COS-D407. *Scientific Modeling and Model Validation*

Hands-on excercises

Week 4

University of Helsinki, Finland

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Source: https://github.com/christina-bohk-ewald/2021-COS-D407-scientific-modeling-and-model-validation

Table of content:

1. Some preparations in R

1.1 Open a new script for week 4 in R (e.g., *week-4.R*) and save it to a folder of your choice (e.g., *course-COS-D407*).

1.2 Create a filepath to this folder from where you would like to load data and to where you would like to save your outcome. For example,

```
the_course_COS_D407_path <- c("C:/course-COS-D407")
```

1.3 You can then set the working directory to this path

```
setwd(the_course_COS_D407_path)
```

2. Download and load required input data

In week 4 we apply the demographic scaling model of Bohk-Ewald et al. (2020) for estimating total numbers of COVID-19 infections in Finland. We will start with downloading and loading required input data in R, continue with reading basic functions of the demographic scaling model in R, and finally applying it to estimate the number of people who probably are and have been infected with COVID-19 so far.

2.1 Download confirmed cases and reported deaths attributable to COVID-19 as of today

Please go to the website of the Johns Hopkins University CSSE. The files

- *time_series_covid19_confirmed_global.csv*
- *time_series_covid19_deaths_global.csv*

contain confirmed cases and reported deaths, respectively, for many countries on a daily basis since January 22, 2020. Please download these two files and save them in your project folder.

2.2 Load COVID-19 data

Please load the numbers of confirmed cases and reported deaths from COVID-19 in R using the function *read.csv* of the R-package *openxlsx*.

```
require(openxlsx)

confirmed <- read.csv("time_series_covid19_confirmed_global.csv",header=TRUE,
stringsAsFactors = FALSE)
confirmed[1:2,1:6]
```

```
##   Province.State Country.Region      Lat     Long X1.22.20 X1.23.20
## 1                    Afghanistan 33.93911 67.70995        0        0
## 2                        Albania 41.15330 20.16830        0        0
```

```
deaths <- read.csv("time_series_covid19_deaths_global.csv",header=TRUE,
stringsAsFactors = FALSE)
deaths[1:2,((ncol(deaths)-5):ncol(deaths))]
```

```
##   X9.10.20 X9.11.20 X9.12.20 X9.13.20 X9.14.20 X9.15.20
## 1     1420     1420     1420     1420     1425     1426
## 2      324      327      330      334      338      340
```

2.3 Download and load abridged life tables

Please go to the UNWPP2019 website, download abridged life tables for both sexes together, save them into your project folder, and then load them into R.

```
lt_1950_2020 <- read.xlsx("WPP2019_MORT_F17_1_ABRIDGED_LIFE_TABLE_BOTH_SEXES.xlsx",
sheet = 1,startRow = 17)
```

Brief data description. The data object *lt_1950_2020* contains abridged life tables for both sexes for all UN countries.

Explore this data object and find out how large Finnish remaining life expectancy at birth has been 1950-55 through 2015-19.

```
## lt_1950_2020[1:2,]

colnames(lt_1950_2020)
```

```
##  [1] "Index"
##  [2] "Variant"
##  [3] "Region,.subregion,.country.or.area.*"
##  [4] "Notes"
##  [5] "Country.code"
##  [6] "Type"
##  [7] "Parent.code"
##  [8] "Period"
##  [9] "Age.(x)"
## [10] "Age.interval.(n)"
## [11] "Central.death.rate.m(x,n)"
## [12] "Probability.of.dying.q(x,n)"
## [13] "Probability.of.surviving.p(x,n)"
## [14] "Number.of.survivors.l(x)"
## [15] "Number.of.deaths.d(x,n)"
## [16] "Number.of.person-years.lived.L(x,n)"
## [17] "Survival.ratio.S(x,n)"
## [18] "Person-years.lived.T(x)"
## [19] "Expectation.of.life.e(x)"
## [20] "Average.number.of.years.lived.a(x,n)"
```

```
lt_1950_2020[which(lt_1950_2020[,"Region,.subregion,.country.or.area.*"]=="Finland" &
  lt_1950_2020["Age.(x)"]==0),c("Period","Expectation.of.life.e(x)")]
```

```
##          Period Expectation.of.life.e(x)
## 4823  1950-1955       66.401073999999994
## 10349 1955-1960       68.189361000000005
## 15875 1960-1965       69.067266000000004
## 21401 1965-1970       69.716247999999993
## 26927 1970-1975       70.930030000000002
## 32453 1975-1980       72.714505000000003
## 37979 1980-1985       74.326365999999993
## 43505 1985-1990       74.788223000000002
## 49031 1990-1995       75.841427999999993
## 54557 1995-2000       77.144569000000004
## 60083 2000-2005       78.400789000000003
## 65609 2005-2010       79.548135000000002
## 71135 2010-2015       80.705350999999993
## 76661 2015-2020       81.646075999999994
```

