# Actuarial Science with <br> 2. life insurance \& mortality tables 

## Arthur Charpentier

joint work with Christophe Dutang \& Vincent Goulet and Rob Hyndman's demography package

## UQĀM .illQuantact <br> Université du Québec à Montréal

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## Some (standard) references

Pitacco, E., Denuit, M., Haberman, S.
\& Olivieri, A. (2008) Modeling Longevity
Dynamics for Pensions and Annuity Business Oxford University Press

Schoen, R. (2007)
Dynamic Population Models
Springer Verlag

Modelling Longevity Dynamics for Pensions and Annuity Business



Dynamic Population Models

## A possible motivation?



## Lexis diagram, age and time

From Lexis (1880), idea of visualizing lifetime, age $x$, time $t$ and year of birth $y$


## Lexis diagram, age and time

Idea : Life tables $L_{x}$ should depend on time, $L_{x, t}$.
Let $D_{x, t}$ denote the number of deaths of people aged $x$, during year $t$, data frame DEATH and let $E_{x, t}$ denote the exposure, of age $x$, during year $t$, data frame EXPOSURE, from http://www.mortality.org/

## The Human Mortality Database

| John R. Wilmoth, Director University of California, Berkeley |
| :--- |
| Vladimir Shkolnikov, Co-Director Max Planck Institute for Demographic Research |
| The Human Mortality Database (HMD) was created to provide detailed mortality and |
| population data to researchers, students, journalists, policy analysts, and others interested in |
| the history of human longevity. The project began as an outgrowth of earlier projects in the |
| Department of Demography at the University of California, Berkeley, USA, and at the Max |
| Planck Institute for Demographic Research in Rostock, Germany (see history). It is the work |
| of two teams of researchers in the USA and Germany (see research teams), with the help of |
| financial backers and scientific collaborators from around the world (see acknowledgements). |

## Lexis diagram, age and time

Remark : be carefull of age 110+
> DEATH\$Age=as.numeric (as.character (DEATH\$Age))
> DEATH\$Age[is.na(DEATH\$Age)]=110
> EXPOSURE\$Age=as.numeric (as.character (EXPOSURE\$Age))
> EXPOSURE\$Age[is.na(EXPOSURE\$Age)]=110

Consider force of mortality function

$$
\mu_{x, t}=\frac{D_{x, t}}{E_{x, t}}
$$

> MU=DEATH[,3:5]/EXPOSURE[,3:5]
> MUT=matrix(MU[,3], length(AGE), length(ANNEE))
> persp(AGE[1:100], ANNEE, log(MUT[1:100,]),

+ theta=-30,col="light green",shade=TRUE)



## Tables, per year $t$ and Survival lifetimes

Let us study deaths occurred in year=1900 or $2000, x \mapsto \log \mu_{x, t}$ when $t=1900$ or 2000.
> D=DEATH [DEATH\$Year==year,] ; E=EXPOSURE [EXPOSURE\$Year==year,]
> MU = D[,3:5]/E[,3:5]
> plot(0:110,log(MU[,1]),type="l", col="red"); lines (0:110, $\log (M U[, 2]), c o l=" b l u e ")$
Evolution of $x \mapsto L_{x, t}=\exp \left(-\int_{0}^{x} \mu_{h, t} d h\right)$ when $t=1900$ or 2000 ,
> $\mathrm{PH}=\mathrm{PF}=$ matrix $(\mathrm{NA}, 111,111)$
$>$ for $(x$ in $0: 110)\{$
$+\operatorname{PH}[x+1,1:(111-x)]=\exp (-\operatorname{cumsum}(\operatorname{MU}[(x+1): 111,2]))$
$+\operatorname{PF}[x+1,1:(111-x)]=\exp (-\operatorname{cumsum}(M U[(x+1): 111,1]))\}$
> $\mathrm{x}=0$; plot (1:111, $\mathrm{PH}[\mathrm{x}+1],, y l i m=c(0,1)$, type="l", col="blue")
> lines(1:111,PF[x+1,],col="red")

