Modelling the COVID-19 pandemic

Exercises Accompanying the Course Reaction Transport Modelling in the Hydrosphere

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The COVID-19 pandemic

Problem formulation

One of the most pervasive events in 2020 (and 2021) has been the COVID-19 pandemic, the disease caused by the SARS-CoV-2 ("Corona virus"), which almost halted the social and economic activity all over the world. Despite substantial efforts to contain the pandemic, the Corona virus spread all over Europe, causing many casualties.

The measures taken by the governments in the European countries to a large extent relied on the forecasts of mathematical models that describe the dynamics of infectious diseases (such as measles, rubella, flu, covid). In this exercise, we will first explain the ingredients of the simplest version of such models. Then, you will expand the model, adapt it to the COVID-19 pandemic, and make it as realistic as possible. You will do this based on the information we obtained from an expert from the Institute of Tropical Medicine ("Instituut voor Tropische Geneeskunde", ITG) in Antwerp, Belgium, who provided us with some insights into the characteristics of the COVID-19 pandemic. Because she is *not* a modeller, a considerable part of this exercise will involve figuring out the appropriate values for the model parameters. This will give you a "taste of a modeller's life".

S.I.R. models

Typically, the models used to investigate the spread of infectious diseases are called S.I.R. models. They describe the number of *S*usceptible, *I*nfected and *R*ecovered individuals in a population. Susceptible individuals are vulnerable to get the disease but are not (yet) infected. Infected individuals can recover, but some will die from the disease. Recovered individuals, at least initially, cannot become infected anymore.

As spreading the infection is *not* something that is actively pursued by the infected individuals, the *infection rate* can be modeled as if it were an *elementary chemical reaction*. That is, the infection rate depends on the probability of infected and susceptible people interacting, and the probability that an infection occurs as a result of this interaction. Thus, we describe the infection rate (in units of $ind.\ d^{-1}$, where *ind* stands for the number of individuals) with the following rate expression:

$$Infection = b \cdot I \cdot S.$$

Here, b is a rate constant that describes the infection rate (it has units of $ind^{-1}\ d^{-1}$), and I and S are the number of infected and susceptible individuals, respectively.[1]

Recovery from, and mortality of, infected individuals are modeled as simple first-order processes:

$$Recovery = g \cdot I,$$

[1] In some S.I.R. models the rate parameter b is replaced by β/N, where β has units of d^{-1} and N is the population density.

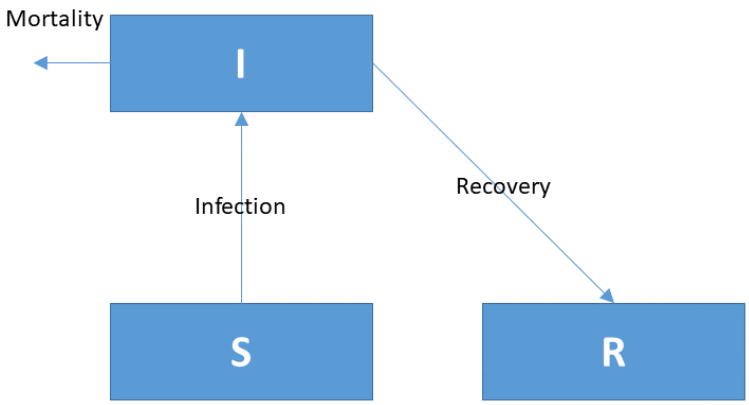


Figure 1: Conceptual scheme of the simplest SIR model.

$$Mortality = m \cdot I,$$

where g and m are the recovery and mortality rate constants, respectively.

The mass balance equations that describe the change in time of each population class are as follows:

$$\frac{dS}{dt} = -Infection,$$

$$\frac{dI}{dt} = Infection - Recovery - Mortality,$$

$$\frac{dR}{dt} = Recovery.$$

These equations imply that the rate constants g and m represent the *fraction* of the infected population that either recover or die *per day*, respectively (both in units of d^{-1}). For example, if there were no infection and no mortality ($b = m = 0$), the number of infected individuals would decrease at a rate $dI/dt = -g \cdot I$, i.e., at a rate proportional to the number of infected individuals. Thus, by normalizing this rate to the number of infected individuals $[(dI/dt)/I]$, we obtain the *fraction* of the infected population that recover per day, which is equal to g.

