

Mortality Modelling with R

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Slides Available at:

https://github.com/amvillegas/LT100_2020

Aims

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

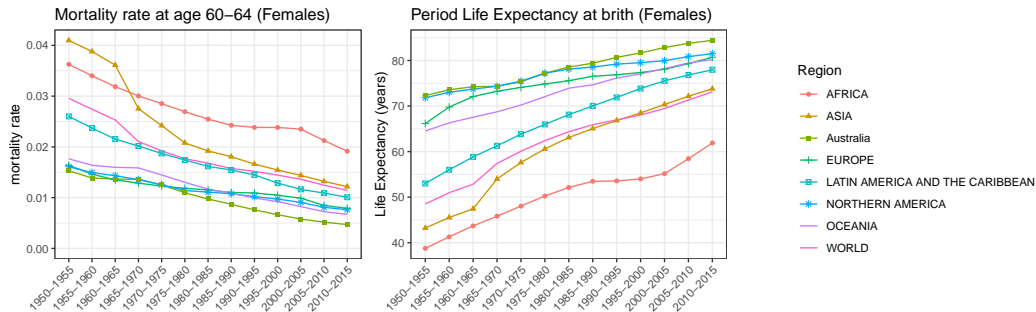
- ▶ Obtain mortality data from Human Mortality Database
- ▶ Fit stochastic mortality models (including Lee-Carter model)
- ▶ Compare goodness of fit of mortality models
- ▶ Forecast future mortality rates (deterministic and using Monte Carlo simulations)
- ▶ Compute demographic and actuarial quantities

Agenda

- ▶ Motivation
- ▶ Review of mortality modelling methodologies
- ▶ 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

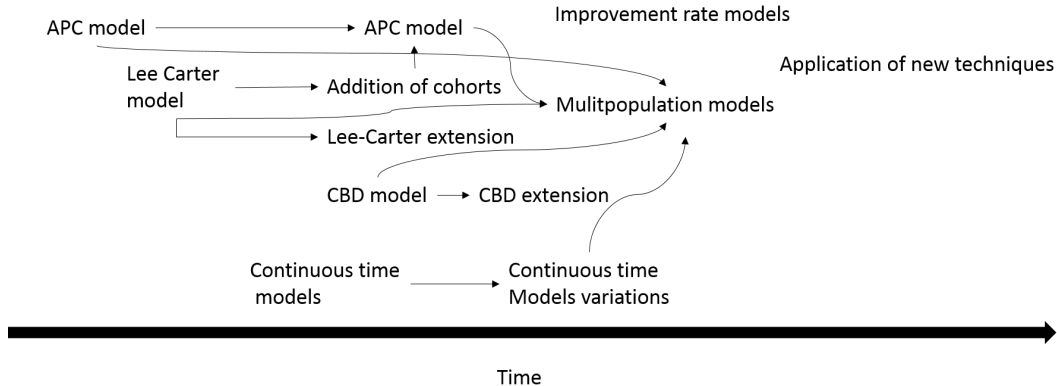
- ▶ Good-news!
- ▶ Important social and financial implications for governments, insurers, individuals.
- ▶ Need to model and project these trends

Mortality forecasting methodologies

A good overview of methodologies is given in the review papers by Booth and Tickle (2008), Wong-Fillips 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

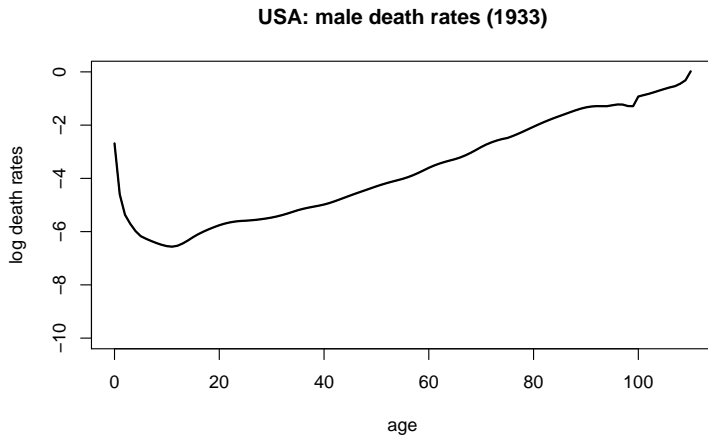
A timeline of “recent” mortality modelling methodologies



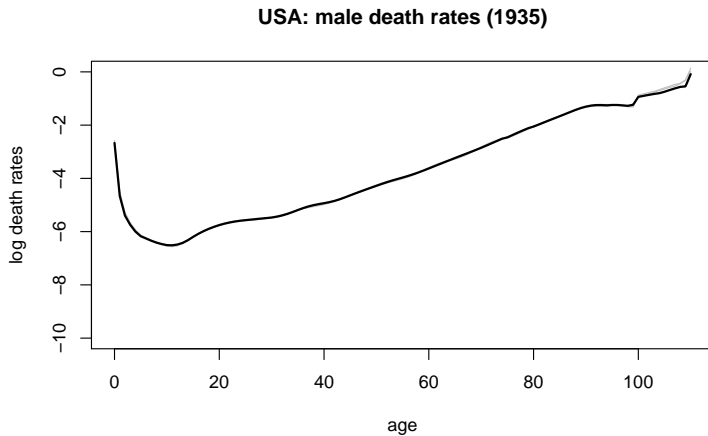
Advances in single population mortality modelling

- ▶ **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))