## Tables, per year $t$ and Survival lifetimes



## Tables, per year $t$ and Survival lifetimes

Survival probability in 1900


Survival probability in 2000


## Survival lifetimes and rectangularization'



## Life table and transversality



## Life table and transversality

It might be interesting to follow a cohort, per year of birth $x-t$,
> Nannee <- max(DEATH\$Year)
> naissance <- 1950
> taille <- Nannee - naissance
> Vage <- seq(0,length=taille+1)
> Vnaissance <- seq(naissance,length=taille+1)
> Cagreg <- DEATH\$Year*1000+DEATH\$Age
> Vagreg <- Vnaissance*1000+Vage
> indice <- Cagreg\%in\%Vagreg
> DEATH[indice,]
Year Age Female Male Total
56621950018943.0525912 .3844855 .43
$\begin{array}{llllll}5774 & 1951 & 1 & 2078.41 & 2500.70 & 4579.11\end{array}$
$\begin{array}{llllll}5886 & 1952 & 2 & 693.20 & 810.32 & 1503.52\end{array}$
$\begin{array}{llllll}5998 & 1953 & 3 & 375.08 & 467.12 & 842.20\end{array}$
$\begin{array}{llllll}6110 & 1954 & 4 & 287.04 & 329.09 & 616.13\end{array}$
$\begin{array}{llllll}6222 & 1955 & 5 & 205.03 & 246.07 & 451.10\end{array}$
$\begin{array}{llllll}6334 & 1956 & 6 & 170.00 & 244.00 & 414.00\end{array}$

## Life table and transversality



## Lee \& Carter (1992) model

Assume here (as in the original model)

$$
\log \mu_{x, t}=\alpha_{x}+\beta_{x} \cdot \kappa_{t}+\varepsilon_{x, t},
$$

with some i.i.d. noise $\varepsilon_{x, t}$. Identification assumptions are usually

$$
\sum_{x=x_{m}}^{x_{M}} \beta_{x}=1 \text { and } \sum_{t=t_{m}}^{t_{M}} \kappa_{t}=0
$$

Then sets of parameters $\boldsymbol{\alpha}=\left(\alpha_{x}\right), \boldsymbol{\beta}=\left(\beta_{x}\right)$ and $\boldsymbol{\kappa}=\left(\kappa_{t}\right)$, are obtained solving

$$
\left(\hat{\alpha}_{x}, \hat{\beta}_{x}, \kappa_{t}\right)=\arg \min \sum_{x, t}\left(\ln \mu_{x t}-\alpha_{x}-\beta_{x} \cdot k_{t}\right)^{2} .
$$

## Using demography package

Package demography can be used to fit a Lee-Carter model
> library (forecast)
> library (demography)
> YEAR=unique (DEATH\$Year) ; $\mathrm{nC}=$ length (YEAR)
> AGE =unique (DEATH\$Age); nL=length (AGE)
> MUF =matrix (DEATH\$Female/EXPOSURE\$Female,nL,nC)
> MUH =matrix(DEATH\$Male/EXPOSURE\$Male,nL,nC)
> POPF=matrix (EXPOSURE\$Female,nL,nC)
> POPH=matrix (EXPOSURE\$Male,nL,nC)
Then wo use the demogdata format
> BASEH <- demogdata(data=MUH, pop=POPH, ages=AGE, years=YEAR, type="mortality",

+ label="France", name="Hommes", lambda=1)
> BASEF <- demogdata(data=MUF, pop=POPF,ages=AGE, years=YEAR, type="mortality",
+ label="France", name="Femmes", lambda=1)


## Estimation of $\boldsymbol{\alpha}=\left(\alpha_{x}\right)$ and $\boldsymbol{\beta}=\left(\beta_{x}\right)$

The code is simply LCH <- lca(BASEH)
> plot(LCH\$age,LCH\$ax,col="blue"); plot(LCH\$age,LCH\$bx,col="blue")


## Estimation and projection of $\boldsymbol{\kappa}=\left(\kappa_{t}\right)$ 's

Use library (forcast) to predict future $\kappa_{t}$ 's, e.g. using exponential smoothing
> library (forecast)
> Y <- LCH\$kt
$>(E T S<-$ ets $(Y))$
$\operatorname{ETS}(A, N, N)$

Call:
ets $(\mathrm{y}=\mathrm{Y})$

Smoothing parameters:
alpha $=0.8923$

Initial states:
$1=71.5007$
sigma: 12.3592

AIC AICc BIC

```
1042.0741042 .1901047 .420
```

> plot(forecast(ETS,h=100))

But as in Lee \& Carter original model, it is possible to fit an $\operatorname{ARMA}(1,1)$ model, on the differentiate series $\left(\Delta \kappa_{t}\right)$

$$
\Delta \kappa_{t}=\phi \Delta \kappa_{t-1}+\delta+u_{t}-\theta u_{t-1}
$$

It is also possible to consider a linear tendency

$$
\kappa_{t}=\alpha+\beta t+\phi \kappa_{t-1}+u_{t}-\theta u_{t-1} .
$$

```
> (ARIMA <- auto.arima(Y,allowdrift=TRUE))
```

