

# Determination of detection rates, hospitalizations, ICU admissions, death rates of severe and critical cases from Spanish data sets.

## Comparison with other countries.

The Spanish Government has published detailed age stratified data on hospital and critical care admissions. I looked into the data to get sensible estimates of hospitalization. It happens that the Spanish serological survey also came out, age stratified and quite detailed. Using these, and additional information from a published article of ICU admissions in Italy, one can derived all relevant rates/probabilities and, through comparison with other countries, say something on the reliability of the data.

### Spanish population pyramid

Get age pyramid for Spain (5 years age groups) these estimates are produced via processed WorldPop data (2020 estimates)

```
age.pyram.17 <- as.matrix( read.table("Data/Spain_5km_stats.dat",  
                                     header=FALSE) )  
age.pyram.17 <- unlist(age.pyram.17[,3])
```

Build reduced age pyramid (10 years age groups) by aggregating

```
get.10y.from.5y <- function( ap.17 ) {  
  ap.9 = c()  
  for (jj in seq(1,16,2)) ap.9 <- cbind(ap.9, ap.17[jj]+ap.17[jj+1])  
  ap.9 <- cbind(ap.9, ap.17[17])  
}  
age.pyram.9 <- get.10y.from.5y( age.pyram.17 )
```

### Spanish survey data

Take data from Spanish survey: number of tested and percentage of positive

```
# Data from spanish survey  
spanish.survey.count.20 <- c(268, 1693, 2857, 3425, 3221, 2805, 2606, 3050, 4000,  
                             5174, 5330, 5263, 5187, 4560, 3568, 2931, 2161, 1410,  
                             968, 420)  
spanish.survey.perc.20 <- c(1.1, 2.2, 3.0, 3.9, 3.8, 4.5, 4.8, 3.8, 4.6,  
                             5.3, 5.7, 5.8, 6.1, 5.9, 6.2, 6.9, 6.1, 5.1, 5.6, 5.8)
```

Estimate the number of positives in survey

```
spanish.survey.posit.20 <- spanish.survey.count.20 * spanish.survey.perc.20 / 100.0
```

Reduce survey data to 17 age groups

```
spanish.survey.count.17 <- spanish.survey.count.20[2:18]  
spanish.survey.count.17[1] <- spanish.survey.count.17[1] + spanish.survey.count.20[1]  
spanish.survey.count.17[17] <- spanish.survey.count.17[17] + spanish.survey.count.20[19] +
```

```
spanish.survey.count.20[20]
```

```
spanish.survey.posit.17 <- spanish.survey.posit.20[2:18]
spanish.survey.posit.17[1] <- spanish.survey.posit.17[1] + spanish.survey.posit.20[1]
spanish.survey.posit.17[17] <- spanish.survey.posit.17[17] + spanish.survey.posit.20[19] +
  spanish.survey.posit.20[20]
```

Estimate positive counts on national basis using the 17 age groups

```
spanish.survey.perc.17 <- spanish.survey.posit.17 / spanish.survey.count.17
spanish.estimate.count.17 <- spanish.survey.perc.17 * age.pyram.17
print(paste('Check: 5% ~', sum(spanish.estimate.count.17)/(sum(age.pyram.17))*100.0) )
```

```
## [1] "Check: 5% ~ 5.01960542302666"
```

## Admission to ICU and overall (severe + critical) death rates

Information from Spain at 16.05.2020 - 10 years age groups. This is age stratified information on 239,125 cases, and includes hospital admissions, ICU admissions (from hospitalized), and deaths (both ICU and hospital, for a total of 19,186 deaths). The age stratified information is a subset of the total cases (about 70%) for which information on sex and age is available.

```
cases.total.9 <- c(877, 1637, 13461, 22639, 35135, 42794, 34360, 32443, 37463+18316)
cases.hosp.9 <- c(279, 277, 1477, 3811, 8666, 14075, 17264, 20794, 18842+6346)
cases.ICUs.9 <- c(39, 23, 89, 274, 740, 1562, 2534, 2261, 332+56)
cases.deaths.9 <- c(2, 5, 23, 63, 201, 611, 1695, 4632, 7872+4082)
```

The same report provides further information on all cases, setting the total death toll to 27,650. Using this information, we rescale the deaths to account for the true death toll. This is supported by the fact that the rate of hospitalization and ICU admission for the wider set is similar to that for the age stratified set.

```
total.deaths <- 27650
cases.deaths.9 <- cases.deaths.9*total.deaths/(sum(cases.deaths.9))
```

Distribute total cases to 5-years age classes distributing by age prevalence

```
cases.total.17 <- c()
cases.deaths.17 <- c()
for (ii in 1:8) {
  ratio <- age.pyram.17[(2*ii-1):(2*ii)]
  ratio <- ratio[1]/(ratio[1]+ratio[2])
  cases.total.17 <- c(cases.total.17, cases.total.9[ii]*ratio, cases.total.9[ii] -
    cases.total.9[ii]*ratio)
  cases.deaths.17 <- c(cases.deaths.17, cases.deaths.9[ii]*ratio, cases.deaths.9[ii] -
    cases.deaths.9[ii]*ratio)
}
cases.total.17 <- c( cases.total.17, cases.total.9[9] )
cases.deaths.17 <- c( cases.deaths.17, cases.deaths.9[9] )
print( paste("Check: ", sum(cases.total.9), '=', sum(cases.total.17)) )
```

```
## [1] "Check: 239125 = 239125"
```

```
print( paste("Check: ", sum(cases.deaths.9), '=', sum(cases.deaths.17)) )
```

```
## [1] "Check: 27650 = 27650"
```

Determine detection (sympt) rate. This is the rate of detection of cases, not truly asymptomatic rates. This is given by the count of detected cases divided by the count of totally infected plus the dead individuals (which are there but would not appear in the count of individuals affected by COVID19). We get the rates for 5y and 10y age groups.

```
sympt.rate.17 <- cases.total.17 / (spanish.estimate.count.17+cases.deaths.17)
print(sympt.rate.17)

## [1] 0.008645652 0.005906960 0.007618587 0.007819069 0.056692914 0.053150070
## [7] 0.091717091 0.075771140 0.076235827 0.070889071 0.093356488 0.088773572
## [13] 0.095621079 0.091024193 0.101862331 0.114905481 0.289321537

sympt.rate.9 <- cases.total.9 / get.10y.from.5y(spanish.estimate.count.17+cases.deaths.17)
print(sympt.rate.9)

##           [,1]      [,2]      [,3]      [,4]      [,5]      [,6]
## [1,] 0.006969417 0.007714531 0.05481979 0.08218449 0.07347925 0.0911016
##           [,7]      [,8]      [,9]
## [1,] 0.09347181 0.1072366 0.2893215
```

Derive estimated critical admissions (raw estimate) from Spanish cases

```
hosp_to_ICUs.9 <- cases.ICUs.9/cases.hosp.9
```

## ICU death rates using Italian data

Estimates of ICU deaths are based on a study published recently on about 1600 patients admitted to ICU in Lombardy, Italy [Grasselli, G., et al. (2020). Baseline Characteristics and Outcomes of 1591 Patients Infected With SARS-CoV-2 Admitted to ICUs of the Lombardy Region, Italy. JAMA 323, 1574–1581]. The patients in the study were admitted between the 20th of February and the 18th of March (28 days), and the study reports on their status on the 25th of March (35 days).