TASKS

1. Implement the simple S.I.R. model in R

The above model is the simplest S.I.R. model possible. It is not very realistic, and not very handy to be used as a decision-making tool. Nevertheless, you should start with implementing this model in *R* (R core team 2020) and solve it with the deSolve package (Soetaert et al., 2010). Use the template R markdown file *RTM_0D.Rmd* to implement this model.[2]

- Run the model for 365 days, using the following parameters (not patterned to the covid pandemic!):

Name	Value	Description	Unit
b	0.00000002	infection parameter	$ind^{-1}\ d^{-1}$
g	0.07	recovery parameter	d^{-1}
m	0.007	mortality parameter	d^{-1}

- Calculate the total population size in the model. This will allow you to keep track of the number of people that died from the disease. Think of an alternative way to keep track of these people. In this model we will ignore birth and mortality due to non-covid causes.
- Calculate the *average duration of the infectious period*, τ, i.e., the average number of days that an infected person stays infected. Tip: you can deduce this number by considering the meaning of the parameters g and m.[3]
- An often used number to designate the phase of the pandemic is the "Reproduction Number", *RN*. This is the number of people that one infected individual, on average, infects. When this number drops below 1, the number of infections will decrease (a good sign); when $RN > 1$, the number of infected individuals will increase — exponentially — in time (alarming). Add the reproduction number as an ordinary output variable to the model. You will need to derive the equation to estimate this number. Tip: use the rate expression for the number of infections per day to derive *RN*. You will also need to use the value of the parameter τ derived in the previous step.
- Apply the model to the Dutch or Belgian situation. You can start the simulation assuming that all Dutch/Belgian people are susceptible to the disease, and that the spreading of the disease starts with 1000 infected individuals that return from holidays. Assume that, overall, there are 17.5 million Dutch people and 11.5 million Belgians.

2. Vaccination and immunity loss

Add vaccination to the S.I.R. model. For now, you may assume that people that are vaccinated become resistant to the disease in a similar way as those that have recovered from the disease.

- Update your model with the vaccination. Assume that only susceptible individuals are vaccinated.
- For the rate expression, assume that a *fixed fraction* of susceptible people is vaccinated per day (a crude approximation). Study the impact of vaccination by changing the vaccination rate constant from 0 to greater values.

Unfortunately, recovered people can lose their immunity.

[2] You can obtain this file from Rstudio: File → new File → Rmarkdown → from template → RTM_0D. Save this file under a different name. Do not forget to change the heading of this file.

[3] Alternatively, you can derive it by solving the differential equation for I given above assuming that the infection rate is zero ($b = 0$), and starting with a specific number of infected individuals initially (e.g., $I_{ini} = 1000$). You will see how this is done rigorously in an appendix to the answers.

- Add the loss of immunity to the model.
- For the rate expression, assume that a fixed fraction of recovered people loses immunity per day.

3. Pressure on hospitals

One of the concerns at the start of the Covid-pandemic was that our hospitals would be swamped with Covid patients that cannot be treated anymore. A horror scenario is that patients need to wait in an ambulance (as in the UK), or be treated in corridors of the hospitals (as in Italy). Also, when hospitals have too many Covid patients, the treatment of non-Covid patients will be jeopardised.

The number of hospital beds is 60,000 in Belgium and 55,000 in the Netherlands, so these numbers are to be kept in mind when taking measures to keep the pandemic manageable.

- Update your model to include the number of patients *hospitalised* due to Covid-related complications.
- Find suitable rate expressions for the rates in and out of the new compartment.

4. Updated model

Based on tasks 2 and 3, you should now arrive at an updated version of your model, including the conceptual scheme, mass balance equations and rate expressions. Discuss your ideas with the lecturers before you proceed with the next step.

5. Finding realistic parameter values

As mentioned earlier, large part of modelling involves figuring out realistic values for the model parameters. You will do this now based on the information we received from the ITG expert. These are her quotes:

