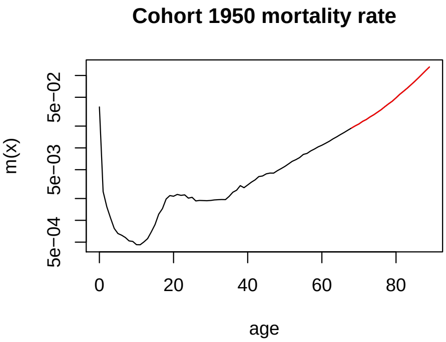
LC
APC
CBD
M7
mortality rate (log scale)
0.005
0.020
0.050
0.200
x = 85
x = 75
x = 65
1980
2000
2020
2040
year

Obtaining projected life tables for a cohort

```r
chosen_cohort <- 1950

#observed rates for ages 0-59
hist_rates <- extractCohort(USmale$Dxt/USmale$Ext,
                            cohort = chosen_cohort)[1:60]

#fitted historical rates for ages 60-67
lc_fit_rates <- extractCohort(fitted(LCfit, type = "rates"),
                              cohort = chosen_cohort)
#forcasted rates for ages 68-89
lc_for_rates <- extractCohort(LCfor$rates,
                             cohort = chosen_cohort)
#all rates
lc_rates_1950 <- c(hist_rates,lc_fit_rates, lc_for_rates)
```

Obtaining projected life tables for a cohort

```
plot(0:89, lc_rates_1950 ,type = "l", log = "y", xlab = "age",
     ylab = "m(x)", main = "Cohort 1950 mortality rate")
lines(68:89, lc_for_rates, col = "red")
```



Computing life expectancies using **lifecontingencies**

```
#Transform mx to qx
lc_qx_1950 <- mx2qx(lc_rates_1950)
#Create lifetable
lc_lifetable_1950 <- probs2lifetable(probs = lc_qx_1950,
                                     type = "qx",
                                     name = "LC-1950")
exn(lc_lifetable_1950,x=65)
```

```
## [1] 17.373
```

Computing life expectancies using **lifecontingencies**

```
#Transform mx to qx
lc_qx_1950 <- mx2qx(lc_rates_1950)
#Create lifetable
lc_lifetable_1950 <- probs2lifetable(probs = lc_qx_1950,
                                     type = "qx",
                                     name = "LC-1950")
exn(lc_lifetable_1950,x=65)
```

```
## [1] 17.373
```

Model	LC	APC	CBD	M7
LE at age 65	17.3729974	17.4886457	17.254208	17.5034425
LE at age 75	10.3314105	10.6308337	10.3993284	10.5521274

Summary

- This has been a whistle-stop introduction to fitting mortality models in R
- Useful example for using **StMoMo** in the package vignette at https://cran.r-project.org/web/packages/StMoMo/vignettes/StMoMoVignette.pdf
  - Also, references within this useful for understanding more about mortality models
- Useful examples of integrating **StMoMo** with **lifecontingencies** at https://rdrr.io/cran/lifecontingencies/f/inst/doc/mortality_projection.pdf

Summary

- **StMoMo provides** easy implementation and comparison of a wide range of models making it useful for:
  - Actuaries analysing longevity risk $\rightsquigarrow$ Model risk
  - Use in the classroom
- Standard packages are starting point – however, to go beyond them you need to understand the principles behind their operation

Work in progress

- Available in the development version and expected to be released in next six months
  - Selection of models using cross-validation
  - Construction of models using regularisation techniques
- Sister packages **iMoMo** for mortality improvement rate modelling
  - Expected to be released in the next year
- Other development plans
  - Multipopulation models
  - Model combination

Cross validation and regularisation

Mortality Models: Key research questions

1. What model features are desired for different applications?

2. Why do we only consider a fixed set of models?

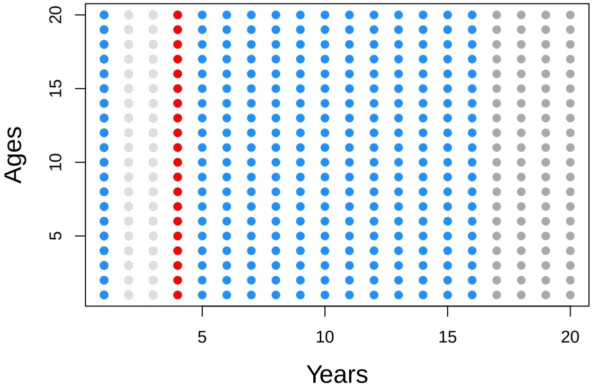
3. How can we be confident we have selected the best model?

Objective

Provide a comprehensive framework to **construct**, **select**, and **evaluate** discrete-time mortality models for forecasting applications, using various **statistical learning** and predictive analytics techniques.

