Compartmental models in mathematical epidemiology

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Definitions

Definition

Epidemic is the occurrence in a community or region of cases of an illness, specific health-related behavior, or other health-related events clearly in excess of normal expectancy.

Definition

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.

Definition

A *susceptible* is a member of a population who is at risk of becoming infected by a disease.

Disease progression

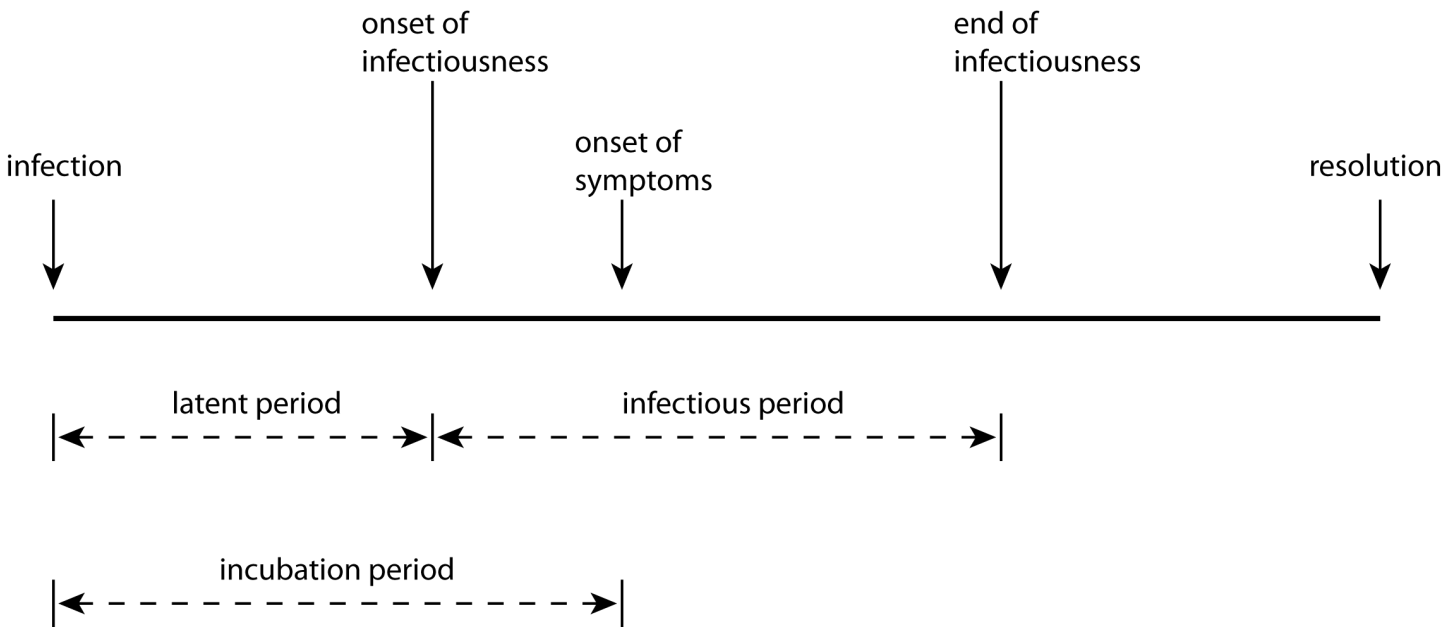
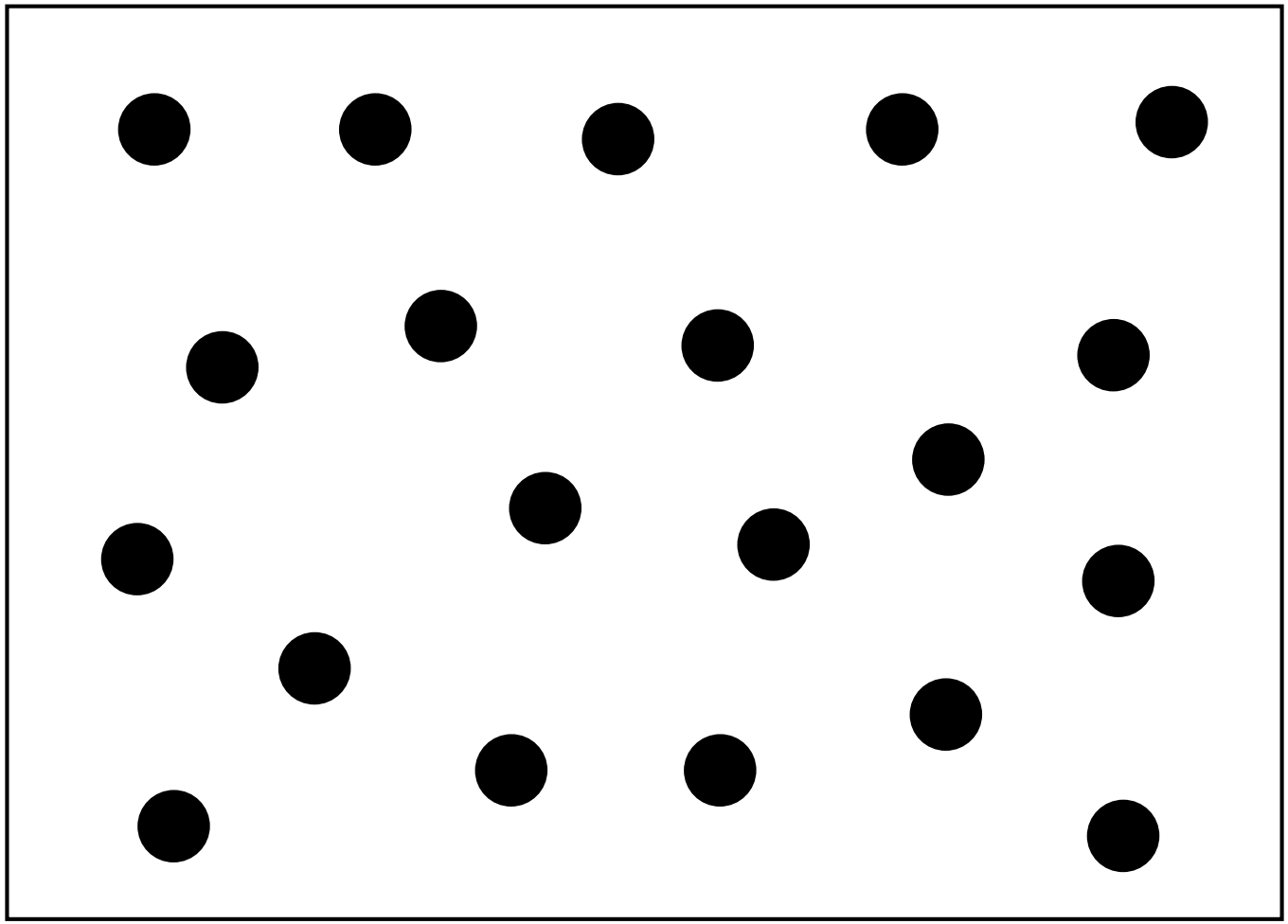
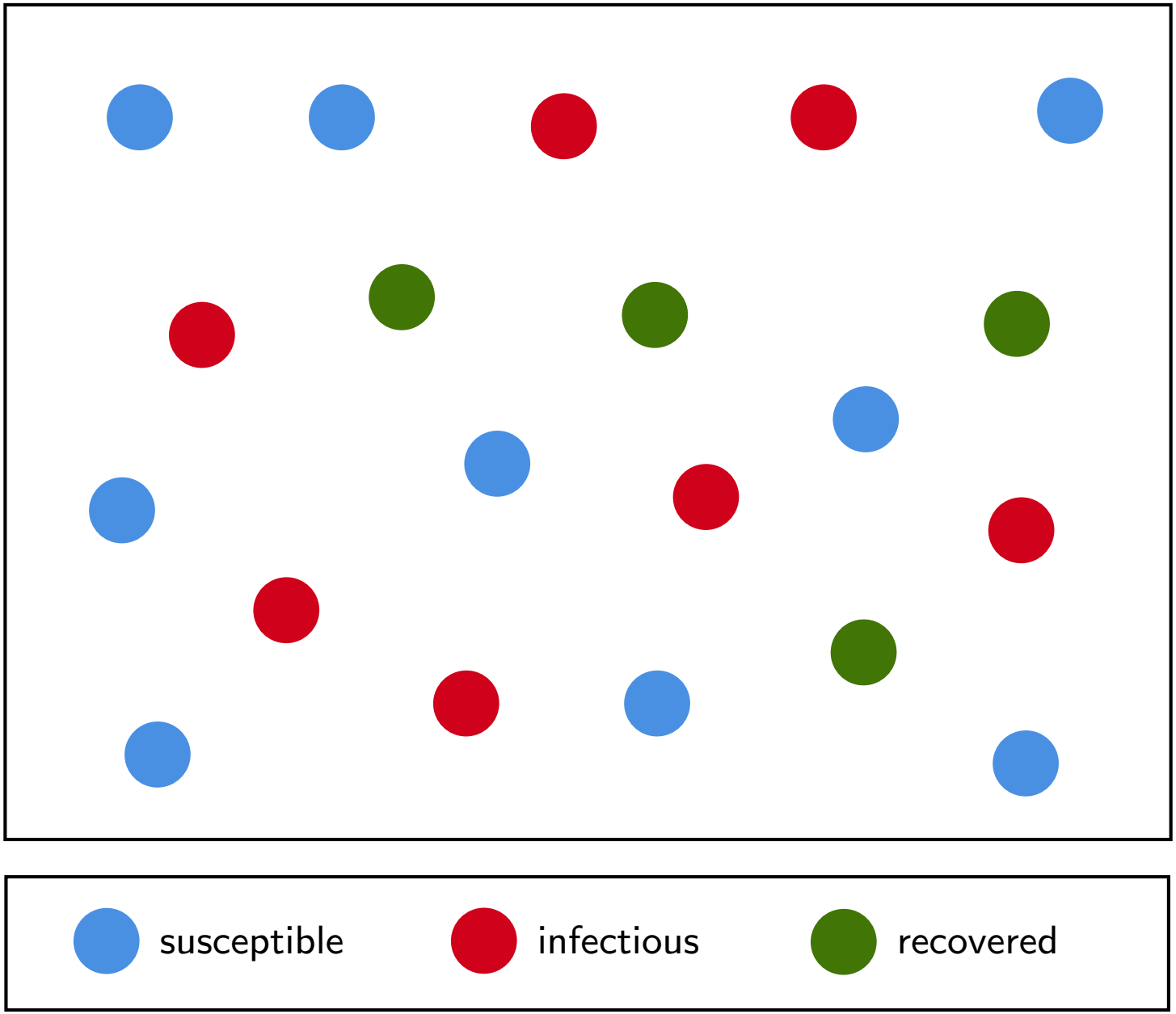


