StMoMo: An R Package for **St**ochastic **Mo**rtality **Mo**delling

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

Who is MoMo?

StMoMo: Stochastic Mortality Modelling

Who is MoMo?

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

Who is MoMo?

Stochastic **Mo**rtality **Mo**delling — StMoMo

Who is MoMo?

StMoMo: An R package for **St**ochastic **Mo**rtality **Mo**delling

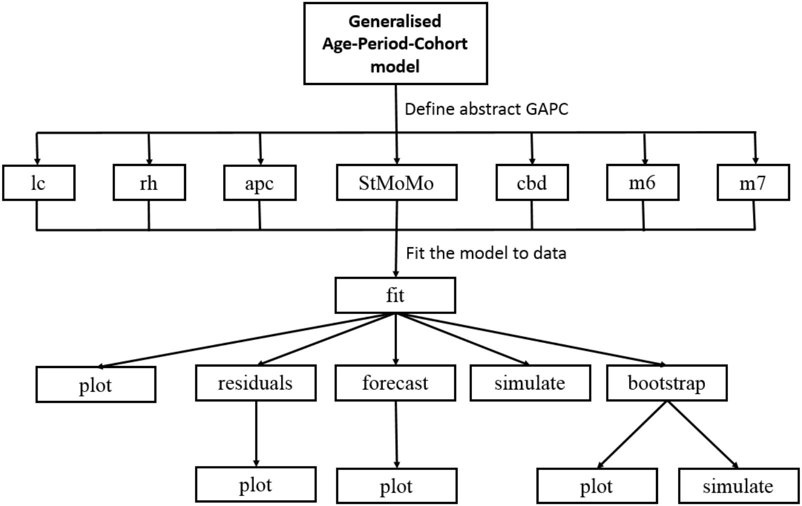
- On CRAN:
  http://cran.r-project.org/web/packages/StMoMo/
- Development version on Github:
  https://github.com/amvillegas/StMoMo
- To install the stable version on R CRAN:

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

- To load within R:

```
library(StMoMo)
```

Overview of the structure of **StMoMo**



Generalised Age-Period-Cohort stochastic mortality models

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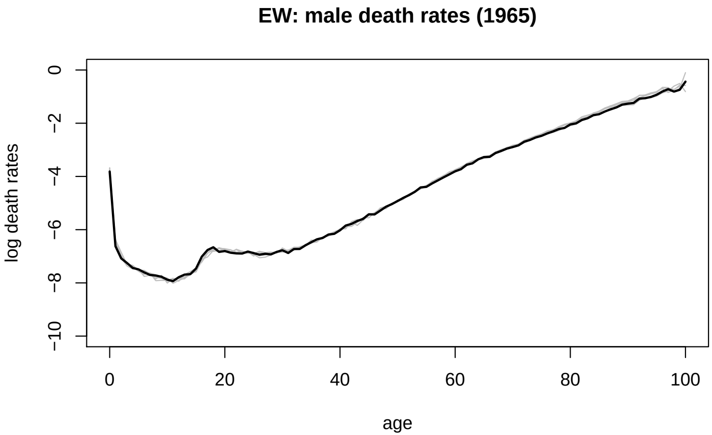

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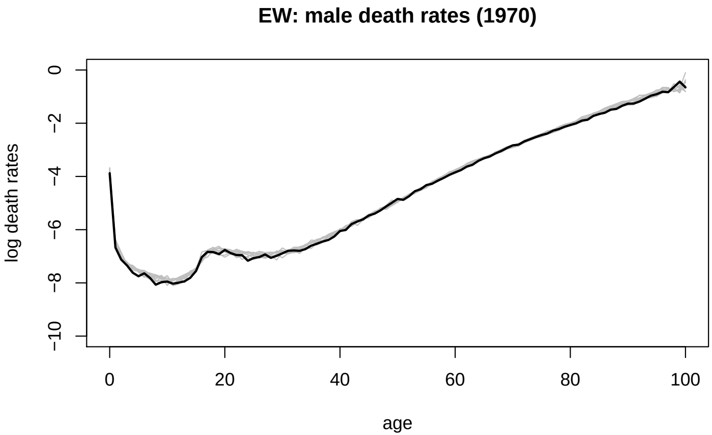

