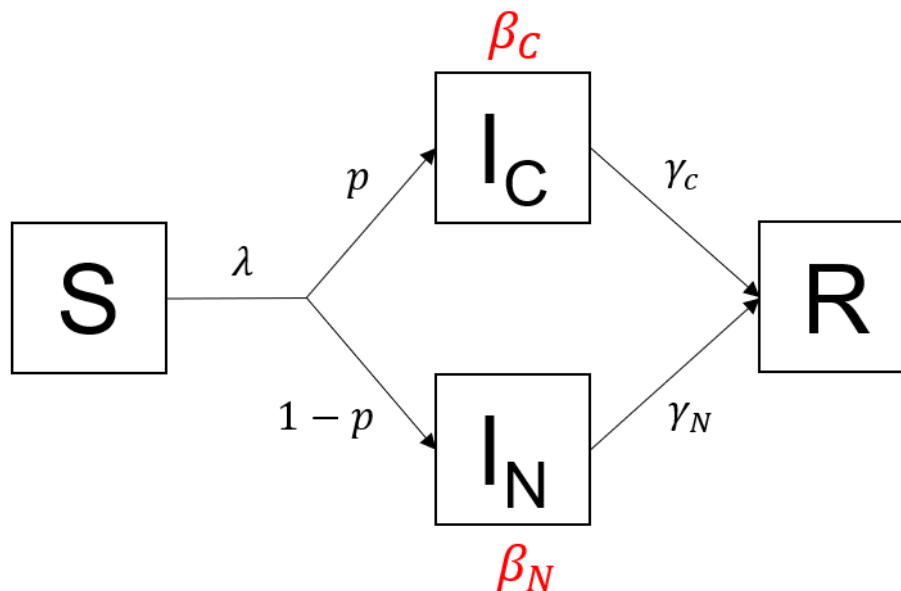


## Calculating more complex forms of $R_0$

To derive  $R_0$  for more complex models, it is useful to remember:

- the definition of  $R_0$ : it is the **average** number of secondary infections caused by a single infected case (index case) in a totally susceptible population
- the principle of competing hazards, which you covered in week 1

### Example 1: symptomatic and asymptomatic infection



This is the example you saw in the video – here we are going to give further explanations on how to derive  $R_0$  for this model.

In this variation of the SIR model, infected people are stratified into 2 compartments: people in the  $I_C$  compartment are coughing, whereas people in the  $I_N$  compartment show no symptoms. The proportion of infected people with a cough is  $p$ , which means the proportion of asymptomatic infected people is  $1-p$ . Coughing people transmit infection at a rate  $\beta_C$  and recover at a rate  $\gamma_C$ , whereas asymptomatic people transmit infection at a rate  $\beta_N$  and recover at a rate  $\gamma_N$ .

With 2 compartments being a source of infection, we can approach the problem by first calculating separately the average number of secondary infections caused by a single coughing case  $I_C$ , and the average number of secondary infections caused by a single asymptomatic case  $I_N$ .

For this, we only need to apply the general principle introduced in the lecture: For any infected compartment,  $\beta$  is (by definition) the average number of secondary infections caused per **unit time**, and  $1/\gamma$  is the average duration of infection.

Take a simple example: if someone infectious is infecting 2 people per day on average, and they are infectious for 5 days on average, this means they cause 10 secondary infections overall, over their whole infectious period.