- Q1. "People that are infected by Covid-19 stay infectious on average for 10 days."
- Q2. "In Belgium and the Netherlands, the reproduction number RN at the start of the pandemic was between 2 and 4. A good guess is to take RN initially equal to 2.5."
  - You cannot use this number directly in your model. However, based on the analysis you made earlier in this exercise (Task 1), you can use it to estimate the infection parameter b.
- Q3. "The immunity of the recovered people is only temporary. It is assumed that people are only immune for about 6 months after recovery from the disease".
  - Use the same approach as in Task 1 (where you figured out how the average duration of infection, τ, is related to the rate constants g and m) to estimate a realistic value for the rate constant describing immunity loss.
- Q4. "It is estimated that 20% of infected people lack any symptoms; of the 80% that do show symptoms, 20% are seriously ill and are hospitalized."
  - Use this quote to estimate the rate constant describing the rate of hospitalisation, h. Hint: Consider that the 20% of the 80% amounts to the number of people that are hospitalized *at some point during the time* when they are infected. Thus, you will need the parameter τ to estimate h as a value *per day*.
- Q5. "On average, patients stay 10 days in the hospital. One quarter of the hospitalised patients are in the intensive care unit (ICU) where they have a probability of 30% to die from the disease. You can assume that all patients who die in hospital die while in ICU."
  - Use this quote to estimate the average mortality and the recovery rate *per day* of the hospitalised individuals.

- Q6. "Of all people that become infected, about 1% to 3% die."
  - This mortality rate is the *average* mortality experienced by *all* infected individuals, i.e., the "free-roaming" and hospitalised individuals. It is not possible to use this number directly. However,
  - you can assume that the total mortality for the free-roaming infected individuals is low, i.e., 0.1%.
  - Create an output variable that estimates the mean mortality of the entire infected population (hospitalised and "free-roaming") to check that this mean indeed fluctuates between 1% and 3%.

6. Implementation in R

Implement the updated model in *R*. Use the rate parameters derived from the expert's quotes.

7. Scenarios

Run several scenarios, patterned to the Belgian situation. There are 11.5 million Belgians, and the spreading of the disease starts with 1000 infected individuals that return from holidays.

- The first (worst case) scenario is where no measures at all are taken, and there is no vaccination.
- The second scenario ("social distancing") is where the number of contacts is reduced so that the probability of infection is only 60% of its original value.
- Last scenario is similar to the previous one, but there is additionally a certain fraction of the population vaccinated per day ("social distancing with vaccination"). Assume that 0.5% of the susceptible individuals are vaccinated per day (this is a crude approximation).

Compare all runs.

- How do these different scenarios affect the mortality rate?
- What are the implications of "social distancing" measures on the number of hospitalized and deceased people?
- What are the implications of the *combined* "social distancing with vaccination" measures, and of the "vaccination" alone (i.e., without "social distancing")?
- Explore different levels of social distancing combined with different vaccination rates. What vaccination rates are needed to achieve "meaningful" results while keeping the society as "free" as possible (i.e., no social distancing measures)?
- Discuss among each other how the model helps you understand the reaction of the different societies around the world to the COVID-19 pandemic over the past year.

ANSWERS

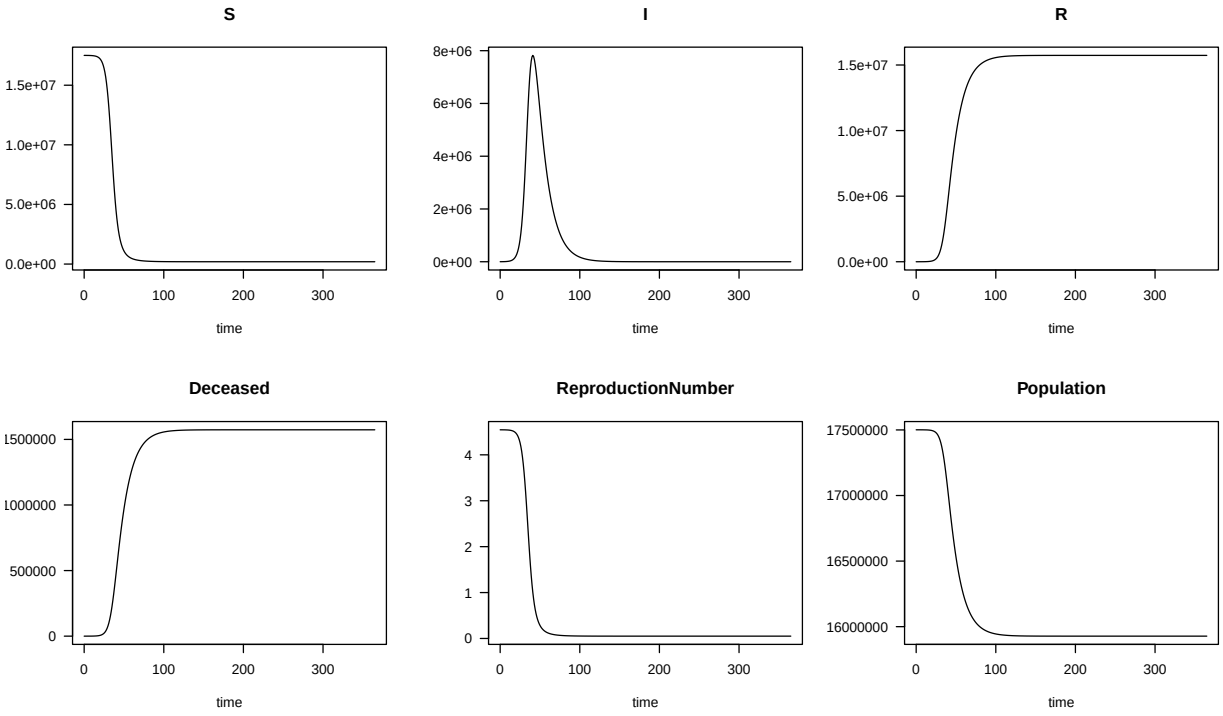
Task 1. The simple SIR model, implemented in R

