Epidemic Models Practical 1 (Lecture 6): Deterministic compartmental models in homogeneous populations

Accompanying R codes (for verification only!): EpiPractical 1 – Section1.R (Basic SIR model without demography), EpiPractical 1 – Section2.R (Basic SIR model with demography) , EpiPractical 1 – Section3.R (more complex models)

Approximate time: 1 hour

Outline:

In this practical you will learn

- Coding different types of deterministic epidemiological models
- How to explore properties of epidemiological models and interpret their results

1. The basic SIR model without demography

Case study PRRS: A pig farmer with a herd of 1000 pigs initially diagnosed 1 piglet showing symptoms of PRRS virus infections. Over the next few days, the number of pigs with PRRS symptoms increased dramatically. After about 2 weeks over half of the herd was infected. Within 2 months the epidemic had apparently become extinguished. The farmer recorded every third day the number of piglets diagnosed with PRRS, which is shown by the dots in the figure below.
We can model the PRRS outbreak in this herd using an SIR model. Using statistical inference (see upcoming lecture later this week), the average infectious period ($1/\gamma$) was estimated as 8.2 days and the transmission rate β was estimated as 0.83 per day. Figure 1 shows that the SIR model with these parameters produces a prevalence curve that is in good agreement with the data.
Let's code the model and explore some of its properties:

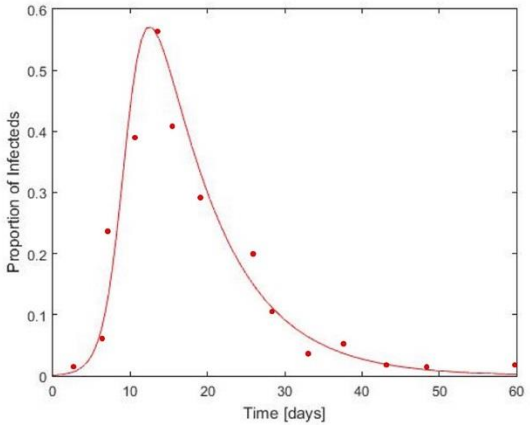

Figure 1: Observed proportion of infected piglets (dots) and modelled prevalence profiles generated by the SIR model with $\beta = 0.83$ per day and $1/\gamma = 8.2$ days and 1 initially infected piglet introduced into a population of 999 susceptible pigs.

1.1 Setting up the model. Write down the equations for the SIR model without demography and demonstrate that the population size is constant (i.e. dN/dt = 0). Calculate the value for R0 for the model with the values for β and γ given above. What does this imply for the risk of the epidemic kicking off?

1.2. Coding the model.

Open R and install the package deSolve. Create a new text file and Create a function that returns the derivatives dS/dt ,dI/dt and dR/dt as a list by typing in:

```
#SIR model without demography – practical 1
library(deSolve)
SIR.mod <- function(t,var,par) {
#Rename variables and parameters
S<- var[1]
I<- var[2]
R<- var[3]
N<- S+I+R
beta<- par[1]
gamma<-par[2]
#The model equations
dS<- - beta*S*I
dI <- beta*S*I-gamma*I
dR<- gamma*I
#return the three derivatives in a list
list(c(dS,dI,dR)) }
```

Next, define parameter values and initial conditions by tying in

```
beta <-0.83
gamma <- 1.0/8.2
SIR.par <- c(beta,gamma)
SIR.init <- c(0.999, 0.001, 0)
SIR.t <- seq(0,60, by=0.1)
```

Note that the initial conditions SIR.init represent 1 infected individual in a population of 999 susceptible and no recovered individuals.

Next, calculate the numerical solutions for the SIR model by calling the numerical solver `lsoda()`. Note that the command below converts the output of the `lsoda` function (a matrix object) to a dataframe, which allows variable naming.

```
SIR.sol <- as.data.frame(lsoda(SIR.init, SIR.t, SIR.mod, SIR.par))
```

And rename your variables for further use

```
names(SIR.sol)[2:4]<-c("S","I","R")

SIR.sol$N<-apply(SIR.sol[,2:4],1,sum)
```

Next, generate a plot that shows the 3 solutions for the fraction of susceptibles (in green), infected (in red) and recovered (in black) over time using the commands plot(), lines(), legend() and col(). Save this plot as SIR_mod1.