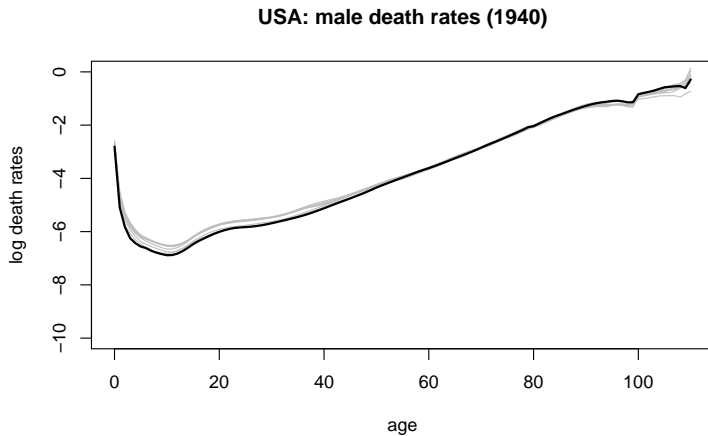
Lee-Carter model



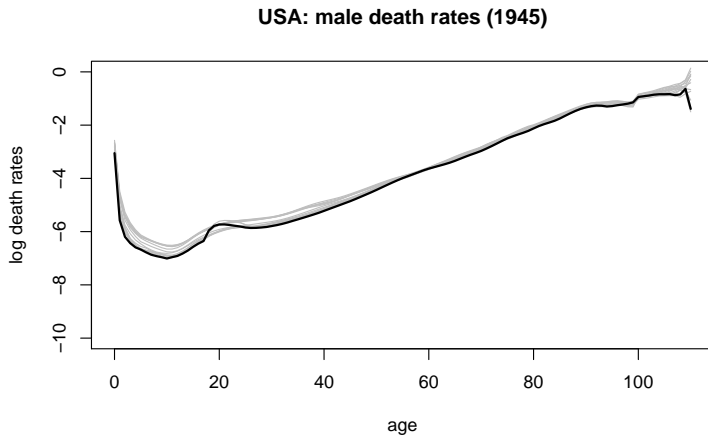
Lee-Carter model



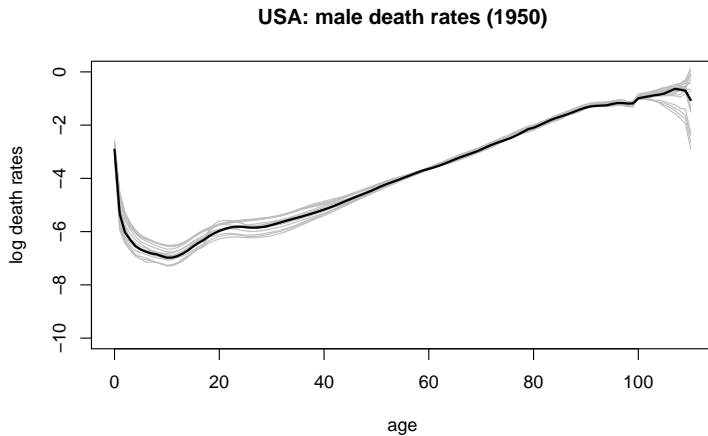
Lee-Carter model



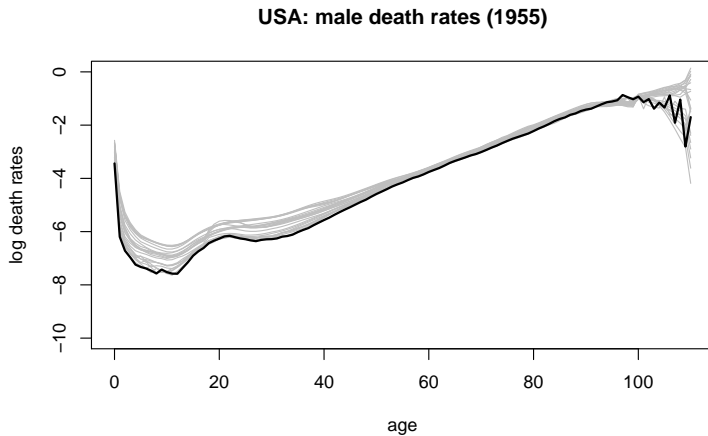
Lee-Carter model



Lee-Carter model

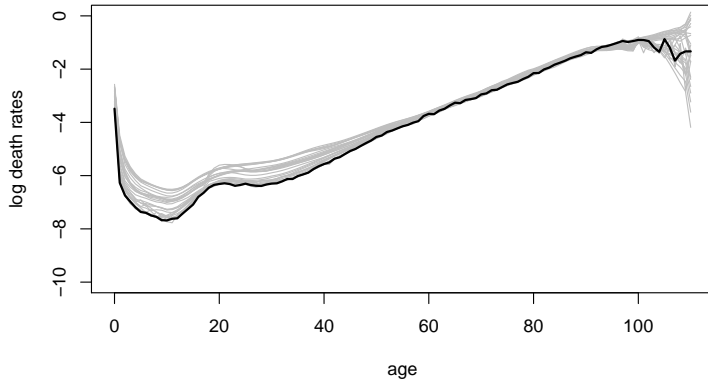


Lee-Carter model

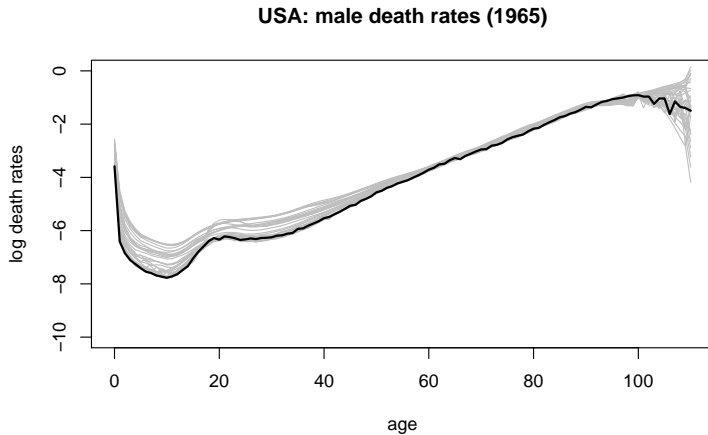


Lee-Carter model

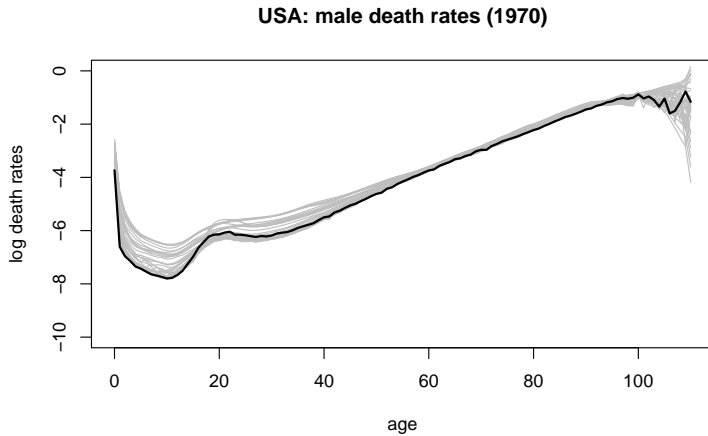
USA: male death rates (1960)



