

Chapter 2 (Solutions)

How are models set up?

I. An introduction to difference equations

2.1 a) The difference equations are as follows:

$$\begin{aligned} \text{Humans: } \quad S_{t+1}^h &= S_t^h - \lambda_t^h S_t^h + r i_t^h \\ i_{t+1}^h &= i_t^h + \lambda_t^h S_t^h - r i_t^h \\ \text{Mosquitoes } \quad S_{t+1}^v &= S_t^v + b - \lambda_t^v S_t^v - \mu S_t^v \\ i_{t+1}^v &= i_t^v + \lambda_t^v S_t^v - \mu i_t^v \end{aligned}$$

Note that the compartments are defined to be the proportions, rather than the numbers of mosquitoes or humans that are susceptible or infected. Since b is the *per capita* birth rate into the mosquito population, we just need to add b into the equation for susceptible mosquitoes to account for births into the population.

b) The risk of infection among humans needs to account for the prevalence of infected mosquitoes, the number of mosquitoes per human, the biting rates of mosquitoes, and the probability that a bite by a mosquito leads to infection in a human.

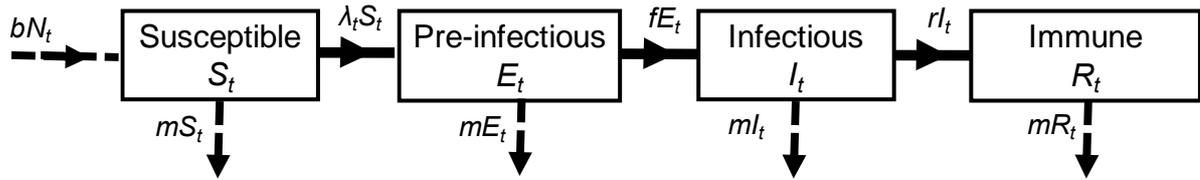
The risk of infection among mosquitoes needs to account for the biting rate of mosquitoes, the probability that a bite by a mosquito leads to infection in a mosquito, and the prevalence of infectious humans.

2.2 We use the symbols b and m to denote the *per capita* birth and death rates respectively, and the symbol N_t to denote the population size at time t .

a) The equations can be rewritten as follows:

$$\begin{aligned} S_{t+1} &= bN_t + S_t - \lambda_t S_t - mS_t \\ E_{t+1} &= E_t + \lambda_t S_t - f E_t - mE_t \\ I_{t+1} &= I_t + f E_t - r I_t - mI_t \\ R_{t+1} &= R_t + r I_t - mR_t \end{aligned}$$

The diagram for this model is provided below, where the expressions next to or above the arrows reflect the number of individuals who move between categories per unit time:



b) The model describes the transmission dynamics of an immunizing infection, and is therefore sufficient for describing the general patterns in incidence for measles and rubella, which are both immunizing infections. There are several ways of making the model more realistic than it is at present:

1. Stratify the compartments by age;
2. Include age-dependent contact between individuals;
3. Include changes in mixing patterns during the course of a year because of school holidays and school terms;
4. Assume that infectious individuals have a different mortality rate from those who are susceptible or are immune;
5. Include maternal immunity.

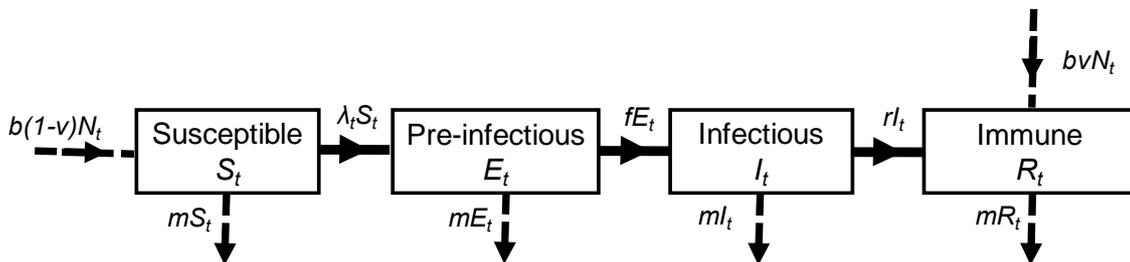
These issues are discussed in later chapters.

c) The equations would be rewritten as follows:

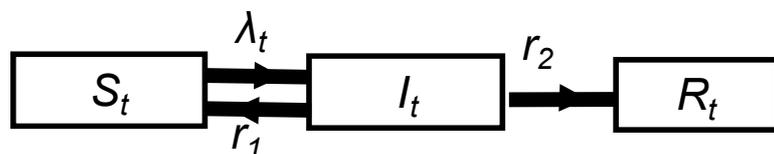
$$\begin{aligned}
 S_{t+1} &= S_t + b(1-v)N_t - \lambda_t S_t - mS_t \\
 E_{t+1} &= E_t + \lambda_t S_t - fE_t - mE_t \\
 I_{t+1} &= I_t + fE_t - rI_t - ml_t \\
 R_{t+1} &= R_t + bvN_t + rI_t - mR_t
 \end{aligned}$$

i.e. the proportion of newborns that is immunized enters the immune compartment and the remainder enters the susceptible compartment.

The diagram for this model is provided below, where the expressions next to or above the arrows reflect the number of individuals who move between categories per unit time:



2.3 The following shows the general structure of the model.



This model doesn't fall naturally into any of the categories presented in Figure 2.2. In fact, it has been called a "compound model" and has been used to describe hookworm data (see chapter 5).