- To calculate the average duration of the infection period, τ, the short answer is $\tau = 1/(g+m)$. This parameter corresponds to what is typically called the *residence time*. A rigorous mathematical derivation of the residence time is given in the Appendix, which shows that, for a first-order removal process characterized by the rate constant k, the residence time is $\tau = 1/k$. Applying this to the situation here, the rate constant characterizing the "removal" of infected individuals is $g+m$ (g due to recovery, m due to mortality), yielding the value of $\tau = 1/(g+m)$.
- The reproduction number (RN) can be estimated from the infection rate, which is the *total* number of infections per day. Dividing the infection rate by the number of infected individuals, we get the number of people that *one* infected individual infects on average *per day*. We need to multiply this with the average duration of the infectious period (parameter τ) to arrive at RN. Thus, $RN = \tau * Infection/I$, which yields
$$RN = \frac{b}{g+m} S.$$
- To keep an eye on the total number of deceased individuals, we introduce a new state variable that integrates the mortality rate over time:
$$\frac{dDeceased}{dt} = Mortality$$

Here is the implementation in R:

```
require(deSolve)    # the R-package for solving the model

# initial conditions, units of number of individuals (in the Netherlands)
state.SIR   <- c(S = 17500000, I = 1000, R = 0, Deceased = 0)

# model parameters
parms.SIR   <- c(
  b = 0.00000002,    # [1/ind/d], infection parameter
  g = 0.07,          # [1/d],     recovery rate of infected individuals
  m = 0.007          # [1/d],     mortality rate of infected individuals
)

# model function
SIR <- function(t, state, parameters) {
  with (as.list(c(state, parameters)), {

    # rate expressions
    Infection  <- b*S*I
    Recovery   <- g*I
    Mortality  <- m*I

    # mass balance equations
    dS          <- -Infection
    dI          <-  Infection - Recovery - Mortality
    dR          <-  Recovery
    dDeceased   <-  Mortality    # to track number of deceased people

    # average duration of infection and the Reproduction number
```

```
    tau  <- 1/(g+m)
    RN <- b*tau*S

    return (list(c(dS, dI, dR, dDeceased),  # the time derivatives
                 ReproductionNumber = RN,    # extra output variables
                 Population = S + I + R))
  })
}

# running the model
time.seq   <- seq(from = 0, to = 365, by = 1)    # time sequence, in days

# default run, business as usual scenario
out <- ode(y = state.SIR, times = time.seq, func = SIR, parms = parms.SIR)

# plot the results
plot(out, las = 1, col=1:2, lty=1)
```



Task 2. Vaccination and immunity loss

- If we assume that the vaccination protects people against infection in a similar way as those recovered from the disease, we do not need to add a new state variable. Vaccinated people are added to the *R*ecovered population without "passing through" the *I*nfected population. The rate expression is:

$$Vaccination = v \cdot S,$$

where v is the fraction of the *S*usceptible population that is vaccinated *per day*.

- Immunity loss causes a transition from *R*ecovered back to *S*usceptible, and it is expressed as:

$$ImmunityLoss = l \cdot R.$$

  Here, l is the fraction of *R*ecovered population that becomes *S*usceptible per day.