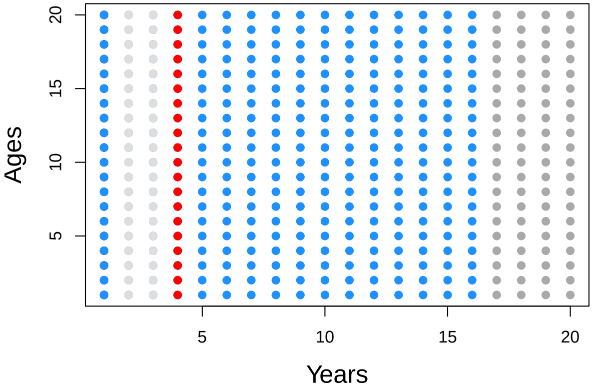
- **Construction** based on regularisation techniques
- **Selection** based on cross-validation techniques

Selection of mortality models using cross validation



- **Training/Test Set**
- **Test Set Width**: Depending on forecasting Horizon
- **Metric**: MSE on the test set

Selection of mortality models using cross validation



- **Training/Test Set**
- **Test Set Width**: Depending on forecasting Horizon
- **Metric**: MSE on the test set

Selection of mortality models using cross validation

```r
# install.packages("devtools")
# devtools::install_github("amvillegas/StMoMo",
#                                  ref = "GroupLasso")

#CV for 1 year ahead
LCcv1 <- cv.StMoMo(LC, h = 1, data=USmale, ages.train=ages.fit,
            years.train=years.fit, type = "lograte")
APCcv1 <- cv.StMoMo(APC, h = 1, data=USmale, ages.train=ages.fit,
            years.train=years.fit, type = "lograte")
CBDcv1 <- cv.StMoMo(CBD, h = 1, data=USmale, ages.train=ages.fit,
            years.train=years.fit, type = "lograte")
M7cv1 <- cv.StMoMo(M7, h = 1, data=USmale, ages.train=ages.fit,
            years.train=years.fit, type = "lograte")
```

Selection of mortality models using cross validation

```
#CV for 10 year ahead
LCcv10 <- cv.StMoMo(LC, h = 10, data=USmale, ages.train=ages.fit,
                    years.train=years.fit, type = "lograte s")
APCcv10 <- cv.StMoMo(APC, h = 10, data=USmale, ages.train=ages.fit,
                    years.train=years.fit, type = "logrates")
CBDcv10 <- cv.StMoMo(CBD, h = 10, data=USmale, ages.train=ages.fit,
                    years.train=years.fit, type = "logrates")
M7cv10 <- cv.StMoMo(M7, h = 10, data=USmale, ages.train=ages.fit,
                    years.train=years.fit, type = "logrates")
```

Selection of mortality models using cross validation

```
LCcv1$cv.mse
```

```
## [1] 0.001367588
```

```
LCcv10$cv.mse
```

```
## [1] 0.004095502
```

Selection of mortality models using cross validation

```
LCcv1$cv.mse
```

```
## [1] 0.001367588
```

```
LCcv10$cv.mse
```

```
## [1] 0.004095502
```

Criterion	LC	APC	CBD	M7
AIC	56814	32063	74754	**27575**
BIC	57388	32892	75286	**28775**
CV 1-year	0.0014	0.0007	0.0017	**0.0005**
CV 10-year	0.0041	**0.0033**	0.0050	0.0046

Construction: "Formalised" Model-Building Framework

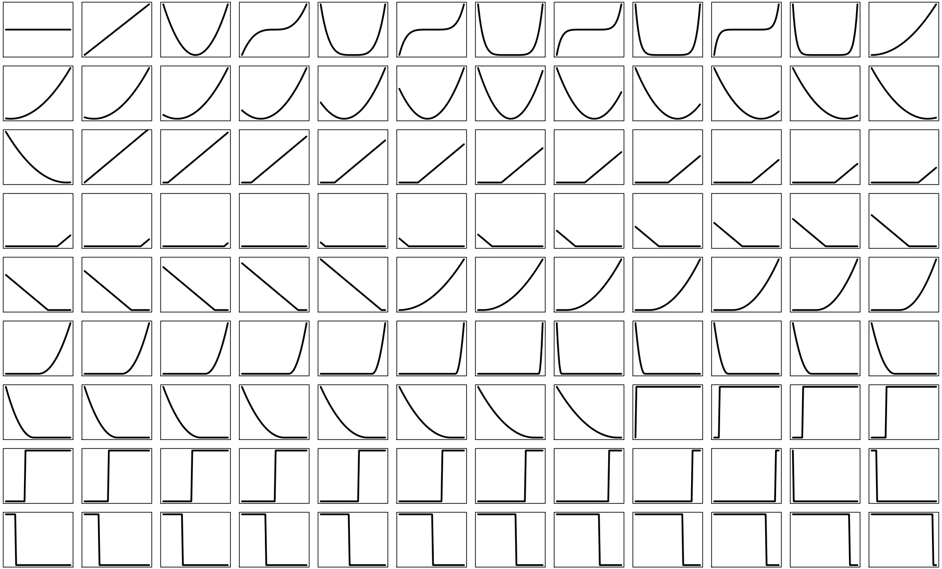
We start with a **huge** model,

$$\ln(\mu_{x,t}) = \alpha_x + \sum_{i=1}^{B} f^{(i)}(x)\kappa_t^{(i)} + \gamma_{t-x},$$

where the suite of basis functions $(f^{(i)}(x))$ included are:

$$f^{(i)}(x) = \begin{cases} 1, & \text{Unit} \\ (x-\bar{x})^n & \text{Polynomial} \\ (x-n)^+ & \text{Call} \\ (n-x)^+ & \text{Put} \\ 1_{x<n} & \text{Below} \\ 1_{x>n} & \text{Above} \end{cases} \quad . \tag{1}$$

