# Age-dependent models

Let’s create a synthetic population following the frequencies of people in each age group as given by UN data: <https://population.un.org/wpp/Download/Standard/Population/>

We should note that the UN data is in thousands, so we need to scale the population accordingly.

Given the population age structure, we can easily calculate the number of age groups, A.

*# population structure in 2020*

popstruc <- read.csv("pop\_structure\_X.csv", header = TRUE)

*# convert from 1000s to total numbers*

popstruc[, 2] <- popstruc[, 2] \* 1000

A <- length(popstruc[, 2])

Here, we are also not sticking to a constant population size assumption. We can the same data source to inform the number births per time unit given the age of the mother. Again, notice the strange units the data comes in and what we need to do to inform the model parameters appropriately. Same thing can be said for mortality per person per time unit, our “natural” mortality (i.e., not disease induced).

*# births by age of mother*

popbirth <- read.csv("pop\_birth\_X.csv", header = TRUE)

*# convert from 1000s per 5 year period to per person per day*

popbirth[, 2] <- 1000 \* popbirth[, 2] / (5 \* popstruc[, 2] \* 365.25)

*#natural mortality per person per year*

popmort <- read.csv("pop\_mort\_X.csv", header = TRUE)

*# convert from 1000s per 5 year period to per person per day*

popmort[, 2] <- 1000 \* popmort[, 2] / (5 \* popstruc[, 2] \* 365.25)

mort <- popmort[, 2]

As we have done before, let’s import the relevant age contact matrices into the model. Note that there is a difference in the number of age groups in the population structure vs the contact data, where the contact matrices are cropped at 75+.

c\_home <- as.matrix(read.csv("contact\_home\_X.csv", header = FALSE))

c\_school <- as.matrix(read.csv("contact\_school\_X.csv", header = FALSE))

c\_work <- as.matrix(read.csv("contact\_work\_X.csv", header = FALSE))

c\_other <- as.matrix(read.csv("contact\_other\_X.csv", header = FALSE))

nce <- A - length(c\_home[1, ])

How is the code filling in the remaining age group contacts?

for (i in (A + 1 - nce):A){

  for (j in 1:(A - nce)){

    contact\_home[i, j] <- c\_home[(A - nce), j]

    contact\_school[i, j] <- c\_school[(A - nce), j]

    contact\_work[i, j] <- c\_work[(A - nce), j]

    contact\_other[i, j] <- c\_other[(A - nce), j]

  }

}

for (i in 1:(A - nce)){

  for (j in (A + 1 - nce):A){

    contact\_home[i, j] <- c\_home[i, (A - nce)]

    contact\_school[i, j] <- c\_school[i, (A - nce)]

    contact\_work[i, j] <- c\_work[i, (A - nce)]

    contact\_other[i, j] <- c\_other[i, (A - nce)]

  }

}

for (i in (A + 1 - nce):A){

  for (j in (A + 1 - nce):A){

    contact\_home[i, j] <- c\_home[(A - nce),(A - nce)]

    contact\_school[i, j] <- c\_school[(A - nce),(A - nce)]

    contact\_work[i, j] <- c\_work[(A - nce),(A - nce)]

    contact\_other[i, j] <- c\_other[(A - nce),(A - nce)]

  }

}

One very important aspect of an age-dependent model is how you implement transition between age groups. How would you describe the way it is implemented in the script?

*# per year ageing matrix*

dd <- seq(1:A) / seq(1:A)

ageing <- t(diff(diag(dd), lag = 1) / (5 \* 365.25))

ageing <- cbind(ageing, 0 \* seq(1:A)) *# no ageing from last compartment*

Next, we can just write down our set of initial conditions and parameter values. Note that we can initialise infection in specific age groups. Do you think that could potentially have an impact in the seeding of infections?