Task 3. Hospitalisations

The easiest way to track the number of people in hospitals is

- To distinguish between (1) infected individuals that are hospitalised (H) and (2) the "free-roaming" infected individuals[4] (I).
- Thus, the hospitalisation rate is calculated by assuming that a certain fracton of *infected* individuals end up in a hospital *per day* (parameter h), which gives

$$Hospitalisation = h \cdot I.$$

  These people are removed from the "free-roaming" infected population (I) and added to the hospitalised population (H).
- For simplicity, we assume that hospitalised patients do *not* infect other people. Thus, the infection rate remains to be given by $b \cdot S \cdot I$ (i.e., independent of H).
- The recovery rate of hospitalised individuals is not necessarily the same as that of the "free-roaming" infected individuals. However, we assume it is still described by the first-order kinetics:

$$RecoveryH = g_H \cdot H,$$

  where g_H is the corresponding rate constant.
- Unfortunately, the severeness of their symptoms significantly increases the mortality rate of hospitalised individuals (mortality parameter m_H). Again, we assume the rate is first-order:

$$MortalityH = m_H \cdot H.$$

Task 4. Updated model

The conceptual diagram describing the full COVID-19 model and the corresponding set of differential equations are therefore:

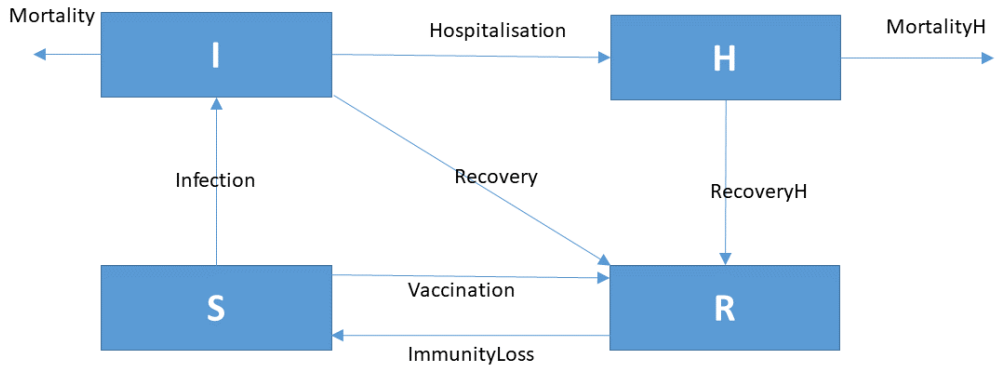


Figure 2: Conceptual scheme of the Covid-19 model

$$\frac{dS}{dt} = ImmunityLoss - Infection - Vaccination$$

[4]We borrow here a word commonly used in ecology, as even the experts could not come up with a good term.

$$\frac{dI}{dt} = Infection - Mortality - Recovery - Hospitalisation$$
$$\frac{dR}{dt} = Recovery + RecoveryH + Vaccination - ImmunityLoss$$
$$\frac{dH}{dt} = Hospitalisation - MortalityH - RecoveryH$$

Task 5. Better parameter values (the Belgian situation)

The quotes from the expert are used as follows:

- People that are infected and not in a hospital stay infectious for 10 days. Therefore, we have $\tau = 10\ d$. Using the result in Task 1, we therefore have $1/(g+m) = 10\ d$. As we will see later, the mortality rate constant for the "free-roaming" infected population is much lower than the recovery rate constant ($m << g$). Therefore, we have $g = 0.1\ d^{-1}$.
- We assume the reproduction number (RN) at the start of the pandemic to be $RN = 2.5$. In Task 1, we have determined that $RN = b \cdot \tau \cdot S$, which implies for the infection parameter b the value of $b = RN/S_{ini}/\tau = 2.5/11.5 \times 10^6/10 \approx 2.2 \times 10^{-8}\ ind^{-1}\ d^{-1}$, where we used $S_{ini} = 11.5 \times 10^6$ for the Belgian population. It may be useful to realise (or note) that the reproduction number does *not* depend on the number of infected people, but rather on the *behavior* of these people, as subsumed in the parameter b.
- Using the same argument as in Task 1, the rate constant for the immunity loss is estimated as $l = 1/(6 \times 30) = 0.00555\ d^{-1}$.
- If 80% of infected people have symptoms, of which 20% are seriously ill and are hospitalized, we can deduce that the probability of an infected individual being hospitalized is $0.8 \times 0.2 = 0.16$. However, this corresponds to the *entire* duration of the infectious period. Thus, the *hospitalisation* rate constant is $h = 0.16/\tau = 0.016\ d^{-1}$.
- The mortality rate for the hospitalised people takes into account the fact that all deaths are in the intensive care units, and this comprises 25% of the total hospitalisations. People in ICU have a probability of 30% to die. This over a period of 10 days. So, the mortality rate constant for the hospitalised people becomes $m_H = 0.3 \times 0.25/10 = 0.0075\ d^{-1}$.
- Because the average stay of infected people in the hospital is 10 days, we have $10 = 1/(g_H + m_H)$. This is based on the same argument as used in Task 1. Using this expression and the value for m_H, we obtain $g_H = 1/10 - m_H = 0.0925\ d^{-1}$.
- For the total mortality of "free-roaming" infected individuals of 0.1%, the parameter m becomes $m = 0.001/\tau = 0.0001\ d^{-1}$.

