Compartmental models in mathematical epidemiology

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Introduction

It will be better if we define some terminologies in epidemiology before we start modeling. Even though there are many things to consider when it comes to the concepts of epidemiology, I will give necessary definitions that are needed to understand the modeling covered in this paper. Let us start with a word from the title of the talk. What is epidemiology? *Epidemiology* is the study of the determinants, occurrence, and distribution of health and disease in a defined population. Note that here the terminology is used for the human population. If a defined population is animal populations, then the study is called *epizootiology* (or *epizoology*). Here, we are going to consider an epidemic; therefore, let us give a definition. According to the Cambridge Dictionary, an *epidemic* is the appearance of a particular disease in a large number of people at the same time (*epizootic* for animal populations). We will examine the mathematical modeling of infectious diseases, so there are certain words to know the meanings, allowing us to understand the assumptions made for the models. The following meanings for words are taken from 'A Dictionary of Epidemiology' by Miquel Porta, the only dictionary I found for Epidemiology. A *host* is a person or other living animal, including birds and arthropods, that provides subsistence or lodgment to an infectious agent under natural conditions. A *susceptible* is a member of a population who is at risk of becoming infected by a disease. I think this is enough for an undergraduate mathematics student, like myself, at least to start the topic. Please note that as the cases become complex, more terminology will be needed, and if needed, I will add the necessary ones.

Disease progression

In the reference book, it was stated the objective of a mathematical model of an infectious disease is to describe the transmission process of the disease. The transmission is the passage of a pathogen[1] from an infectious individual to the population of susceptibles through modes of transmission, such as airborne, droplet transmission, and direct or indirect physical contact. We will observe that depending on the means of transmission, there will be changes in mathematical models. However, we now focus on the disease progression, one of the most important aspects to consider when mathematically modeling the disease.

[1] any organism, agent, factor, or process capable of causing disease

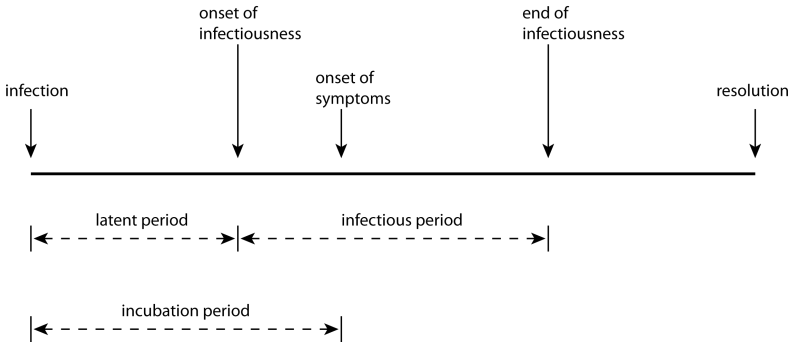
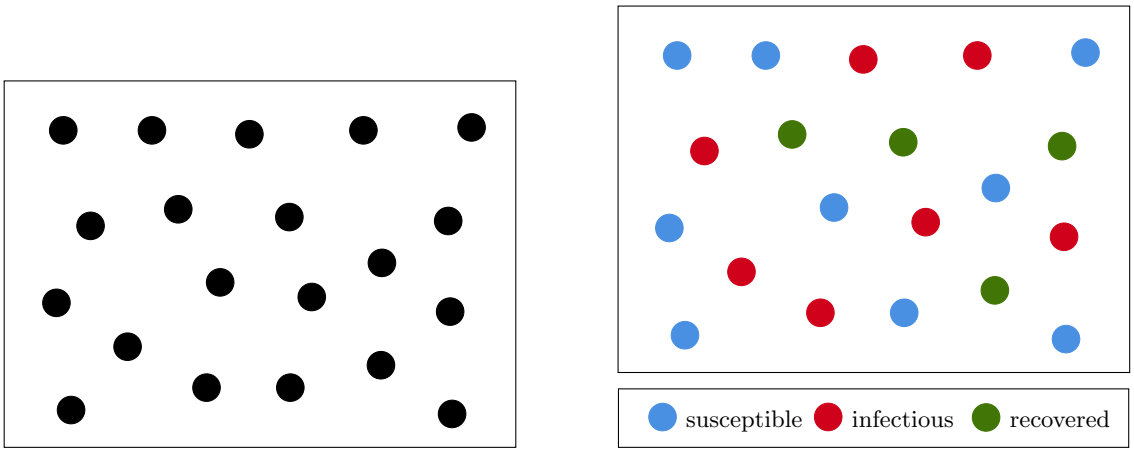


Figure 1: Disease Progression [Dobson, 2020].

