Lesson 5: Basic reproduction number R_0 estimation

Learning objective: The learning goal of this lesson is to formulate the basic reproduction number R_0 equation for simple contact-based disease models using the Next Generation Matrix method.

Self-learning steps: Following the sections of this lesson, first, the student will learn about the basic reproduction number R_0 concept. Once the concept is understood, the learner will find the steady state for the population and linearize the equations around the poputation of susceptibles. Second, the student will go step by step through the process of consructing the next generation matrix by means of the transmission and transition matrices. Finally, the student will get eigenvalues for the final next generation matrix and the R_0 number. The student will need to spend 3 hours to learn how to formulate the basic reproduction number R_0. Once this construction method is understood, the learner can build R_0 equations for any disease model.

Additional resources for the lecture: Additional learning resources about the concept, estimation and formulation of the basic reproduction number R_0 can be found on link 9 in section "Readings and other resources".

5.1. Introduction

Analysis of infection models commonly use Ro, the basic reproduction number, to analyze the expected intensity of an infection. It represents the average number of new cases of an infection caused by one typical infected individual in a population of only susceptible individuals. If $Ro > 1$, then the infection is expected to grow,

while for $Ro < 1$, the infection is espected to be limited or die out.

5.2. Method of calculation

This analysis focuses on infection models based on systems of coupled ordinary differential equations, which are dubbed compartment models. In these models, each variable (capital letters) represents a number of individuals in some category such as susceptibles (S), infected (I), dead (D).

SI and SID models posed below; the task is to estimate Ro for each model following the next generation matrix (NGM) method.

1. Find the steady state for the population with no infected individuals or no infectious elements.
2. Linearize the equations around a population with some number of susceptibles ($S = N$), where N is the initial number of susceptibles in the population, and small numbers of infected ($I \ll N$) or infectious elements ($D, P, F \ll N$).
3. Consider the subset of the equations that involve the infectious processes. That is, ignore the $\frac{dS}{dt}$ equation.
4. Separate the terms in the remaining equations into two parts: transmission, represented by a matrix $\mathbf{T}$, and transistions, represented by a matrix Σ^{-1}.
5. Construct the next-generation matrix (NGM) for the large domain ($\mathbf{K_L} = -\mathbf{T} \cdot \Sigma^{-1}$).
6. Calculate the eigenvalues for $\mathbf{K_L}$. The dominant eigenvalue is Ro.

5.3. Models

SI model. Contact between S and I

This model is the Kermack-McKendrick model with susceptable (S) individuals becoming infected due to contact with infected (I) individuals. Infected individuals die at rate m while susceptible individuals suffer no mortality. Implicit in this model is that the time span of the analysis is short compared to the time scale for natural mortality or reproduction.

$$\frac{dS}{dt} = -\beta I S$$
$$\frac{dI}{dt} = \beta I S - m I$$

The governing equation for a non-infected population ($I = 0$) is $\frac{dS}{dt} = 0$. The population is constant at the initial population level of N.

The linearized equations around the steady state have $S = N$ and $I \ll N$. The resulting linearized equations are

$$\frac{dS}{dt} = -\beta I N$$
$$\frac{dI}{dt} = \beta I N - m I$$

The I equation represents the disease transmission processes. The transmission variables are $\vec{x} = (I)$, a one-dimensional vector. The Transmission matrix is $\mathbf{T} = (\beta N)$ and the transition matrix, representing all other processes is $\Sigma^{-1} = (-m)$.

The linearized model is
$$\frac{d\vec{x}}{dt} = (\mathbf{T} + \Sigma) \cdot \vec{x}$$

The matrix $\mathbf{K_L}$ is calculated from $\mathbf{T}$ and the inverse of which is $\Sigma^{-1} = -1/m$. So,

$$\mathbf{K_L} = -\mathbf{T} \cdot \Sigma^{-1} = -(\beta N)(-1/m) = \beta N/m$$

The eigenvalue is calculated as the roots of the equation $\mathbf{K_L} - \lambda \mathbf{I} = 0$, where in this case, $\mathbf{I}$ is the identity matrix, not the number of infected.

Since $\mathbf{K_L}$ in this case is a 1x1 matrix, the eigenvalue equation is

$$\lambda = \beta \, N / m.$$

That is, the basic reproduction number equation is

$$Ro = \frac{\beta \, N}{m}$$

SID model. Contact between S and D

This model represents disease transmission by contact of susceptibles with the bodies of those who died of the infection. Dead individuals are removed at a rate (d) which could represent decay, reduction of infectiousness of the dead bodies, physical removal of the bodies, or other such processes.

The governing equations are

$$\frac{d \, S}{dt} = -\beta \, D \, S$$
$$\frac{d \, I}{dt} = \beta \, D \, S - m \, I$$
$$\frac{d \, D}{dt} = m \, I - d \, D$$

The equation for a non-infected population ($I = D = 0$) is $\frac{d \, S}{dt} = 0$. The population is constant at the initial population level of N.

The linearized equations around the steady state have $S = N$ and $I, D \ll N$. The resulting linearized equations for the infection processes are

$$\frac{d \, I}{dt} = \beta \, I \, N - m \, I$$
$$\frac{d \, D}{dt} = m \, I - d \, D$$

The transmission vector is $\vec{x} = (I, D)$. Transmission and transition matrices along with the inverse of the transition matrix are

$$\mathbf{T} = \begin{pmatrix} 0 & \beta\,N \\ m & 0 \end{pmatrix} \quad \Sigma = \begin{pmatrix} -m & 0 \\ 0 & -d \end{pmatrix} \text{ and } \Sigma^{-1} = \begin{pmatrix} -1/m & 0 \\ 0 & -1/d \end{pmatrix}$$

The large domain NGM is

$$\mathbf{K_L} = -\mathbf{T} \cdot \Sigma^{-1} = \begin{pmatrix} 0 & \beta\,N/d \\ 1 & 0 \end{pmatrix}$$

The eigenvalues are the solution of

$$\begin{vmatrix} -\lambda & \beta\,N/d \\ 1 & -\lambda \end{vmatrix} = 0,$$

where the vertical bars indicate the determinant. The resulting equation is

$$\lambda^2 - \beta\,N/d = 0 \text{ with positive solution } \lambda = \sqrt{\beta\,N/d}.$$

That is, the basic reproduction number equation is

$$Ro = \sqrt{\frac{\beta\,N}{d}}$$