initP <- sum(popstruc[, 2]) *# population size*

ageindcase <- 20 *# age of index case (years)*

aci <- floor((ageindcase / 5) + 2) *# age class of index case*

*# MODEL INITIAL CONDITIONS*

initI <- 0 \* popstruc[, 2]*# Infected and symptomatic*

initE <- 0 \* popstruc[, 2] *# Incubating*

initE[aci] <- 1 *# place random index case in E compartment*

initR <- 0 \* popstruc[, 2] *# Immune*

initH <- 0 \* popstruc[, 2] *# hospitalised*

initM <- 0 \* popstruc[, 2] *# died*

initC <- 0 \* popstruc[, 2] *# Cumulative cases (true)*

initCM <- 0 \* popstruc[, 2] *# Cumulative deaths (true)*

initS <- popstruc[, 2] - initE - initI -

          initR - initH - initM *# Susceptible (non-immune)*

Following the implementation of the age-dependent model using indices for differential equations (as you did for the spatial model), run the ode function and plot:

* Total population size
* Daily reported incidence
* Hospital occupancy
* Cumulative mortality per age group

*# total population*

pop <- out[, (Sindex + 1)] + out[, (Eindex + 1)] + out[, (Iindex + 1)] +

       out[, (Rindex + 1)] + out[, (Hindex + 1)]

tpop <- rowSums(pop)

time <- as.Date(out[, 1] + startdate)

*# daily incidence*

inc <- parameters["report"] \* parameters["gamma"] \* out[, (Eindex + 1)]

dailyinc <- rowSums(inc)

hospreq <- rowSums(out[, (Hindex + 1)]) *# requirement for hospital beds*

cmortality <- rowSums(out[, (CMindex + 1)]) *# cumulative mortality*

*## plot incidence over time*

plot(rowSums(inc))

*# plot hospital occupancy against the number of hospital beds available*

plot(hospreq)

*#### age groups*

deaths <- (out[, CMindex + 1])

colnames(deaths) <- c("0-4", "5-9", "10-14", "15-19", "20-24",

            "25-29", "30-34", "35-39", "40-44", "45-49", "50-54",

            "55-59", "60-64", "65-69", "70-74", "75-79", "80-84",

            "85-89", "90-94", "95-99", "100+")

deaths\_prop <- round(tail(deaths, 1), 0) / sum(round(tail(deaths, 1), 0))

barplot(deaths\_prop)

Now, lets include two interventions in the model: social distancing (that works like a lockdown) and shielding of the elderly. For that we will need a different set of parameters and a new model function.

parameters\_intervention <- parameters

parameters\_intervention["social\_distancing\_start"] <- 20

parameters\_intervention["social\_distancing\_end"] <- 80

parameters\_intervention["social\_distancing\_effect"] <- 0.15

parameters\_intervention["shielding\_start"] <- 1e100

parameters\_intervention["shielding\_end"] <- 80

shielding\_effect <- seq(0, 100, by = 5)

Look at how those are implemented in the model. Social distancing affects contacts across all age groups, whereas shielding needs to be a vector, reflecting reduced contacts for each age groups once that intervention is active.

social\_distancing <- ifelse(t > social\_distancing\_start &

        t < social\_distancing\_end,

        social\_distancing\_effect, 1)

      shielding <- if (t > shielding\_start &

        t < shielding\_end) {

          (1 - shielding\_effect)

        }else {

           rep(1, A)

        }

lam <- p \* social\_distancing \*

        contacts %\*% (shielding \* (rho \* E + I + rhos \* H) / P)

Compare the social distancing strategy against shielding. Under what conditions (parameters ranges) and intervention logistics is the shielding strategy a viable strategy?

plot(rowSums(deaths), type = "l", col = "red")

lines(rowSums(deaths\_interv), type = "l", col = "blue")

lines(rowSums(deaths\_interv\_shielding), type = "l", col = "seagreen")

legend("topright", legend = c("Control", "Lockdown", "Shielding"), lwd = 1,

    col = c("red", "blue", "seagreen"))

What epidemiological metric would you focus on? Should it be unidimensional, i.e., only care about deaths?