Copy of Italian data: (n) -> number of cases, (d) -> number of deaths, (s) -> number of active cases

```
# Derive estimated critical death rate from Italian data
ita.ICUn.9 <- c(2, 2, 56, 56, 142, 423, 596, 340, 22)
ita.ICUd.9 <- c(0, 0, 4, 4, 16, 63, 174, 136, 12)
ita.ICUs.9 <- c(2, 2, 32, 32, 91, 270, 353, 164, 8)
```

Estimate must take into account that a fraction of those still in hospital will die. Assume the usual  $dI/dt$  for an equivalent SIR model, with  $R_0(t)$  linearly decreasing between  $R_0 = 3$  and 1 [Riccardo, F., et al. (2020). Epidemiological characteristics of COVID-19 cases in Italy and estimates of the reproductive numbers one month into the epidemic. MedRxiv 2020.04.08.20056861.]. This implies  $I(t) \propto \exp(\int_0^t (R_0(\tau) - 1) \gamma d\tau)$ .

$$R_0(t) = R_0 + (1 - R_0)t/T \quad \text{where } R_0 = 3, \text{ and } T = 28 \text{ days}$$

$$\frac{dI}{I} = (R_0(t) - 1)\gamma dt = (R_0 - 1)(1 - t/T)\gamma dt$$

$$\Rightarrow$$

$$I(t) \propto \exp((R_0 - 1)t(1 - t/2T)\gamma)$$

First build a function that returns  $I(t)/I(0)$ , then a function that returns the entry time of n severe admissions to ICU. Use simple rejection method to draw from the normalized  $I(t)$ . Use  $\gamma = 1/7$ : this is the approximated equivalent SIR model.

```
epigrowth <- function(t, RO, gamma) {
  # alpha = (RO-1)*gamma
  # return(exp(alpha*t)/alpha)
```

```

    return( exp( (R0-1)*t*(1-t/(2*28))*gamma ) )
}

# Returns numbers distributed according to I(t)/I(0). These are hospitalization times
repgrowth <- function( n, R0, gamma ) {
  maxobj <- optimize(function(x) {return(epigrowth(x, R0, gamma))},
                      interval=c(0, 28), maximum=TRUE)

  x.max <- maxobj$maximum
  y.max <- maxobj$objective
  y.min <- 1
  theta = y.max - y.min
  vec <- c()
  for (jj in 1:n) {
    repeat {
      x = runif(1)*28
      y = runif(1) < epigrowth(x, R0, gamma)/theta
      if (y) {
        break
      }
    }
    vec <- c(vec, x)
  }
  return(vec)
}

```

Search for death rate that produces the expected deaths by the 25th of May. The final number of deaths in ICU will be higher than the number of deaths registered up to the 25th.

```

findRate <- function(rate, age) {
  vals <- c()
  nn = floor(ita.ICUn.9[age]*rate)
  if (nn > 0) {
    for (jj in 1:1000) {
      t.to.death.ITA <- rpois(nn, 7)
      t.hospital.ITA <- repgrowth(nn, R0=3.0, gamma=1.0/7.0)
      # From 20-02-2020 to 18-03-2020 (included)
      vals <- cbind( vals, sum(t.to.death.ITA+t.hospital.ITA <= 35) )
    }
  } else {
    vals = 0
  }
  return( mean(vals)-ita.ICUd.9[age] )
}

pg1 <- txtProgressBar(min=1, max=length(ita.ICUn.9), style=3)
critic_to_death.9 <- c()
for (age in 1:length(ita.ICUn.9)) {
  setTxtProgressBar(pg1, age)
  rate <- uniroot(findRate, c(0,1), age)$root
  critic_to_death.9 <- cbind(critic_to_death.9, rate)
}

```

## |

|

```
print( critic_to_death.9 )

##      rate rate      rate      rate      rate      rate      rate      rate
## [1,]    0    0 0.08920068 0.0892212 0.1267597 0.1632134 0.3187713 0.4357162
##           rate
## [1,] 0.5936063

print( paste('Check:',sum(critic_to_death.9*ita.ICUn.9), '>', sum(ita.ICUd.9) ) )

## [1] "Check: 448.221307041633 > 409"
```

## Finalizing data

Estimate deaths in ICUs and hospital in Spain using Italian rates. Estimate death rates for severe cases

```
ICUs.deaths.9 <- (cases.ICUs.9 * critic_to_death.9)
hosp.deaths.9 <- cases.deaths.9 - ICUs.deaths.9
# Death rates from non-ICU cases
hosp_to_death.9 <- hosp.deaths.9 / (cases.hosp.9-cases.ICUs.9)
```

Hospitalization rates are the crude rates, given cases.total is the number of detected cases.

```
symp_to_hosp.9 <- (cases.hosp.9-cases.ICUs.9)/cases.total.9
symp_to_ICUs.9 <- cases.ICUs.9/cases.total.9
print("Sympt to hosp")
```

```
## [1] "Sympt to hosp"
```

```
print(symp_to_hosp.9)
```

```
## [1] 0.2736602 0.1551619 0.1031127 0.1562348 0.2255870 0.2924008 0.4286962
## [8] 0.5712480 0.4446118
```

```
print(symp_to_ICUs.9)
```

```
## [1] 0.044469783 0.014050092 0.006611693 0.012103008 0.021061619 0.036500444
## [7] 0.073748545 0.069691459 0.006956023
```

```
print(cases.hosp.9/cases.total.9*hosp_to_ICUs.9)
```

```
## [1] 0.044469783 0.014050092 0.006611693 0.012103008 0.021061619 0.036500444
## [7] 0.073748545 0.069691459 0.006956023
```

```
print("The last two should be the same")
```

```
## [1] "The last two should be the same"
```

Output all rates, assuming 17 age groups (simulation ready... more or less: see at the end)

```
symp_to_hosp.17 <- c(rbind(symp_to_hosp.9, symp_to_hosp.9))[1:17]
symp_to_ICUs.17 <- c(rbind(symp_to_ICUs.9, symp_to_ICUs.9))[1:17]
hosp_to_ICUs.17 <- c(rbind(hosp_to_ICUs.9, hosp_to_ICUs.9))[1:17]
hosp_to_death.17 <- c(rbind(hosp_to_death.9, hosp_to_death.9))[1:17]
critic_to_death.17 <- c(rbind(critic_to_death.9, critic_to_death.9))[1:17]
dat <- data.frame( age=seq(0,16*5, by=5), srate=sympt.rate.17,
                  s2h=symp_to_hosp.17, s2c=symp_to_ICUs.17,
                  h2d=hosp_to_death.17, c2d=critic_to_death.17 )
#write.csv(dat, file="../../Data/Other/rates.csv", row.names=FALSE)
tail( dat, n=18 )
```