Construction: Our Model



Construction: GLM Representation

$$\eta_{x,t} = \ln(\mu_{x,t}) = \alpha_x + \sum_{i=1}^{B} f^{(i)}(x)\kappa_t^{(i)} + \gamma_c,$$

can be expressed as a GLM (Currie 2014),

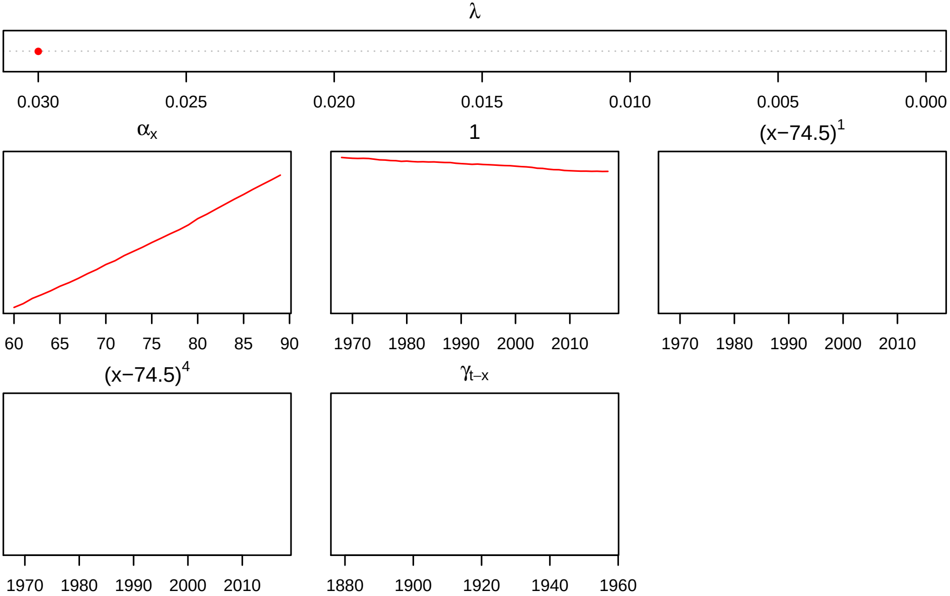
$$\eta = \mathbf{X}\beta = \sum_{j=0}^{B+1} \mathbf{X}_j \boldsymbol{\beta}_j, \qquad \mathbf{X} = [\mathbf{X_0} : \mathbf{X_1} : \mathbf{X_2} : \ldots : \mathbf{X_B} : \mathbf{X_{B+1}}],$$

where,

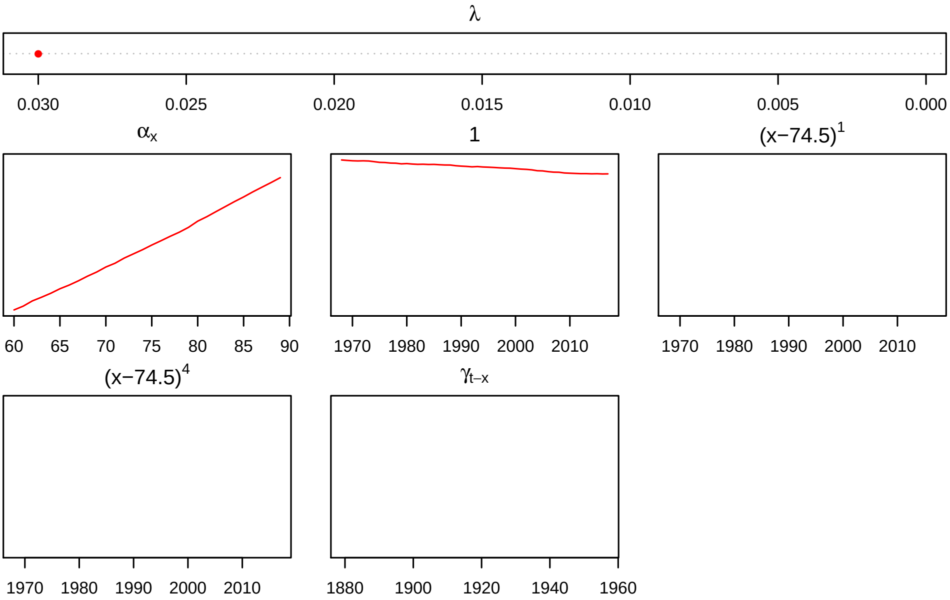
$$\boldsymbol{\beta} = \{\boldsymbol{\beta_i}\}_{i=0}^{B+1}, \quad \boldsymbol{\beta_0} = \{\alpha_x\}_{x=1}^{n_x}, \quad \boldsymbol{\beta_i} = \{\kappa_t^{(i)}\}_{t=1}^{n_t}, \quad \boldsymbol{\beta_{B+1}} = \{\gamma_c\}_{c=1}^{n_c}.$$

