COS-R403. Special Research Methods. *Forecasting I: Introduction*

Hands-on excercises

Day 3 of intensive 5-day course

University of Helsinki, Finland

04.05.2020–08.05.2020

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Source: https://github.com/christina-bohk-ewald/2020-COS-R403-forecasting-I-introduction

Table of content:

1. Some preparations in R

1.1 Open a new script for day 3 in R and save it to a folder of your choice.

1.2 Create a filepath to a folder where you would like to save your outcome. For example,

```
the.plot.path <- c("C:/plots")
```

1.3 You can then set the working directory to this outcome path

```
setwd(the.plot.path)
```

2. Load, explore, and plot US female mortality

On day 3 we delve deeper into the field of mortality forecasting. We first look more closely at the age profile of mortality over time. We do this exemplarily for US women.

2.1 Please install and load the fds package.

The *fds* package allows you, for example, to easily access data of the Human Mortality Database.

```
library(fds)
```

2.2 Load US female mortality by single years of age and calendar year

```
usa_wom <- read.hmd(country=params$country, sex="Female", file = "Mx_1x1.txt",
username=your_username, password=your_password, yname="mortality rates")
```

Please note that you need to insert your personal username and password to access the Human Mortality Database.

Brief data description. *usa_wom* contains mortality for single years of age, 0 through 110, and calendar year, 1933 through 2017, from the HMD.

Something to think about. What does *Mx_1x1* mean? What other kinds of data formats does the Human Mortality Database provide?

2.3 Explore data object *usa_wom*. For example,

```
head(usa_wom[[2]][,as.character(1933:1940)])
```

```
##       1933     1934     1935     1936     1937     1938     1939     1940
## 0 0.054177 0.060211 0.053557 0.055160 0.053895 0.050748 0.046848 0.046847
## 1 0.008866 0.009894 0.008334 0.008082 0.007856 0.007401 0.005904 0.005263
## 2 0.004025 0.004540 0.003766 0.003923 0.003690 0.003322 0.002644 0.002471
## 3 0.002869 0.002979 0.002756 0.002675 0.002513 0.002233 0.001896 0.001679
## 4 0.002230 0.002236 0.002326 0.002154 0.001951 0.001785 0.001544 0.001359
## 5 0.001852 0.001858 0.001929 0.001758 0.001604 0.001458 0.001310 0.001158
```

Something to explore. How do you extract data from *usa_wom*, for example for age 80 and calendar year 1980?

2.4 Plot US female mortality rates on log scale

We visualize US female mortality to better understand how it has developed over age and time.

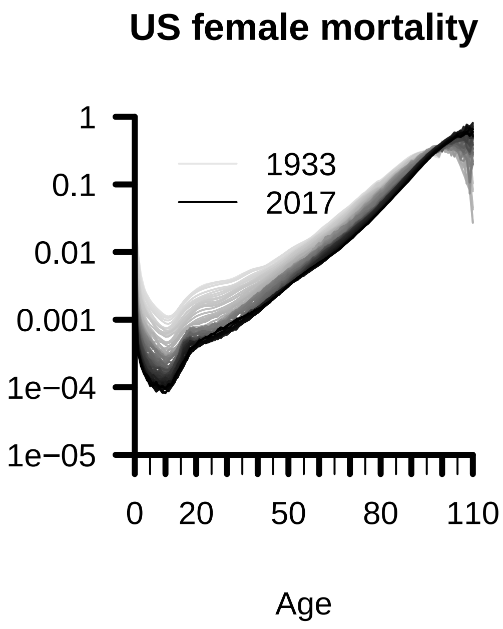
We first create a color palette that ranges from gray to black between the calendar years 1933 and 2017.

```
colfunc <- colorRampPalette(c(gray(0.9), "black"))

blackgray <- colfunc(length(1933:2017))
```

Something to explore. How does the function *colorRampPalette* work? How do you make sure that the color palette contains exactly as many colors between gray and black as you have calendar years?

In a second step we depict US female mortality on a logarithmic scale.

```
par(fig = c(0,1,0,1), las=1, mai=c(0.8,0.8,0.8,0.8))

plot(x=-100,y=-100,xlim=c(0,110),ylim=c(log(0.00001,base=exp(1)),log(1,base=exp(1))),
xlab="Age",ylab="",main="US female mortality", cex=0.8, axes=FALSE)

for(year in 1933:2017){
    lines(x=0:110,y=log(usa_wom[[2]][,as.character(year)],base=exp(1)),
col=blackgray[(year-1932)])
}

legend(x=5,y=log(0.75,base=exp(1)),col=c(blackgray[1],blackgray[length(1933:2017)]),
lty=1,horiz=FALSE,bty="n",c("1933","2017"))

axis(side=1,at=seq(0,110,5),labels=FALSE,lwd=1,pos=log(0.00001,base=exp(1)))

axis(side=1,at=seq(0,110,10),labels=seq(0,110,10),lwd=3,pos=log(0.00001,base=exp(1)))

axis(side=2,at=log(c(0.00001,0.0001,0.001,0.01,0.1,1),base=exp(1)),
labels=c(0.00001,0.0001,0.001,0.01,0.1,1),lwd=3,pos=0)
```



Something to explore. How do you display mortality on a logarithmic scale? What parameters / elements of the plot are affected? What is the advantage of visualizing mortality on a logarthmic scale?