Task 6. Implementation in R

```
# the R-package for solving the model
require(deSolve)

# model parameters for Belgian case
parms      <- c(
  tau  = 10,          # [d], duration of the infectious period, free-roaming individuals
  tauH = 10,          # [d], duration of the infectious period, hospitalized individuals
  b = 2.5/11.5e6/10, # [1/ind/d], infection parameter, assuming RN=2.5, b=RN/Sini/d
  v = 0.0,            # [1/d] vaccination rate (no vaccines initially)
  g = 1/10,           # [1/d] recovery rate of free-roaming infected individuals, g=1/d
```

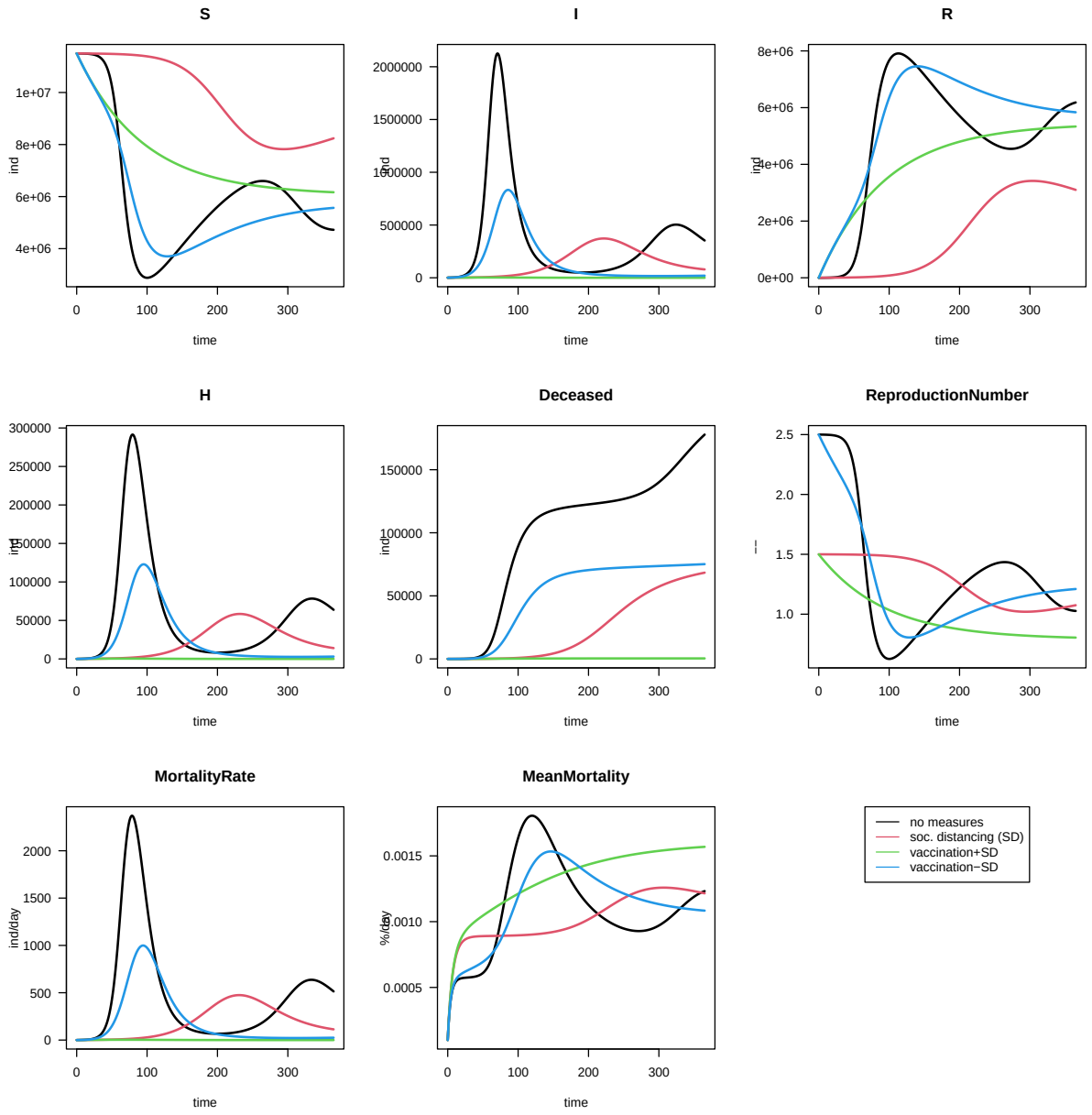
```
  m = 0.001/10,      # [1/d] mortality rate of free-roaming infected people, m=0.001/d
  l = 1/180,         # [1/d] immunity loss rate, l=1/(6*30)
  h = 0.2*0.8/10,    # [1/d] hospitalisation rate, h=0.8*0.2/d
  mH = 0.25*0.3/10,  # [1/d] mortality rate of hospitalised individuals, mH=0.25*0.3/dH
  gH = 1/10-0.25*0.3/10 # [1/d] recovery rate of hospitalised individuals, gH=1/dH-mH
)

# the model function
Corona <- function(t, state, parameters) {
  with (as.list(c(state, parameters)), {

    # rate expressions - units of [ind/day]
    Infection          <- b*S*I
    Vaccination        <- v*S
    Recovery           <- g*I
    Mortality          <- m*I    # Daily mortality of "free-roaming" infected
    ImmunityLoss       <- l*R    # Daily loss of immunity of recovered individuals
    Hospitalisation    <- h*I    # Daily rate of hospitalizations of infected persons
    MortalityH         <- mH*H   # Mortality rate of hospitalised persons
    RecoveryH          <- gH*H   # Recovery rate of hospitalised persons

    # mass balance equations
    dS        <- -Infection - Vaccination + ImmunityLoss
    dI        <-  Infection - Recovery - Mortality - Hospitalisation
    dR        <-  Recovery  + RecoveryH + Vaccination - ImmunityLoss
    dH        <-  Hospitalisation - RecoveryH - MortalityH
    dDeceased <-  Mortality + MortalityH # auxillary, track deceased individuals

    return (list(c(dS, dI, dR, dH, dDeceased),           # the time derivatives
                 ReproductionNumber = tau*Infection/I,   # output variables
                 MortalityRate = Mortality+MortalityH,   # daily mortality rate (ind/d)
                 MeanMortality = (Mortality+MortalityH)/(I+H) # fraction of infected
                                                              # that die per day
                 ))
  })
}
```