2.4 Load global pattern over age of COVID-19 deaths

Dudel et al. (2020) provide in their supplementary material data for age-specific death counts attributable to COVID-19, which has been served as a basis for calculating a global average pattern over age for total death counts as input for the demographic scaling model. You can download this *global average pattern over age* from the GitHub repository for this course.

```
global_age_dist_deaths <- source("global_age_dist_deaths.R")
## global_age_dist_deaths
```

Brief data description. The data object *global_age_dist_deaths* contains the global pattern over 10-year age groups of COVID-19 deaths.

Note that we follow here the original methodology of the demographic scaling model that has been introduced in the paper of Bohk-Ewald et al. (2020). Another way is to use COVID-19-related death counts by age that have been reported to the COVerAGE database (as presented on Monday).

2.5 Load infection fatality rates from Verity et al. (2020)

Verity and colleagues (2020, page 5) report infection fatality rates by 10-year age groups for Hubei, China, on page 5. Please create a data object *ifr_by_age_china_verity* that contains these data or download it from the GitHub repository for this course.

```
ifr_by_age_china_verity <- read.table("infection-fatality-rates-by-age-china-Verity.txt",
header=FALSE, stringsAsFactors = FALSE)

ifr_by_age_china_verity
```

```
##   V1      V2       V3       V4
## 1  0 1.6e-05 1.85e-06 0.000249
## 2 10 7.0e-05 1.50e-05 0.000500
## 3 20 3.1e-04 1.40e-04 0.000920
## 4 30 8.4e-04 4.10e-04 0.001850
## 5 40 1.6e-03 7.60e-04 0.003200
## 6 50 6.0e-03 3.40e-03 0.013000
## 7 60 1.9e-02 1.10e-02 0.039000
## 8 70 4.3e-02 2.50e-02 0.084000
## 9 80 7.8e-02 3.80e-02 0.133000
```

Brief data description. The data object *ifr_by_age_china_verity* contains the modal estimate as well as the lower and upper bound of the 95 percent credible interval for the infection fatality rates of Hubei, China, by 10-year age groups.

3. Estimate COVID-19 infections in Finland

3.1 Source basic functions of the demographic scaling model

You can find the basic functions of the demographic scaling model in the file *basic-functions-week-4.R* in the GitHub repository for this course. They contain the functions:

- *to_ungroup* to interpolate IFR estimates of Verity et al. (2020) into single years of age
- *get_ungrouped_ex_2015_2020* to ungroup remaining life expectancy
- *map_ifr_betw_ref_and_one_coi_thanatAge* to scale IFRs from a reference country (here: China; Verity et al. (2020)) onto a country of interest based on remaining life expectancy
- *aggregate_mapped_ifr_10y* to aggregate scaled IFRs into 10-year age groups
- *disaggregate_deaths_one_coi_10y* to disaggregate total deaths into 10-year age groups

You may have a look at these basic functions if you wish. But it is also fine to just source (or load) them via the file *basic-functions-week-4.R*:

```
source("basic-functions-week-4.R")
```