Something to think about. How would you describe the development of US female mortality over age and time? Do you recognize specific patterns, with respect to average level of mortality and change of mortality by age and over time)?

3. Fit and forecast mortality with the Lee-Carter method using the base period 1933-2017

The Lee-Carter method consists of two main steps. It first fits a model to observed mortality by age and time on the log scale and it then uses the time index of this fitted model to forecast mortality years ahead.

3.1 Fit Lee-Carter model to US female mortality, 1933–2017

In a first major step we fit the Lee-Carter model to observed US female mortality. To do this, we implement the steps 1.1 through 1.8 of the *morning lecture* of course day 3.

Step 3.1.1:

usa_wom contains mortality by age in rows and calendar year in columns.

Step 3.1.2:

```
log_usa_wom <- log(usa_wom[[2]],base=exp(1))
```

Step 3.1.3:

```
mean_log_usa_wom <- rowMeans(log_usa_wom)

ax <- mean_log_usa_wom
```

Step 3.1.4:

```
centered_log_usa_wom <- log_usa_wom - ax
```

Step 3.1.5.1:

```
svd_centered_log_usa_wom <- svd(t(centered_log_usa_wom))

names(svd_centered_log_usa_wom)
```

```
## [1] "d" "u" "v"
```

Step 3.1.5.2:

```
sum_v <- sum(svd_centered_log_usa_wom$v[,1])

bx <- svd_centered_log_usa_wom$v[,1]/sum_v
```

Step 3.1.5.3:

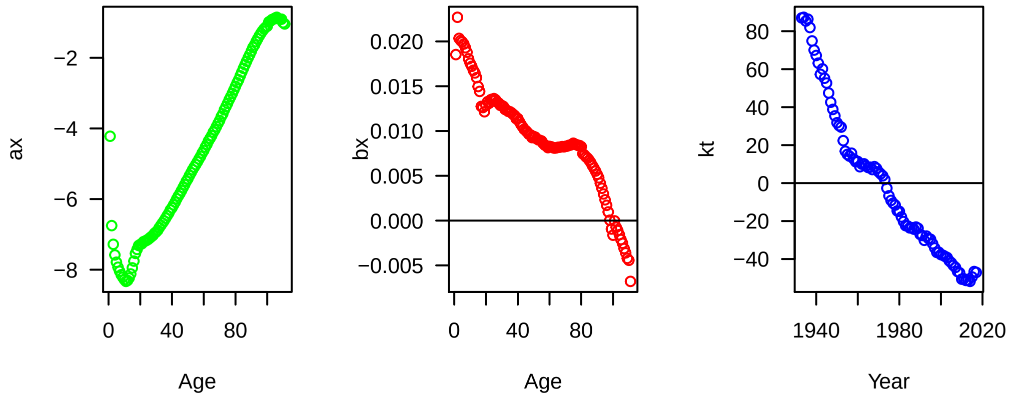
```
kt <- svd_centered_log_usa_wom$d[1] * svd_centered_log_usa_wom$u[,1] * sum_v
```

Step 3.1.5.4:

```
sum(bx)

sum(kt)
```

Step 3.1.6:

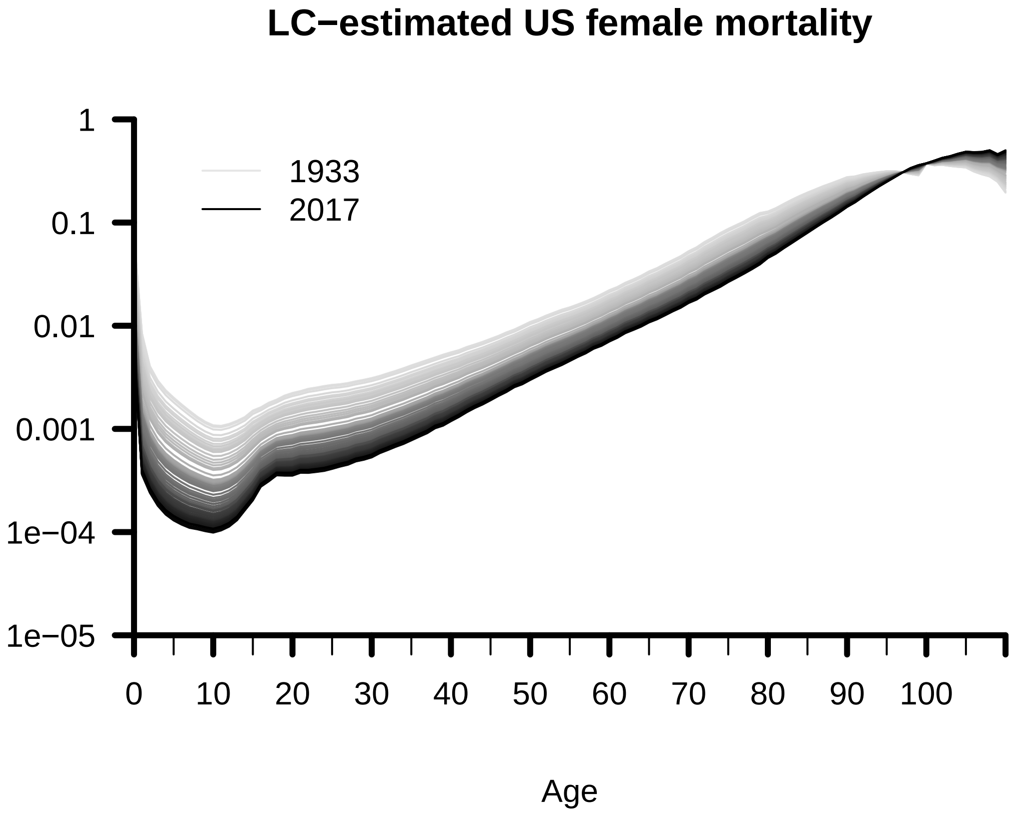
```
par(mfrow=c(1,3), las=1)

plot(ax,xlab="Age",col="green")

plot(bx,xlab="Age",col="red")
abline(h=0)

plot(x=1933:2017,y=kt,xlab="Year",col="blue")
abline(h=0)
```