Task 7. Scenarios

The model is applied to the Belgian case:

```
# the R-package for solving the model
require(deSolve)

# initial conditions, units of number of individuals (in Belgium)
state      <- c(S = 11500000, I = 1000, R = 0, H = 0, Deceased = 0)

time.seq   <- seq(from = 0, to = 365, by = 1)

# default run, business as usual
out <- ode(y = state, times = time.seq, func = Corona, parms = parms)

# run with reduced infection rate to 60% (social distancing)
```

```r
parms2 <- parms
parms2["b"] <- parms2["b"]*0.6
out2 <- ode(y = state, times = time.seq, func = Corona, parms = parms2)

# add vaccination
parms3 <- parms2
parms3["v"] <- 0.005
out3 <- ode(y = state, times = time.seq, func = Corona, parms = parms3)

# vaccination but without social distancing
parms4 <- parms
parms4["v"] <- 0.005
out4 <- ode(y = state, times = time.seq, func = Corona, parms = parms4)

par(oma = c(0,2,0,0))
plot(out, out2, out3, out4, xlab = "time", lwd = 2, lty = 1, las = 1, mfrow=c(3,3),
     ylab=c("ind","ind","ind","ind","ind","--","ind/day","%/day",""))
plot.new()
legend("top", col = 1:4, lty = 1,
       legend = c("no measures", "soc. distancing (SD)",
                  "vaccination+SD", "vaccination-SD"))
```



Final remarks

The simulations performed above are only realistic at the start of the pandemic. This is because they assume that the model parameters remain constant. However, in reality the parameters are frequently changed because the society *does* take measures, which themselves evolve in time. While such changes in parameter values are perfectly possible to implement in *R*, it would go far beyond the scope of this introductory course in modelling to explore them. Nevertheless, the exercise gives you a "taste" of how models can help design strategies in this type of circumstances.