Series: Y
ARIMA(0,1,0) with drift
Call: auto.arima(x = Y, allowdrift = TRUE)
Coefficients:

```
        drift
        -1.9346
s.e. 1.1972
sigma^2 estimated as 151.9: log likelihood = -416.64
AIC = 837.29 AICc = 837.41 BIC = 842.62
> plot(forecast(ARIMA,h=100))
```


## Projection of $\widehat{\kappa}_{t}$ 's

Forecasts from ETS(A,N,N)


Forecasts from ARIMA(0,1,0) with drift


## Shouldn't we start modeling after 1945 ?

Starting in 1948, LCHO <- lca(BASEH,years=1948:2005)


## Projection of $\widehat{\kappa}_{t}$ 's

Forecasts from ARIMA(0,1,0) with drift


Forecasts from ARIMA(1,1,0) with drift


## Projection of life expectancy, born in 2005

> LCHT=lifetable(LCHf); plot( $0: 100$, LCHT\$ex[,5],type="l", col="red")
> LCHTu=lifetable(LCHf, "upper"); lines ( $0: 100$, LCHTu\$ex[,5],lty=2)
> LCHTl=lifetable(LCHf,"lower"); lines(0:100,LCHTl\$ex[,5],lty=2)

Life expectancy in 2005


## Residuals in Lee \& Carter model

Recall that

$$
\log \mu_{x, t}=\alpha_{x}+\beta_{x} \cdot \kappa_{t}+\varepsilon_{x, t}
$$

Let $\widehat{\varepsilon}_{x, t}$ denote pseudo-residuals, obtained from estimation

$$
\widehat{\varepsilon}_{x, t}=\log \mu_{x, t}-\left(\widehat{\alpha}_{x}+\widehat{\beta}_{x} \cdot \widehat{\kappa}_{t}\right) .
$$

> RES=residuals(LCH,"pearson")
> colr=function(k) rainbow(110) [k*100]
> couleur=Vectorize(colr)(seq(.01,1,by=.01))
> plot(rep(RES\$y,length(RES\$x)), (RES\$z), col=couleur[rep(RES\$x,

+ each=length (RES\$y))-RES\$x[1]+1])
> plot(rep(RES\$x,each=length(RES\$y)),t(RES\$z),col=couleur [rep(RES\$y,length(RES\$x))+1])


## Residuals in Lee \& Carter model



## Residuals in Lee \& Carter model



## LifeMetrics Functions

LifeMetrics is based on R functions that can be downloaded from JPMorgan's website, that can be uploaded using source("fitModels.r").

Standard functions are based on two matrices etx (for the exposure) and dtx for death counts, respectively at dates $t$ and ages $x$.

Recall that, with discrete notation,

$$
m(x, t)=\frac{\# \text { deaths during calendar year } t \text { aged } x \text { last birthday }}{\text { average population during calendar year } t \text { aged } x \text { last birthday }}
$$

Note that not only the Lee-Carter model is implemented, but several models,
Lee \& Carter (1992), $\log m(x, t)=\beta_{x}^{(1)}+\beta_{x}^{(2)} \kappa_{t}^{(2)}$,
Renshaw \& Haberman (2006), $\log m(x, t)=\beta_{x}^{(1)}+\beta_{x}^{(2)} \kappa_{t}^{(2)}+\beta_{x}^{(3)} \gamma_{t-x}^{(3)}$,
Currie (2006), $\log m(x, t)=\beta_{x}^{(1)}+\kappa_{t}^{(2)}+\gamma_{t-x}^{(3)}$,
CAirns, Blake \& Dowd (2006), $\operatorname{logit}\left(1-e^{-m(x, t)}\right)=\kappa_{t}^{(1)}+(x-\alpha) \kappa_{t}^{(2)}$, CAIRNS et al. (2007), logit $\left(1-e^{-m(x, t)}\right)=\kappa_{t}^{(1)}+(x-\alpha) \kappa_{t}^{(2)}+\gamma_{t-x}^{(3)}$.

## LifeMetrics Functions

For Lee \& Carter model,
> res <- fit701 (x, y, etx, dtx, wa)
where wa is a (possible) weight function. Here, assume that wa=1.
Remark : we have to remove very old ages,
> DEATH <- DEATH[DEATH\$Age<90,]
> EXPOSURE <- EXPOSURE[EXPOSURE\$Age<90,]
> XV <- unique (DEATH\$Age)
> YV <- unique(DEATH\$Year)
> ETF <- t(matrix(EXPOSURE[,3],length(XV), length(YV)))
$>$ DTF <- t(matrix (DEATH [,3], length (XV), length(YV)))
> ETH <- t(matrix (EXPOSURE[,4], length(XV), length(YV)))
$>$ DTH <- t(matrix (DEATH[,4], length(XV), length(YV)))
> WA <- matrix(1,length(YV),length(XV))
> LCF <- fit701 (xv=XV,yv=YV,etx=ETF,dtx=DTF,wa=WA)
> LCH <- fit701 (xv=XV, yv=YV, etx=ETH,dtx=DTH, wa=WA)

