

# MB IA Assessed Practical 2 (Easter 2019)

*Revised version 21 March 2019*

## 1 Aims

Analyse the dynamics of the simple epidemic model (SIR) defined by the following system of differential equations:

$$\begin{aligned}\frac{dS}{dt} &= -\beta SI \\ \frac{dI}{dt} &= \beta SI - \gamma I\end{aligned}$$

This assessed practical makes use of the different programming methods you learned in the Lent term. The step-by-step questions will guide you to produce figures similar to those in the lecture notes (Lecture 5 - Simple epidemic models).

## 2 Assessment

Your report, in the form of an R markdown document (in .Rmd format) should be submitted electronically via Moodle, before 17.00 on 9th May 2019.

Please make sure to include your name and CRSid in the body of your report; you should also include your CRSid in the name of the file, which should be titled ‘MathBiolAssessedPractical2\_XXXX’ (replacing the XXXX with your CRSid)

Your assignment will be marked by loading the R markdown into a clean environment and checking what is produced; you might therefore wish to check that your code works in an entirely self-contained manner and does not rely on details of the environment that were altered during development (e.g. by shutting R, starting R, loading your .Rmd file and knitting it).

Notes:

- This assignment does not require any external data files, so there is no need to specify a working directory (in other words, don’t use the `setwd` function).
- As a pre-requisite, the `deSolve` package must be installed on your computer; however there is no need to include the `install.packages("deSolve")` command in your .Rmd file.
- The code you have to write is very similar to that from the last two practicals (which are available on Moodle). Keep in mind that there may be different ways to write code to get correct results. The practical will be assessed primarily on the results.
- To get started, open RStudio, check if `deSolve` is installed on your computer (look under the Packages tab); if not, install it. Then, create a new “R Markdown” file in RStudio, enter “MB Assessed Practical 2” as the title and your name as the author, and select html output. In the new file, leave the header as it is and delete the default contents starting with `## R Markdown`.
- Remember to write the R code inside “chunks” (click on the Insert icon and select R). Use a new chunk to write and run the R code for each question.

## 3 Assistance

Assistance will be available from demonstrators during an optional, ‘drop-in’ practical class that will be held on 25/4/2019, between 14.00 and 18.00, in the Titan Teaching Rooms. Please note that the purpose of this class is to provide help with any difficulties you have encountered while starting to prepare your report; you should not aim to compose the whole report from start to finish during the class.

## 4 Questions

1. Write a function `R0(beta,gamma,N)` which takes three arguments ( $\beta$ ,  $\gamma$  and the population size  $N$ ) and returns the basic reproductive ratio  $R_0 = \beta N / \gamma$ .
2. Write code to generate a plot of  $R_0$  against the recovery rate  $\gamma$  ranging from 0.1 to 2, with fixed values  $\beta = 0.01$  and  $N = 100$ . Then, using the `abline` function, add a horizontal line to show the threshold  $R_0 = 1$  on the same plot.
3. Write a function `SIR_dydt(t,y,parms)` which takes three arguments (time  $t$ , current values of the variables, and values of the model parameters) and returns a list whose only element is a vector with the values of the derivatives  $dS/dt$  and  $dI/dt$  (see Practical 15).
4. Before trying to solve the model, you should test that your `SIR_dydt` function works correctly. According to the model definition,  $dS/dt$  should always be negative, whereas  $dI/dt$  will only be positive if  $\beta S > \gamma$  and  $I > 0$ .
  - a. Setting  $\beta = 0.01$ ,  $\gamma = 0.4$ ,  $I = 1$ , write a for loop that prints the value of  $dI/dt$  for  $S$  ranging from 10 to 100 in steps of 10.
  - b. Based on the last output, what is the critical density of susceptible individuals required for an epidemic?
5. Load the `deSolve` library. Using the function `ode()`, compute the solution of the SIR model with  $N = 100$ ,  $\beta = 0.01$ ,  $\gamma = 0.4$ , initial conditions  $S(0) = 99.9$ ,  $I(0) = 0.1$ , and a vector of time points ranging from 0 to 50. Plot the solution in the (S,I) phase plane.
6. Create a vector containing the number of recovered individuals at the same time points as in question 5. Plot all three variables (S, I and R) against time. Your plot should look similar to Figure 5.4 in Lecture 5 (you can use different line styles or different colours).
7. This question aims to estimate the final epidemic size  $f$  without using the differential equations. Recall from lecture 5 (Epidemic models) that  $f$  is the non-zero solution of the following equation:

$$1 - f - e^{-R_0 f} = 0$$

- a. Write a function `fes_eq(f,r0)` which calculates the left-hand-side of the equation, given the values of  $f$  and  $R_0$ .
- b. Using  $R_0 = 2.5$ , plot the left-hand side of the equation against  $f$ , for  $f$  ranging from 0 to 1.
- c. Using  $R_0 = 2.5$ , write a `while()` loop that goes through values of  $f$  from 1 downwards in steps of 0.001, stopping when the value of `fes_eq(f,r0)` becomes non-negative. Print the resulting value of  $f$ .
- d. Using your code from questions (a) and (c), write a function `fes_sol(r0)` which returns an approximate value of the final epidemic size  $f$  for any given value of  $R_0$ .
- e. Plot the final epidemic size as a function of  $R_0$ , for  $R_0$  ranging from 1 to 6. You should obtain a graph similar to Figure 5.5 in the Lecture notes.