- Estimate parameters with group lasso using the R package **grpreg** (Breheny and Huang 2013)

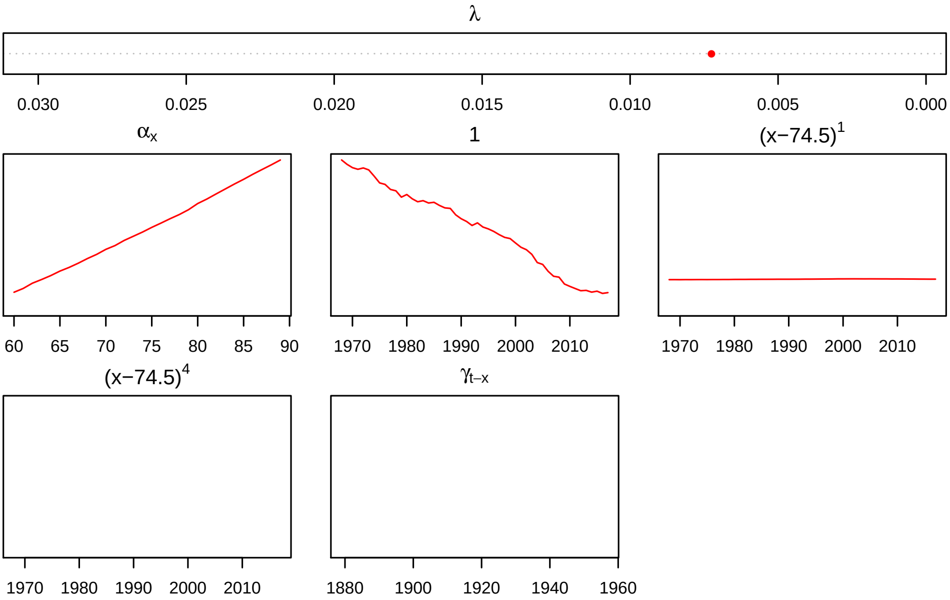
Construction: Estimated Parameters (USA Males)



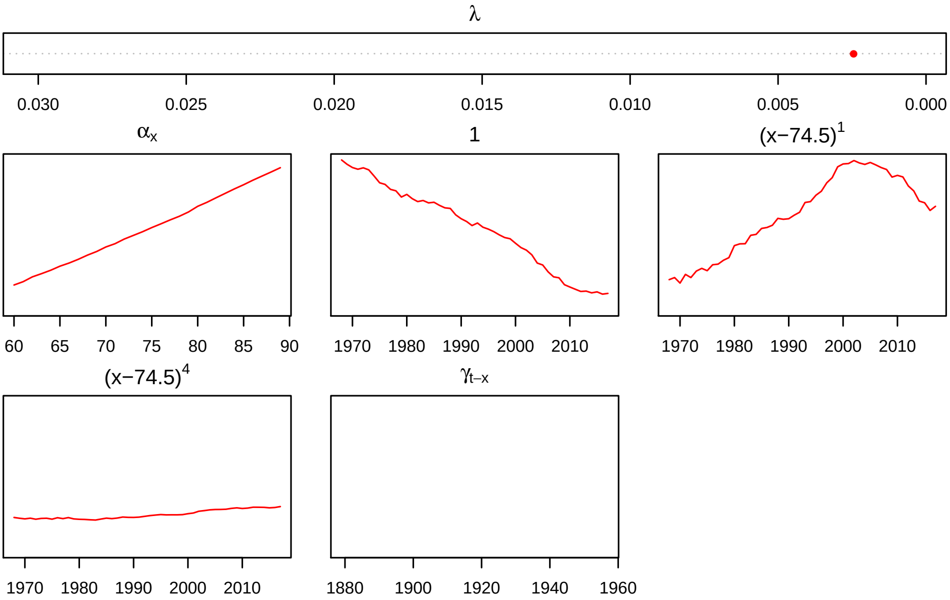
Construction: Estimated Parameters (USA Males)