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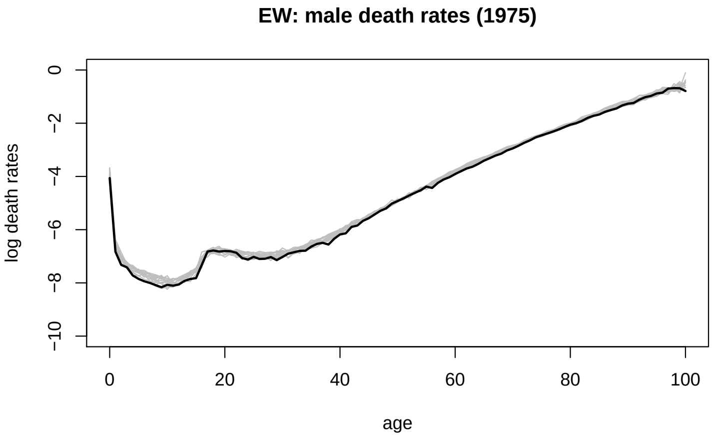

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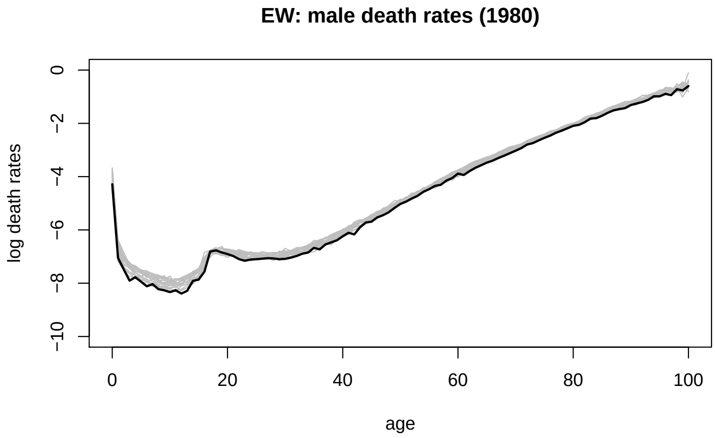

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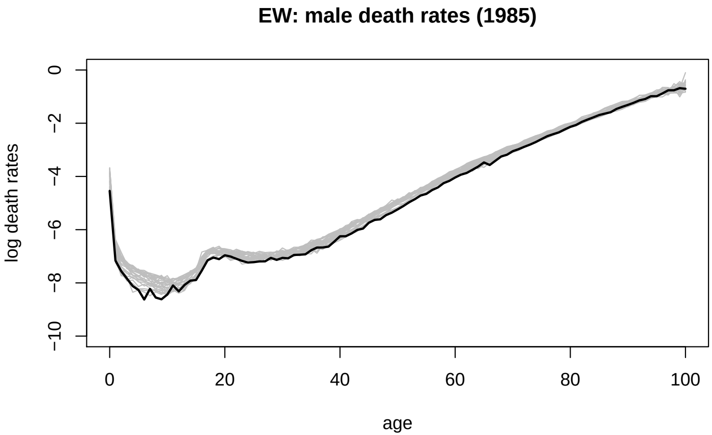

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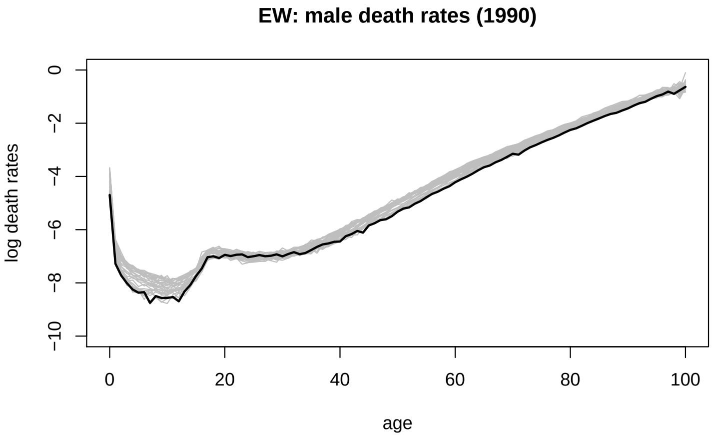