##	age	srate	s2h	s2c	h2d	c2d
## 1	0	0.008645652	0.2736602	0.044469783	0.01200963	0.00000000
## 2	5	0.005906960	0.2736602	0.044469783	0.01200963	0.00000000
## 3	10	0.007618587	0.1551619	0.014050092	0.02836919	0.00000000
## 4	15	0.007819069	0.1551619	0.014050092	0.02836919	0.00000000
## 5	20	0.056692914	0.1031127	0.006611693	0.01816117	0.08920068
## 6	25	0.053150070	0.1031127	0.006611693	0.01816117	0.08920068
## 7	30	0.091717091	0.1562348	0.012103008	0.01875775	0.08922120
## 8	35	0.075771140	0.1562348	0.012103008	0.01875775	0.08922120
## 9	40	0.076235827	0.2255870	0.021061619	0.02471233	0.12675973
## 10	45	0.070889071	0.2255870	0.021061619	0.02471233	0.12675973
## 11	50	0.093356488	0.2924008	0.036500444	0.04999652	0.16321338
## 12	55	0.088773572	0.2924008	0.036500444	0.04999652	0.16321338
## 13	60	0.095621079	0.4286962	0.073748545	0.11099737	0.31877131
## 14	65	0.091024193	0.4286962	0.073748545	0.11099737	0.31877131
## 15	70	0.101862331	0.5712480	0.069691459	0.30703479	0.43571619
## 16	75	0.114905481	0.5712480	0.069691459	0.30703479	0.43571619
## 17	80	0.289321537	0.4446118	0.006956023	0.68537289	0.59360625

The interesting aspect of these rates is that they are not strictly dependent on the knowledge of the detection rate. In other words,  $\text{sympt.rate.17} * \text{symp\_to\_hosp.17}$  is the rate an average infected individual will be hospitalized (severe case), independently on being symptomatic or asymptomatic. That means that as long as we have a detection rate, or better a symptomatic rate that is compatible with (meaning greater than) the hospitalization rate, we can rescale one of the terms of the multiplication according to what the other term becomes. What is invariant is the product. By splitting the product into detection rate and hospitalization rate, we retain the information on the detection rate: this could be used for comparison between countries.

## Comparisons and checks

We can compare the resulting rates with with the Infectious Fatality Ratio (IFR) from the Verity paper [Verity, R., et al. (2020). Estimates of the severity of coronavirus disease 2019: a model-based analysis. The Lancet Infectious Diseases.], and with other countries. This will provide an insight into the reliability of the estimates obtained above.

### Comparing with Verity IFR

How do expected deaths for Spain based on above numbers compare with those predicted with Verity IFR?

```
expected.deaths.17 <- age.pyram.17*sympt.rate.17*(symp_to_hosp.17*hosp_to_death.17+
                                                    symp_to_ICUs.17*critic_to_death.17)
print(sum(expected.deaths.17))
```

```
## [1] 455244.7
```

```
IFR <- c(0.00161, 0.00695, 0.0309, 0.0844, 0.161, 0.595, 1.93, 4.28, 7.80)/100.0
print(sum(age.pyram.9*IFR))
```

```
## [1] 633294.1
```

Here we are using a rough estimate of the number of deaths if 100% of the population were affected. The Verity IFR predicts a higher death toll, about 1.5 times higher. It is worth exploring where the difference comes from

```
expected.deaths.9 <- get.10y.from.5y( expected.deaths.17 )
print((age.pyram.9*IFR-expected.deaths.9)/expected.deaths.9)
```

```
##           [,1]      [,2]      [,3]      [,4]      [,5]      [,6]      [,7]      [,8]
## [1,] -0.3219686  1.046304  1.286695  1.537729  1.654119  2.172103  1.902605  0.9328091
##           [,9]
## [1,] -0.1271078
```

```
print(sum(age.pyram.9*IFR))
```

```
## [1] 633294.1
```

```
print(sum(expected.deaths.9))
```

```
## [1] 455244.7
```

The general consensus is that death in Spain (as in many European countries) are underestimated as they typically miss many elderly dying home or in care homes with typical COVID19 symptoms. However, here the bulk of the difference does not come from the oldest age groups, but from middle aged groups. This poses a doubt, which requires comparison with other countries.

We can have a look at two other data sets from European countries: from Italy and Germany.. At the 20th of May there were 31017 deaths in Italy, all age attributed. Germany has similarly recorded age for all deaths and is in fully updated at 23rd of March (Note: German data are reported in German from Robert Kock Institute; their age stratified data is reported in form of a plot. I sidlined retrieving data from the plot by accessing Wikipedia data which looks appropriate.) We can take the age pyramid of the two countries and rescale appropriately to check how Italian and German deaths would have appeared in Spain by accounting for demographic differences.

```
buildDataset <- function( deaths.9, pyram.17, def.pyram.9 ) {
  pyram.9 <- get.10y.from.5y(pyram.17)
  deaths.rescaled.9 <- (deaths.9/pyram.9)*def.pyram.9
  deaths.rescaled.9 <- deaths.rescaled.9*27650/sum(deaths.rescaled.9)
  return (deaths.rescaled.9)
}

# Rescaling for Spanish data (no rescale needed here!)
cases.deaths.rescaled.9 <- cases.deaths.9

# Loading and rescaling of Italian data
ITA <- c(4, 0, 14, 61, 268, 1101, 3219, 8447, 12691+5212)
ita.age.pyram.17 <- as.matrix( read.table("Data/Italy_5km_stats.dat",
                                         header=FALSE) )[,3]
ita.deaths.rescaled.9 <- buildDataset( ITA, ita.age.pyram.17, age.pyram.9 )

# Loading and rescaling of German data
GER <- c(1, 2, 8, 20, 62, 279, 761, 1844, 3689+1496+50)
ger.age.pyram.17 <- as.matrix( read.table("Data/Germany_5km_stats.dat",
                                         header=FALSE) )[,3]
ger.deaths.rescaled.9 <- buildDataset( GER, ger.age.pyram.17, age.pyram.9 )

# Datasets and Plots
ver.projections.9 <-
  as.vector((age.pyram.9*IFR)*sum(cases.deaths.rescaled.9)/sum(age.pyram.9*IFR))
df1 <- data.frame( age=seq(0,8*10,10), ita=as.vector(ita.deaths.rescaled.9),
                  ger=as.vector(ger.deaths.rescaled.9),
                  esp=cases.deaths.rescaled.9,
                  ver=ver.projections.9)
tail(df1, n=10)
```

```
##   age      ita      ger      esp      ver
```