Step 3.1.7: We choose *none adjustment*.

Step 3.1.8:

```
fitted_log_usa_wom <- matrix(NA,nr=length(0:110),nc=length(1933:2017))

rownames(fitted_log_usa_wom) <- 0:110

colnames(fitted_log_usa_wom) <- 1933:2017

for(year in 1:85){
    fitted_log_usa_wom[,year] <- ax+bx*kt[year]
}

par(fig = c(0,1,0,1), las=1, mai=c(0.8,0.8,0.8,0.8))

plot(x=-100,y=-100,xlim=c(0,110),ylim=c(log(0.00001,base=exp(1)),log(1,base=exp(1))),
xlab="Age",ylab="",main="LC-estimated US female mortality",axes=FALSE)

for(year in 1933:2017){
    lines(x=0:110,y=fitted_log_usa_wom[,as.character(year)],
col=blackgray[(year-1932)])
}

legend(x=5,y=log(0.75,base=exp(1)),col=c(blackgray[1],blackgray[length(1933:2017)]),
lty=1,horiz=FALSE,bty="n",c("1933","2017"))

axis(side=1,at=seq(0,110,5),labels=FALSE,lwd=1,pos=log(0.00001,base=exp(1)))
axis(side=1,at=seq(0,110,10),labels=seq(0,110,10),lwd=3,pos=log(0.00001,base=exp(1)))

axis(side=2,at=log(c(0.00001,0.0001,0.001,0.01,0.1,1),base=exp(1)),
labels=c(0.00001,0.0001,0.001,0.01,0.1,1),lwd=3,pos=0)
```



Something to think about. Please explain in your own words how the Lee-Carter model is fitted to observed US female mortality data in steps 3.1.1 through 3.1.8.

Something more to think about. How would you describe and intepret the pattern of α_x, β_x, and κ_t in step 3.1.6, also considering observed US female mortality as shown in section 2.4?

Going a little further into this direction: comparing observed and LC-estimated US female mortality in section 2.4 and step 3.1.8, what mortality developments does the Lee-Carter model capture and what does it not capture?

3.2 Forecast US female mortality, 2018–2067, with the Lee-Carter method

In a second major step we use the fitted Lee-Carter model to forecast US female mortality via the time index κ_t. To do this, we implement the steps 2.1 through 2.3 of the *morning lecture* of course day 3.

Step 3.2.1:

```
fit_kt_model <- summary(lm(kt[2:85]-kt[1:84] ~ 1))

kt_drift <- fit_kt_model$coefficients[1,1]

sec <- fit_kt_model$coefficients[1,2]
```

```
see <- fit_kt_model$sigma

fitted_kt <- kt[1:84] + kt_drift

residuals_kt <- fit_kt_model$residuals
```

Some explanatory notes for step 3.2.1—that is, to estimate κ_t in base period with a time series model:

- Use *~1* in the *lm* function to fit linear model with an intercept only
- *kt_drift* is equal to the average of the first order differences of κ_t in base period
- *sec* is the standard error of the model coefficient (*kt_drift*)
- *see* is the square root of the estimated variance of the residuals (/ random error)

Below are some alternative ways to determine *kt_drift* and *see* to better understand their meaning:

```
kt_drift <- mean(diff(kt))

residuals_kt <- kt[2:85]-(kt[1:84]+kt_drift)

see <- sqrt((1/(84-1))*sum(residuals_kt^2))
```

Something to explore. How similar are the values for *kt_drift* and *see* based on the alternative ways to derive them (shown above)?