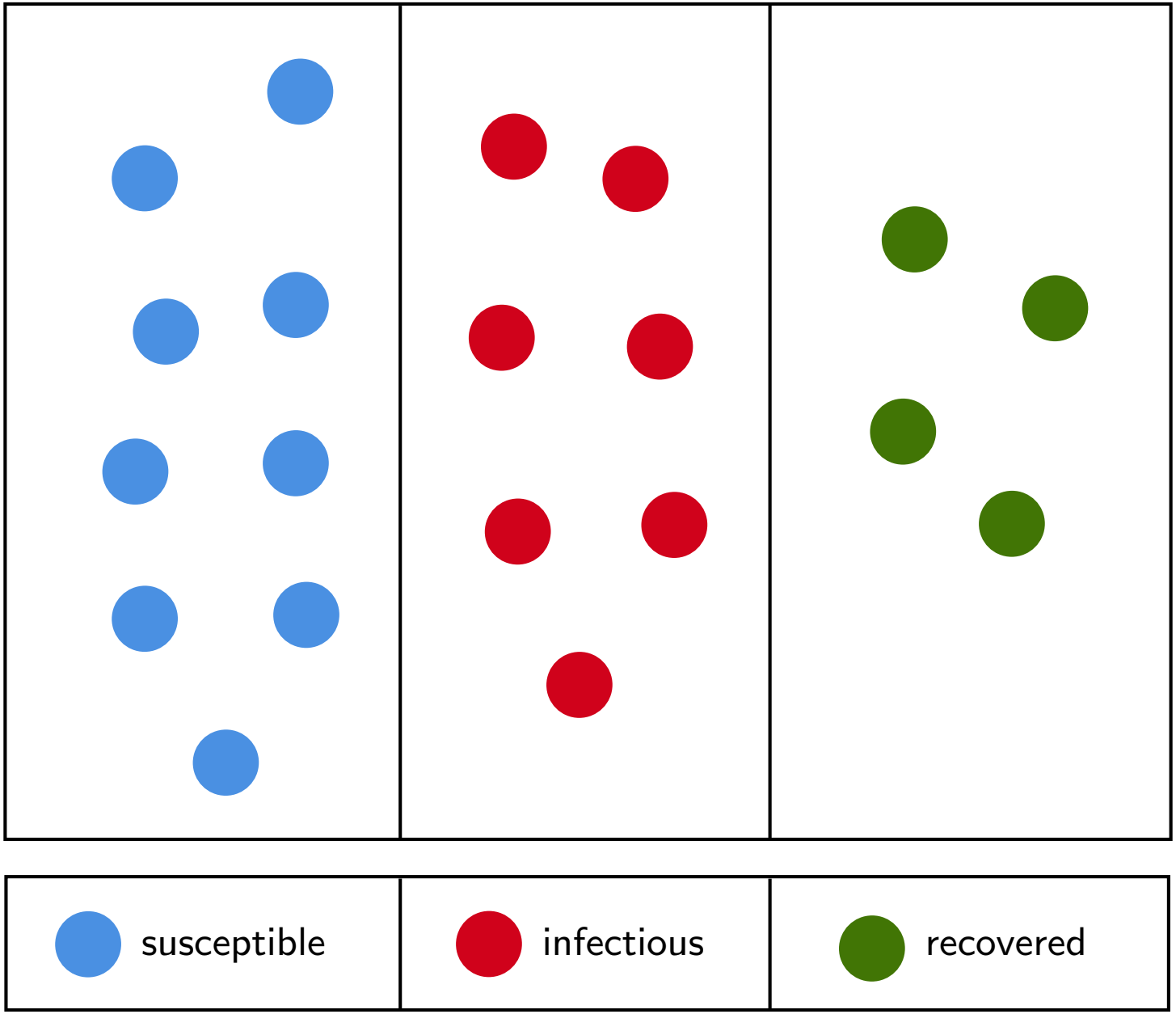
Figure: Disease Progression [Dobson, 2020].