The figure 1 clearly illustrates disease progression. There is no need to define the latent, incubation, and infectious periods, as they are clearly shown in the figure. Please note that the lengths of the latent, incubation, and infectious periods, as well as the ways they overlap, vary for different diseases. For example, the incubation period for ebola is shorter than the latent period, while for measles, the incubation period is longer than the latent period. (For detailed information, please refer to 'Epidemic Modelling – Some Notes, Maths, and Code' by Simon Dobson, if you are interested.) It is crucial to examine the progression of a specific disease because the model changes. For example, in some diseases where the incubation period is longer than the latent period, individuals remain asymptomatic, meaning they can infect others without showing any symptoms. It is essential to consider this scenario, as it significantly changes the model, a topic that will be discussed in more detail in the SEIR model.

Compartmental models

To understand the idea of modeling the disease, let us consider the simplest case. Assume a constant number of host population (see Figure 2a). The dots in the figure represent humans in the population.



(a) Host population

(b) Host population divided into three different groups

When asked to model, the first thing that comes to our minds is to split the population into three groups: susceptibles, infected, and recovered. I clearly show the groups different colors, blue, red and green (see Figure 2b). What we are interested in is knowing the number of people in each group at any given time. It is straightforward to see that as people come into contact, the numbers in each group change. Let us discuss the concept known as *compartmental models for infectious diseases*, which essentially involves the same principles we have been applying.

The host population is partitioned into mutually exclusive groups, referred to as *compartments*, based on the nature of the disease. Let us denote

$$S\text{: susceptible class}, \quad I\text{: infectious class}, \quad R\text{: recovered class}.$$

Here, we are examining the simplest compartmental model, which is known as the *SIR model*. We illustrate the transmission process using the diagram, called a *transfer diagram.*(see Figure 3)

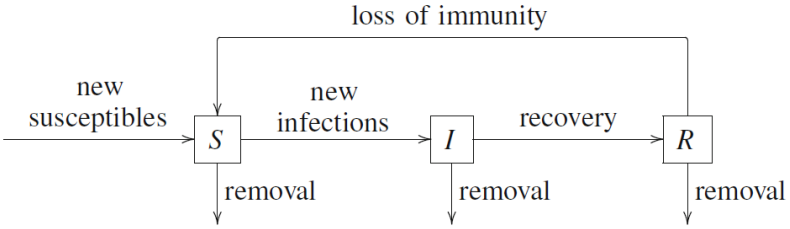


Figure 3: Transfer diagram for the SIR model [Li, 2018].

Recall that our aim is to obtain the number of hosts in each compartment at any given time t. We denote the numbers in each compartment by $S(t)$, $I(t)$, $R(t)$. We can construct a compartmental model by considering the net change in the number of individuals in each compartment in an interval $[t, t + \Delta t]$.

$$\begin{aligned}
\Delta S(t) &= \text{new susceptibles} + \text{transfer from } R - \text{new infections} - \text{removal from } S \\
\Delta I(t) &= \text{new infections} - \text{transfer into } R - \text{removal from } I \\
\Delta R(t) &= \text{transfer from } I - \text{transfer into } S - \text{removal from } R
\end{aligned}$$

If we divide both sides of the above equations by Δt and let $\Delta t \to 0$, we obtain the following differential equations.

$$\begin{aligned}
S'(t) &= \text{influx of new susceptibles} + \text{transfer rate from } R - \text{incidence rate} - \text{removal rate from } S \\
I'(t) &= \text{incidence rate} - \text{transfer rate into } R - \text{removal rate from } I \\
R'(t) &= \text{transfer rate from } I - \text{transfer into } S - \text{removal rate from } R
\end{aligned} \tag{1}$$

To determine the right-hand side of the system of ODEs, assumptions for the infectious disease should be provided. Then, using these assumptions, we can define the right-hand side.