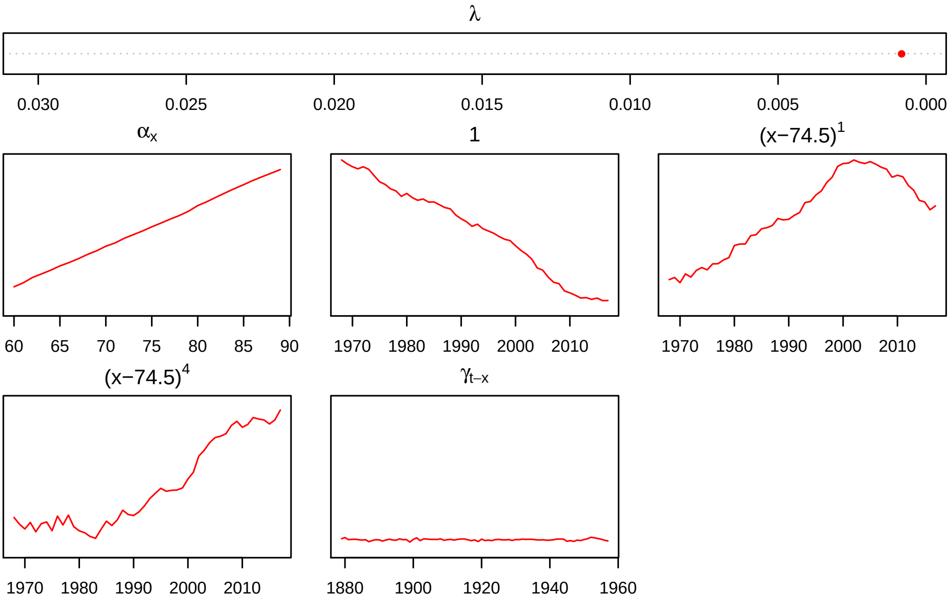
Construction: Estimated Parameters (USA Males)



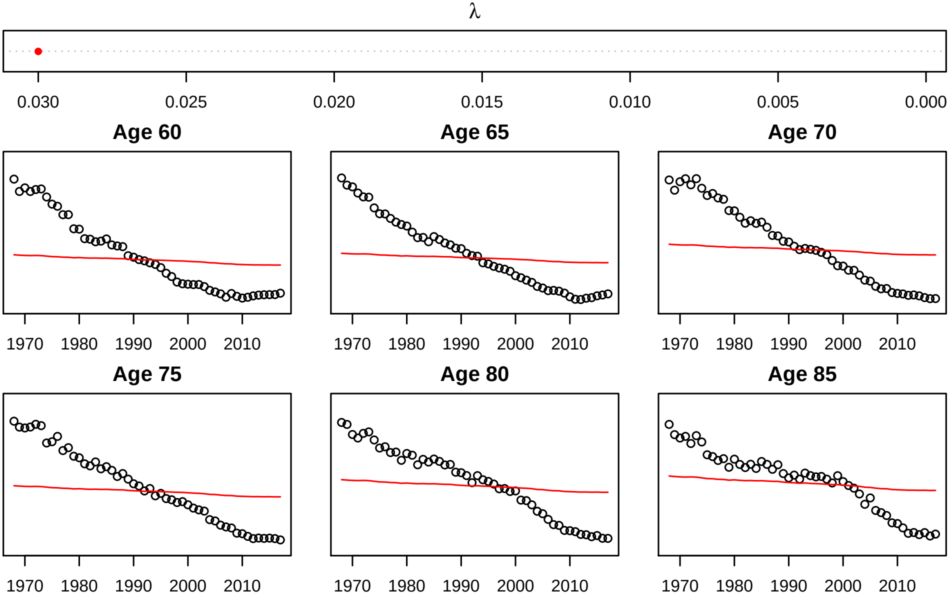
Construction: Estimated Parameters (USA Males)



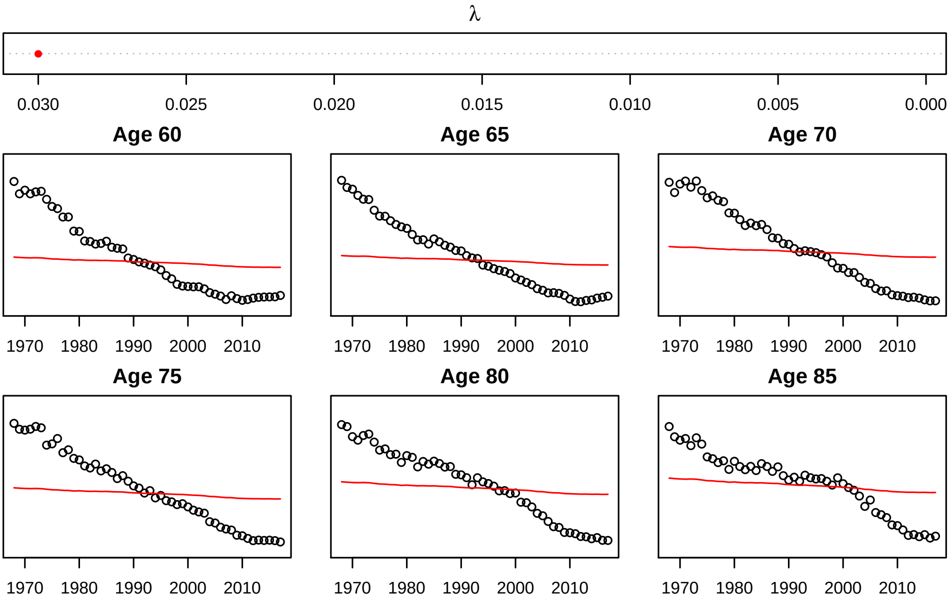
Construction: Estimated Parameters (USA Males)