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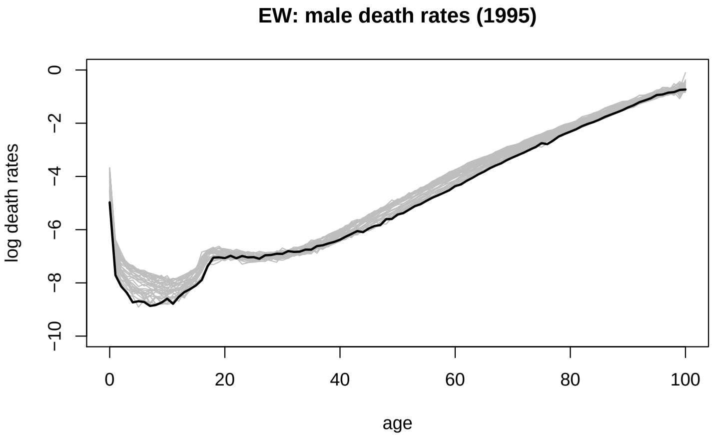

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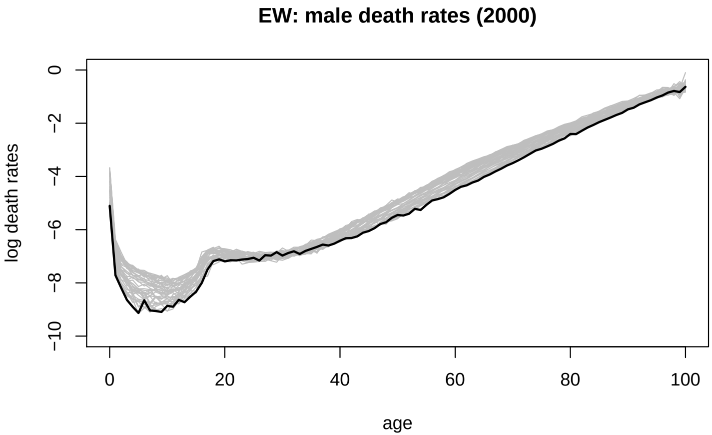

Generalised Age-Period-Cohort stochastic mortality models

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

Generalised Age-Period-Cohort stochastic mortality models

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

Generalised Age-Period-Cohort stochastic mortality models

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

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Generalised Age-Period-Cohort stochastic mortality models

$$\log \mu_{xt} = \alpha_x + \sum_{i=1}^{N} \beta_x^{(i)} \kappa_t^{(i)}$$

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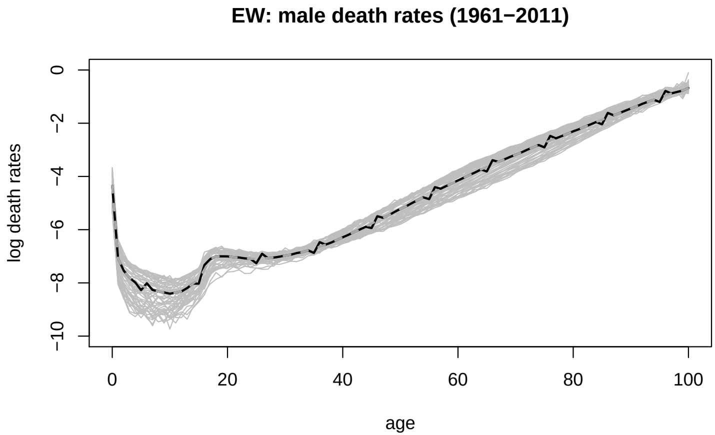

$$\log \mu_{xt} = \alpha_x + \sum_{i=1}^{N} \beta_x^{(i)} \kappa_t^{(i)} + \gamma_{t-x}$$