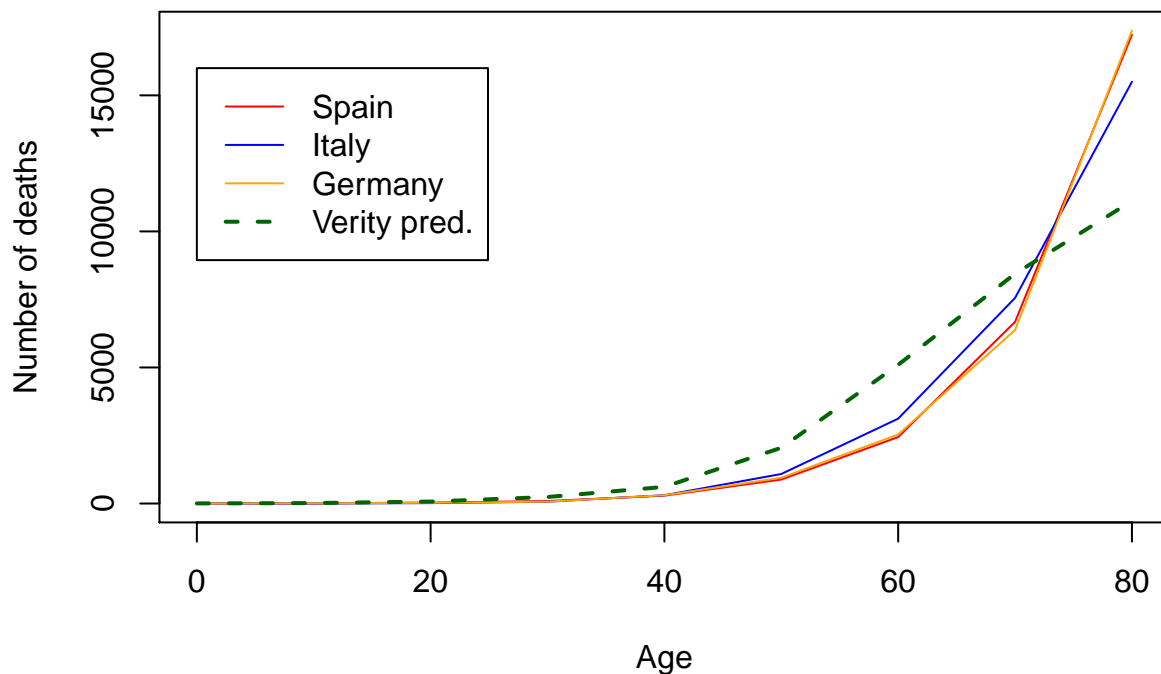
```
## 1  0      4.676917      3.815410      2.882310      3.478736
## 2 10      0.000000      8.544874      7.205775      16.717433
## 3 20     14.227736     25.248381     33.146565     71.174361
## 4 30     66.761145     68.737791     90.792766    239.274128
## 5 40    304.152275    304.233308    289.672157    610.868171
## 6 50   1084.241525   947.347881   880.545710   2049.188886
## 7 60   3119.473622  2536.680508  2442.757740  5097.205014
## 8 70   7556.523628  6376.405180  6675.430001  8444.863393
## 9 80  15499.943151 17378.986666 17227.566976 11117.229877
```

```
print(colSums(df1))
```

```
##   age   ita   ger   esp   ver
##  360 27650 27650 27650 27650
```

```
max.y = max(df1)
plot(c(0,80), c(0,max.y), type="n", xlab="Age", ylab="Number of deaths",
     main="Projected deaths according to Spanish age pyramid")
lines(df1$age, df1$esp, col="red", type='l')
lines(df1$age, df1$ita, col="blue")
lines(df1$age, df1$ger, col="orange")
lines(df1$age, df1$ver, col="darkgreen", lw=2, lt=2)
legend(0, 16000, c("Spain", "Italy", "Germany", "Verity pred."),
      col=c("red", "blue", "orange", "darkgreen"), lty=c(1,1,1,2), lw=c(1,1,1,2))
```

## Projected deaths according to Spanish age pyramid



It is evident that after rescaling, the Spanish, German and Italian sets have more similarity than the predictions from the Verity IFR. It also appears interesting that German and Spanish data sets are almost superimposing, suggesting that the Spanish dataset is sufficiently robust. This also reassures on the fact



that initially we proportionally redistributed, over all the age groups, the difference between the 27650 cases and the 19186 cases that had age information. However, it would be important to compare with additional countries. We add here a similar comparison with the additional sets from Portugal, Switzerland and Canada.

```
POR <- c(0, 0, 1, 0, 15, 41, 118, 258, 384+513)
por.age.pyram.17 <- as.matrix( read.table("Data/Portugal_5km_stats.dat",
                                         header=FALSE) )[,3]
por.deaths.rescaled.9 <- buildDataset( POR, por.age.pyram.17, age.pyram.9 )

CHZ <- c(0, 0, 0, 5, 4, 34, 114, 320, 1084)
chz.age.pyram.17 <- as.matrix( read.table("Data/Switzerland_5km_stats.dat",
                                         header=FALSE) )[,3]
chz.deaths.rescaled.9 <- buildDataset( CHZ, chz.age.pyram.17, age.pyram.9 )

# Loading and rescaling of Italian data
CAN <- c(0, 0, 3, 10, 36, 116, 382, 949, 3982+2153+1828)
can.age.pyram.17 <- c(1929522, 1993849, 1905977, 2067651, 2495075, 2575863,
                    2579123, 2501565, 2379067, 2363496, 2664738,
                    2725718, 2363696, 2019832, 1538354, 1056484, 817778)
can.deaths.rescaled.9 <- buildDataset( CAN, can.age.pyram.17, age.pyram.9 )

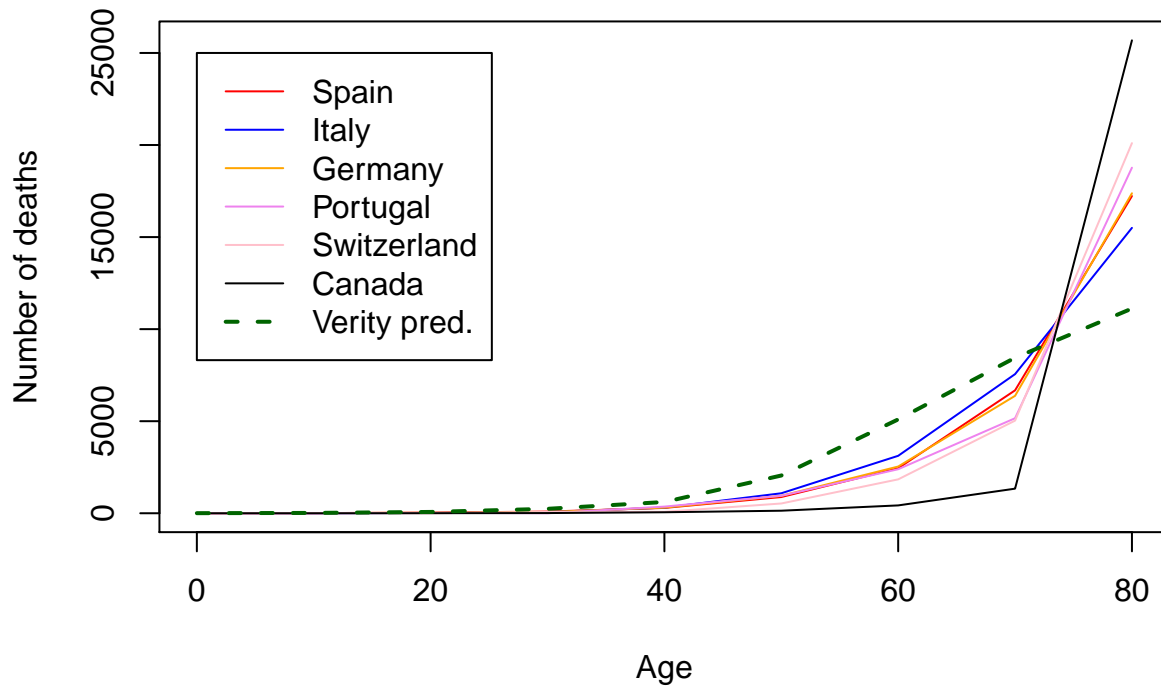
df2 <- data.frame( age=seq(0,8*10,10), por=as.vector(por.deaths.rescaled.9),
                  chz=as.vector(chz.deaths.rescaled.9),
                  can=as.vector(can.deaths.rescaled.9))

df0 <- merge(df1, df2, by.x='age', by.y='age')
```