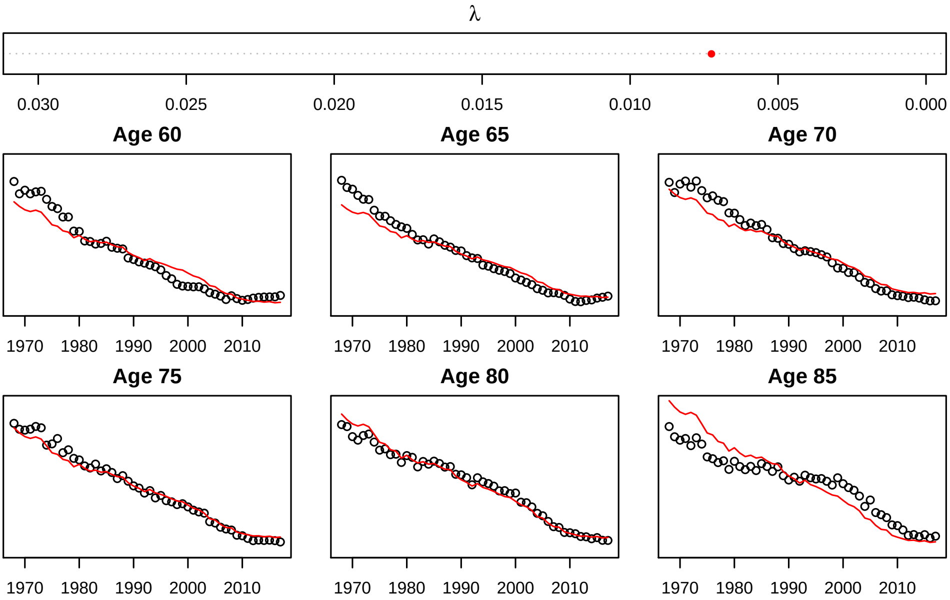
Construction: Fitted Values (USA Males)



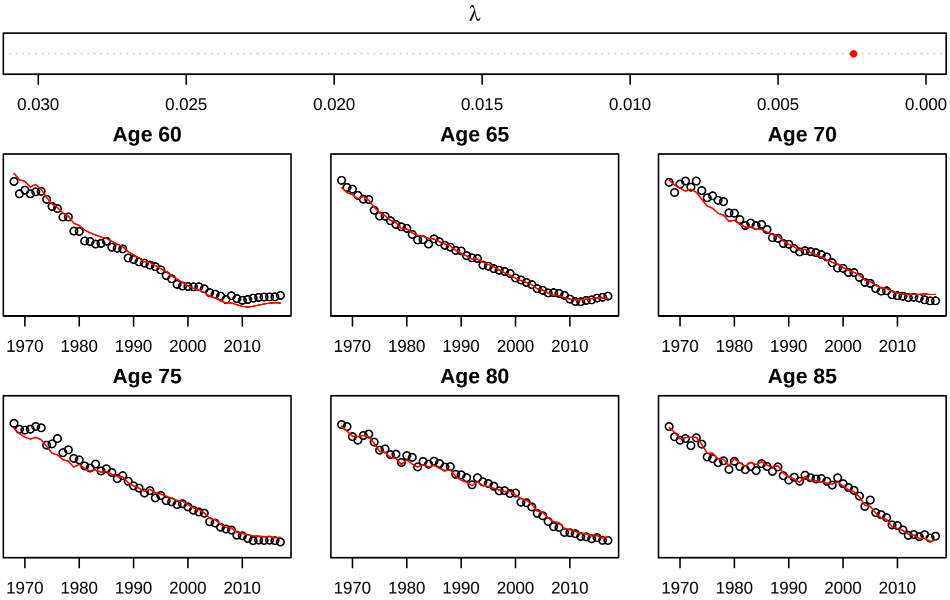
Construction: Fitted Values (USA Males)



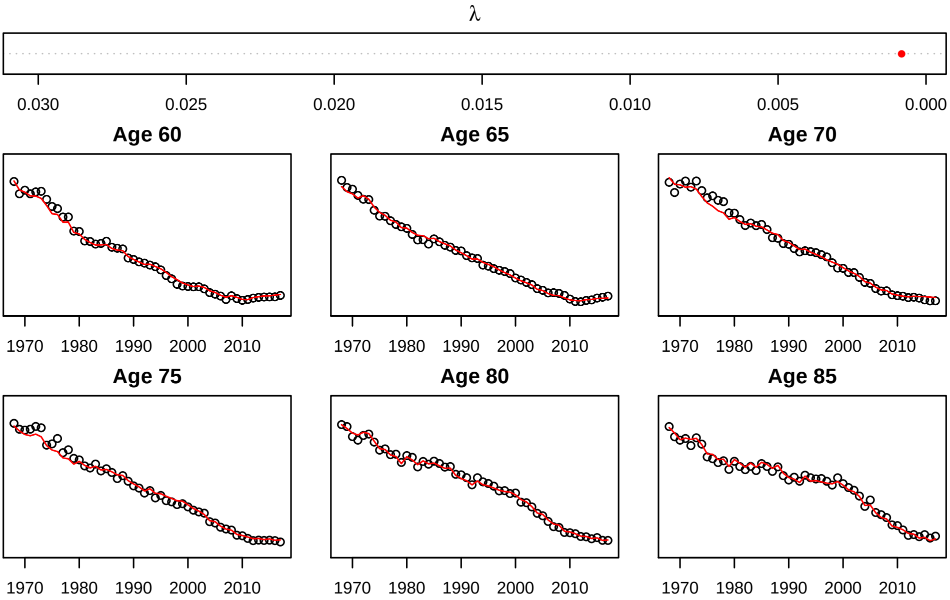
Construction: Fitted Values (USA Males)