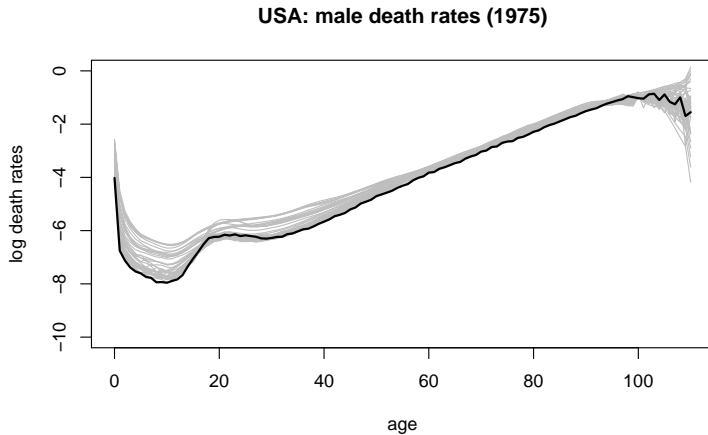
Lee-Carter model



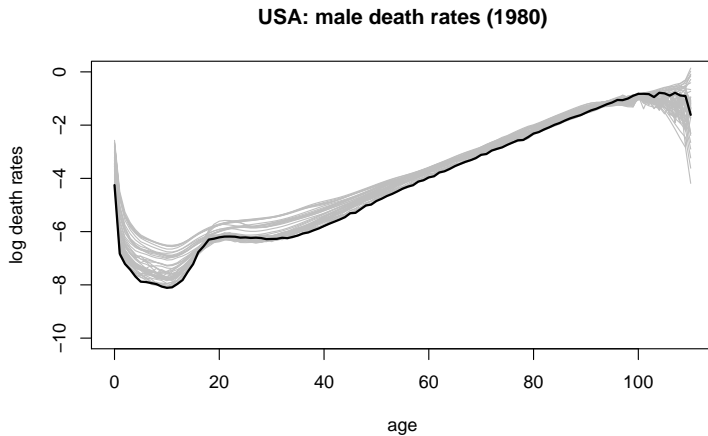
Lee-Carter model



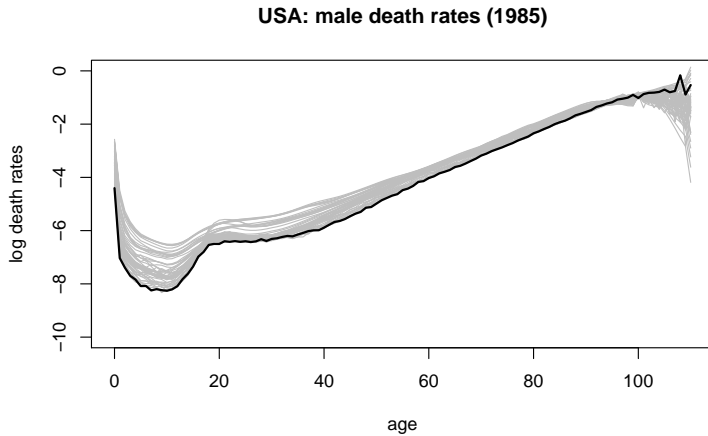
Lee-Carter model



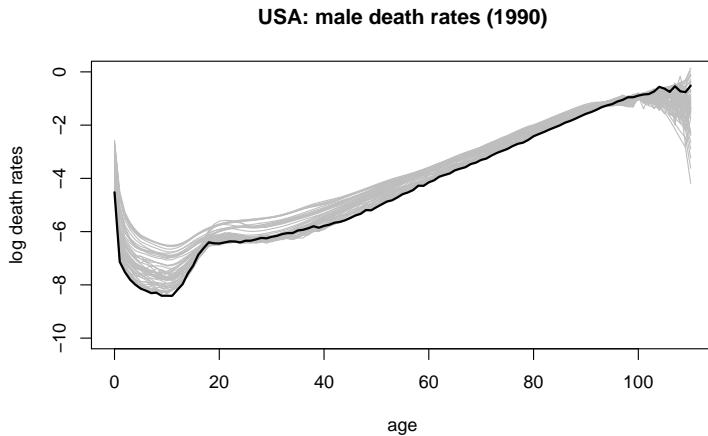
Lee-Carter model



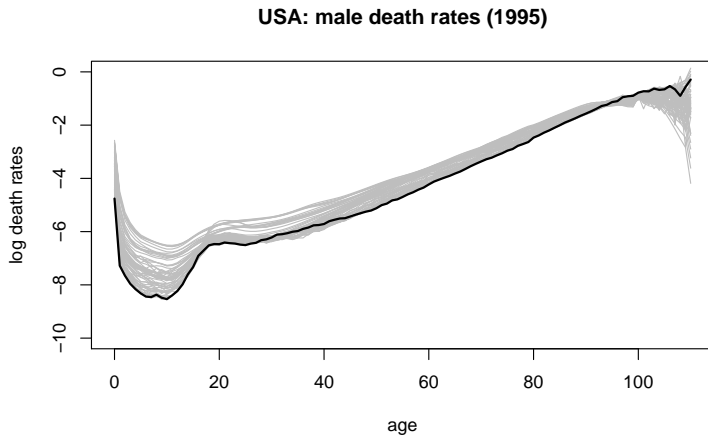
Lee-Carter model



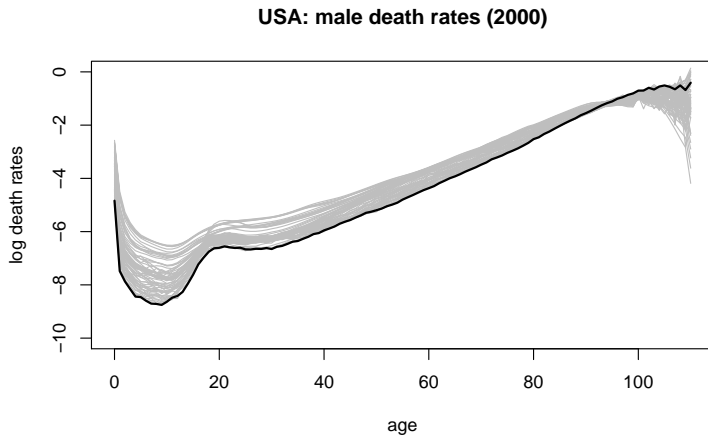
Lee-Carter model



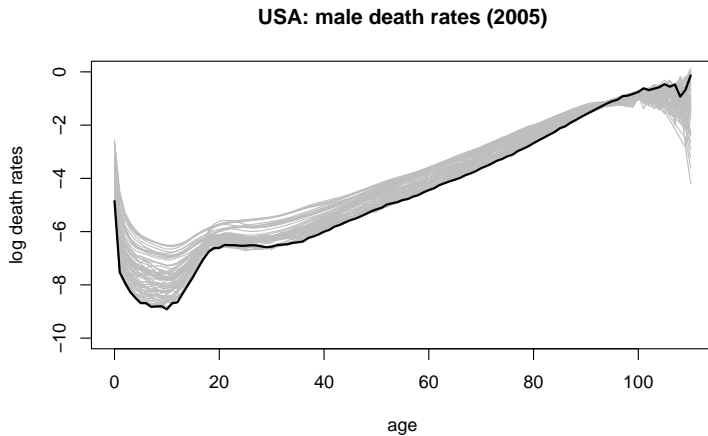
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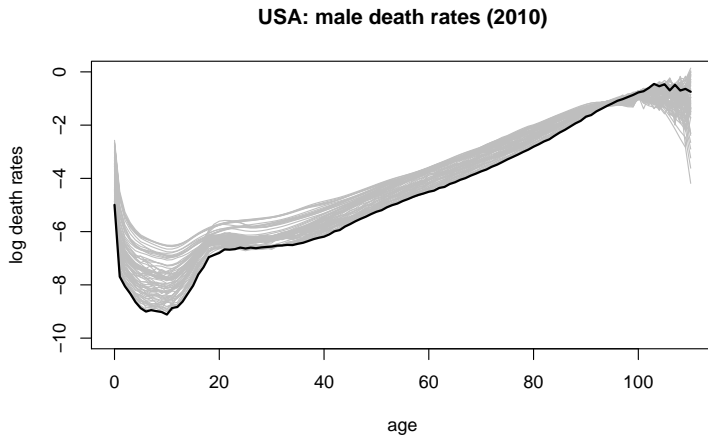
Lee-Carter model