3.2 Apply the demographic scaling model with data for Finland

```
#
## 1. Ungroup China's IFR:
#

ungrouped_mode_ifr_by_single_age_china_sp <- to_ungroup(to_ungroup=
                ifr_by_age_china_verity[,2],nr_grouped_years=10)

ungrouped_low95_ifr_by_single_age_china_sp <- to_ungroup(to_ungroup=
                ifr_by_age_china_verity[,3],nr_grouped_years=10)

ungrouped_up95_ifr_by_single_age_china_sp <- to_ungroup(to_ungroup=
                ifr_by_age_china_verity[,4],nr_grouped_years=10)

#
## 2. Scale IFRs from a RC onto a COI via remaining life expectancy:
#

mapped_mode_ifr_thanatAge <- map_ifr_betw_ref_and_one_coi_thanatAge(coi="Finland",
    lt_1950_2020=lt_1950_2020,
    ungrouped_ifr_by_single_age_china_sp=ungrouped_mode_ifr_by_single_age_china_sp)

## and fill in the few NA values:

pos_na <- which(is.na(mapped_mode_ifr_thanatAge[1,]))
    if(length(pos_na)>0){
        for(pos in 1:length(pos_na)){
            if(pos_na[pos] < 6){
                mapped_mode_ifr_thanatAge[1,pos_na[pos]] <-
                    min(mapped_mode_ifr_thanatAge[1,],na.rm=TRUE)
            }
            if(pos_na[pos] >= 6){
                mapped_mode_ifr_thanatAge[1,pos_na[pos]] <-
                    mapped_mode_ifr_thanatAge[1,pos_na[pos]-1]
            }
        } ## for pos
    } ## if

#
## 3. Put scaled IFRs into 10-year age groups:
#

mapped_mode_ifr_thanatAge_10y <- aggregate_mapped_ifr_10y(disaggregated_mapped_ifr=
                        mapped_mode_ifr_thanatAge)

#
## 4. Disaggregate total COVID-19-related deaths into 10-year age groups:
#

deaths_by_age <- disaggregate_deaths_one_coi_10y(coi="Finland")
```

```
#
## 5. Estimate COVID-19 infections over time:
#

inf_mode <- colSums( deaths_by_age / mapped_mode_ifr_thanatAge_10y )
```

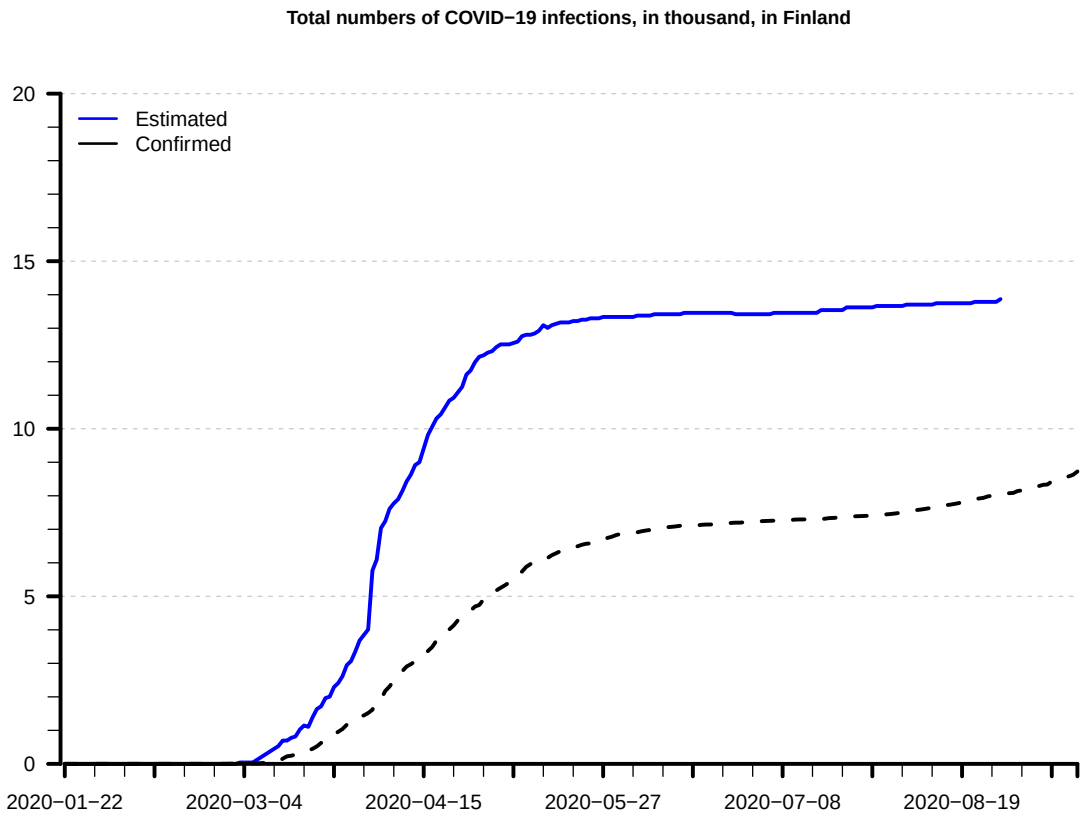
Think about how you could extend this R-code in order to estimate the total numbers of COVID-19 infections for other countries and how to provide uncertainty estimates for them.