Kermack-McKendrick model

As mentioned earlier, the model is constructed based on assumptions or hypotheses. Consider the following hypothesis about the transmission process of an infectious disease and its host population.

1. Transmission occurs horizontally through direct contact between hosts.
2. Mixing of individual hosts is homogeneous. In particular, the incidence rate can be expressed as $\lambda I(t)S(t)$, where λ is called the *transmission coefficient*.
3. Rate of transfer from a compartment is proportional to the population size of the compartment. For instance, the recovery rate can be written as $\gamma I(t)$, for a rate constant γ.
4. Infected individuals become infectious upon infection with no latency period.

5. There is no loss of immunity and no possibility of reinfection.

6. There is no input of new susceptibles and no removal from any compartments.

Notice that assumption 6 implies that the total host population remains constant. Even though we have considered assumptions that impose certain restrictions, these assumptions are plausible for a disease spread within the student population on a campus. When all the terms are substituted in (1), we obtain the following system of differential equations.

$$\begin{aligned} S'(t) &= -\lambda IS, \\ I'(t) &= \lambda IS - \gamma I, \\ R'(t) &= \gamma I, \end{aligned}$$

with initial conditions

$$S(0) = S_0, \quad I(0) = I_0, \quad R(0) = 0.$$

This system of ordinary differential equations is called the *Kermack-McKendrick epidemic model* (the transfer diagram for the model is given in Figure 4).

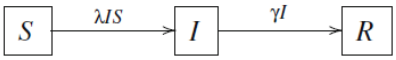


Figure 4: Transfer diagram for a simple SIR model [Li, 2018].

In the derived model, the functions $S(t)$, $I(t)$, and $R(t)$, as well as the model parameters λ and γ, are nonnegative, given that the functions $S(t)$, $I(t)$, and $R(t)$ denote the number of people. In addition, some observations can be made without solving the system. Let us denote the total host population by $N(t)$. Since we assume that the total host population is constant, then $N(t) = S_0 + I_0$. As λ, S, and I are nonnegative, it is easy to notice that $S'(t) \leq 0$, implying that $S(t)$ is a decreasing function. We have defined the epidemic, but can we ascertain the conditions under which the epidemic occurs by examining this model? Yes, we can. In the model, we have the differential equation given by

$$I'(t) = I(\lambda S - \gamma). \tag{2}$$

When defining an epidemic, we state that it occurs when there is a large number of people affected simultaneously. Alternatively, we can express that an epidemic occurs when there is a rapid increase in the number of infectious individuals. Mathematically speaking, this implies that an epidemic occurs when $I'(t) > 0$. By using the equation (2), we observe that this occurs when $\lambda S - \gamma > 0$, or $S > \frac{\gamma}{\lambda}$. As we have observed that $S(t)$ is a decreasing function, it follows that $S_0 > \frac{\gamma}{\lambda}$. Therefore, we conclude that an epidemic occurs if $S_0 > \frac{\gamma}{\lambda}$. This phenomenon is known as *threshold phenomena*, and a threshold value $\frac{\gamma}{\lambda}$ is called the *critical community size.*

One may wonder how we arrive at the terms λIS and γI in the model. This question will be addressed in the next sections.

Transfer rates

The model we have discussed assumes proportional transfer rates between compartments. However, our assumption that the recovery rate is in proportion to the size of the infectious population is by no means universal. Let us understand what it means for transfer rates to be proportional.

Let us consider a general compartment, denoted as C, with a total population size of $N(t)$. Individuals in this compartment exit at a rate of $rN(t)$, where r is a positive constant.

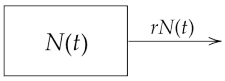


Figure 5: A compartment C.