The lengths of the latent, incubation, and infectious periods, as well as the ways they overlap, vary for different diseases.

Compartmental models




susceptible
infectious
recovered


susceptible
infectious
recovered

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

S: susceptible class, I: infectious class, R: recovered class

Here, we consider the simplest compartmental model called the *SIR* model. We illustrate the transmission process using the diagram, called a transfer diagram.

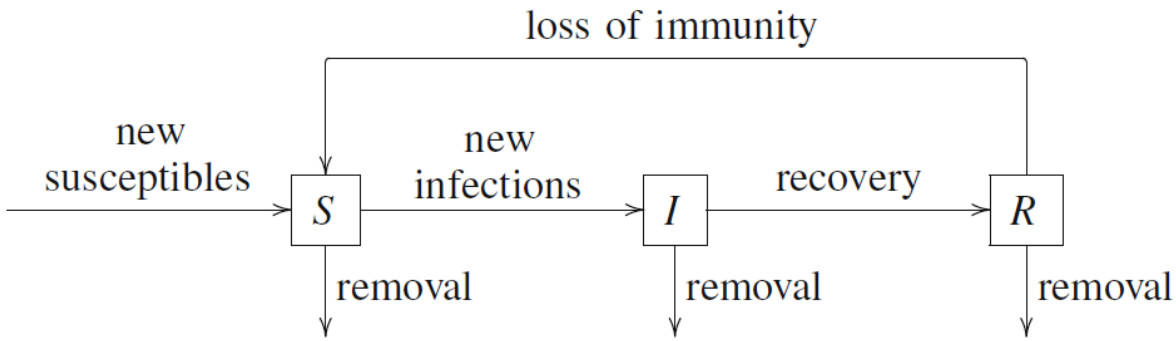


Figure: Transfer diagram for the SIR model [Li, 2018].

We can construct a compartmental model by considering the net change in the number of individuals in each compartment in an interval $[t, t + \Delta t]$.

$$\Delta S(t) = \text{new susceptibles} + \text{transfer from } R - \text{new infections} - \text{removal from } S$$

$$\Delta I(t) = \text{new infections} - \text{transfer into } R - \text{removal from } I$$

$$\Delta R(t) = \text{transfer from } I - \text{transfer into } S - \text{removal from } R$$

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

$$S'(t) = \text{influx of new susceptibles} + \text{transfer rate from } R - \text{incidence rate} - \text{removal rate from } S$$

$$I'(t) = \text{incidence rate} - \text{transfer rate into } R - \text{removal rate from } I$$

$$R'(t) = \text{transfer rate from } I - \text{transfer rate into } S - \text{removal rate from } R$$

Depending on our hypotheses about disease transmission and population transfer, the expression of the terms can vary.

Kermack-McKendrick model

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.
7. The total host population remains constant.

Substituting all the terms, 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.

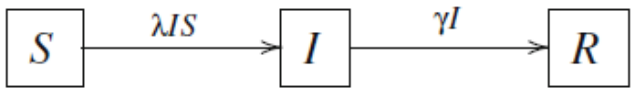


Figure: Transfer diagram for a simple SIR model [Li, 2018].

Transfer rates

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.

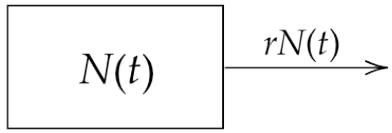


Figure: A compartment C [Li, 2018].

Then $N(t)$ satisfies

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

which has the solution

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

As our focus is on the population transfer out of C, we consider

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

If we let X denote the random variable of the *residence time* of an individual in compartment C, we notice that

$$F(t) = P(X \leq t).$$

We observe that the assumption of a proportional exit rate is equivalent to the residence time of an individual in compartment C having an exponential distribution.

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

The expected value of X is

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

which corresponds to the mean residence time under the assumption of a proportional exit rate.
For transfers from compartment I to R, the infectious period of individuals follows an exponential distribution

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

and the mean infectious period is $\frac{1}{\gamma}$.

How do we derive the model equations when the infectious periods of individuals follow the distribution $F(t)$?

We consider the associated survival function

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

The number of individuals who are infected at time τ and remain infectious at time t is given by

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

Hence, at time t, the number of individuals present in the I compartment 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 cumulative number of individuals who are already infected at $\tau = 0$ and remain infectious at time $t > 0$.