Step 3.2.2:

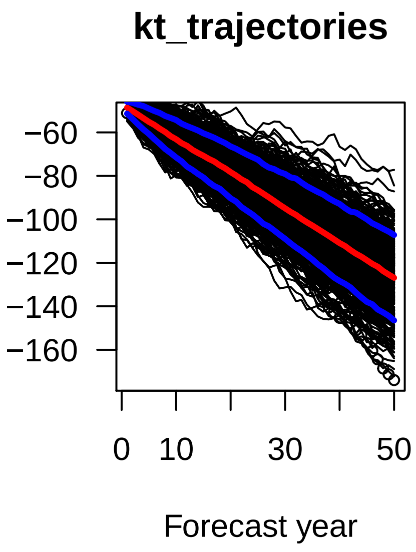
```
h <- 50

nsim <- 1000

kt_trajectories <- matrix(NA,nr=nsim,nc=h)

set.seed(1234)

for(run in 1:nsim){
    for(year in 1:1){
        current_epsilon <- rnorm(n=1,mean=0,sd=see)
        kt_trajectories[run,year] <- (kt[length(kt)] + kt_drift +
current_epsilon)
    }
    for(year in 2:h){
        current_epsilon <- rnorm(n=1,mean=0,sd=see)
        kt_trajectories[run,year] <- (kt_trajectories[run,(year-1)] + kt_drift +
current_epsilon)
    }
}

kt_trajectories_median <- apply(kt_trajectories,2,median)

kt_trajectories_low80 <- apply(X=kt_trajectories,2,FUN=function(X){quantile(X,probs=0.1)})

kt_trajectories_up80 <- apply(X=kt_trajectories,2,FUN=function(X){quantile(X,probs=0.9)})
```

Some explanatory notes for step 3.2.2—that is, to probabilistically forecast κ_t years ahead based on simulation:

- h is the length of the forecast horizon
- *nsim* is the number of tracectories to be simulated, N
- *kt_trajectories* is a matrix that stores simulated trajectories for κ_{t+s}
- *set.seed(1234)* sets a seed to make random simulation reproducible
- *rnorm()* is the random normal distribution for ϵ_t
- *kt_trajectories_median* contains median forecast of κ_{t+s}
- *kt_trajectories_low80* contains lower boundary of the 80% prediction interval of κ_{t+s}
- *kt_trajectories_up80* contains upper boundary of the 80% prediction interval of κ_{t+s}

Something to think about. How do you explain in your own words the procedure to simulate trajectories for κ_t years ahead? How do you interpret the 80% prediction intervals of κ_t?

```
par(fig = c(0,1,0,1), las=1, mai=c(0.8,0.8,0.8,0.8))

plot(1:h,kt_trajectories[1,], xlab="Forecast year",ylab="",main="kt_trajectories",cex=0.7)

for(run in 2:500){
    lines(1:h,kt_trajectories[run,])
}

lines(1:h,kt_trajectories_median,col="red",lwd=3)

lines(1:h,kt_trajectories_low80,col="blue",lwd=3)

lines(1:h,kt_trajectories_up80,col="blue",lwd=3)
```



Something more to do here. How do you determine & display the 95% prediction interval of κ_t?

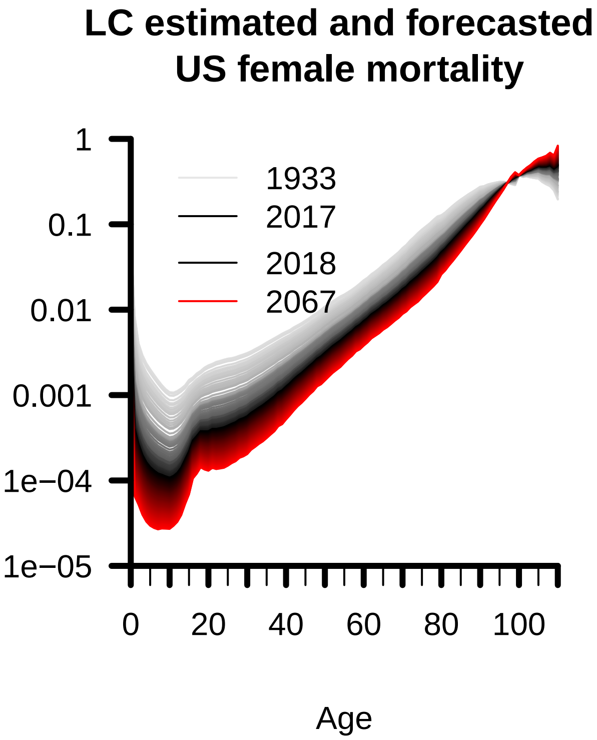
Step 3.2.3

```
forecast_log_usa_wom_median <- matrix(NA,nr=length(0:110),nc=length(2018:2067))

rownames(forecast_log_usa_wom_median) <- 0:110

colnames(forecast_log_usa_wom_median) <- 2018:2067

forecast_log_usa_wom_low80 <- matrix(NA,nr=length(0:110),nc=length(2018:2067))

rownames(forecast_log_usa_wom_low80) <- 0:110

colnames(forecast_log_usa_wom_low80) <- 2018:2067

forecast_log_usa_wom_up80 <- matrix(NA,nr=length(0:110),nc=length(2018:2067))

rownames(forecast_log_usa_wom_up80) <- 0:110

colnames(forecast_log_usa_wom_up80) <- 2018:2067

for(year in 1:h){
    forecast_log_usa_wom_median[,year] <- ax+bx*kt_trajectories_median[year]

    forecast_log_usa_wom_low80[,year] <- ax+bx*kt_trajectories_low80[year]

    forecast_log_usa_wom_up80[,year] <- ax+bx*kt_trajectories_up80[year]
}
```