Construction: Fitted Values (USA Males)



Construction: Fitted Values (USA Males)



Implementation in StMoMo - Define model

```
#Create big model
strikes <- seq(65,85,5)
bModel <- StMoMo(link = "log-Gaussian", staticAgeFun = TRUE,
                periodAgeFun = c("1", genPoly(1:5), genCall(strikes),
                                 genPut(strikes)),
                cohortAgeFun = "1")
bModel
```

```
## Gaussian model with predictor: log m[x,t] = a[x] + k1[t] +
f2[x] k2[t] + f3[x] k3[t] + f4[x] k4[t] + f5[x] k5[t] + f6[x]
k6[t] + f7[x] k7[t] + f8[x] k8[t] + f9[x] k9[t] + f10[x] k10[t] +
f11[x] k11[t] + f12[x] k12[t] + f13[x] k13[t] + f14[x] k14[t] +
f15[x] k15[t] + f16[x] k16[t] + g[t-x]
```

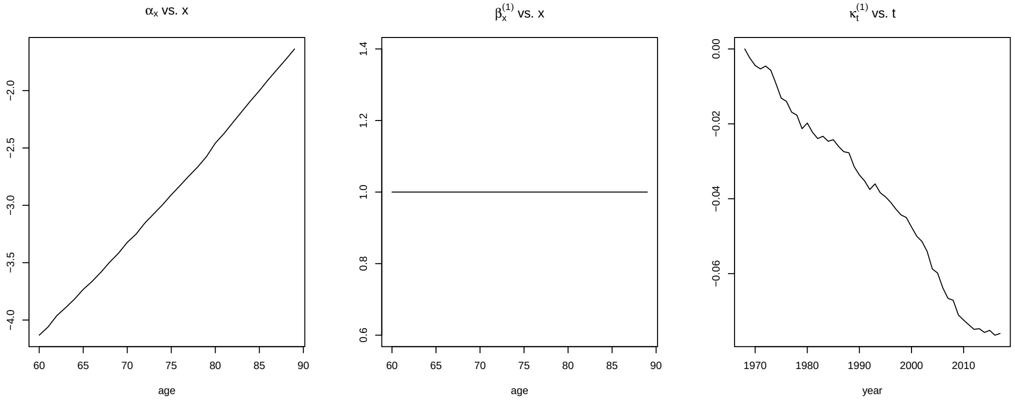
Implementation in StMoMo - Fit model with grouped penalised regularisation

```r
#lambda grid
lambda <- exp(seq(log(0.03), log(0.0005), length.out = 50))
#Penalise all term
bMgrpfit <- grpfit(bModel, lambda = lambda, data = USmale,
                   ages.fit = ages.fit, years.fit = years.fit)
```

```
## StMoMo: Start fitting with grpreg
## StMoMo: Finish fitting with grpreg
```

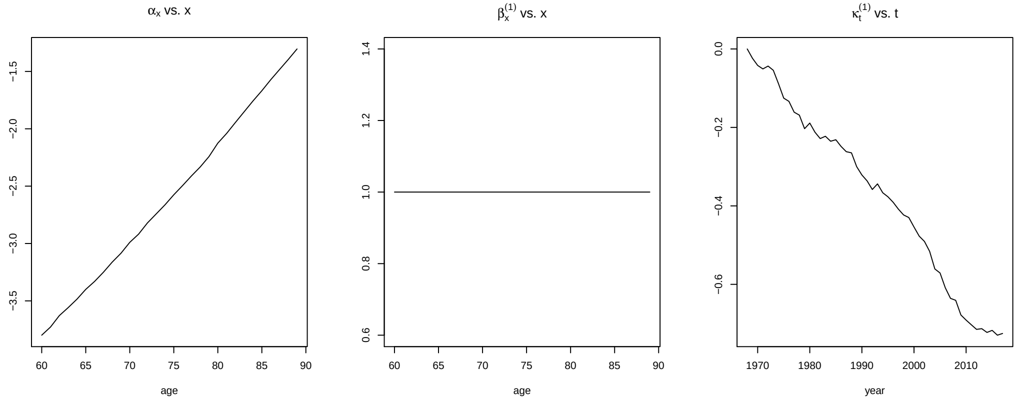
Implementation in StMoMo - Parameter paths

```r
plot(extractStMoMo(bMgrpfit, 1), nCol = 3)
```