Plots follow

```
max.y=max(df0)
plot(c(0,80), c(0, max.y), type='n', xlab="Age", ylab="Number of deaths",
     main = "Projected deaths according to Spanish age pyramid")
lines(df0$age, df0$esp, type='l', col="red")
lines(df0$age, df0$ita, col="blue")
lines(df0$age, df0$ger, col="orange")
lines(df0$age, df0$por, col="violet")
lines(df0$age, df0$chz, col="pink")
lines(df0$age, df0$can, col="black")
lines(df0$age, df0$ver, col="darkgreen", lw=2, lty=2)
legend(0,25000, c("Spain", "Italy", "Germany", "Portugal", "Switzerland",
                 "Canada", "Verity pred."), col=c("red", "blue",
                 "orange", "violet", "pink", "black", "darkgreen"),
      lty=c(1,1,1,1,1,1,2), lw=c(1,1,1,1,1,1,2))
```

## Projected deaths according to Spanish age pyramid



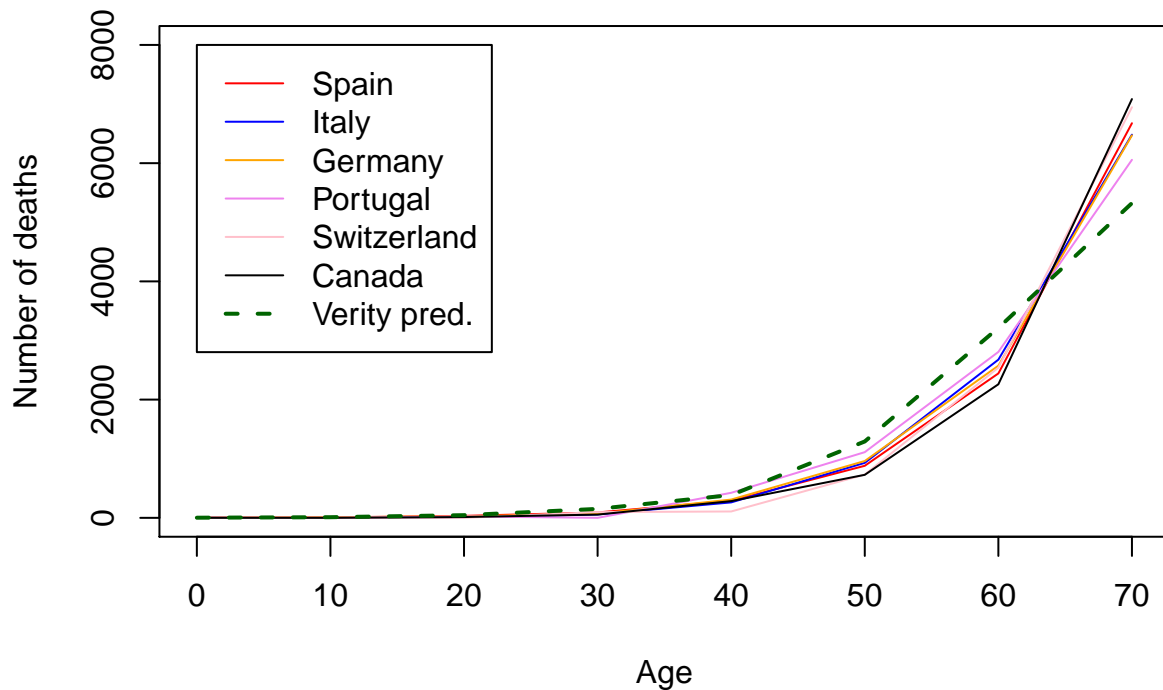
With respect to the other countries, Canada is remarkably different. However, cases are here renormalized so that we are taking age stratified cases in one country and compare with the Spanish case by accounting for demography and matching the total count number.

According to Wikipedia, the majority of deaths in eardarly in Canada occurred in long-term care home with “factors such as outside visitors, communal living spaces, and staff being transferred among multiple facilities, as particular vulnerabilities”. Estimates suggest that “as many of 79 percent of Canada’s COVID-19 fatalities occurred in long-term care homes”. So it is a problem common to many countries that was particularly exacerbated in Canada. Hence, do the curves resemble each other if we exclude the 80+ category? We can normalize up to the 70s and observe how close the curves are:

```
makePlot <- function(nn) {
  colours=c("red","blue", "orange","violet", "pink", "black", "darkgreen")
  max.y = 8000
  plot(c(0,(nn-1)*10), c(0,max.y), type="n", xlab="Age", ylab="Number of deaths",
       main = "Projected deaths renormalized to match the total of cases up to 70 y.o.")
  lines(df0$age[1:nn], df0$esp[1:nn]/sum(df0$esp[1:nn])*sum(df0$esp[1:nn]), type='l', col=colours[1])
  lines(df0$age[1:nn], df0$ita[1:nn]/sum(df0$ita[1:nn])*sum(df0$esp[1:nn]), type='l', col=colours[2])
  lines(df0$age[1:nn], df0$ger[1:nn]/sum(df0$ger[1:nn])*sum(df0$esp[1:nn]), type='l', col=colours[3])
  lines(df0$age[1:nn], df0$por[1:nn]/sum(df0$por[1:nn])*sum(df0$esp[1:nn]), type='l', col=colours[4])
  lines(df0$age[1:nn], df0$chz[1:nn]/sum(df0$chz[1:nn])*sum(df0$esp[1:nn]), type='l', col=colours[5])
  lines(df0$age[1:nn], df0$can[1:nn]/sum(df0$can[1:nn])*sum(df0$esp[1:nn]), type='l', col=colours[6])
  lines(df0$age[1:nn], df0$ver[1:nn]/sum(df0$ver[1:nn])*sum(df0$esp[1:nn]), type='l', col=colours[7],
        lw=2, lty=2)
  legend(0, 8000, c("Spain","Italy", "Germany", "Portugal", "Switzerland",
                   "Canada", "Verity pred."), col=colours,
        lty=c(1,1,1,1,1,1,2), lw=c(1,1,1,1,1,1,2))
}
```

```
}  
makePlot(8)
```