## LifeMetrics Functions

The output is the following, LC\$kappa1, LC\$beta1, ... LC\$11 for the maximum log-likelihood estimators of different parameters, LC\$mtx is an array with crude death rates, and LC\$mhat with fitted death rates. LC\$cy is the vector of cohort years of birth (corresponding to LC\$gamma3).

It it then possible to plot one of the cofficients against either LC\$x or LC\$y.
> plot(LCF\$x,LCF\$beta1,type="l", col="red")
> lines(LCH\$x,LCH\$beta1, col="blue",lty=2)
> plot(LCF\$x,LCF\$beta2,type="l", col="red")
> lines(LCH\$x,LCH\$beta2, col="blue",lty=2)

> plot(LCF\$y,LCF\$kappa2,type="l", col="red")
> lines(LCH\$y,LCH\$kappa2,col="blue")


## Using the gnm package

(Much) more generally, it is possible to use the gnm package, to run a regression. Assume here that

$$
D_{x, t} \sim \mathcal{P}\left(\lambda_{x, t}\right) \text { where } \lambda_{x, t}=E_{x, t} \exp \left(\alpha_{x}+\beta_{x} \cdot \kappa_{t}\right)
$$

which is a generalized nonlinear regression model.

```
> library(gnm)
> Y=DEATH$Male
> E=EXPOSURE$Male
> Age= DEATH$Age
> Year=DEATH$Year
> I=(DEATH$Age<100)
> base=data.frame(Y=Y[I],E=E[I],Age=Age[I],Year=Year [I])
> REG=gnm(Y~}\mathrm{ factor(Age)+Mult((factor(Age)),factor(Year)),
    data=base,offset=log(E),family=quasipoisson)
Initialising
Running start-up iterations..
Running main iterations.
Done
```


## Using the gnm package

> names(REG\$coefficients[c(1:5,85:90)])
[1] "(Intercept)" "factor(Age)1" "factor(Age)2" "factor(Age)3"
[5] "factor(Age)4" "factor(Age)84" "factor(Age)85" "factor(Age)86"
[9] "factor(Age)87" "factor(Age)88" "factor(Age)89"
> names(REG\$coefficients[c(91:94,178:180)])
[1] "Mult(., factor(Year)).factor(Age)0" "Mult(., factor(Year)).factor(Age)1"
[3] "Mult(., factor(Year)).factor(Age)2" "Mult(., factor(Year)).factor(Age)3"
[5] "Mult(., factor(Year)).factor(Age)87" "Mult(., factor(Year)).factor(Age)88"
[7] "Mult(., factor(Year)).factor(Age)89"
> nomvar <- names (REG\$coefficients)
> nb3 <- substr(nomvar, nchar(nomvar) -3, nchar (nomvar))
> nb2 <- substr (nomvar, nchar (nomvar) -1, nchar (nomvar))
> nb1 <- substr (nomvar, nchar (nomvar), nchar (nomvar))
> nb <- nb3
> nb[substr(nb, 1, 1) =="g"]<- nb1[substr(nb,1,1)=="g"]
> nb[substr (nb, 1, 1) =="e"]<- nb2[substr (nb, 1, 1) =="e"]
> nb <- as.numeric(nb)
> I <- which(abs(diff(nb))>1)




## Using Lee \& Carter projections

Using estimators of $\alpha_{x}{ }^{\prime}$ 's, $\beta_{x}$ 's, as well as projection of $\kappa_{t}$ 's, it is possible to obtain projection of any actuarial quantities, based on projections of $\mu_{x, t}$ 's. E.g.
> A <- LCH\$ax; B <- LCH\$bx
> K1 <- LCH\$kt; K2 <- LCH\$kt[99]+LCHf\$kt.f\$mean; K <- c (K1,K2)
> MU <- matrix(NA,length(A), length (K))
$>$ for $(i$ in 1:length(A))\{ for( $j$ in 1:length $(K))\{$
$+\operatorname{MU}[i, j]<-\exp (A[i]+B[i] * K[j])\}\}$