Some explanatory notes for step 3.2.3—that is, to probabilistically forecast $m_{x,t}$ on the log scale 50 years ahead, based on estimated α_x, estimated β_x, and on simulated trajectories of κ_t:

- *forecast_log_usa_wom_median* contains the median forecasts of $m_{x,t}$
- *forecast_log_usa_wom_low80* contains the lower boundary of the 80% prediction intervals of $m_{x,t}$
- *forecast_log_usa_wom_up80* contains the upper boundary of the 80% prediction intervals of $m_{x,t}$

```
colfunc <- colorRampPalette(c("black","red"))

blackred <- colfunc(length(1:50))

par(fig = c(0,1,0,1), las=1, mai=c(0.8,0.8,0.8,0.8))

plot(x=-100,y=-100,xlim=c(0,110),ylim=c(log(0.00001,base=exp(1)),log(1,base=exp(1))),
xlab="Age",ylab="",main="LC estimated and forecasted \n US female mortality",
axes=FALSE, cex=0.6)

    for(year in 1933:2017){
        lines(x=0:110,y=fitted_log_usa_wom[,as.character(year)],
col=blackgray[(year-1932)])
    }

    for(year in 2018:2067){
        lines(x=0:110,y=forecast_log_usa_wom_median[,as.character(year)],
col=blackred[(year-2017)])
    }
    legend(x=5,y=log(0.99,base=exp(1)),col=c(blackgray[1],blackgray[length(1933:2017)]),
lty=1,horiz=FALSE,bty="n",c("1933","2017"))

    legend(x=5,y=log(0.1,base=exp(1)),col=c(blackred[1],blackred[50]),lty=1,horiz=FALSE,
bty="n",c("2018","2067"))

    axis(side=1,at=seq(0,110,5),labels=FALSE,lwd=1,pos=log(0.00001,base=exp(1)))

    axis(side=1,at=seq(0,110,10),labels=seq(0,110,10),lwd=3,pos=log(0.00001,base=exp(1)))

    axis(side=2,at=log(c(0.00001,0.0001,0.001,0.01,0.1,1),base=exp(1)),
labels=c(0.00001,0.0001,0.001,0.01,0.1,1),lwd=3,pos=0)
```



Something to think about. How would you describe and intepret the pattern of LC-forecasted US female mortality until 2067?

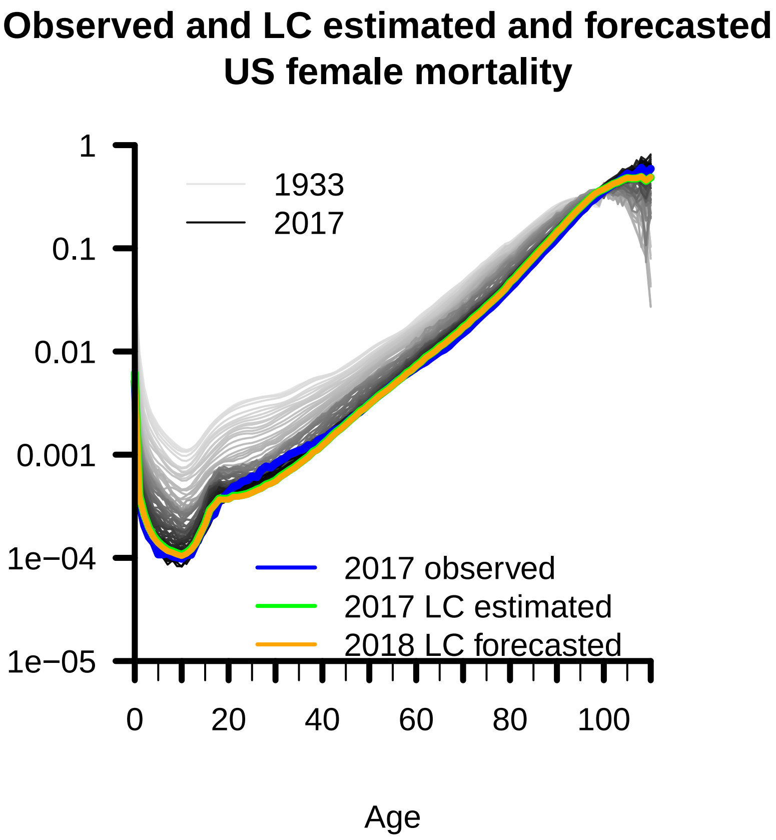
Something more to think about. Compare observed, LC-estimated, and LC-forecasted US female mortality in section 2.4, step 3.1.8, and step 3.2.3, respectively. In what way does the LC-forecast reflect LC-estimated and also observed US female mortality?