SAVE THE R-FILE!
(See file EpiPractical 1 - Section 1.R, if you want to cheat ☺)

1.3. Exploring the model

Inspect the graph generated above to answer the following questions:

- **At what time does the epidemic reach its peak and what is the maximum proportion of infected at this peak time?**
- **How long does it take until less than 5% of piglets remain infected?**
- **How many pigs become infected in total?**
- **Verify, both analytically (by using the fact that the derivative is zero at the peak) and by inspecting the graph that the epidemic reaches its peak when S = γ / β**

1.4. Modelling different scenarios

Generate a new R-file (or add new code to the existing file) in which you modify the code above to explore the following scenarios:

1.4a. (Effect of initial conditions) Pig farms often experience recurrent PRRS outbreaks. Imagine the above farm already experiences the second outbreak within this year, which again is caused by one initially infected pig with the same virus strain. But this time only 50% of pigs are susceptible (i.e. almost 50% are already immune). Will the second outbreak be as severe as the first outbreak?
Modify the code above to generate the equivalent plot for the time profiles as the one above and compare the two plots by comparing the total proportion of infected and the time and value for peak prevalence.
[Tip: generate new initial conditions by defining a set of values SIR.init.a <- ….**]**

What is the proportion of immune pigs required for the second outbreak not to occur? Based on this, what recommendation would you provide to the farmer in terms of restocking his population?

1.4b (Effect of a more virulent virus strain): Now model the epidemics as if the 2nd outbreak was caused by a pig infected with a more virulent PRRS virus strain that doubles the above transmission rate, and all other pigs are susceptible to this strain**. Compare the severity and duration of the first and second epidemic.**

1.4c (Effect of treatment) How much would R0, the maximum and total proportion of infecteds drop if the desperate farmer managed to get hold of a treatment that cures each pig after 2 days of infection?
How fast would the treatment need to act to completely prevent an outbreak?

2. The SIR model with demography

The SIR model with birth and death is given by the equation

$$\frac{dS}{dt} = \mu - \beta S I - \mu S$$

$$\frac{dI}{dt} = \beta S I - \gamma I - \mu I$$

$$\frac{dR}{dt} = \gamma I - \mu R$$

2.1. Verify that the population size of the above model is constant and that this model has two equilibria, where the disease free equilibrium is (S*,I*,R) = (1,0,0) and the endemic equilibrium is $(S^*, I^*, R^*) = (\frac{1}{R_0}, \frac{\mu}{\beta}\ (R_0 - 1), 1 - \frac{1}{R_0} - \frac{\mu}{\beta}\ (R_0 - 1))$**.** [Tip: Start by setting the above equations for the infectives equal to zero and solve for S*]

2.2. Start a new R text file to code the SIR model with demography.
Copy the code for the above SIR model without demography and modify it by writing a function SIRwithDemo.mod() that calculates the derivatives dS, dI, dR corresponding to the model with demography above, and solve it with the numerical solver lsoda()
Next, generate the profiles for the proportion of susceptible (S), infected (I) and recovered or removed (R) individuals over time for the following parameter values and initial conditions:

```
beta <- 1.66
gamma <- 1 / 2
mu <- 10/365
SIR.par <- c(beta,gamma, mu)
SIR.init <- c(0.5, 0.001, 1-0.5-0.001)
SIR.t <- seq(0,100, by =0.1)
```

- **What effect do birth and death have on the epidemiological profiles in the short and long-term?**
- **How many days pass approximately between the first and 2nd peak?**
- **Calculate R0 and the endemic equilibrium for the parameters given above.**
- **What happens if you increase the birth and death rate μ, in particular if μ approaches 1?**
- **What is the threshold value for the natural birth and death rate μ to prevent the disease outbreak altogether?**

3. Optional section: Adding complexity to the SIR model.

Sketch a diagram, showing the compartments and the flows between them, and write down the model equations and modify the R-code above to model the following scenarios and answer the corresponding questions in bold:

3a. Loss of immunity

Assume the assumption of lifelong immunity does not hold in the above SIR model with demography. Instead recovered individuals are only immune for a relatively short period of time before they become susceptible again.

How does the duration of the immune period affect disease prevalence, the period of oscillations and the final size of the epidemic (where the final size is defined as S(0)-S(infinity))?

3b. Inclusion of a latent period: The SEIR model

For many infections, individuals don't start to immediately transmit the infection upon becoming infected. Instead, there is a period of time during which the pathogen reproduces within the host but the host is not infectious. Hence the host cannot be categorized as susceptible, infectious or recovered, but we need to include another compartment, referred to 'Exposed' for individuals that are infected but not yet infectious.

Compare the infection profiles for the SEIR model with the equivalent SIR model (ignoring the exposed compartment). What effect does this additional compartment have on the equilibrium and on the early stages of the epidemics?