## Projected deaths renormalized to match the total of cases up to 70 y.



The plot still shows some variability in death incidence, but such variability is less dramatic and probably determined by stochastic effects and difference in age mixing. The Verity predictions are still somehow off. With this, we can thus assume that the the assumptions made about Spanish data are fine and we can save the rate to an external file.

```
#dat$s2h <- dat$s2h * 27650/19186.0 # <- C++ prgrammer idiosyncrasy  
#dat$s2c <- dat$s2c * 27650/19186.0  
#dat$srates <- dat$srates * 27650.0/19186  
  
print( paste('Check: 27650 =',sum(cases.total.17 * (dat$s2h*dat$h2d + dat$s2c*dat$c2d)) ) )  
  
## [1] "Check: 27650 = 27650"  
  
write.csv(dat, file="Output/rates.csv", row.names=FALSE)  
tail( dat, n=18 )
```

##	age	srates	s2h	s2c	h2d	c2d
## 1	0	0.008645652	0.2736602	0.044469783	0.01200963	0.00000000
## 2	5	0.005906960	0.2736602	0.044469783	0.01200963	0.00000000
## 3	10	0.007618587	0.1551619	0.014050092	0.02836919	0.00000000
## 4	15	0.007819069	0.1551619	0.014050092	0.02836919	0.00000000
## 5	20	0.056692914	0.1031127	0.006611693	0.01816117	0.08920068
## 6	25	0.053150070	0.1031127	0.006611693	0.01816117	0.08920068
## 7	30	0.091717091	0.1562348	0.012103008	0.01875775	0.08922120

```
## 8 35 0.075771140 0.1562348 0.012103008 0.01875775 0.08922120
## 9 40 0.076235827 0.2255870 0.021061619 0.02471233 0.12675973
## 10 45 0.070889071 0.2255870 0.021061619 0.02471233 0.12675973
## 11 50 0.093356488 0.2924008 0.036500444 0.04999652 0.16321338
## 12 55 0.088773572 0.2924008 0.036500444 0.04999652 0.16321338
## 13 60 0.095621079 0.4286962 0.073748545 0.11099737 0.31877131
## 14 65 0.091024193 0.4286962 0.073748545 0.11099737 0.31877131
## 15 70 0.101862331 0.5712480 0.069691459 0.30703479 0.43571619
## 16 75 0.114905481 0.5712480 0.069691459 0.30703479 0.43571619
## 17 80 0.289321537 0.4446118 0.006956023 0.68537289 0.59360625

sum(cases.deaths.17/(dat$rate*(dat$s2h*dat$h2d+dat$s2c*dat$c2d)))/sum(age.pyram.17)

## [1] 0.05072134

sum((spanish.estimate.count.17+cases.deaths.17)*dat$rate)

## [1] 239125

sum((spanish.estimate.count.17+cases.deaths.17)*dat$rate*(dat$s2h*dat$h2d+dat$s2c*dat$c2d))

## [1] 27650

sum(cases.deaths.17/(dat$rate*(dat$s2h*dat$h2d+dat$s2c*dat$c2d))-cases.deaths.17)

## [1] 2642226

sum(spanish.estimate.count.17)

## [1] 2642226
```

We can assume that all rates up to 70 y.o. are reasonably reliable, whilst death rates for 80+ is less reliable and strongly dependent on social factors.

## What to expect for Kenya

For Kenya, we can get a rough estimate of the expected deaths by applying the rates to the Kenyan age pyramid. Note that we multiply by the Spanish detection rate, but this is not important as what is fixed by the Spanish survey is the product of the detection rate by the hospitalization (severe or critical) rates. Thus, the assumption we are doing here is that hospitalization and acceptance to critical care are the same as European countries, irrelevant of the detection rate.

We can also take into account that only about 90% of the population will be infected in case of no control or insufficient control measures.

```
ken.age.pyram.17 <- as.matrix( read.table("Data/Kenya_5km_stats.dat",
                                         header=FALSE) )[,3]
kenya.projected.deaths.17 <- ken.age.pyram.17* dat$rate *
  (dat$s2h*dat$h2d+dat$s2c*dat$c2d)*0.9
print(paste('Total projected deaths:', floor(sum(kenya.projected.deaths.17)+0.5)))

## [1] "Total projected deaths: 44443"

print( data.frame( age=seq(0,80,5), deaths=kenya.projected.deaths.17 ) )
```

```
##   age   deaths
## 1    0  171.9144
## 2    5  112.6474
## 3   10  180.9363
```

```
## 4    15    162.2380
## 5    20    557.3178
## 6    25    453.5652
## 7    30   1180.0940
## 8    35    816.4306
## 9    40   1324.9549
## 10   45    904.5755
## 11   50   2190.9842
## 12   55   1584.7147
## 13   60   4586.2059
## 14   65   3154.7765
## 15   70   6412.4167
## 16   75   4284.8350
## 17   80  16363.9278
```

## Estimating number of infected worldwide

We could use the number of deaths and the serological survey to estimate the fraction of the population infected by COVID-19. For instance Italy:

```
ita.est.17 <- ita.age.pyram.17*dat$rate*(dat$s2h*dat$h2d+dat$s2c*dat$c2d)
ita.est.17 <- ita.est.17*sum(ITA)/sum(ita.est.17)
print(get.10y.from.5y(ita.est.17))
```

```
##           [,1]      [,2]      [,3]      [,4]      [,5]      [,6]      [,7]      [,8]
## [1,] 6.047914 10.00824 42.39897 120.032 280.2244 908.5053 2508.025 6766.375
##           [,9]
## [1,] 20375.38
```

```
print(ITA)
```

```
## [1]      4      0     14     61    268   1101   3219   8447 17903
```

```
sum(GER) / sum((get.10y.from.5y(ger.age.pyram.17)*symp.rate.9*
  (symp_to_hosp.9*hosp_to_death.9+symp_to_ICUs.9*critic_to_death.9)))*100.0
```

```
## [1] 1.113964
```

This of course works if deaths are registered similarly among nations. In addition, to apply this in general, we would need information on the distribution of cases by age for each country. This is not available for all countries, so we adopt a very rough approach by assuming that the cases do follow the expected distribution. This would not be correct, for instance, for Canada, and is likely to be a bit far-fetched. However, if we do insist in this approach, we can obtain an estimate of the fraction of the population who would result positive to a serological study in each country. We can use the JHSSE data set for the number of deaths (just to be sure I use data corresponding to 2 days earlier than the last day reported) and the UN estimates of population pyramids.