4. Transition between actual and forecasted US female mortality, 2017-2018

It is always a good idea to test forecasts with respect to their plausibility. Below we test the transition between observed and LC-forecasted US female mortality in two subsequent calendar years, 2017 and 2018:

```
par(fig = c(0,1,0,1), las=1, mai=c(0.8,0.8,0.8,0.8))

plot(x=-100,y=-100,xlim=c(0,110),ylim=c(log(0.00001,base=exp(1)),log(1,base=exp(1))),
xlab="Age",ylab="",main="Observed and LC estimated and forecasted \n US female mortality",
axes=FALSE, cex=0.6)
```

```
    for(year in 1933:2017){
        lines(x=0:110,y=log_usa_wom[,as.character(year)],
col=blackgray[(year-1932)])
    }

    lines(x=0:110,y=log_usa_wom[,as.character(2017)],col="blue",lwd=4)

    lines(x=0:110,y=fitted_log_usa_wom[,as.character(2017)],col="green",lwd=4)

    lines(x=0:110,y=forecast_log_usa_wom_median[,as.character(2018)],col="orange",lwd=3)

    legend(x=5,y=log(0.99,base=exp(1)),col=c(blackgray[1],blackgray[length(1933:2017)]),
lty=1,horiz=FALSE,bty="n",c("1933","2017"))

    legend(x=20,y=log(0.00019,base=exp(1)),col=c("blue","green","orange"),lty=1,horiz=FALSE,
bty="n",c("2017 observed","2017 LC estimated","2018 LC forecasted"),lwd=2)

    axis(side=1,at=seq(0,110,5),labels=FALSE,lwd=1,pos=log(0.00001,base=exp(1)))

    axis(side=1,at=seq(0,110,10),labels=seq(0,110,10),lwd=3,pos=log(0.00001,base=exp(1)))

    axis(side=2,at=log(c(0.00001,0.0001,0.001,0.01,0.1,1),base=exp(1)),
labels=c(0.00001,0.0001,0.001,0.01,0.1,1),lwd=3,pos=0)
```



Something to think about. Explain difference btw observed & LC-foreasted mortality in 2017 and 2018.

5. Avoid jump-off bias using observed mortality in jump-off year, 2017, and normalizing κ_t

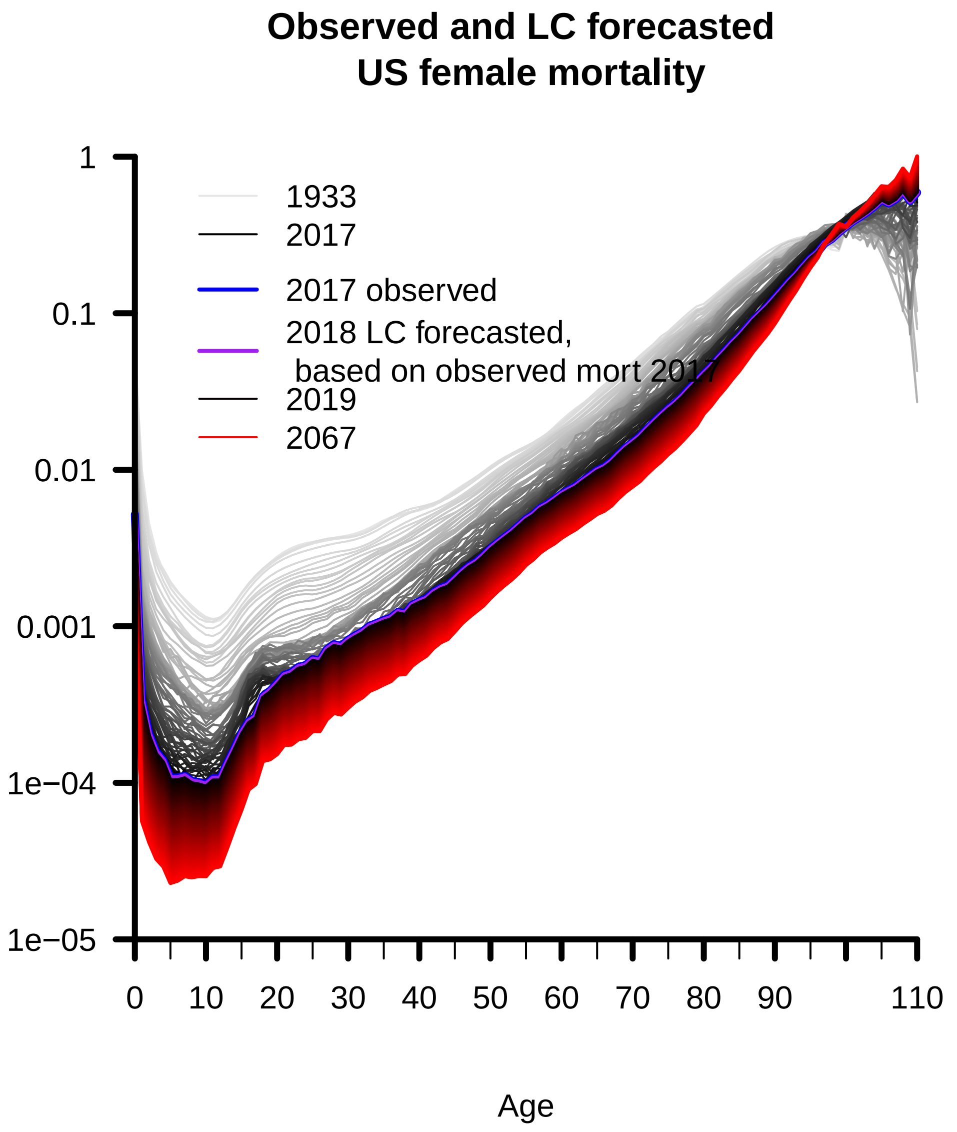
To avoid the jump-off bias between observed and LC-forecasted US female mortality, we simply replace α_x with mortality of the latest observed calendar year, 2017, and we also normalize the entire time series of κ_t to be zero in 2017.