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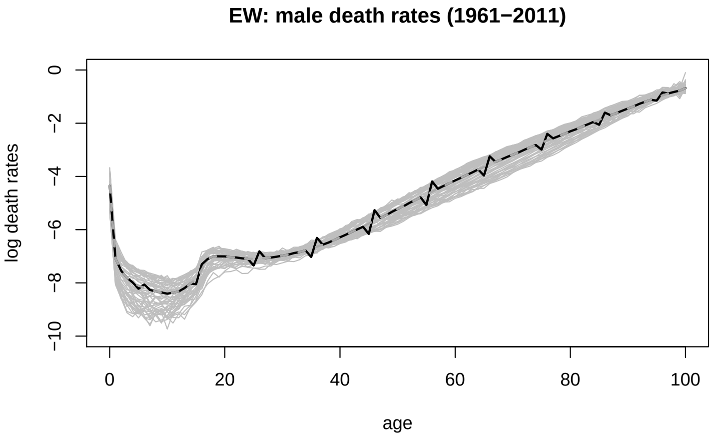

$$\log \mu_{xt} \quad = \quad \alpha_x \quad + \quad \sum_{i=1}^{N} \beta_x^{(i)} \kappa_t{}^{(i)} \quad + \quad \beta_x^{(0)} \gamma_{t-x}$$

Model definition

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

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

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```
LC <- lc()
CBD <- cbd(link = "log")
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] = k1[t] +
f2[x] k2[t] + f3[x] k3[t] + g[t-x]
```

Model fitting: Data

Sample data for England & Wales males aged 0-100 for the period 1961-2011

```
Dxt <- EWMaleData$Dxt
Ext <- EWMaleData$Ext
ages <- EWMaleData$ages    #0-100
years <- EWMaleData$years #1961-2011
```

Model fitting: Data

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ages <- EWMaleData$ages    #0-100
years <- EWMaleData$years #1961-2011
```

```
Dxt
```

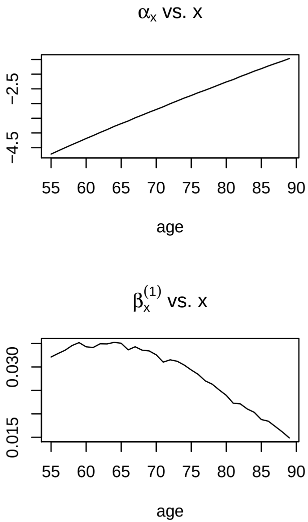
```
##    1961  1962  1963  1964 1965 1966 1967 1968 1969
## 0 9988 10573 10401 10011 9518 9357 8673 8705 8331
## 1  665   598   665   588  571  616  549  552  567
## 2  398   353   378   354  354  389  374  381  381
## 3  249   259   261   254  292  301  281  316  275
```

Model fitting: England and Wales males 55-89

```
#Fit models
LCfit <- fit(LC, Dxt = Dxt, Ext = Ext, ages = ages,
        years = years, ages.fit = 55:89)
CBDfit <- fit(CBD, Dxt = Dxt, Ext = Ext, ages = ages,
        years = years, ages.fit = 55:89)
M7fit <- fit(M7, Dxt = Dxt, Ext = Ext, ages = ages,
        years = years, ages.fit = 55:89)
```

Parameter estimates

```r
plot(LCfit)
```



Goodness-of-fit: Residuals

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

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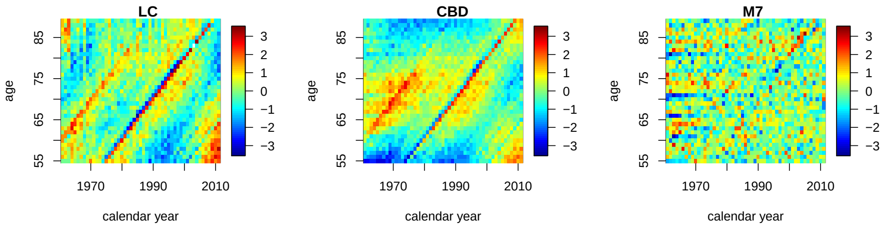
```

```
plot(LCres, type="colourmap", reslim=c(-3.5, 3.5))
plot(CBDres, type="colourmap", reslim=c(-3.5, 3.5))
plot(M7res, type="colourmap", reslim=c(-3.5, 3.5))
```



Forecasting

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

$$\boldsymbol{\kappa}_t = \boldsymbol{\delta} + \boldsymbol{\kappa}_{t-1} + \boldsymbol{\xi}_t^{\kappa}$$

- **Cohort effect for M7:** ARIMA$(2, 0, 0)$ with non-zero intercept

$$\gamma_c = \delta_0 + \phi_1\gamma_{c-1} + \phi_2\gamma_{c-2} + \epsilon_c$$

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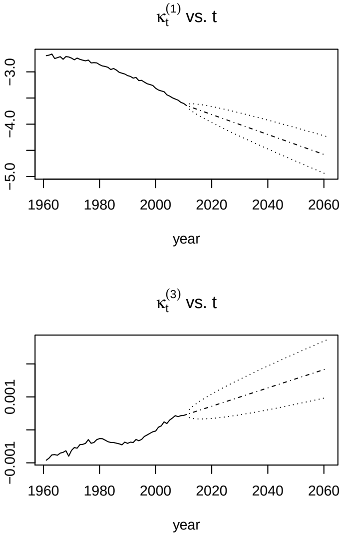
$$\gamma_c = \delta_0 + \phi_1\gamma_{c-1} + \phi_2\gamma_{c-2} + \epsilon_c$$