It is then possible to extrapolate $k \mapsto{ }_{k} p_{x}$ 's
> $\mathrm{t}=2000$
$>\mathrm{x}=40$
$>s=\operatorname{seq}(0,99-x-1)$

```
> MUd=MU[x+1+s,t+s-1898]
> (Pxt=cumprod(exp(-diag(MUd))))
    [1] 0.99838440 0.99663098 0.99469369 0.99248602 0.99030804 0.98782725
    [7] 0.98417947 0.98017722 0.97575106 0.97098896 0.96576107 0.96006617
[13] 0.95402111 0.94749333 0.94045500 0.93291535 0.92484762 0.91622709
[19] 0.90707101 0.89726011 0.88690981 0.87577047 0.86405282 0.85159220
[25] 0.83850049 0.82472277 0.81011757 0.79478797 0.77847592 0.76144457
[31] 0.74364218 0.72457570 0.70474824 0.68387491 0.66193090 0.63903821
[37] 0.61469237 0.58924560 0.56257772 0.53478172 0.50577349 0.47480005
[43] 0.44324965 0.41055038 0.37750446 0.34390607 0.30973747 0.27613617
[49] 0.24253289 0.21038508 0.17960626 0.14970800 0.12276231 0.09902686
[55] 0.07742879 0.05959964 0.04495042 0.03281240 0.02366992
```

and then we can derive projections of several actuarial (or demography) quantities. E.g. remaining lifetimes
> $\mathrm{x}=40$
> E=rep(NA,150)
> for ( t in 1900:2040)\{
$+s=s e q(0,90-x-1)$
$+\mathrm{MUd}=\mathrm{MU}[\mathrm{x}+1+\mathrm{s}, \mathrm{t}+\mathrm{s}-1898]$
$+\operatorname{Pxt}=\operatorname{cumprod}(\exp (-\operatorname{diag}(M U d)))$

+ ext=sum (Pxt)
$+E[t-1899]=e x t\}$
> plot(1900:2049,E)
or expected present value of deferred whole life annuities, purchased at age 40, deferred of 30 years
$>\mathrm{r}=.035: \mathrm{m}=70$
$>\mathrm{VV}=\mathrm{rep}(\mathrm{NA}, 141)$
$>$ for (t in 1900:2040) \{
$+s=\operatorname{seq}(0,90-x-1)$
$+\mathrm{MUd}=\mathrm{MU}[\mathrm{x}+1+\mathrm{s}, \mathrm{t}+\mathrm{s}-1898]$
$+\operatorname{Pxt}=\operatorname{cumprod}(\exp (-\operatorname{diag}(M U d)))$
$+h=\operatorname{seq}(0,30)$
$+\mathrm{V}=1 /(1+\mathrm{r})-(\mathrm{m}-\mathrm{x}+\mathrm{h}) * \operatorname{Pxt}[\mathrm{~m}-\mathrm{x}+\mathrm{h}]$
$+V V[t-1899]=\operatorname{sum}(V, n a . r m=T R U E)\}$
> plot(1900:2040,VV)



## Mortality rates as functional time series

It is possible to consider functional time series using rainbow package
> library (rainbow)
> rownames $($ MUH $)=A G E$
> colnames (MUH) =YEAR
$>$ rownames (MUF) $=$ AGE
> colnames (MUF) =YEAR
> MUH=MUH[1:90,]
> MUF=MUF[1:90,]
> MUHF=fts(x = AGE[1:90], $y=\log (M U H)$, xname $=$ "Age", yname $=$ "Log Mortality Rate")
> MUFF=fts(x = AGE[1:90], y = log(MUF), xname = "Age", yname = "Log Mortality Rate")
> fboxplot(data = MUHF, plot.type = "functional", type = "bag")

Using principal components, it is possible to detect outliers
> fboxplot(data = MUHF, plot.type = "bivariate", type = "bag")



## Cohort effect and Lee \& Carter model

A natural idea is to include (on top of the age $x$ and the year $t$ ) a cohort factor, based on the year of birth, $t-x$

$$
\log \mu_{x, t}=\alpha_{x}+\beta_{x} \cdot \kappa_{t}+\gamma_{x} \cdot \delta_{t-x}+\eta_{x, t}
$$

as in Renshaw \& Haberman (2006).
Using gnm function, it is possible to estimate that model, assuming again that a log-Poisson model for death counts is valid,

```
> D=as.vector(BASEB)
> E=as.vector(BASEC)
> A=rep(AGE,each=length(ANNEE))
> Y=rep(ANNEE,length(AGE))
> C=Y-A
> base=data.frame(D,E,A,Y,C,a=as.factor(A),
+ y=as.factor(Y),c=as.factor(C))
> LCC=gnm(D~a+Mult(a,y)+Mult(a,c),offset=log(E), family=poisson,data=base)
```