Lee-Carter model



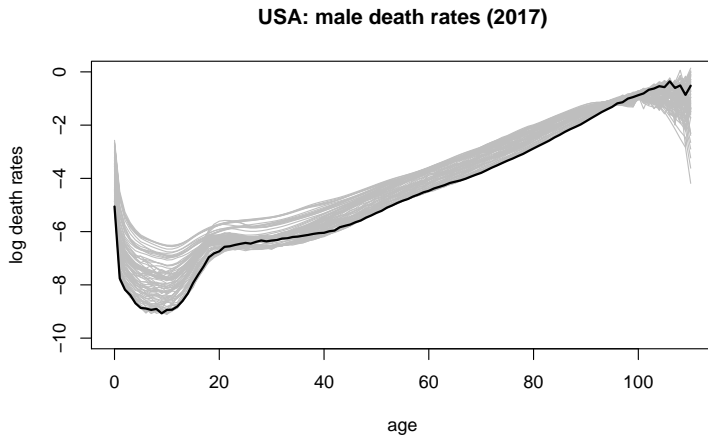
Lee-Carter model



Lee-Carter model

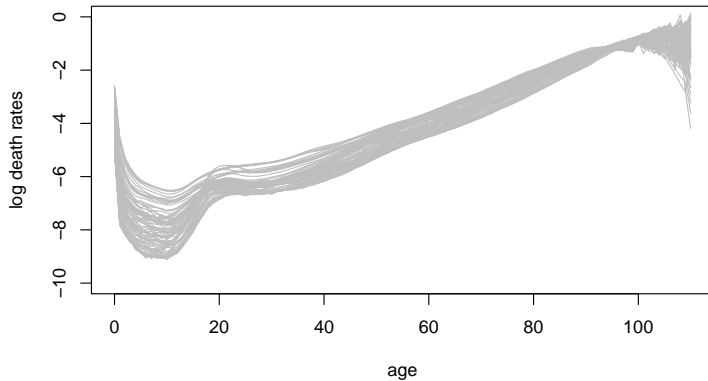


Lee-Carter model



Lee-Carter model

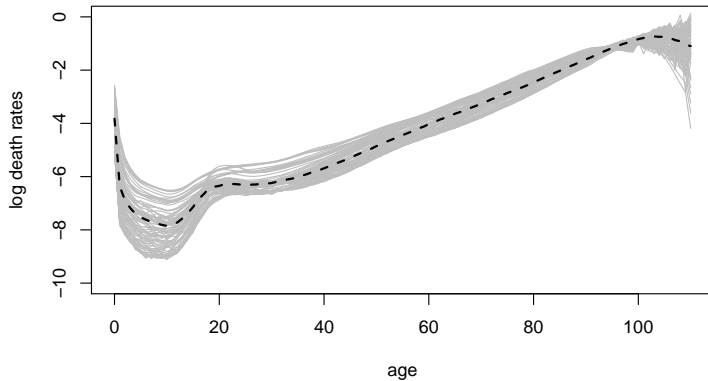
USA: male death rates (1933–2017)



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

Lee-Carter model

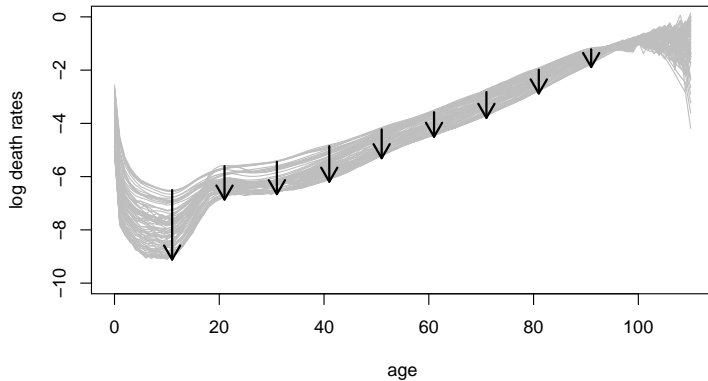
USA: male death rates (1933–2017)



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

Lee-Carter model

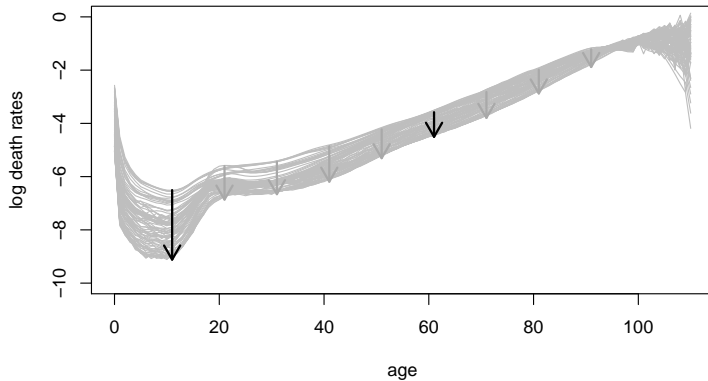
USA: male death rates (1933–2017)



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

Lee-Carter model

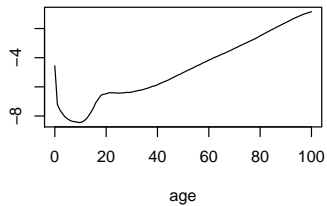
USA: male death rates (1933–2017)



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

Lee-Carter model

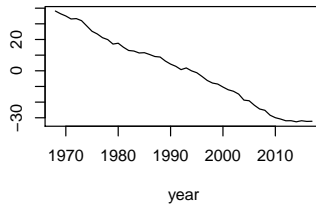
α_x vs. x



$\beta_x^{(1)}$ vs. x



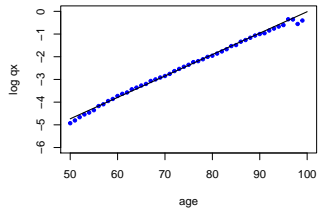
$\kappa_t^{(1)}$ vs. t



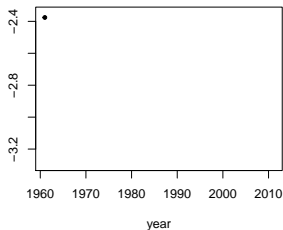
Cairns-Blake-Dowd model

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

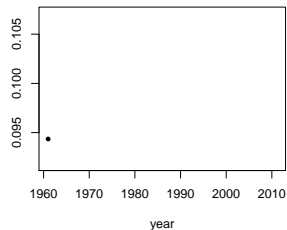
EW: death probability male (1961)



$\kappa_t^{(1)}$ vs t



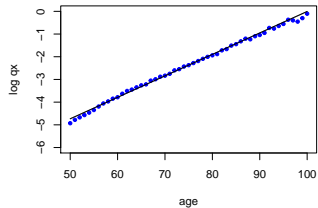
$\kappa_t^{(2)}$ vs t



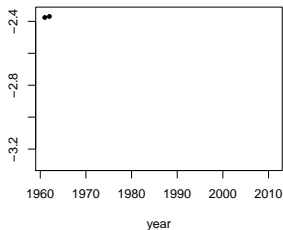
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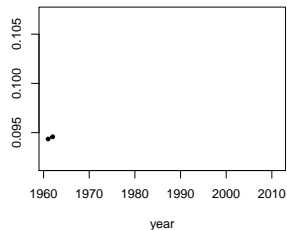
EW: death probability male (1962)



$\kappa_t^{(1)}$ vs t



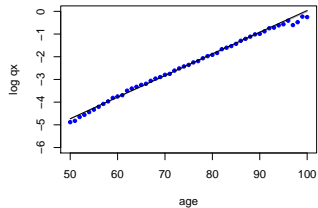
$\kappa_t^{(2)}$ vs t



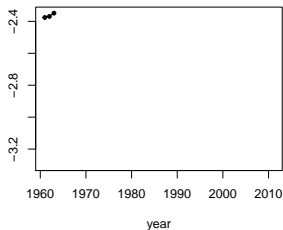
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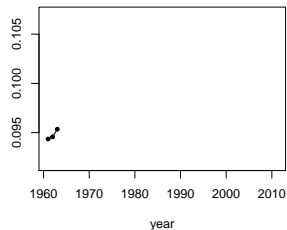
EW: death probability male (1963)



$\kappa_t^{(1)}$ vs t



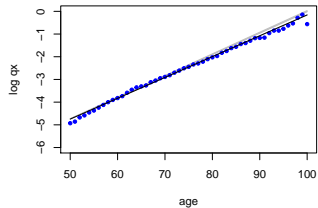
$\kappa_t^{(2)}$ vs t



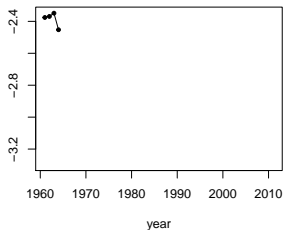
Cairns-Blake-Dowd model

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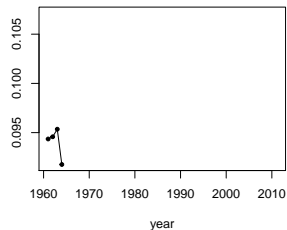
EW: death probability male (1964)



