

## Assignment 1

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I was already registered at [www.mortality.org](http://www.mortality.org). I used the following function, that is included in "HMDHFDplus" library, to download single years, single period death counts and exposure of Italy.

```
library(HMDHFDplus)
```

```
italy_death <- readHMDweb(CNTRY = "ITA", item = "Deaths_1x1",  
                          username = "***", password = "***")  
italy_exp <- readHMDweb(CNTRY = "ITA", item = "Exposures_1x1",  
                       username = "***", password = "***")
```

In order to create two matrices from the two data frame downloaded from [www.mortality.org](http://www.mortality.org), I defined two vectors: years and ages with duplicate elements removed. I used these two vectors to identify rows and columns of D and E that are respectively the matrix of deaths and exposures with counts for each year and age for the whole population.

```
x <- c(0,1, seq(2,110,1))  
years <- unique(italy_death$Year)  
ages <- unique(italy_death$Age)
```

```
D <- matrix(italy_death$Total, nrow = length(ages), dimnames = list(ages,  
years))  
E <- matrix(italy_exp$Total, nrow = length(ages), dimnames = list(ages,  
years))
```

I used the following function to calculate life expectancy at birth and the nominator of coefficient of variation of the life distribution of death. This function needs as input a vector of years and two matrices about deaths and exposures and it gives as output a list. This list is composed by a data frame (complete life table with life expectancy and the numerator of the coefficient of variation) and a summary with life expectancy at birth and the final expression of the coefficient of variation.

```
LTfun <- function (x, Dx, Nx) {  
  
  nx <- c(diff(x), Inf)  
  nmx <- Dx / Nx  
  npx <- exp(-nx*nmx)  
  nqx <- 1-npx  
  lx <- cumprod(c(1, npx[-length(npx)]))  
  ndx <- c(diff(-lx), lx[length(lx)])  
  nLx <- -nx*ndx/log(npx); nLx[is.nan(nLx)] <- 0  
  Tx <- rev(cumsum(rev(nLx)))  
  ex <- Tx/lx
```

```

cv <- sqrt(cumsum(ndx*(x+0.5-ex)^2))

list(
  lt = data.frame(
    x, nx, nm, npx, nqx, lx, ndx, nLx, Tx, ex, cv
  ),
  summary = c(e0 = ex[[1]], m = x[which.max(ndx)], ltr = 1/ex[[1]], cv0 =
cv[[1]]/ex[[1]])
)
}

```

Before to use the function I created an empty list called e0t where to insert the result of the function with deaths and exposures of Italy. In order to fill the list I used a for loop as long as the number of the columns of D (or E is equivalent). Then I saved the life expectancies at birth and the coefficient of variation, both per year, in two vectors.

```

e0t <- vector(mode = 'list', length = ncol(D))

for (i in 1:ncol(D)) {
  e0t[[i]] <- LTFun(x = ages, Dx = D[,i], Nx = E[,i])
}

e0_final <- sapply(e0t, function(x) {x$summary['e0']})
cv_final <- sapply(e0t, function(x) {x$summary['cv0']})

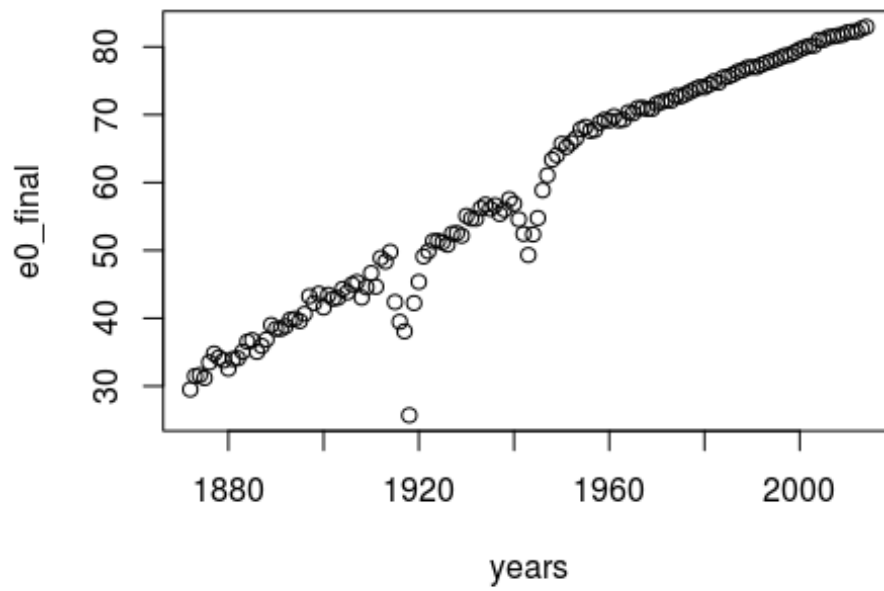
```

Shown below there are some plot of e0, cv and e0 vs cv. As we can see in the last graphic, it seems to be a linear relationship between life expectancy at birth and coefficient of variation. As the e0 increases, the cv decreases.