But: as we have mentioned several times, models are just an abstraction of reality, and they cannot capture everything!

References

R Core Team (2020). R: A language and environment for statistical computing. R Foundation for Statistical Computing, Vienna, Austria. URL https://www.R-project.org/.

Karline Soetaert, Thomas Petzoldt, R. Woodrow Setzer (2010). Solving Differential Equations in R: Package deSolve. Journal of Statistical Software, 33(9), 1–25. URL http://www.jstatsoft.org/v33/i09/ DOI 10.18637/jss.v033.i09

Appendix — Residence time for a first-order removal process

Here we show how to calculate the *residence time* (τ) for a first-order removal process. We consider a process that transfers individuals from the category "infected" to the category "recovered" ($I \rightarrow R$). We assume that the rate of this process is described by the first-order kinetics, i.e., the removal rate is $k \cdot I$, where k is the rate constant and I is the number of infected individuals. The mass balance equation describing the time evolution of I is then given as

$$\frac{dI}{dt} = -k \cdot I.$$

The solution to this differential equation is an exponentially decreasing function

$$I(t) = I_{ini} \cdot e^{-kt},$$

where I_{ini} is the initial value of I.

Suppose that we have initially 1000 individuals ($I_{ini} = 1000$) and the rate constant is $k = 0.1\ d^{-1}$. Using the equation above, the number of infected individuals on day zero will be $I(0) = 1000 \cdot e^{-0} = 1000$, on day one it will be $I(1) = 1000 \cdot e^{-0.1 \cdot 1} = 905$, on day two it will be $I(2) = 1000 \cdot e^{-0.1 \cdot 2} = 819$, etc.

If we now select a *random* individual from the population of 1000 individuals, it is clear that the *probability* that the individual is in the category "infected" decreases exponentially with time in the *same way* as the total number of infected individuals. For a given time point, t, we denote by $p(t)$ the probability that the individual who started initially as infected *remains* infected until the time point t. Thus, we have

$$p(t) = A \cdot e^{-kt},$$

where A is the normalization constant such that

$$\int_0^\infty p(t)\, dt = 1.$$

Using the above function for $p(t)$, this integral can rather easily be calculated. We obtain:

$$1 = \int_0^\infty p(t)\, dt = \int_0^\infty A\, e^{-kt}\, dt = \frac{A}{k} \quad \rightarrow \quad A = k.$$

Now we apply some knowledge about probabilities. Specifically, if we have a *discrete random* variable that takes the value of t_i with a probability of p_i, then the *mean value* (often denoted as $\langle t \rangle$) of this random variable is calculated as

$$\langle t \rangle = \sum_{i=1}^{\infty} t_i \cdot p_i.$$

If the random variable is *continuous*, the mean value is calculated from the integral

$$\langle t \rangle = \int_0^\infty t \cdot p(t)\, dt.$$

Combining the results above, we can calculate the *average time during which a randomly selected individual is in the category "infected"*, which we denote as τ. This parameter is often called the *residence time*, as it describes the average time a substance "resides" in the source compartment before it is removed. We obtain[5]

$$\tau = \int_0^\infty t \cdot p(t)\, dt = k \int_0^\infty t \cdot e^{-kt}\, dt = k\, \frac{1}{k^2} = \frac{1}{k}.$$

This shows that for a first-order removal process, the *residence time* is the *reciprocal* of the rate constant: $\tau = 1/k$.

To demonstrate that $\tau = 1/(g+m)$, we use the simple SIR model and calculate τ by approximating the integrals numerically by sums, where we follow an initial population of 1000 infected individuals, assuming that there are no further infections ($b = 0$).

```
parms2      <- parms.SIR
parms2["b"] <- 0
out2 <- ode(y = state.SIR, times = time.seq, func = SIR, parms = parms2)
# probability of being categorized as "infected" at time point t:
Prob <- out2[,"I"]/sum(out2[,"I"])
# average time to be categorized as "infected":
tau  <- sum(Prob*time.seq)
```

The average duration of infection calculated numerically from the probability is $\tau = 12.49$ days. The value calculated from parameters g and m is $\tau = 1/(g+m) = 12.99$ days.

[5]Note that in the second last step, we looked up the value of the integral in a table of integrals: $\int_0^\infty t\, e^{-kt}\, dt = 1/k^2$.