$\kappa_t^{(1)}$ vs t



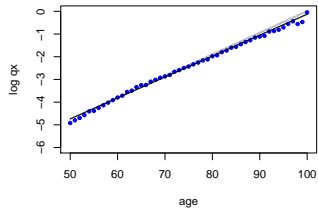
$\kappa_t^{(2)}$ vs t



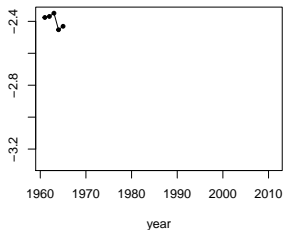
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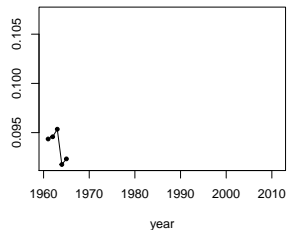
EW: death probability male (1965)



$\kappa_t^{(1)}$ vs t



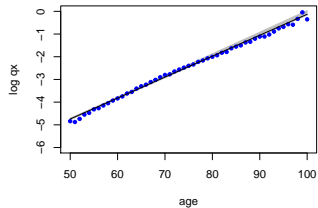
$\kappa_t^{(2)}$ vs t



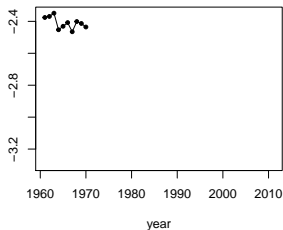
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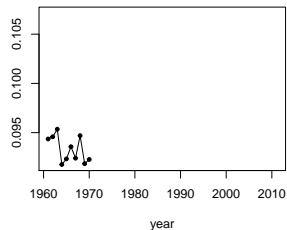
EW: death probability male (1970)



$\kappa_t^{(1)}$ vs t



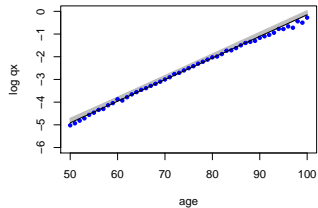
$\kappa_t^{(2)}$ vs t



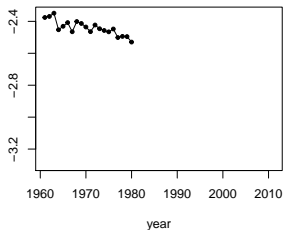
Cairns-Blake-Dowd model

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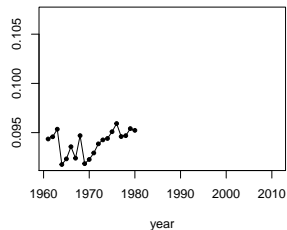
EW: death probability male (1980)



$\kappa_t^{(1)}$ vs t



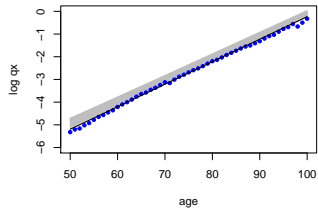
$\kappa_t^{(2)}$ vs t



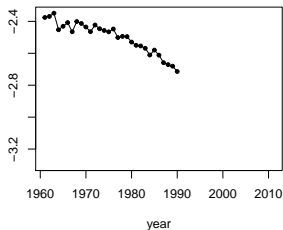
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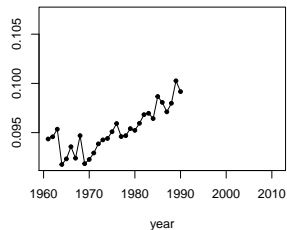
EW: death probability male (1990)



$\kappa_t^{(1)}$ vs t



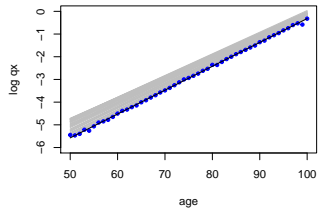
$\kappa_t^{(2)}$ vs t



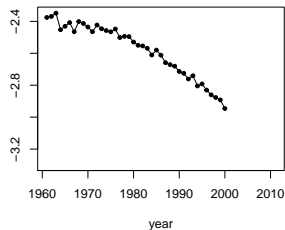
Cairns-Blake-Dowd model

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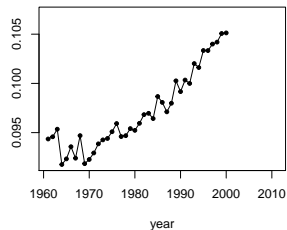
EW: death probability male (2000)



$\kappa_t^{(1)}$ vs t



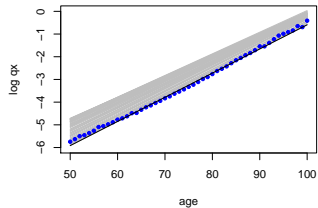
$\kappa_t^{(2)}$ vs t



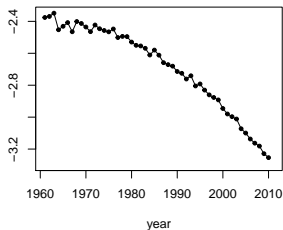
Cairns-Blake-Dowd model

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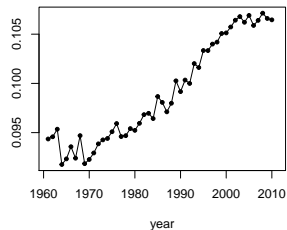
EW: death probability male (2010)



$\kappa_t^{(1)}$ vs t



$\kappa_t^{(2)}$ vs t



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:

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

2. Systematic Component:

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

- ▶ 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

$$\kappa_t = \delta + \kappa_{t-1} + \xi_t^\kappa, \quad \kappa_t = \begin{pmatrix} \kappa_t^{(1)} \\ \vdots \\ \kappa_t^{(N)} \end{pmatrix}, \quad \xi_t^\kappa \sim N(\mathbf{0}, \Sigma),$$

- 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 packages we use:

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

- ▶ To load within 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

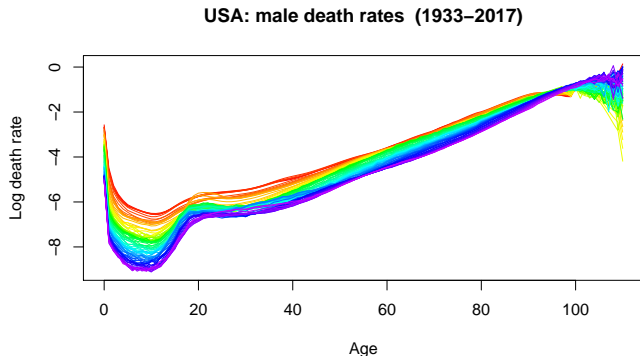
```
library(demography)
USdata <- hmd.mx(country = "USA", username = "username",
                 password = "password")
```

USdata

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

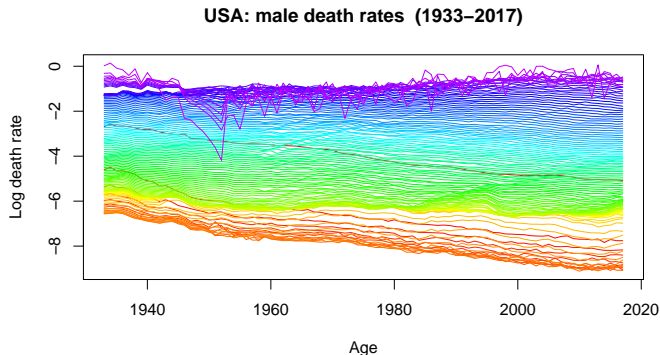
USA Data from Human Mortality Database

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



USA Data from Human Mortality Database

```
library(demography)
USdata <- hmd.mx(country = "USA", username = "username",
                  password = "password")
plot(USdata, series = "male", plot.type = "time")
```



StMoMo: Stochastic Mortality Modelling

Who is MoMo?