More generally, we can write:

$$\begin{aligned} \text{Total number of secondary infections} \\ = \text{Secondary infections per unit time} \times \text{average infectious period} \end{aligned}$$

Which, in terms of model parameters, is the same as:

$$\beta \times \frac{1}{\gamma}$$

This is the same as the logic covered in the lectures. Now – thinking about the model above, we concentrate first on a coughing index case (in the  $I_C$  compartment). The average number of secondary infections caused by such a case equals:

$$\frac{\beta_C}{\gamma_C}$$

Similarly, the average number of secondary infections caused by an asymptomatic index case (in the  $I_N$  compartment) equals:

$$\frac{\beta_N}{\gamma_N}$$

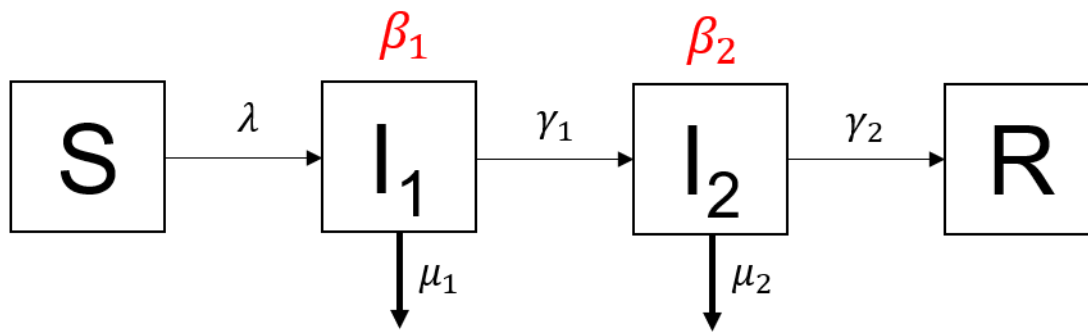
Now, remember that  $R_0$  is an average over the population, meaning that we need to take an average over coughing and non-coughing individuals. We know that a proportion  $p$  of infected people are coughing. So a population average of the terms above is simply:

$$R_0 = p \frac{\beta_C}{\gamma_C} + (1 - p) \frac{\beta_N}{\gamma_N}$$

Of course, if there is an equal number of people in both compartments, this simplifies to a normal mean:

$$R_0 = 0.5 \frac{\beta_C}{\gamma_C} + 0.5 \frac{\beta_N}{\gamma_N}$$

## Example 2: progressive infection



In the second example, we again have 2 compartments transmitting the infection, but this time they represent consecutive stages of an infection. People in the first stage of the infection  $I_1$  transmit infection at a rate  $\beta_1$ , die at a rate  $\mu_1$ , and leave the first stage of infection at a rate  $\gamma_1$ . They progress into the second stage of infection,  $I_2$ . People in the stage  $I_2$  transmit infection at a rate  $\beta_2$ , die at a rate  $\mu_2$ , and recover at a rate  $\gamma_2$ . This kind of structure could apply, for example, to a disease that has an initial asymptomatic stage ( $I_1$ ), where infected people are infectious without symptoms, and a more advanced diseased stage ( $I_2$ ), where they develop symptoms, and potentially higher infectiousness.

The approach to calculating  $R_0$  is similar to before: first, we calculate the average number of secondary infections caused by an index case from each compartment separately. This time, when calculating the average duration in any compartment, we have to take account of the fact that there are now 2 competing rates involved,  $\gamma$  and  $\mu$ .

The average number of secondary infections caused by an index case in  $I_1$  is:

$$\frac{\beta_1}{\gamma_1 + \mu_1}$$

And the average number of secondary infections caused by an index case in  $I_2$  is:

$$\frac{\beta_2}{\gamma_2 + \mu_2}$$

Again, we need to take a population average of both. Of course, we know that every infected person (100%) passes through the first stage of infection, but what proportion of infected people reaches the second stage? Because of the rate  $\mu_1$ , some individuals may die before progressing to  $I_2$ .

Here, you just need to apply the same principle you learnt in the lecture on competing hazards to calculate the case fatality ratio. The proportion who progresses to the second stage before dying is:

$$\frac{\gamma_1}{\gamma_1 + \mu_1}$$

Bringing all this together into a population average of secondary infections gives, for  $R_0$ :

$$R_0 = \frac{\beta_1}{\gamma_1 + \mu_1} + \frac{\gamma_1}{\gamma_1 + \mu_1} \times \frac{\beta_2}{\gamma_2 + \mu_2}$$