Read global datasets on deaths and population pyramids

```
library(dplyr)
```

```
##
## Attaching package: 'dplyr'
##
## The following objects are masked from 'package:stats':
##
##   filter, lag
```

```
## The following objects are masked from 'package:base':
##
## intersect, setdiff, setequal, union
```

```
SELECTED.DATE <- 'X5.31.20'
deaths <- read.csv("Data/time_series_covid19_deaths_global.csv", header=TRUE,
                  stringsAsFactors = FALSE)
pops <- read.csv("Data/WPP2019_POP_F07_1_POPULATION_BY_AGE_BOTH_SEXES.csv",
                header=TRUE, skip=16, stringsAsFactors = FALSE)
```

Perform some modification to match country names and exclude non-matching/missing countries.

```
d.countries <- unique(deaths$Country.Region)

names <- colnames(pops)
names[3] <- "Country"
colnames(pops) <- names
# Reset some country names (incomplete)
pops[pops$Country == "Iran (Islamic Republic of)",]$Country <- "Iran"
pops[pops$Country == "Russian Federation",]$Country <- "Russia"
pops[pops$Country == "Republic of Korea",]$Country <- "South Korea"
pops[pops$Country == "United States of America",]$Country <- "US"
pops[pops$Country == "Syrian Arab Republic",]$Country <- "Syria"

p.countries <- unique(pops$Country)
commonCountries <- d.countries[(d.countries %in% p.countries)]
deaths <- select( deaths[which(deaths$Country.Region %in% commonCountries),],
                 Country.Region, Province.State, SELECTED.DATE )
```

Group countries that are detailed in terms of provinces/territories (for some countries this is incorrect, i.e. the UK, but the difference is quite small) and merge the two data sets

```
deaths <- summarise_at( group_by(deaths, Country.Region), vars(SELECTED.DATE), sum)
pops <- pops[which(pops$Country %in% commonCountries),]
full <- merge(pops, deaths, by.x='Country', by.y='Country.Region', all=TRUE)
full <- full[full$Reference.date..as.of.1.July. == 2020,]
```

Build estimates by distributing deaths to age groups and reverting transformation to positives using Spanish survey data. Also add projected deaths for 90% infected population

```
format.rate <- function(x) {return(floor(10000*x+0.5)/100.0)}
transRate.9 <- sympt.rate.9*(symp_to_hosp.9*hosp_to_death.9+symp_to_ICUs.9*critic_to_death.9)
globalEstimates <- data.frame( Country=as.character(),
                              positive=as.numeric(), stringsAsFactors = FALSE )
transRate.17 <- sympt.rate.17*(symp_to_hosp.17*hosp_to_death.17+symp_to_ICUs.17*critic_to_death.17)

distributeCases <- function( total, distr ) {
  normdistr <- distr / sum(distr)
  return(total*normdistr)
}

getEstimates <- function( row ) {
  pyramid.21 <- as.numeric(gsub(" ", "", row[9:29]))
  pyramid.17 <- pyramid.21[1:17]*1000 # in thousands
  pyramid.17[17] <- pyramid.17[17] + sum(pyramid.21[18:21])*1000 # idem
  t.deaths <- as.numeric(gsub(" ", "", row[SELECTED.DATE]))
  d.deaths <- distributeCases(t.deaths, transRate.9*get.10y.from.5y(pyramid.17))
}
```

```

globalEstimates <- rbind(globalEstimates, data.frame( Country=row$Country,
  Positives=format.rate(sum(d.deaths / transRate.9-d.deaths) /
    sum(pyramid.17)),
  Deaths=t.deaths,
  Projection=sum(pyramid.17*transRate.17*0.9) ))
}
dummy <- by(full, 1:nrow(full), getEstimates) # This avoids output
globalEstimates <- globalEstimates[order(-globalEstimates$Positives),]
print(globalEstimates)

```

##	Country	Positives	Deaths	Projection
## 16	Belgium	10.05	9467	84066.6919
## 157	United Kingdom	7.47	38571	461507.7854
## 140	Spain	6.62	27127	365936.8856
## 44	Ecuador	6.59	3358	45764.1713
## 74	Ireland	6.19	1652	23893.2369
## 144	Sweden	5.41	4395	72604.5553
## 76	Italy	5.38	33415	553271.6847
## 54	France	5.07	28805	506443.3423
## 159	US	4.97	104381	1879640.8476
## 128	Sao Tome and Principe	4.74	12	227.4781
## 106	Netherlands	4.52	5975	118021.6806
## 118	Peru	4.19	4506	96661.2467
## 72	Iran	3.92	7797	178600.3126
## 82	Kuwait	3.90	212	4898.1778
## 22	Brazil	3.85	29314	683620.3832
## 156	United Arab Emirates	3.39	264	7049.1781
## 90	Luxembourg	2.98	110	3305.9537
## 145	Switzerland	2.81	1920	61154.2812
## 29	Canada	2.79	7374	235887.1829
## 99	Mexico	2.65	9930	336718.1783
## 115	Panama	2.29	336	13176.1907
## 153	Turkey	1.63	4540	249685.1048
## 43	Dominican Republic	1.57	502	28625.1643
## 122	Qatar	1.57	38	2190.0193
## 42	Djibouti	1.48	24	1459.4112
## 121	Portugal	1.45	1410	86775.2361
## 111	North Macedonia	1.32	133	9013.2426
## 41	Denmark	1.30	574	39515.0898
## 32	Chile	1.17	1054	80399.4091
## 67	Honduras	1.09	212	17476.8663
## 11	Bahamas	1.07	11	923.5872
## 58	Germany	1.06	8540	719087.2975
## 129	Saudi Arabia	1.04	503	43633.3164
## 47	Equatorial Guinea	0.96	12	1125.0466
## 12	Bahrain	0.94	19	1816.8163
## 7	Armenia	0.92	131	12789.9495
## 9	Austria	0.92	668	64753.0637
## 123	Romania	0.89	1266	126927.1364
## 113	Oman	0.85	49	5208.4570
## 5	Antigua and Barbuda	0.78	3	344.4527
## 28	Cameroon	0.77	191	22307.7633
## 68	Hungary	0.75	526	62874.4840
## 1	Afghanistan	0.73	257	31846.3170