Then, we have the following initial value problem.

$$N'(t) = -rN(t), \quad N(0) = N_0.$$

The solution to this problem is

$$N(t) = N_0 e^{-rt}, \quad \text{or} \quad e^{-rt} = \frac{N(t)}{N_0}. \tag{3}$$

The equality (3) shows that e^{-rt} is the fraction of the host population that remains in compartment C. In probabilistic terms, it represents the probability of an individual being in C at time t. As our focus is on the population transfer out of C, we consider

$$F(t;r) = \begin{cases} 1 - e^{-rt}, & t \geq 0, \\ 0, & t < 0. \end{cases}$$

This gives us the fraction of the population that has left compartment C during the time period $[0, t)$, or the probability of an individual who has left compartment C during $[0, t)$. If we denote X as a random variable representing the *residence time* of an individual in compartment C, then

$$F_X(t) = p(X \leq t).$$

It is clear to see that $F(t;r)$ is the cumulative distribution function of the exponential distribution. So, the residence time of an individual in compartment C follows an exponential distribution. We can also write the probability density function for the random variable X.

$$f(t;r) = \begin{cases} re^{-rt}, & t \geq 0, \\ 0, & t < 0. \end{cases}$$

The probability density function $f(t;r)$ shows the proportion of individuals with residence time t. We can also find the expected value of X, which gives us the *mean residence time*.

$$E[X] = \int_{-\infty}^{\infty} tf(t)\,dt = \frac{1}{r}.$$

For transfers from compartment I to R, the residence time is the period between the time of infection and the time of recovery, which is the *infectious period*. Then the infectious periods of individuals follow an exponential distribution.

$$F(t;\gamma) = \begin{cases} 1 - e^{-\gamma t}, & t \geq 0, \\ 0, & t < 0, \end{cases}$$

where $\frac{1}{\gamma}$ is the *mean infectious period*. Similarly, for transfers from compartment R to S, the residence time is the *immune period* during which recovered individuals are protected from reinfection. Then the immune periods of individuals follow an exponential distribution.

$$F(t;\delta) = \begin{cases} 1 - e^{-\delta t}, & t \geq 0, \\ 0, & t < 0, \end{cases}$$

where $\frac{1}{\delta}$ is the *mean immune period*.

We have seen that if we assume the proportional exit rate, then we have an exponential distribution for the residence time of an individual in a compartment. But how do we derive the model equations when the infectious periods of individuals follow the distribution $F(t)$? Let us derive the model equations when the infectious periods of individuals follow the distribution $F(t)$. Notice that the change in assumption for the infectious period does not impact the equation for $S(t)$ in the simple SIR model we have shown. Based on this assumption, we will re-derive the equations for $I(t)$ and $R(t)$. Let $F_X(t)$ be the probability distribution function for residence time X. Then,

$$G(t) = 1 - F_X(t) = P(X > t).$$

is the associated *survival function*. The function $G(t)$ gives us the fraction of the population that has remained in the compartment during the time period $[0, t)$, or the probability of an individual who has remained in the compartment during $[0, t)$. For any given time $\tau > 0$, $G(t - \tau)$ is the fraction of individuals who became infected at time τ and are still infectious at time t $(t > \tau)$. Therefore, the number of people infected at time τ and remaining infectious at time t is given by

$$\lambda I(\tau)S(\tau)G(t - \tau).$$

Then we can find the number of people accumulated in compartment I since $\tau = 0$ is

$$I(t) = I_0(t) + \int_0^t \lambda I(\tau)S(\tau)G(t - \tau)\, d\tau,$$

where $I_0(t)$ is the number of people who are already infected at $\tau = 0$ and remain infectious at time t. Similarly, we can also obtain equation for compartment R.

$$R(t) = R_0(t) + \int_0^t \lambda I(\tau)S(\tau)(1 - G(t - \tau))\, d\tau.$$

When $F(t) = 1 - e^{-\gamma t}$, we obtain

$$I(t) = I_0(t) + \int_0^t \lambda I(\tau)S(\tau)e^{-\gamma(t-\tau)}\, d\tau, \quad I_0(t) = I(0)e^{-\gamma t}.$$

Once the derivative is taken with respect to t, we get

$$I'(t) = I_0'(t) + \frac{d}{dt}\int_0^t \lambda I(\tau)S(\tau)e^{-\gamma(t-\tau)}\, d\tau, \quad I_0'(t) = -\gamma I_0(t).$$