In a first step we normalize κ_t to be 0 in the jump-off year 2017:

```r
kt_base_forecast <- c(fitted_kt , kt_trajectories_median)

names(kt_base_forecast) <- 1934:2067 ## to 1934 ... to 2067

kt_base_forecast_normalized <- kt_base_forecast -  kt_base_forecast[as.character(2017)]

kt_base_forecast_low <- c(fitted_kt, kt_trajectories_low80)

names(kt_base_forecast_low) <- 1934:2067 ## to 1934 ... to 2067

kt_base_forecast_low_normalized <-
kt_base_forecast_low -  kt_base_forecast_low[as.character(2017)]

kt_base_forecast_up <- c(fitted_kt , kt_trajectories_up80)

names(kt_base_forecast_up) <- 1934:2067 ## to 1934 ... to 2067

kt_base_forecast_up_normalized <-
kt_base_forecast_up -  kt_base_forecast_up[as.character(2017)]
```

In a second step we forecast US female mortality replacing α_x with $m_{x,t=2017}$ and using normalized time series of κ_t. As a result, the transition of US female mortality from the latest observed calendar year 2017 to the first forecast year 2018 appears to be much smoother:

```r
par(fig = c(0,1,0,1), las=1, mai=c(0.8,0.8,0.8,0.8))

plot(x=-100,y=-100,xlim=c(0,110),ylim=c(log(0.00001,base=exp(1)),log(1,base=exp(1))),
xlab="Age",ylab="",main="Observed and LC forecasted \n US female mortality",
axes=FALSE, cex=0.6)

    for(year in 1933:2017){
        lines(x=0:110,y=log_usa_wom[,as.character(year)],
col=blackgray[(year-1932)])
    }

    lines(x=0:110,y=log_usa_wom[,as.character(2017)],col="blue",lwd=4)

    lines(x=0:110,
y=(log_usa_wom[,as.character(2017)]+bx*kt_base_forecast_normalized[as.character(2018)]),
col="purple",lwd=3)

    for(year in 2019:2067){
        lines(x=0:110,
y=(log_usa_wom[,as.character(2017)]+bx*kt_base_forecast_normalized[as.character(year)]),
col=blackred[(year-2017)],lwd=2)
    }
    legend(x=5,y=log(0.99,base=exp(1)),col=c(blackgray[1],blackgray[length(1933:2017)]),
lty=1,horiz=FALSE,bty="n",c("1933","2017"))

    legend(x=5,y=log(0.35,base=exp(1)),col=c("blue","purple"),lty=1,horiz=FALSE,
bty="n",c("2017 observed","2018 LC forecasted,\n based on observed mort 2017"),lwd=2)

    legend(x=5,y=log(0.05,base=exp(1)),col=c(blackred[2],blackred[50]),lty=1,horiz=FALSE,
bty="n",c("2019","2067"))

    axis(side=1,at=seq(0,110,5),labels=FALSE,lwd=1,pos=log(0.00001,base=exp(1)))

    axis(side=1,at=seq(0,110,10),labels=seq(0,110,10),lwd=3,pos=log(0.00001,base=exp(1)))

    axis(side=2,at=log(c(0.00001,0.0001,0.001,0.01,0.1,1),base=exp(1)),
labels=c(0.00001,0.0001,0.001,0.01,0.1,1),lwd=3,pos=0)
```



Something to think about. How would you explain in your own words the procedure to avoid jump-off bias within the Lee-Carter methodology?

