Imperial College London – Zambart

Workshop on *Analysing and modelling epidemic data*

Practical: Expanding the SIR model.

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Adapted using materials from Prof Nim Arinaminpathy

The aims of the practical are:

- To introduce yourselves to the rationale for expanding a mathematical model.
- To explore the concepts of constant vs varying hazards in a dynamic transmission model.

In this hand-out, generally:

▶ Indicates an instruction.

▶ Indicates a useful tip or note.

▶ Indicates a question.

Example 1: open SIR model

► *Navigate to the odin interface* https://shiny.dide.ic.ac.uk/infectiousdiseasemodels-lusaka-2022/ *in Chrome or Safari.*

► *In the Thursday section, "Expanding the SIR model", click on "Example 1".*

Thus far, we have been working with a simple SIR model where the population is 'closed'. This means we assume the total number of people in the (*N)* model remains constant throughout the simulations, 'flowing' between three compartments:

$$\frac{dS}{dt} = -\beta \frac{SI}{N}$$

$$\frac{dI}{dt} = \beta \frac{SI}{N} - \gamma I$$

$$\frac{dR}{dt} = \gamma I$$

In this sense, the 'hazards' of transitioning across model states are unchanged (albeit the force of infection is dynamic, given change in model states over time!). However simple, the SIR model has been very useful to explore some key concepts of dynamic disease transmission. Here, we will expand it to explore concepts of varying hazards.

► *In groups of four, discuss what kinds of varying hazards you could incorporate in a transmission model to make it useful for analysing an outbreak? How would you adapt the model to account for these varying hazards? (5 min)*

Before moving on to more complex adaptations, let's first 'open up' the model population. By this we mean we need to account for births and background (i.e. all-cause) mortality. Note that, in order to do so, we are assuming all new individuals are born into the *Susceptible* compartment, yet **all** compartments are subject to background mortality.

$$\frac{dS}{dt} = bN - \beta\frac{SI}{N} - \mu S$$

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

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

► *Code the above ODEs into the* **Editor tab** *and compile your code with the parameters and initial conditions provided.*

► *Once you are happy with your code, go to the* **Visualise tab** *and run the model for 1,825 days (5 years).*

► **Question 1:** what do you observe towards the end of the simulations that differs from what you have seen thus far by modelling closed populations? Now, rerun the model for 15,000 days (~41 years). What do you observe?

► *Go back to the* **Editor tab** *and modify your ODEs to allow immunity to wane over time* σ.

► *Remember this is a new parameter we need to declare. First, declare the parameter by typing in the code below at the end of your script* ***exactly as follows:***

```
waning_t <- user(1) # average number of years natural immunity lasts for
sigma <- 1 / (waning_t * 365) # natural immunity waning rate (match time frame of the model)
```

► *Second, add the new sigma parameter to your differential equations in the appropriate places.*

► *Once you are happy with your code, compile it and run the model for 500 days. Plot* R_t *on a secondary Y axis again.*

► You might find it useful to consider where individuals are flowing out from (-) and where are they flowing to (+).

► **Question 2:** How is R_t changing over the course of the outbreak? How does this correspond with changes in the model compartments (*I*, *S, R*)? How do changes in those compartments impact the underlying force of infection? What happens if you increase/decrease the average duration of immunity (plot *I* only) by 10%? Does varying the mean birth rate have the same effect over the model duration (500 days)? Lastly, if you run the model for 2000 days with baseline parameters, what do you observe (plot only *I*)?

Example 2: age-stratified SIR model

Well done! Between yesterday and today, you have been learning about modifications to your SIR model to model time-varying hazards. We are now going to account for age, which is a key driver of varying hazards in infectious disease transmission.

We know populations don't mix equally. For example, both younger and older individuals in a population tend to interact much more within their age groups. This has important implications in the control of infectious diseases, as vaccination campaigns would usually account for this to decide who to target in the population.

► *Navigate to the odin interface* https://shiny.dide.ic.ac.uk/infectiousdiseasemodels-lusaka-2022/ *in Chrome or Safari.*

► *In the Thursday section, "Expanding the SIR model", click on "Example 2".*

This is an example of an age-stratified SIR model, with only three age compartments. Note that all compartments in the population are now multiplied by 3! This is because we are explicitly accounting for the fact that this is a heterogeneous population of individuals. Furthermore, in lines 65-76 we are defining their age-specific force of infection.

► ***DO NOT RUN THE MODEL YET! Answer Question 3 without running the model.***

► **Question 3:** What do the age-specific forces of infection ($\lambda_1, \lambda_2, \lambda_3$) tell you about how the population interacts? Assume age groups are 1: children, 2: adults, and 3: the elderly.

► *Now you can run the model!*

► *First, hide the pop_n (1,2,3) and lambda_n (1,2,3) variables in the* **Editor tab**.

► *Next, go to the* **Visualise tab** *and run the model for 200 days.*

► *Visualise either one age group at a time (e.g. S_1, I_1 and R_1) or one disease stage at a time (e.g. I_1, I_2 and I_3).*

► **Question 4:** As a proportion of the total population, which age group is most affected by the epidemic? Which age group is most affected when considered as a proportion of the population in that age group? Why do you think that is? How do the peaks of the epidemic change between age groups and how is this determined? Overall, which age group do you think was most affected by this infectious disease?

You can begin to see how accounting for varying hazards is of paramount importance in infectious disease modelling. For example, the above disease dynamics would have important implications for a vaccination campaign. Consider which age group would you target with a vaccine that prevents infection? What if the vaccine was no good at preventing infection, but decreases the risk of severe disease and death?

As we have said in this workshop thus far, the choice of model and building in its complexity should be driven by the research/policy questions we are aiming to answer. A key question is, how fast is the disease spreading; that is, what is its reproduction number and growth rate. A simple parametric calculation of R_o even with just three age compartments would be almost impossible to derive by hand.

► *In your own time, navigate to the odin interface* https://shiny.dide.ic.ac.uk/infectiousdiseasemodels-lusaka-2022/ *in Chrome or Safari.*

► *In the Thursday section, "Expanding the SIR model", download the script "Example 3" and explore the code to derive this disease' R_o* using *the next generation matrix.* You will need to run this in your own computer in an R-Studio session.