Let us use the Leibniz integral rule for differentiation above to obtain

$$\begin{aligned} I'(t) &= I_0'(t) + \lambda I(t)S(t) - \gamma \int_0^t \lambda I(\tau)S(\tau)e^{-\gamma(t-\tau)}\, d\tau = \\ &= -\gamma I_0(t) + \lambda I(t)S(t) - \gamma \int_0^t \lambda I(\tau)S(\tau)e^{-\gamma(t-\tau)}\, d\tau = \\ &= \lambda I(t)S(t) - \gamma \left(I_0(t) + \int_0^t \lambda I(\tau)S(\tau)e^{-\gamma(t-\tau)}\, d\tau \right) = \\ &= \lambda I(t)S(t) - \gamma I(t). \end{aligned}$$

Similarly, we can obtain

$$R'(t) = \gamma I(t).$$

We have re-derived the equations for $I(t)$ and $R(t)$ in the SIR model discussed earlier.

Disease incidence

Now we are going to derive *disease incidence*, which is the rate at which new infections occur. In other words, we will find the number of newly infected people per unit time. This concept is different from *disease prevalence*, which is the proportion of the population found to be infected, including both new and existing cases, at time t.

Let λ be the average number of contacts per person per unit time, and p represent the probability of a contact leading to an infection. Then the incidence is given by

$$p\lambda \cdot \frac{S(t)}{N(t)} \cdot I(t),$$

where $p\lambda$ is the average number of effective contacts produced by each infectious individual and $\frac{S(t)}{N(t)}$ denotes the probability of making contact with a susceptible individual. Let us denote the effective contact number per capita by λ. Then, the incidence becomes

$$\frac{\lambda}{N(t)} I(t)S(t).$$

The incidence changes depending on the nature of the total population size $N(t)$. If N is constant, then the incidence is found to be the same as the first incidence form we examined ($\beta = \frac{\lambda}{N}$). Now, let us consider two simple cases where the total population size $N(t)$ varies with time t. As a first case, let the effective contact number λ be independent of the total population size $N(t)$. Then the incidence is given by

$$\lambda \cdot \frac{I(t)S(t)}{N(t)},$$

where λ is a positive constant. This case occurs when population density is independent of population size. For example, consider a rural population; as the population size increases, rural towns tend to expand to maintain a constant population density. As a second case, let the effective contact number λ be proportional to the total population size $N(t)$; then $\lambda(N) = \beta N$, where β is a constant. Then the incidence is given by

$$\beta I(t)S(t).$$

This case occurs when population density is proportional to population size. For example, consider an urban population in a city confined in space; as the population size increases, the population density will increase proportionally. We have observed that the variation in incidence forms depends on assumptions about how total population density changes as the total population size varies.

Starting now, we will enhance the Kermack-McKendrick model (SIR) we have discussed by incorporating additional concepts to make it more reflective of real-life scenarios.

Demography: birth, death, and population growth

Assuming that the birth or death rate is proportional to the population size, we can derive the corresponding system of differential equations for the model based on these considerations.

$$\begin{aligned} S'(t) &= bN(t) - \lambda I(t)S(t) - d_1 S(t), \\ I'(t) &= \lambda I(t)S(t) - (\gamma + d_2)I(t), \\ R'(t) &= \gamma I(t) - d_3 R(t), \end{aligned}$$

where b represents the natural birth rate constant, while d_1, d_2, and d_3 are death rate constants corresponding to the compartments S, I, and R, respectively. Please note that, in this assumption, the newborn population is directly put into compartment S. However, it is possible for a

newborn to be born infected and be considered in compartment I. This case will be discussed in a later section.

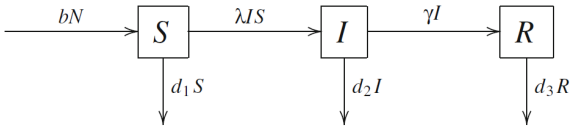


Figure 6: Transfer diagram for an SIR model with birth and death [Li, 2018].