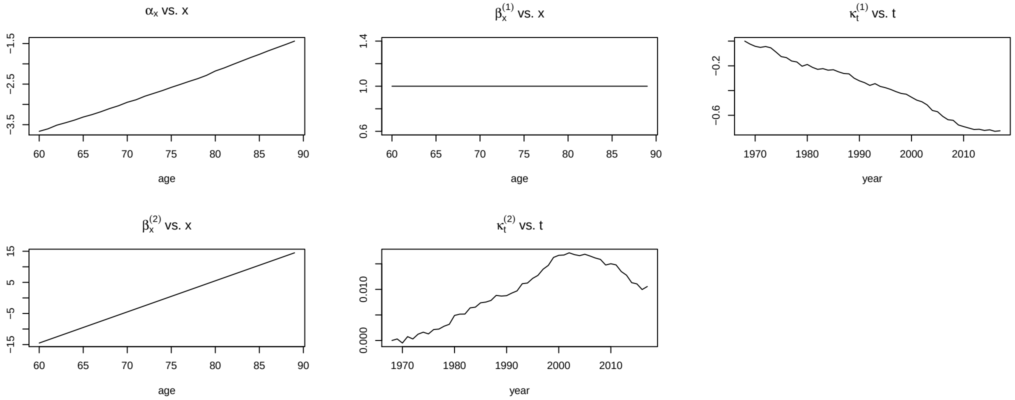
Implementation in StMoMo - Parameter paths

```r
plot(extractStMoMo(bMgrpfit, 17), nCol = 3)
```



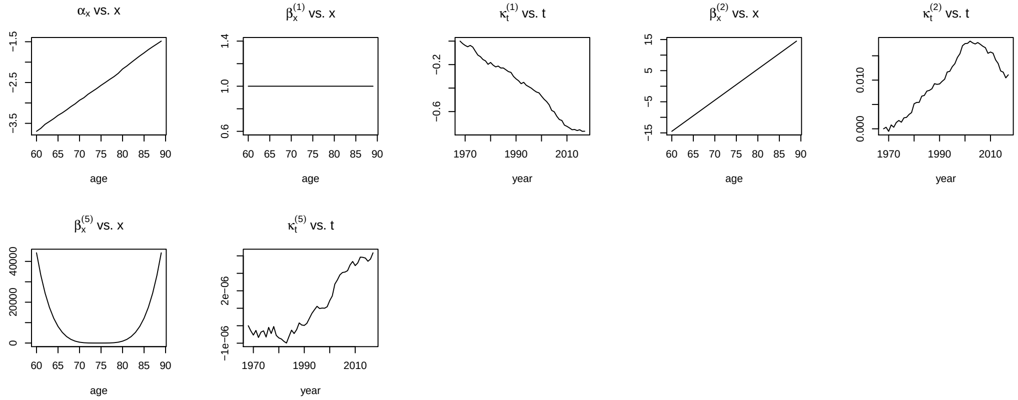
Implementation in StMoMo - Parameter paths

```r
plot(extractStMoMo(bMgrpfit, 30), nCol = 3)
```



Implementation in StMoMo - Parameter paths

```r
plot(extractStMoMo(bMgrpfit, 40), nCol = 5)
```



Improvement rate modelling

The APCi model

- Modelling improvement rates rather than mortality rates is becoming commong
- Consider the APCi model which corresponds broadly to the lates CMI projection approach:

$$-\log \frac{\mu_{xt}}{\mu_{x,t-1}} = \alpha_x + \kappa_t + \gamma_{t-x}$$

Implementation in **iMoMo**

```r
library(iMoMo) #Not yet publicly available
#Define model
APCi <- apci()
APCi
```

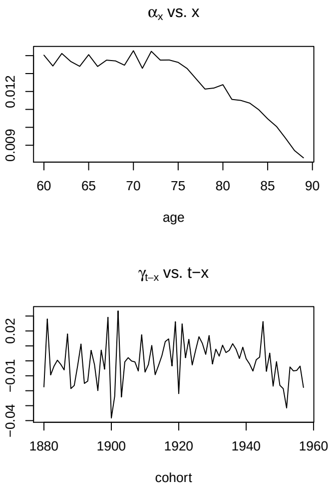
```
## indirect model with predictor: eta[x,t] = a[x] + k1[t] + g[t-x]
```

```r
#fit the model
APCifit <- fit(APCi, data=USmale, ages.fit=ages.fit,
               years.fit=years.fit)
```

```
## StMoMo: Start fitting with gnm
## StMoMo: Finish fitting with gnm
```

Implementation in **iMoMo**

```
plot(APCifit, parametricbx = FALSE)
```



http://cran.r-project.org/web/packages/StMoMo/
https://github.com/amvillegas/StMoMo

Thank you!

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