Similarly, the R equation is given by

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

When $F(t) = 1 - e^{-\gamma t}$, we have $G(t) = e^{-\gamma t}$, and the equation for $I(t)$ is given by

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

where $I_0(t) = I(0)e^{-\gamma t}$. Since $I_0'(t) = -\gamma I_0(t)$, we obtain

$$I'(t) = \lambda I(t) S(t) - \gamma I(t).$$

Similarly, we have

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

Disease incidence

We are going to derive disease incidence. Let

- λ be the average per capita contact number among individuals per unit time,
- p represent the probability that a contact will result in an infection.

Then the incidence is given by

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

If we combine the probability p with the contact number λ, so that λ is the per capita effective contact number, then the incidence is given by

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

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 ($\beta = \frac{\lambda}{N}$). Let us consider two simple cases where the total population size $N(t)$ varies with time t.

1. The effective contact number λ is independent of the total population size. Then the incidence is given by

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

   where λ is a constant.

2. The effective contact number λ is proportional to the total population size, i.e., $\lambda(N) = \beta N$, for a constant β. Then the incidence is given by

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

Demography: birth, death, and population growth

Let's assume that the birth or death rate is proportional to the population size. Then, based on these assumptions, the corresponding system of differential equations for the model is derived.

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

where b is the natural birth rate constant, and d_1, d_2, and d_3 are death rate constants.

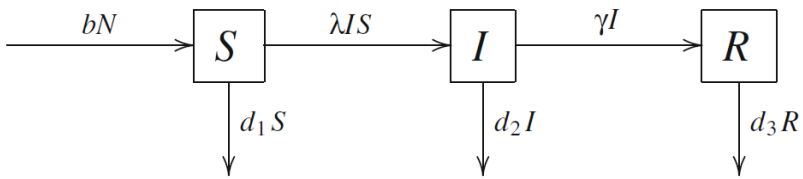


Figure: Transfer diagram for an SIR model with birth and death[Li, 2018].

Unlike previous models, for this model, the total population size changes over time.

$$N'(t) = bN(t) - d_1 S(t) - d_2 I(t) - d_3 R(t).$$

Let us consider the special case when the death rate constants for each compartment are the same (i.e., $d_1 = d_2 = d_3 = d$).

$$N'(t) = (b - d)N(t),$$

which has the general solution

$$N(t) = N_0 e^{(b-d)t},$$

where $N(0) = N_0$.

Disease latency: latent and incubation periods

The host population is partitioned into mutually exclusive groups:

S: susceptible class, I:infectious class,

E: exposed class, R: recovered class.

This leads to the following system of differential equations:

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

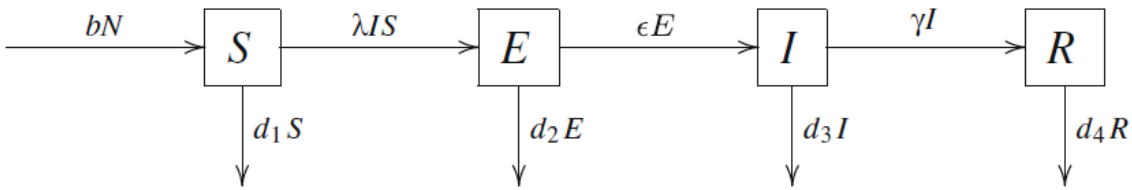


Figure: Transfer diagram for an SEIR model [Li, 2018].

Immunity

In certain diseases, such as COVID-19 caused by the SARS-CoV-2 virus, reinfection occurs after recovery, and loss of immunity results in a transfer of recovered individuals back to the susceptible compartment.

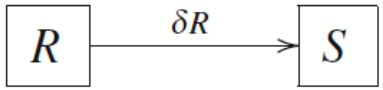


Figure: Transfer diagram from compartment R to S [Li, 2018].

Routes of transmission: horizontal and vertical

The transmission mode is typically characterized as either *vertical* or *horizontal*. Up until now, we have assumed that transmission occurs horizontally through direct contact between hosts. Let us consider a mathematical model that assumes vertical transmission.