Note that, unlike the model we considered earlier, in this model, the host population size changes over time. This can be observed directly from the model itself.

$$N'(t) = S'(t) + I'(t) + R'(t) = bN(t) - d_1S(t) - d_2I(t) - d_3R(t).$$

As a special case, let us consider that the death rate constants for each compartment are the same, i.e., $d_1 = d_2 = d_3 = d$. Then,

$$N'(t) = (b - d)N(t). \tag{4}$$

The general solution to the problem (4) is given by

$$N(t) = N_0e^{(b-d)t}, \tag{5}$$

where $N(0) = N_0$. From (5), it is evident that if $b > d$, then $N(t) \to \infty$ as $t \to \infty$. Conversely, if $b < d$, then $N(t) \to 0$ as $t \to \infty$. Finally, if $b = d$, then $N(t)$ remains constant. This observation holds true in reality: When the birth rate is greater than the death rate, the population tends to grow, and conversely, if the death rate is greater than the birth rate, the population tends to decline over time.

So far, we have only examined cases where population growth or decline is influenced solely by factors related to birth or death. However, it is important to acknowledge that immigration and out-migration should also be taken into account as factors contributing to both the increase and decrease in the total population. Let A be the number of new immigrants per unit time, and also $d_1S(t)$, $d_2I(t)$, $d_3R(t)$ be interpreted as removal rates that include both death and out-migration (refer to 7 for the transfer diagram in this scenario).

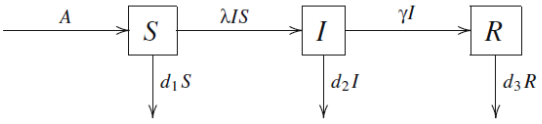


Figure 7: Transfer diagram for an SIR model with migration/immigration and removal [Li, 2018].

The derived system of differential equations for the model, with the transfer diagram shown in 7, is given by

$$\begin{aligned} S'(t) &= A - \lambda I(t)S(t) - d_1S(t), \\ I'(t) &= \lambda I(t)S(t) - (\gamma + d_2)I(t), \\ R'(t) &= \gamma I(t) - d_3R(t), \end{aligned}$$

Please note that we have only considered immigration as a factor that contributes to compartment S. However, individuals arriving in a population may carry infections, and as such, they should be accounted for in compartment I. In the literature, these scenarios have been investigated, and corresponding models have been suggested.

Disease latency: latent and incubation periods

After the host is infected, in some infectious diseases, the host becomes symptomatic, and the host is capable of transmitting the pathogens to others, but only after some time has passed since the initial infection. The period between the time of infection and the time of becoming infectious is called the *latent period*. During the latent period, the host is infectious, but since the host shows no symptoms, we cannot detect it. However, we can include this in our mathematical model. Until now, in the model we have discussed, we considered the case where the host, once infected, directly becomes infectious. In other words, we assumed that the latent period is equal to the incubation period. Now, let us consider the case when these periods do not coincide. Then, we define a new compartment, an *exposed compartment* E (also known as the *latent compartment*), that has a transfer to I satisfying the proportional assumption. The model that includes the exposed compartment E is known as the *SEIR model*.

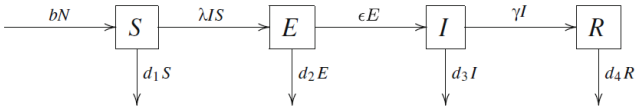


Figure 8: Transfer diagram for an SEIR model [Li, 2018].

These assumptions lead to the following system of differential equations.

$$\begin{aligned} S'(t) &= bN(t) - \lambda I(t)S(t) - d_1 S(t), \\ E'(t) &= \lambda I(t)S(t) - (\epsilon + d_2)E(t), \\ I'(t) &= \epsilon E - (\gamma + d_3)I(t), \\ R'(t) &= \gamma I(t) - d_4 R(t), \end{aligned}$$

where ϵ is a rate constant. The derivation of ϵE is the same as discussed in the transfer rates section. Consequently, the *mean latent period* is $\frac{1}{\epsilon}$.

Immunity

After recovering from an infection, an infected host typically retains a certain level of immunity against reinfection. Some diseases, like measles, grant lasting immunity, preventing reinfection after recovery. However, diseases such as COVID-19, caused by the SARS-CoV-2 virus, exhibit reinfection after recovery, and the loss of immunity leads to a transfer of recovered individuals back to the susceptible compartment.

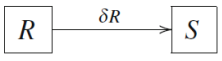


Figure 9: Loss of immunity resulting in individuals in compartment R moving into S [Li, 2018].

