

Modeling of Epidemics

This project is taken from [BB15, chapter 7, 7.P.1]. Infectious disease is disease caused by a biological agent (virus, bacterium, or parasite) that can be spread directly or indirectly from one organism to another. A sudden outbreak of infectious disease that spreads rapidly and affects a large number of people, animals, or plants in a particular area for a limited period of time is referred to as an epidemic. Mathematical models are used to help understand the dynamics of an epidemic, to design treatment and control strategies (such as a vaccination program or quarantine policy), and to help forecast whether an epidemic will occur. In this project, we consider two simple models that highlight some important principles of epidemics.

The SIR Model. Most mathematical models of disease assume that the population is subdivided into a set of distinct compartments, or classes. The class in which an individual resides at time t depends on that individual's experience with respect to the disease. The simplest of these models classifies individuals as either susceptible, infectious, or removed from the population following the infectious period.

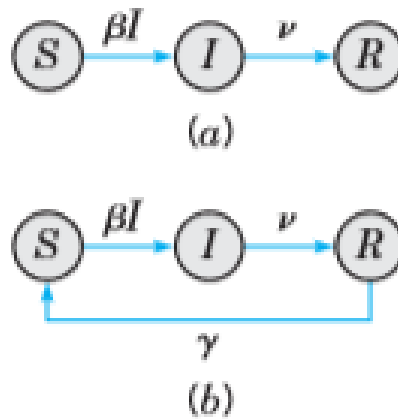


Figure 0.1: (a) The SIR epidemic model and (b) the SIRS epidemic model.

Accordingly, we define the state variables:

$S(t)$ = number of susceptible individuals at time t ,

$I(t)$ = number of infected individuals at time t ,

$R(t)$ = number of post-infective individuals removed from the population at time t (due to immunity, quarantine, or death).

Susceptible individuals are able to catch the disease, after which they move into the infectious class. Infectious individuals spread the disease to susceptibles, and remain in the infectious class for a period of time (the infectious period) before moving into the removed class. Individuals in the removed class consist of those who can no longer acquire or spread the disease. The mathematical model (referred to as the SIR model) describing the temporal evolution of the sizes of the classes is based on the following assumptions:

1. The rate at which susceptibles become infected is proportional to the number of encounters between susceptible and infected individuals, which in turn is proportional to the product of the two populations, βSI . Larger values of β correspond to higher contact rates between infecteds and susceptibles.
2. The rate of transition from class I to class R is proportional to I, that is, νI . The biological meaning of ν is that $1/\nu$ is the average length of the infectious period.
3. During the time period over which the disease evolves there is no immigration, emigration, births, or deaths except possibly from the disease.

4. Assume that for all $t > 0$ the $S(t) + I(t) = N$, that is, the total size of the population.

With these assumptions, the differential equations that describe the number of individuals in the three classes are

$$\begin{aligned}\frac{dS}{dt} &= -\beta \cdot I \cdot S, \\ \frac{dI}{dt} &= \beta \cdot I \cdot S - v \cdot I, \\ \frac{dR}{dt} &= v \cdot I.\end{aligned}$$

It is convenient to restrict analysis to the first two equations since they are independent of R :

$$\begin{aligned}\frac{dS}{dt} &= -\beta \cdot I \cdot S, \\ \frac{dI}{dt} &= \beta \cdot I \cdot S - v \cdot I.\end{aligned}$$

The SIRS Model. A slight variation in the SIR model results by assuming that individuals in the R class are temporarily immune, say, for an average length of time $1/\gamma$, after which they rejoin the class of susceptibles. The governing equations in this scenario, referred to as the SIRS model, are

$$\begin{aligned}\frac{dS}{dt} &= -\beta \cdot I \cdot S + \gamma R, \\ \frac{dI}{dt} &= \beta \cdot I \cdot S - v \cdot I, \\ \frac{dR}{dt} &= v \cdot I - \gamma R.\end{aligned}$$

Project "Modeling of Epidemics" Problems

1. (60 points) The triangular region $\Gamma := \{(S, I) : 0 \leq S + I \leq N\}$ in the SI -plane is depicted below.

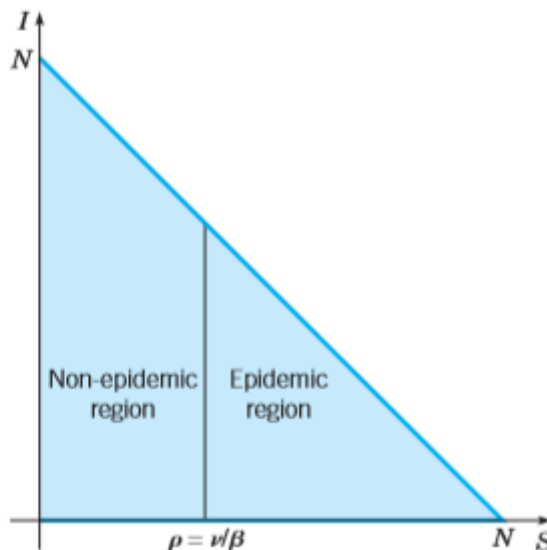


Figure 0.2: The state variables S and I for the SIR models must lie in the region Γ .

- (a) Use an analysis based on direction fields to show that no solution of the system can leave the set Γ . In particular, show that each point on the boundary of Γ is either a critical point of the system, or else the direction field vectors point toward the interior of Γ or are parallel to the boundary of Γ . Here are the steps to show this:
 - i. (10 points) First find the critical points for the system.
 - ii. (10 points) Obtain the linearization around arbitrary point (section 2 in "nonlinear odes").
 - iii. (30 points) Linearize the system around each of the critical points and based on the eigenvalues identify the qualitative behaviour (saddle-unstable, unstable or stable node). Sketch a picture (or just provide the Matlab bonus plot).
 - iv. (10 points) Conclude that each point on the boundary of Γ is either a critical point of the system, or else the direction field vectors point toward the interior of Γ or are parallel to the boundary of Γ .
 - (b) (10 points) Bonus: Draw the direction field using software and identify the separatrix.
2. (20 points) If epidemics are identified with solution trajectories in which the number of infected individuals initially increases, reaches a maximum, and then decreases, use a nullcline analysis to show that an epidemic occurs if and only if $S(0) > v/\beta$.
- (a) (5 points) Use a nullcline analysis to show that an epidemic occurs if and only if $S(0) > v/\beta$.
 - (b) (5 points) As done for the for competing species use the linearization around arbitrary critical point (1.ii above). Identify what constraints on $S(0), v/\beta$ will ensure stable behaviour (i.e. real negative distinct eigenvalues) towards the bottom line of Γ (where $I(t) = 0$).
 - (c) (10 points) Thus v/β is in effect, a threshold value of susceptibles separating Γ into an epidemic region and a nonepidemic region. Explain how the size of the nonepidemic region depends on contact rate and length of infection period.
3. (20 points) By taking a ratio as in the autonomous section, find an implicit equation $H(S, I) = c$ describing the solution trajectories of in S,I-plane (10 points) (section 1 in "nonlinear odes").
- (a) (10 points) Sketch these trajectories in the region Γ .
 - (b) (10 points) Bonus: or plot them using software.
4. (10 points) Bonus: Describe qualitatively the behaviour of S and I as $t \rightarrow +\infty$. In particular, answer the question "Does everyone get infected?" Then explain the statement "The epidemic does not die out due to the lack of susceptibles, but rather due to a lack of infectives."

References

- [BB15] William Boyce and James R. Brannan. *Differential equations: an introduction to modern methods and applications*. John Wiley & Sons, 2015.