## 20	Bosnia and Herzegovina	0.73	153	18759.1661
## 75	Israel	0.69	285	36761.1635
## 53	Finland	0.67	320	42629.8482
## 112	Norway	0.64	236	32730.2562
## 136	Slovenia	0.64	108	15136.5352
## 138	South Africa	0.62	683	99109.0583
## 49	Estonia	0.61	68	9979.9056
## 94	Maldives	0.60	5	754.1156
## 3	Algeria	0.59	653	98885.8436
## 55	Gabon	0.59	17	2581.5521
## 65	Guyana	0.57	12	1881.2376
## 133	Sierra Leone	0.57	46	7292.0681
## 34	Colombia	0.53	916	154661.8760
## 124	Russia	0.53	4693	787496.4357
## 45	Egypt	0.51	959	168963.4577
## 69	Iceland	0.51	10	1758.6142
## 137	Somalia	0.51	78	13890.5133
## 142	Sudan	0.51	286	50599.5250
## 31	Chad	0.46	65	12821.2815
## 87	Liberia	0.46	27	5288.7732
## 95	Mali	0.46	77	15197.3457
## 119	Philippines	0.45	957	191759.4939
## 64	Guinea-Bissau	0.44	8	1642.0581
## 97	Mauritania	0.43	23	4806.4320
## 114	Pakistan	0.43	1483	312402.4559
## 40	Czechia	0.42	320	67969.6834
## 73	Iraq	0.42	205	43479.4034
## 131	Serbia	0.42	243	51689.6857
## 15	Belarus	0.41	235	51184.3591
## 147	Tajikistan	0.40	47	10516.7630
## 120	Poland	0.39	1064	241615.3149
## 14	Barbados	0.36	7	1751.9649
## 26	Cabo Verde	0.34	4	1062.2181
## 109	Niger	0.32	64	18250.4642
## 62	Guatemala	0.31	108	31607.2481
## 24	Burkina Faso	0.30	53	15703.9423
## 37	Croatia	0.30	103	30923.7770
## 89	Lithuania	0.29	70	21484.3718
## 6	Argentina	0.27	539	176470.0408
## 71	Indonesia	0.27	1613	539867.7464
## 17	Belize	0.26	2	689.7100
## 23	Bulgaria	0.26	140	48409.2383
## 39	Cyprus	0.26	17	5852.2637
## 162	Yemen	0.26	80	27307.4632
## 96	Malta	0.25	9	3236.2871
## 101	Montenegro	0.25	9	3182.7649
## 155	Ukraine	0.25	708	254828.2362
## 10	Azerbaijan	0.24	63	24002.9035
## 108	Nicaragua	0.24	35	12991.8012
## 130	Senegal	0.24	42	16028.5658
## 2	Albania	0.22	33	13723.1630
## 35	Comoros	0.21	2	853.5443
## 46	El Salvador	0.21	46	19517.4242
## 66	Haiti	0.21	44	19109.4532



## 102	Morocco	0.21	205	87258.4026
## 13	Bangladesh	0.19	650	313195.6308
## 63	Guinea	0.18	23	11336.7217
## 98	Mauritius	0.18	10	4857.6561
## 60	Greece	0.17	175	93734.6977
## 70	India	0.17	5408	2782406.2346
## 110	Nigeria	0.16	287	164578.0204
## 150	Togo	0.16	13	7204.8818
## 84	Latvia	0.15	24	14162.8672
## 161	Western Sahara	0.15	1	597.4286
## 83	Kyrgyzstan	0.14	16	10583.9001
## 85	Lebanon	0.14	27	17498.4160
## 93	Malaysia	0.14	115	73212.3952
## 151	Trinidad and Tobago	0.14	8	4958.3821
## 81	Kenya	0.13	64	43557.1990
## 152	Tunisia	0.13	48	34389.0667
## 38	Cuba	0.12	83	62406.0861
## 50	Eswatini	0.12	2	1474.7404
## 59	Ghana	0.11	36	30754.5883
## 158	Uruguay	0.10	22	19864.9785
## 77	Jamaica	0.09	9	9286.7445
## 134	Singapore	0.09	23	23856.2007
## 135	Slovakia	0.09	28	28497.7904
## 33	China	0.08	4638	5053997.9433
## 139	South Sudan	0.08	10	11905.5676
## 80	Kazakhstan	0.07	40	50140.6260
## 107	New Zealand	0.07	22	26951.8369
## 8	Australia	0.06	103	146118.2737
## 78	Japan	0.06	898	1374329.4482
## 79	Jordan	0.06	9	13744.1437
## 117	Paraguay	0.06	11	15783.9207
## 143	Suriname	0.06	1	1413.5022
## 36	Costa Rica	0.05	10	17961.9596
## 56	Gambia	0.05	1	1892.9295
## 57	Georgia	0.05	12	21073.4246
## 163	Zambia	0.05	7	13061.2973
## 30	Central African Republic	0.04	2	4172.6568
## 88	Libya	0.04	5	10818.0632
## 21	Botswana	0.03	1	3134.0532
## 160	Uzbekistan	0.03	15	53949.7644
## 18	Benin	0.02	3	12618.0135
## 91	Madagascar	0.02	6	27507.9301
## 92	Malawi	0.02	4	15968.8092
## 146	Syria	0.02	5	27982.8472
## 148	Thailand	0.02	57	305374.1656
## 164	Zimbabwe	0.02	4	14475.1636
## 4	Angola	0.01	4	24075.6658
## 25	Burundi	0.01	1	8949.2832
## 51	Ethiopia	0.01	11	128507.7706
## 103	Mozambique	0.01	2	27634.9694
## 105	Nepal	0.01	8	50640.2223
## 125	Rwanda	0.01	1	12447.6870
## 141	Sri Lanka	0.01	10	70898.9168
## 19	Bhutan	0.00	0	1679.0836

## 27	Cambodia	0.00	0	24100.6791
## 48	Eritrea	0.00	0	4841.9293
## 52	Fiji	0.00	0	1475.5783
## 61	Grenada	0.00	0	356.0056
## 86	Lesotho	0.00	0	3362.8554
## 100	Mongolia	0.00	0	4859.2186
## 104	Namibia	0.00	0	3042.4614
## 116	Papua New Guinea	0.00	0	9342.7927
## 126	Saint Lucia	0.00	0	630.4366
## 127	Saint Vincent and the Grenadines	0.00	0	353.4695
## 132	Seychelles	0.00	0	244.9280
## 149	Timor-Leste	0.00	0	1735.4926
## 154	Uganda	0.00	0	29187.1981

Note that we are using the same approach for Spain, and the resulting percentage is higher than the one measured by the survey. This is a direct consequence of the fact that the implied distribution of cases is not the true one (checked, not shown). Not sure how to associate an error (bootstrapping?).

Summing up all projections we have the expected number of worldwide deaths.

```
print(paste('Expected number of worldwide deaths is:',
            floor(sum(globalEstimates$Projection))/1000000, 'millions'))
```

```
## [1] "Expected number of worldwide deaths is: 22.654741 millions"
```

```
""
```

## References

Spanish survey [ <https://www.mscbs.gob.es/gabinetePrensa/notaPrensa/pdf/13.05130520204528614.pdf> ]

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