Routes of transmission: horizontal and vertical

The transmission mode is typically characterized as either *vertical* or *horizontal*. Mixed transmission can also be added to the characterization, in which symbionts[2] [3] can be transmitted both vertically and horizontally. *Vertical transmission* is defined as the transmission of the infectious

[2] an organism living in symbiosis with another

[3] symbiosis - a relationship between two types of animal or plant in which each provides for the other the conditions necessary for its continued existence

pathogen from the mother to the fetus during the antepartum and intrapartum periods, or to the neonate during the postpartum period via the placenta in utero, body fluid contact during childbirth, or through direct contact owing to breastfeeding after birth [Kotlyar et al., 2021, p. 36]. The article provides a detailed definition, but to summarize, we will be focusing on diseases where the infectious pathogen is directly transmitted from an infected mother to a newborn. Up until now, we have assumed that transmission occurs horizontally through direct contact between hosts. However, in this section, we are going to consider a mathematical model that assumes vertical transmission. Let us assume that a fraction p of newborns from the infected population becomes infected at birth, and the remaining fraction $1-p$ is susceptible. The transfer diagram in Figure 10 illustrates both vertical and horizontal transmission based on our assumption.

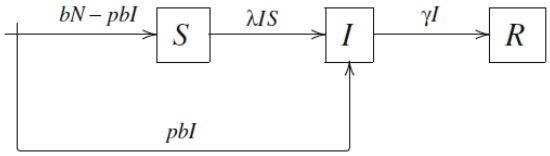


Figure 10: Transfer diagram for an SIR model with vertical transmission [Li, 2018].

Then, the model describing this case is given by

$$\begin{aligned} S'(t) &= bN(t) - pbI(t) - \lambda I(t)S(t), \\ I'(t) &= pbI(t) + \lambda I(t)S(t) - \gamma I(t), \\ R'(t) &= \gamma I(t), \end{aligned}$$

where bN represents the total number of newborns with a natural birth rate b, pbI is the number of newborns infected at birth, and $bN - pbI$ is the number of healthy susceptible newborns.

Disease control and prevention measures

We are going to consider two prevention and control measures, namely immunization, more specifically *vaccination*, and *quarantine*.

Vaccination plays a vital role in both preventing and controlling infections. A successful vaccine offers protection to susceptible hosts against potential infections. Moreover, by vaccinating a substantial portion of the susceptible population, we can decrease the initial number of susceptibles, S_0. To be more precise, if we succeed in reducing S_0 below the threshold value of $\frac{\gamma}{\lambda}$, we can effectively prevent the outbreak of an epidemic. To model the vaccination impact, let us assume that a fraction p of all susceptibles is vaccinated per unit time.

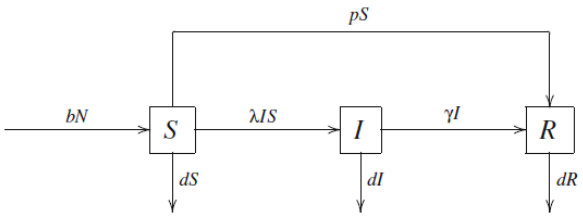


Figure 11: Transfer diagram for an SIR model with vaccination [Li, 2018].

Then we have the following system of differential equations

$$\begin{aligned} S'(t) &= bN - \lambda IS - dS - pS, \\ I'(t) &= \lambda IS - (d+\gamma)I, \\ R'(t) &= pS + \gamma I - dR. \end{aligned}$$

But we also need to consider the case where vaccinations are not perfect, and individuals can still get infected. To model this scenario, we introduce a new compartment V for vaccinated hosts.

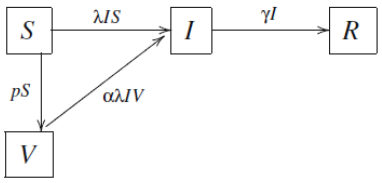


Figure 12: A vaccination model with a leaky vaccine [Li, 2018].

Then we have the following system of differential equations

$$\begin{aligned} S'(t) &= -\lambda IS - pS, \\ V'(t) &= pS - \alpha\lambda IV, \\ I'(t) &= \lambda IS + \alpha\lambda IV - \gamma I, \\ R'(t) &= \gamma I, \end{aligned}$$

where $\alpha \in (0, 1]$ denotes the reduced probability of transmission due to immune protection from the imperfect vaccine. This model is known as the *SVIR* epidemic model.