3.3 Visualize COVID-19 infecton estimates for Finland

Visualize the numbers of COVID-19 infections in Finland over time, accounting for an average time to death of 18 days.

```
dates <- seq(as.Date("22/01/2020", format = "%d/%m/%Y"),
by = "days", length = (ncol(deaths)-4) )
```

```
par(fig = c(0,1,0,1), las=1, mai=c(0.4,0.8,0.8,0.4))

plot(x=-100,y=-100,xlim=c(0,length(5:ncol(deaths))),ylim=c(0,20),xlab="Date",ylab="",cex.main=0.9,
main="Total numbers of COVID-19 infections, in thousand, in Finland",axes=FALSE)

segments(x0=rep(0,4),x1=rep(length(5:ncol(deaths)),4),y0=seq(5,20,5),y1=seq(5,20,5),
lty=2,col=grey(0.8))

lines(x=1:length(5:ncol(deaths)),y=c(inf_mode[-c(1:18)],rep(NA,18))/1000,col="blue",lwd=3)

lines(x=1:length(5:ncol(deaths)),y=confirmed[which(confirmed[,"Country.Region"]=="Finland"),
5:ncol(confirmed)]/1000,col="black",lty=2,lwd=3)

legend(0,20,c("Estimated","Confirmed"),col=c("blue","black"),bty="n",lwd=2,lty=1)

axis(side=1,at=seq(1,length(5:ncol(deaths)),7),labels=FALSE,lwd=1,pos=0)

axis(side=1,at=c(seq(1,length(5:ncol(deaths)),21),length(5:ncol(deaths))),
labels=dates[c(seq(1,length(5:ncol(deaths)),21),
length(5:ncol(deaths)))],lwd=3,pos=0)

axis(side=2,at=seq(0,20,1),labels=FALSE,lwd=1,pos=0)

axis(side=2,at=seq(0,20,5),labels=TRUE,lwd=3,pos=0)
```



Please describe the level and the temporal development of the estimated numbers of COVID-19 infections in Finland, also compared to (1) the numbers of confirmed cases in Finland, and to (2) the corresponding figures in other European countries. As a source of inspiration, you may want to have a look at the press release *How many Finns have really been infected with COVID-19?*.

Again, please think about how you could extend this R-code in order to estimate the total numbers of COVID-19 infections for other countries and how to provide uncertainty estimates for them.

4. Time for you to think both creatively and critically about these COVID-19 infection estimates for Finland.

How would you evaluate the process of the demographic scaling model?

How plausible are the infection estimates, also considering, e.g., the quality of the input data and the key assumptions of the demographic scaling model? As a source of inspiration, you may want to have a look at the paper of Bohk-Ewald et al. (2020).