StMoMo: Stochastic Mortality Modelling

Who is MoMo?



StMoMo: Stochastic Mortality Modelling

Who is MoMo?

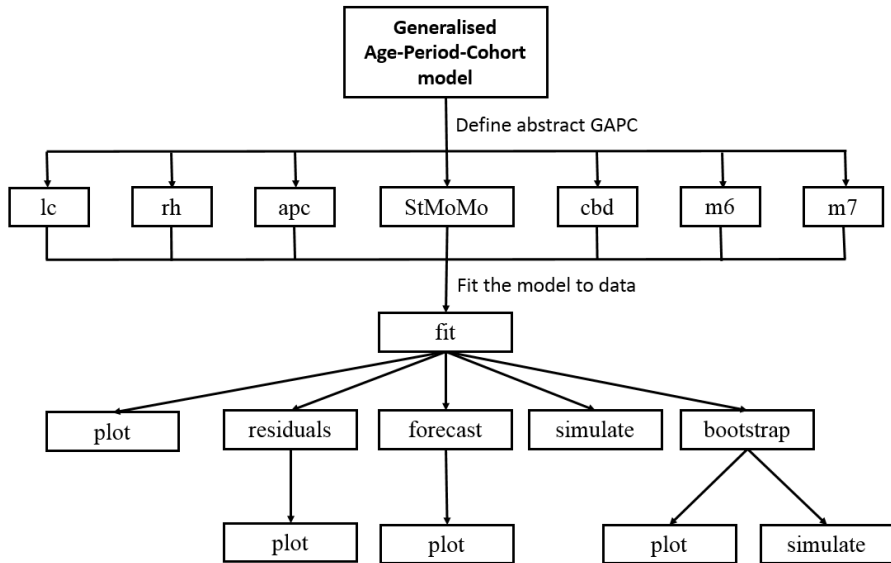


StMoMo: Stochastic Mortality Modelling

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:

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

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

Model definition: Predefined functions for common models

Model definition: Predefined functions for common models

```
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: $\log m[x,t] = a[x] + b1[x] k1[t]$

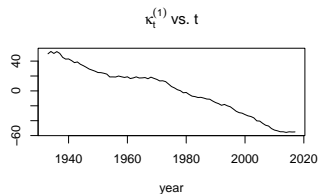
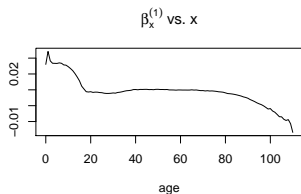
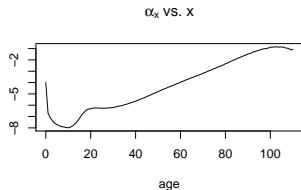
Poisson model with predictor: $\log m[x,t] = k1[t] + f2[x] k2[t]$

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

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



Model fitting: Concentrate on older ages

```
#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)
```

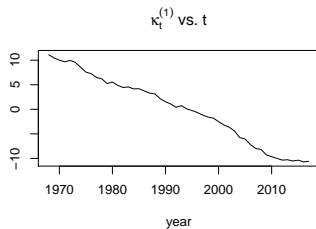
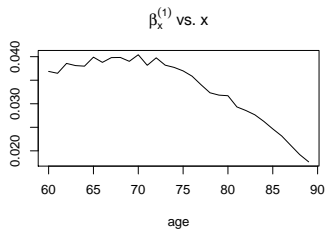
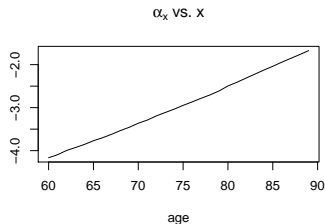
```
CBDfit <- fit(CBD, data=USmale, ages.fit=ages.fit,  
             years.fit=years.fit)
```

```
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)
```

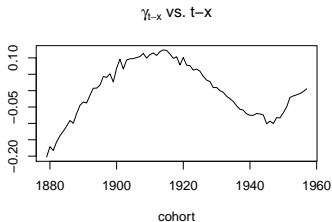
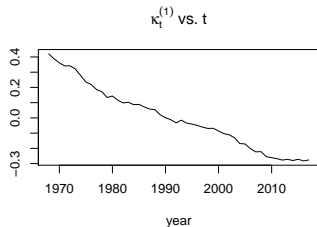
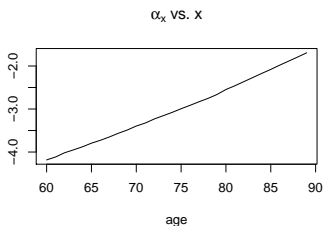
Parameter estimates – LC ($\log \mu_{xt} = \alpha_x + \beta_x^{(1)} \kappa_t^{(1)}$)

```
plot(LCfit)
```



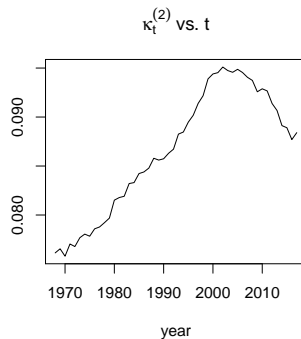
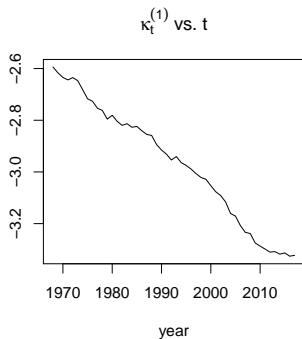
Parameter estimates – APC ($\log \mu_{xt} = \alpha_x + \kappa_t^{(1)} + \gamma_{t-x}$)

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



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

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



Goodness-of-fit: Deviance Residuals

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

Goodness-of-fit: Deviance Residuals

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

```
#Compute residuals
```

```
LCres <- residuals(LCfit)
```

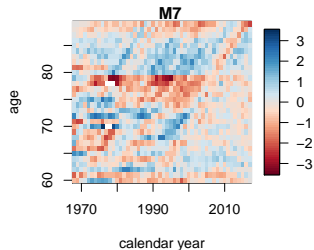
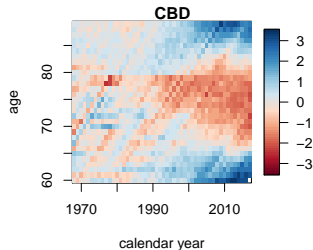
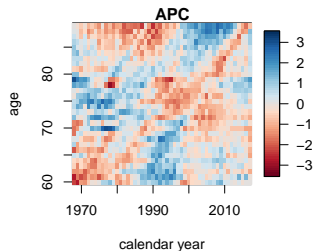
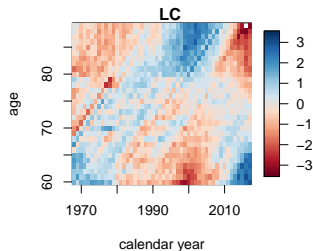
```
APCres <- residuals(APCfit)
```