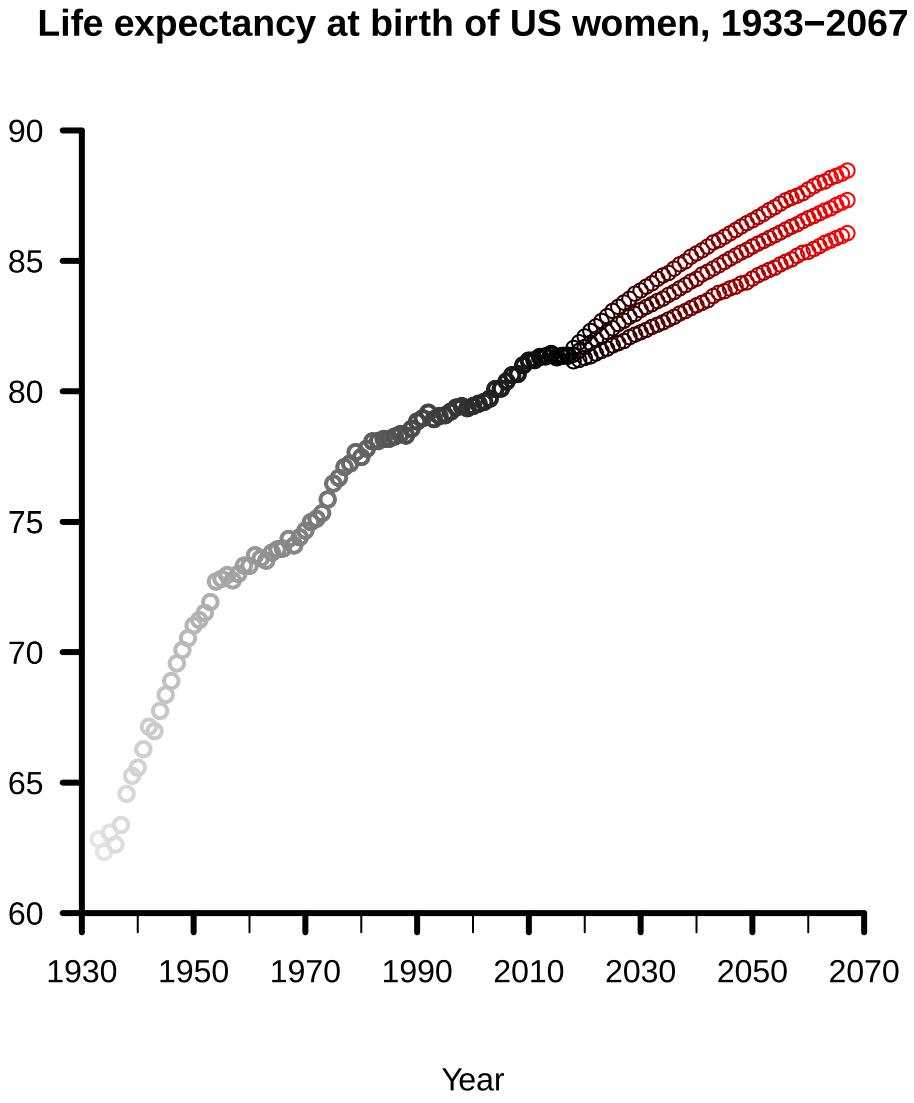
6. How does this look like in terms of life expectancy at birth?

We first write a function to calculate life expectancy at birth.

```
lexp.age.specific <- function(mx,ax){

        qx <- mx/(1+(1-ax)*mx)

            px <- 1-qx

            lx <- c(100000, (cumprod(px)*100000)[1:(length(qx)-1)])

            dx <- c(-diff(lx), lx[length(lx)])

            Lx1 <- lx[-1]+ax[1:(length(ax)-1)]*dx[1:(length(dx)-1)]

            Lx2 <- if(mx[length(mx)] == 0){

                0}else{

                    dx[length(dx)]/mx[length(mx)]

                }

            Lx <- c(Lx1, Lx2)

            Tx <- rev(cumsum(rev(Lx)))

            ex <- Tx/lx

            ex[is.nan(ex)] <- 0

            return(ex)

}
```

We then depict the LC-forecasts of US female life expectancy at birth:

```
par(fig = c(0,1,0,1), las=1, mai=c(0.8,0.8,0.8,0.8))

plot(x=-100,y=-100,xlim=c(1930,2020+50),ylim=c(60,90),xlab="Year",ylab="",
main="Life expectancy at birth of US women, 1933-2067",axes=FALSE)

    axis(side=1,at=seq(1930,2020+50,10),labels=FALSE,lwd=1,pos=60)

    axis(side=1,at=seq(1930,2020+50,20),labels=seq(1930,2020+50,20),lwd=3,pos=60)

    axis(side=2,at=seq(60,90,5),labels=seq(60,90,5),lwd=3,pos=1930)

    max_age <- 110

    lt_ax <- c(0.06,rep(0.5,max_age-1))
    for(year in 1933:2017){

        current.e0 <- lexp.age.specific(usa_wom[[2]][1:max_age,as.character(year)],
lt_ax)[1]

        points(year,current.e0,col=blackgray[(year-1932)],lwd=2)
    }

    for(year in 2018:2067){

        ## Median:

        current.mx <- exp(log(usa_wom[[2]][,as.character(2017)],base=exp(1))+
bx*kt_base_forecast_normalized[as.character(year)])

        current.e0 <- lexp.age.specific(current.mx[1:max_age],lt_ax)[1]

        points(year,current.e0,col=blackred[(year-2017)],lwd=1)

        ## Lower 80:

        current.mx <- exp(log(usa_wom[[2]][,as.character(2017)],base=exp(1))+
bx*kt_base_forecast_low_normalized[as.character(year)])

        current.e0 <- lexp.age.specific(current.mx[1:max_age],lt_ax)[1]

        points(year,current.e0,col=blackred[(year-2017)],lwd=1)

        ## Upper 80:

        current.mx <- exp(log(usa_wom[[2]][,as.character(2017)],base=exp(1))+
bx*kt_base_forecast_up_normalized[as.character(year)])

        current.e0 <- lexp.age.specific(current.mx[1:max_age],lt_ax)[1]

        points(year,current.e0,col=blackred[(year-2017)],lwd=1)
    }
```



Something to think about. How do you describe and interpret the LC-forecast of US female life expectancy at birth?

Something more to think about. How do you generalize the procedure of the LC method so that it would be applicable for other populations?

7. Now is the time to do this again for the US using the base period 1988-2017. As always, feel free to adapt the R code to your own needs and creativity :-)