Quarantine is a method to isolate infected individuals, preventing them from spreading the infection. To integrate quarantine scenario into our mathematical model, we introduce a new compartment Q for the quarantined individuals.

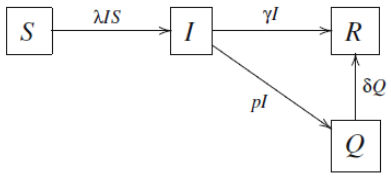


Figure 13: An SIR model with quarantine [Li, 2018].

Then we have the following system of differential equations

$$\begin{aligned} S'(t) &= -\lambda IS, \\ I'(t) &= \lambda IS - (p+\gamma)I, \\ Q'(t) &= pI - \delta Q, \\ R'(t) &= \gamma I + \delta Q, \end{aligned}$$

where $p \in (0, 1]$ represents the fraction of infectious individuals isolated per unit time, and δ is the rate constant for the recovery of quarantined individuals. This model is known as the *SIQR* epidemic model.

The basic reproduction number

The *basic reproduction number*, $\mathcal{R}_0$, is the average number of people who will get infected by one contagious person in a population where all individuals are susceptible to infection. The definition assumes no pre-existing immunity through exposure or vaccination. If $\mathcal{R}_0$ is found to be 2, then a contagious individual will, on average, transmit the disease to 2 other individuals (see Figure 14).

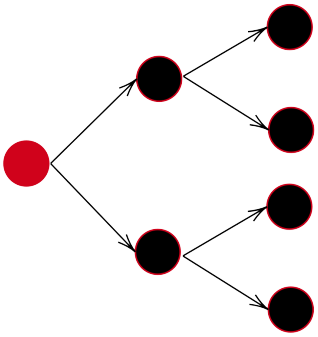


Figure 14: Spreading of a disease when $\mathcal{R}_0 = 2$.

Depending on the model proposed, the basic reproduction number also changes. The general method for deriving $\mathcal{R}_0$ is the *next-generation method*. In this method, the basic reproduction number $\mathcal{R}_0$ is determined by the spectral radius of the *next-generation matrix* G, i.e., $\mathcal{R}_0 = \rho(G)$. In this paper, I am not going to explain what the next-generation matrix is and how to find it.

If we consider the Kermack-McKendrick model, then the basic reproduction number is given by

$$\mathcal{R}_0 = S_0 \frac{\lambda}{\gamma},$$

where λ represents the average number of effective contacts of a single infectious host, S_0 denotes the initial susceptible population, and $\frac{1}{\gamma}$ corresponds to the mean infectious period.

It is evident that when the basic reproduction number, $\mathcal{R}_0$, is less than 1, the number of infected individuals will decrease, leading to the extinction of the disease. In cases where $\mathcal{R}_0$ equals 1, the disease will persist in a stable state, but an epidemic will not occur. However, an epidemic will occur if $\mathcal{R}_0$ exceeds 1. Recall the previous section where we mentioned that the epidemic will occur if $S_0 > \frac{\gamma}{\lambda}$, which is equivalent to stating that $\mathcal{R}_0 > 1$.

References

[Dobson, 2020] Dobson, S. (2020). *Epidemic Modelling - Some Notes, Maths, and Code*. Independent Publishing Network.

[Kotlyar et al., 2021] Kotlyar, A. M., Grechukhina, O., Chen, A., Popkhadze, S., Grimshaw, A., Tal, O., Taylor, H. S., & Tal, R. (2021). *Vertical transmission of coronavirus disease 2019: a systematic review and meta-analysis. American Journal of Obstetrics and Gynecology, 224* (1), 35-53.e3. `https://doi.org/10.1016/j.ajog.2020.07.049`

[Li, 2018] Li, M. Y. (2018). *An Introduction to Mathematical Modeling of Infectious Diseases*. 1st ed. Springer Cham. `https://doi.org/10.1007/978-3-319-72122-4`.

[Porta, 2014] Porta, M. (Ed.). (2014). *A Dictionary of Epidemiology*. Oxford University Press. `https://doi.org/10.1093/acref/9780199976720.001.0001`.