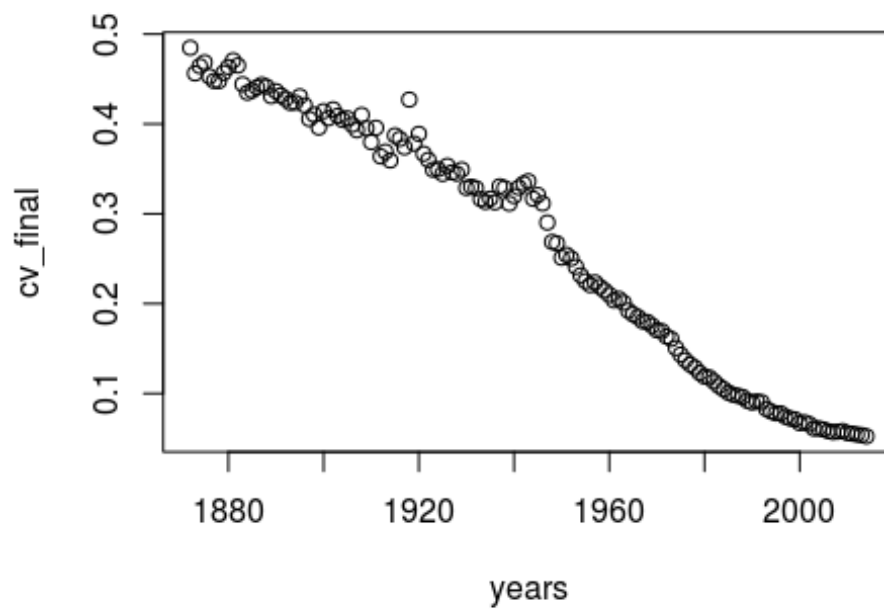
```

plot(years,e0_final)

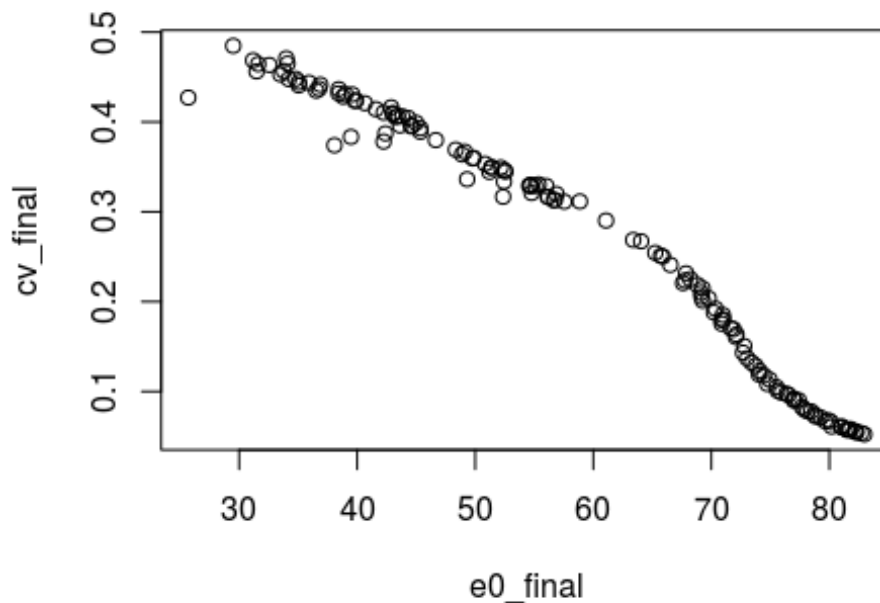
```



```
plot(years,cv_final)
```



```
plot(e0_final,cv_final)
```



As a proof I first calculated the correlation between the two variables and then i fitted a model using cv as dependent variable and e0 as independent variable. The results are shown below.

```
cor(e0_final,cv_final)
```

```
## [1] -0.983238
```

```
model <- lm(cv_final ~ e0_final)
```

```
summary(model)
```

```
##
```

```
## Call:
```

```
## lm(formula = cv_final ~ e0_final)
```

```
##
```

```
## Residuals:
```

```
##      Min       1Q   Median       3Q      Max
```

```
## -0.116608 -0.021382  0.001787  0.019462  0.044295
```

```
##
```

```
## Coefficients:
```

```
##              Estimate Std. Error t value Pr(>|t|)
```

```
## (Intercept)  0.7578109  0.0079202   95.68  <2e-16 ***
```

```
## e0_final    -0.0083350  0.0001302  -64.03  <2e-16 ***
```

```
## ---
```

```
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
##
```

```
## Residual standard error: 0.02569 on 141 degrees of freedom
```

```
## Multiple R-squared:  0.9668, Adjusted R-squared:  0.9665  
## F-statistic: 4100 on 1 and 141 DF,  p-value: < 2.2e-16
```

```
plot(e0_final,cv_final)  
abline(lm(cv_final ~ e0_final), col='red')
```