```
CBDres <- residuals(CBDfit)
```

```
M7res <- residuals(M7fit)
```

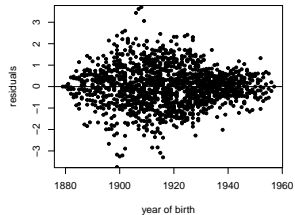
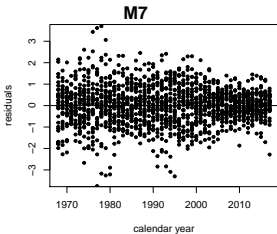
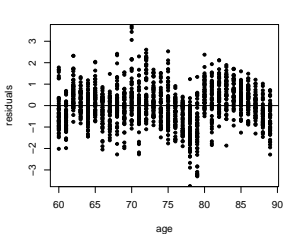
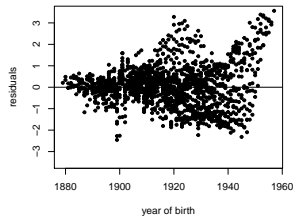
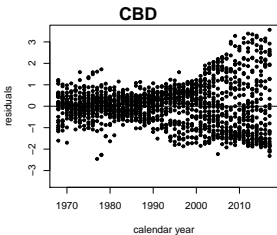
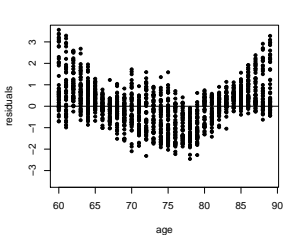
Goodness-of-fit: Residual heatmaps

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



Goodness-of-fit: Residual scatterplots

```
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

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

#Compute residuals

```
AIC(CBDfit)
```

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

```
BIC(CBDfit)
```

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

Criterion	LC	APC	CBD	M7
<i>AIC</i>	56814	32063	74754	27575
<i>BIC</i>	57388	32892	75286	28775

Forecasting and simulation

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

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

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

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

Forecasting

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

Forecasting

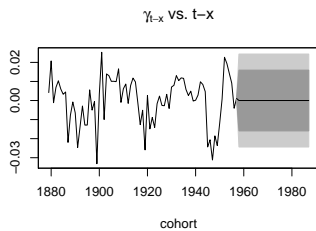
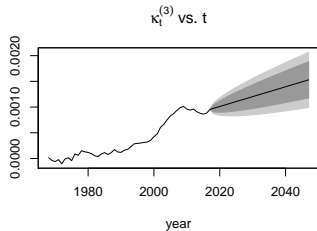
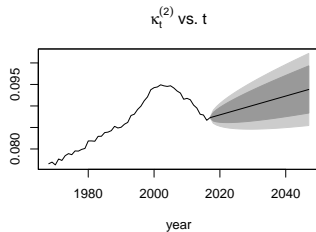
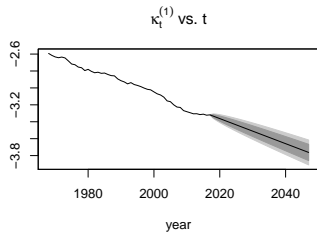
Model	Model for γ_{t-x}
APC	ARIMA(1, 1, 0) with zero mean
M7	ARIMA(0, 0, 0) with zero mean

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)
```

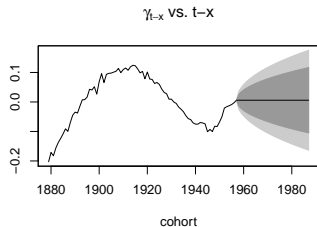
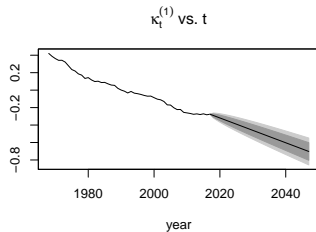
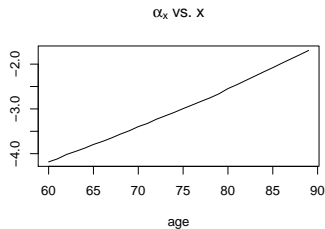
Forecasted period and cohort indexes

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



Forecasted period and cohort indexes

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

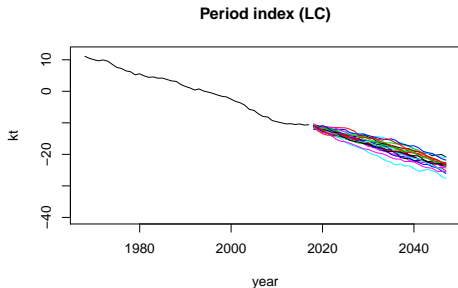


Simulation

```
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)
```

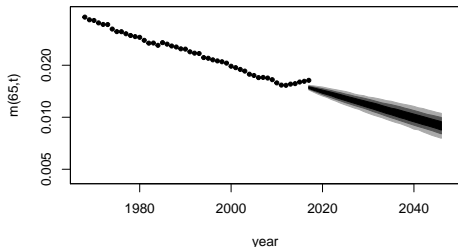
Simulation

```
#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)
```

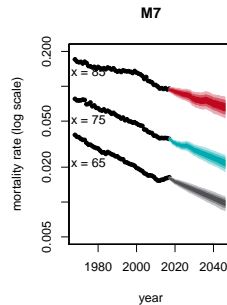
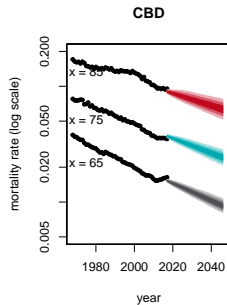
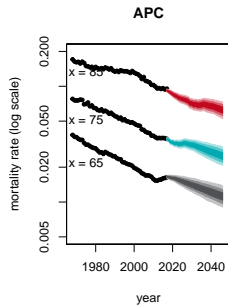
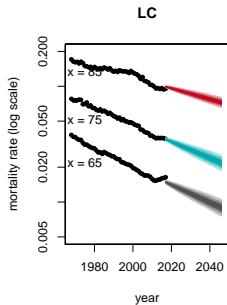


Fancharts

```
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



Obtaining projected life tables for a cohort

```
chosen_cohort <- 1950

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

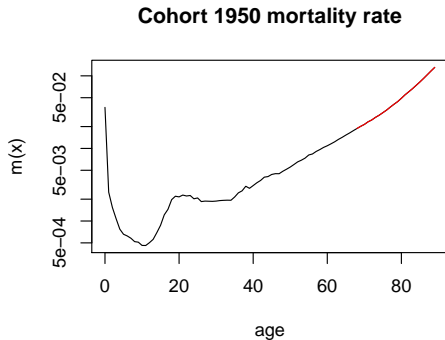
#fitted historical rates for ages 60-67
lc_fit_rates <- extractCohort(fitted(LCfit, type = "rates"),
                             cohort = chosen_cohort)

#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://rdr.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