```
LCfor <- forecast(LCfit, h=50)
CBDfor <- forecast(CBDfit, h=50)
M7for <- forecast(M7fit, h=50, gc.order = c(2,0,0))
```

Forecasted period and cohort indexes

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

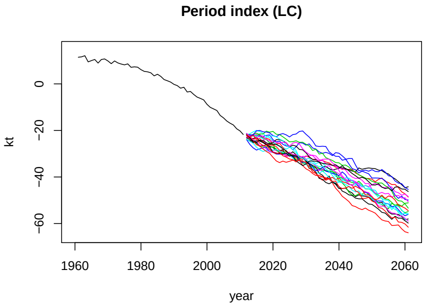


Simulation

```
LCsim <- simulate(LCfit, nsim=500, h=50)
CBDsim <- simulate(CBDfit, nsim=500, h=50)
M7sim <- simulate(M7fit, nsim=500, h=50,
                  gc.order=c(2,0,0))
```

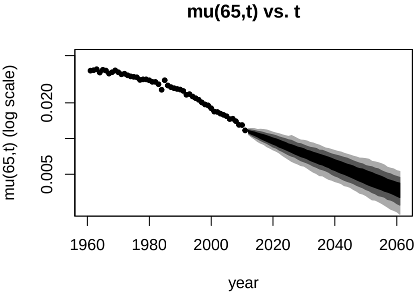
Simulation trajectories

```
#Plot period index trajectories for the LC model
plot(LCfit$years, LCfit$kt[1,],
     xlim=c(1960,2061), ylim=c(-65,15),
     type="l", xlab="year", ylab="kt",
     main="Period index (LC)")
matlines(LCsim$kt.s$years, LCsim$kt.s$sim[1,,1:20],
         type="l", lty=1)
```



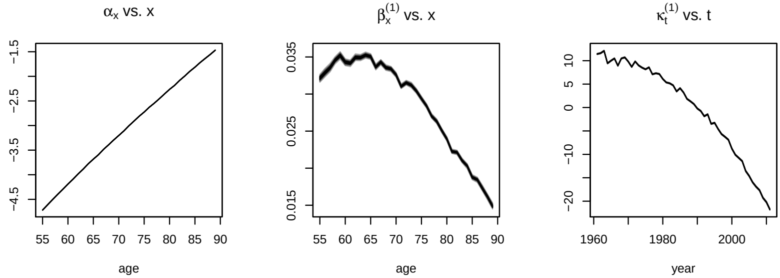
Fancharts

```
library(fanplot)
plot(LCfit$years, (Dxt/Ext)["65",], xlim=c(1960,2061),
     ylim=c(0.0025,0.05), pch=20, log="y", xlab="year",
     ylab="mu(65,t) (log scale)", main="mu(65,t) vs. t")
fan(t(LCsim$rates["65",,]), start=2012,
    probs=c(2.5,10,25,50,75,90,97.5), n.fan=4, ln=NULL,
    fan.col=colorRampPalette(c("black","white")))
```



Parameter uncertainty and bootstrapping

```
LCboot <- bootstrap(LCfit, nBoot = 500)
plot(LCboot, nCol = 3)
```



Conclusion

- **StMoMo** uses the framework of the GAPC family of models to implement the vast majority of stochastic mortality models in the literature
  - Define new models
  - Model fitting
  - Analysis of goodness-of-fit
  - Projection and simulations
  - Bootstrapping and parameter uncertainty

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- Easy implementation and comparison of a wide range of models making it useful for:
  - Actuaries analysing longevity risk
  - Use in the classroom

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

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