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

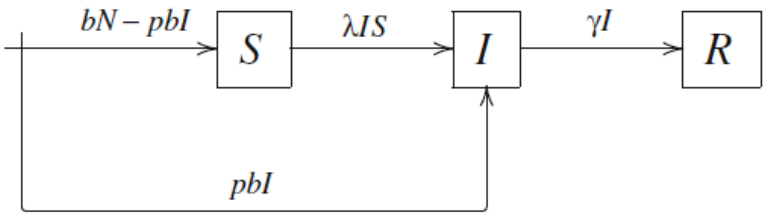


Figure: Transfer diagram for an SIR model with vertical transmission [Li, 2018].

Disease control and prevention measures

If we assume a vaccination rate of p for susceptibles per unit time, we arrive at the following system of differential equations.

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

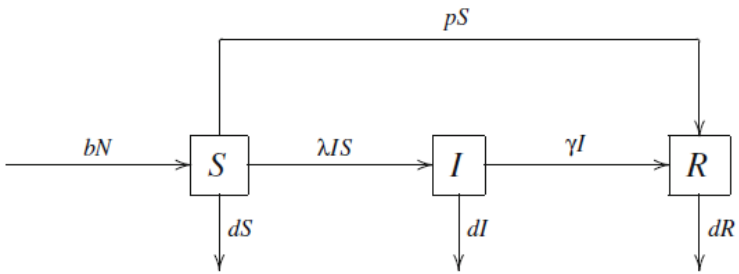


Figure: Transfer diagram for an SIR model with vaccination [Li, 2018].

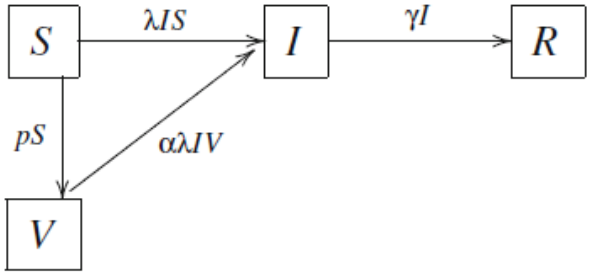


Figure: A vaccination model with a leaky vaccine [Li, 2018].

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

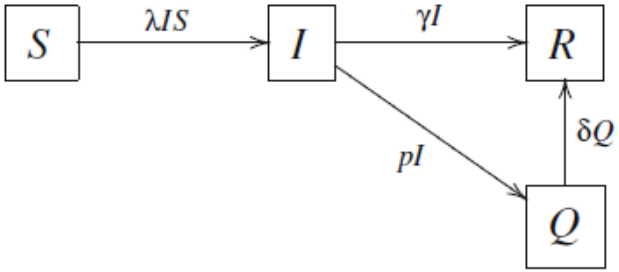


Figure: An SIR model with quarantine [Li, 2018].

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

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.

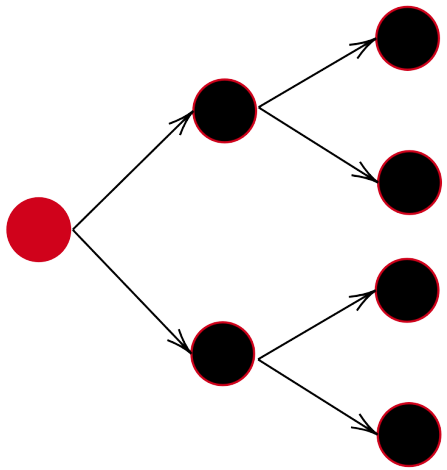


Figure: Spreading of a disease when $\mathcal{R}_0 = 2$.

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

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

Using $\mathcal{R}_0$, the threshold phenomenon can be expressed as follows:

- If $\mathcal{R}_0 \leq 1$, then an epidemic will not occur.
- If $\mathcal{R}_0 > 1$, then an epidemic will occur.

Thank you for your attention!

References

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