```
# 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 = "logrates")
APCcv1 <- cv.StMoMo(APC, h = 1, data=USmale, ages.train=ages.fit,
                  years.train=years.fit, type = "logrates")
CBDcv1 <- cv.StMoMo(CBD, h = 1, data=USmale, ages.train=ages.fit,
                  years.train=years.fit, type = "logrates")
M7cv1 <- cv.StMoMo(M7, h = 1, data=USmale, ages.train=ages.fit,
                  years.train=years.fit, type = "logrates")
```

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 = "logrates")  
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
<i>AIC</i>	56814	32063	74754	27575
<i>BIC</i>	57388	32892	75286	28775
<i>CV 1-year</i>	0.0014	0.0007	0.0017	0.0005
<i>CV 10-year</i>	0.0041	0.0033	0.0050	0.0046

Construction: “Formalised” Model-Building Framework

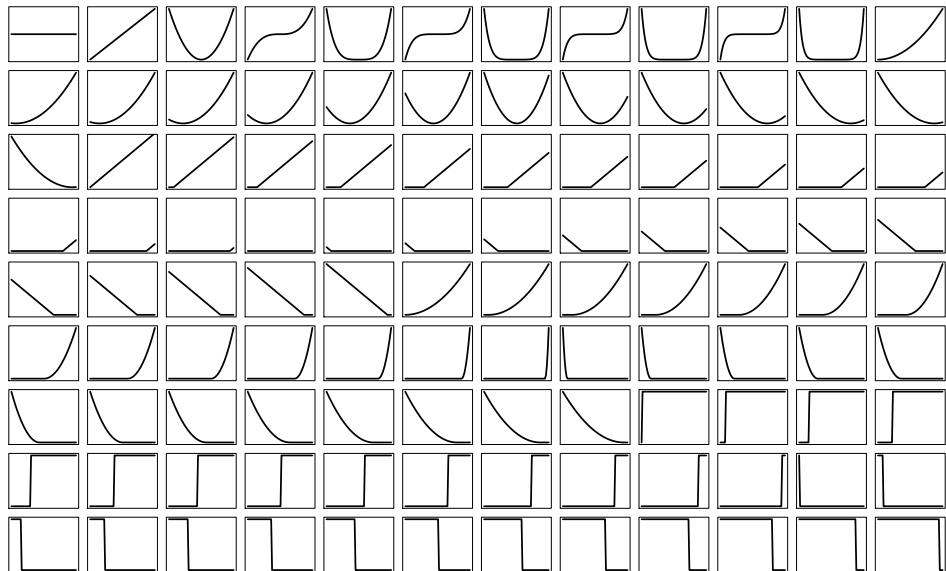
We start with a **huge** model,

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

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

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

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),

$$\eta = \mathbf{X}\beta = \sum_{j=0}^{B+1} \mathbf{X}_j \beta_j, \quad \mathbf{X} = [\mathbf{X}_0 : \mathbf{X}_1 : \mathbf{X}_2 : \dots : \mathbf{X}_B : \mathbf{X}_{B+1}],$$

where,

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

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

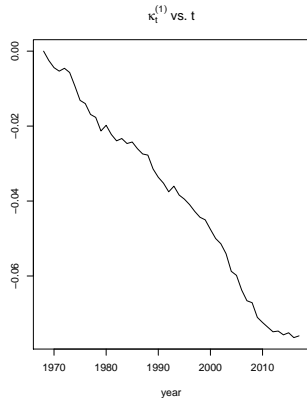
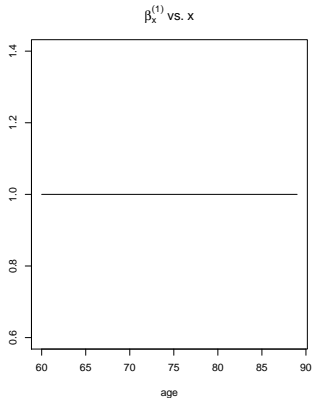
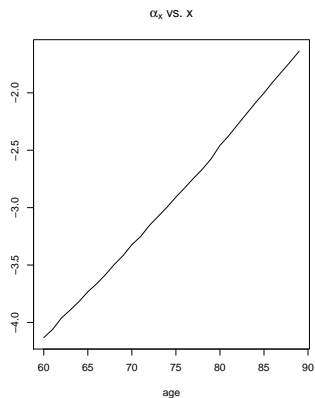
Implementation in StMoMo - Fit model with grouped penalised regularisation

```
#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
```

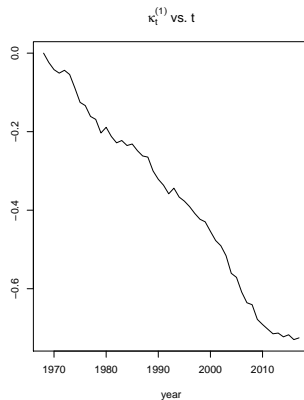
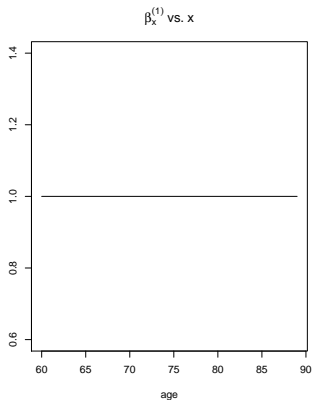
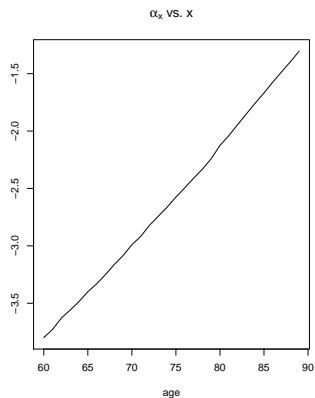
Implementation in StMoMo - Parameter paths

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



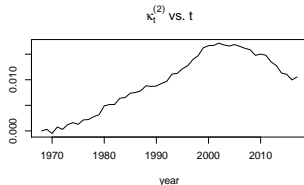
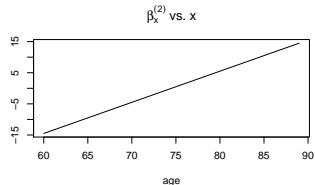
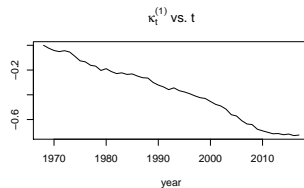
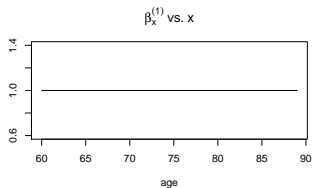
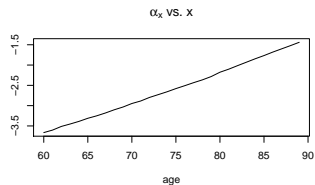
Implementation in StMoMo - Parameter paths

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



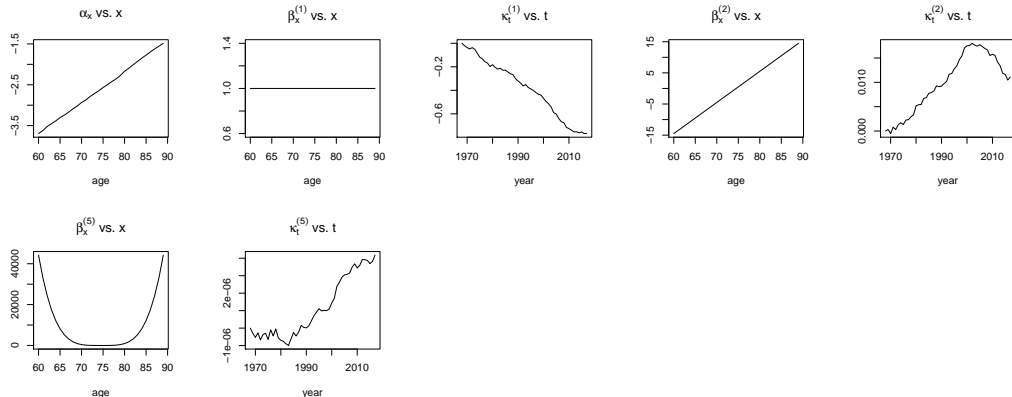
Implementation in StMoMo - Parameter paths

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



Implementation in StMoMo - Parameter paths

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



Improvement rate modelling

The APCi model

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

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

Implementation in iMoMo

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

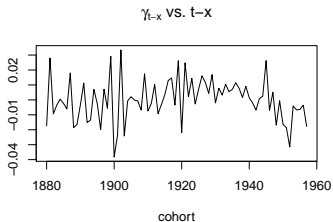
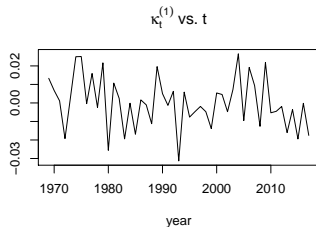
```
## indirect model with predictor:  $\eta[x,t] = a[x] + k1[t] + g[t-x]$ 
```

```
#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>

Thank you!

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