Advanced Studies in Biology, Vol. 3, 2011, no. 7, 309 - 317

Study of Reproductive Number in SIR-SIS Model

S. Seddighi Chaharborj*

Islamic Azad University, Science and Research Branch
Department of Mathematics, Bushehr, Iran
*sarkhosh@math.upm.edu.my

Yousof Gheisari

Islamic Azad University Bushehr Branch, Bushehr, Iran

Abstract

The thresholds for mathematical epidemiology models specify the critical conditions for an epidemic to grow or die out. The reproductive number can provide significant insight into the transmission dynamics of a disease and can guide strategies to control its spread. We define the mean number of contacts, the mean duration of infection, and the mean transmission probability appropriately for certain epidemiological models, and construct a simplified formulation of the reproductive number as the product of these quantities. When the spread of the epidemic depends strongly upon the heterogeneity, and the expressions for the reproductive number become correspondingly more complex. In this article we formulate a model with different heterogeneous structures and demonstrate how to define the mean quantities for an explicit expression for the reproductive number. We derive an explicit formula for the reproductive number employing the spectral radius of the next generation operator.

Keywords: Reproductive number; Infection-free equilibrium; Spectral radius; M-matrix

1 Introduction

One of the fundamental questions of mathematical epidemiology is to find threshold conditions that determine whether an infectious disease will spread in a susceptible population when the disease is introduced into the population. The threshold conditions are characterized by the so called reproductive number, the reproduction number, the reproductive ratio, basic reproductive value, basic reproductive rate, or contact number, commonly denoted by R_0 in

mathematical epidemiology [1, 5, 14]. The concept of R_0, introduced by Ross in 1909 [20], is defined in epidemiological modeling such that if $R_0 < 1$, the modeled disease dies out, and if $R_0 > 1$, the disease spreads in the population. There have been intensive studies in the literature to calculate R_0 for a wide class of epidemiological models of infectious disease [2, 3, 5, 6, 9, 10, 11, 12, 13]. In mathematical models, the reproductive number is determined by the spectral radius of the next generation operator in continuous models and, in particular, is determined by the dominant eigenvalue of the Jacobian matrix at the infection-free equilibrium for models in a finite-dimensional space [8]. It can also be obtained, in certain models, by suitable Lyapunov functions [11]. In this article, we use the SIS and SIR models as a basis [4, 7] and formulate a new heterogeneous models to demonstrate how different cases can be treated so that an appropriate reproductive number can be estimated.

2 Disease Transmission Model with n Patches

In Fig. (1) we consider an new model with different heterogeneous structures for HIV transmission in a population of individuals who are at high-risk for HIV.
The following system of ODEs describes this new model,

$$\begin{aligned}
\frac{dS_1}{dt} &= \mu S_1^0 - \mu S_1 - \delta_1 S_1 - \lambda_1 S_1 + \alpha_1 I_1, \\
\frac{dS_i}{dt} &= \mu S_i^0 - \mu S_i - \delta_i S_i - \lambda_i S_i + \delta_{i-1} S_{i-1} + \alpha_i I_i \quad ; \quad 2 \le i \le n-1, \\
\frac{dS_n}{dt} &= \mu S_n^0 - \mu S_n - \lambda_n S_n + \delta_{n-1} S_{n-1} + \alpha_n I_n, \\
\frac{dI_1}{dt} &= \lambda_1 S_1 - (\mu + \alpha_1 + \gamma_1 + \epsilon_1) I_1, \\
\frac{dI_i}{dt} &= \lambda_i S_i - (\mu + \alpha_i + \gamma_i + \epsilon_i) I_i + \epsilon_{i-1} I_{i-1} \quad ; \quad 2 \le i \le n-1, \\
\frac{dI_n}{dt} &= \lambda_n S_n - (\mu + \alpha_n + \gamma_n) I_n + \epsilon_{n-1} I_{n-1}, \\
\frac{dR_i}{dt} &= \gamma_i I_i - \mu R_i \quad ; \qquad 1 \le i \le n,
\end{aligned} \tag{1}$$

where

$$\lambda_i = r\beta_i \frac{I_i}{I_i + S_i + R_i} \tag{2}$$

Figure (1) illustrates the system (1). This system is nonlinear due to the form of λ_is.

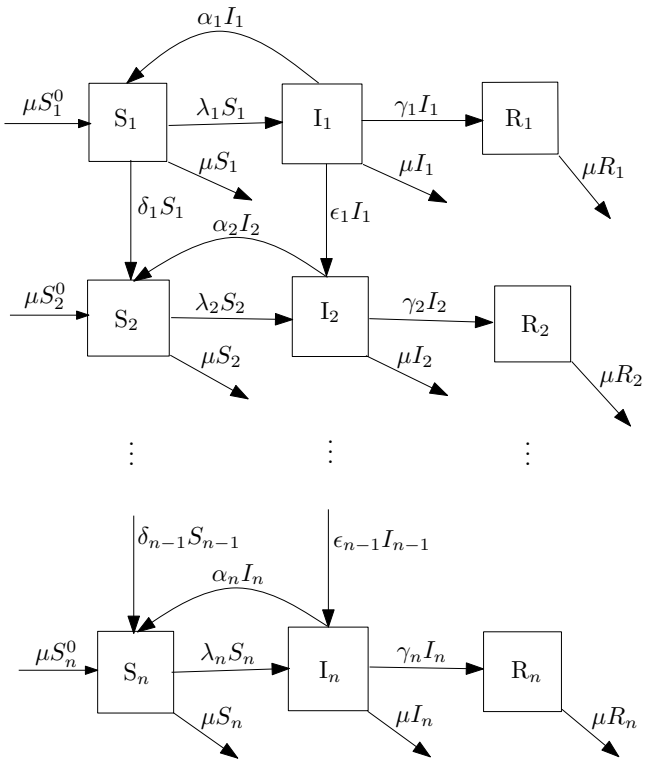

Figure 1: A schematic of system (1). Here S_i's are the susceptibles, I_i's are the infectives, R_i's are the removeds, $\mu > 0$, a constant, is the death rate, $\mu S_i^0 > 0$, constants, are the migration terms, γ_i, constants, are the removal rate from I_i to R_i, α_i, constants, are the removal rate from I_i to S_i, δ_i, constants, are the removal rate from S_i to S_{i+1}, ϵ_i, constants, are the removal rate from I_i to I_{i+1}, and $\lambda_i = r\beta_i \frac{I_i}{S_i+I_i+R_i}$ are the infection rate.

2.1 Reproductive Number

We derive an explicit formula for the reproductive number of infection by determining the spectral radius of the next generation operator of system (1) with (2) as follows.
System (1) has an infection-free equilibrium, given by,

$$E_0 = (S_1,\ S_2,\ S_3, ...,\ S_{n-1},\ S_n,\ I_1 = 0, ...,\ I_n = 0).$$

Where $S_1 = \frac{\mu S_1^0}{\mu+\delta_1}$, and $S_n = \frac{\mu S_n^0 + \delta_{n-1} S_{n-1}}{\mu}$. Linearizing system (1) around the infection-free equilibrium, we have the Jacobian matrix,

$$J = \begin{bmatrix} A & B \\ 0 & C \end{bmatrix}$$

where

$$A = \begin{bmatrix} -\mu-\delta_1 & 0 & 0 & \cdots & 0 & 0 \\ \delta_1 & -\mu-\delta_2 & 0 & \cdots & 0 & 0 \\ 0 & \delta_2 & -\mu-\delta_3 & \cdots & 0 & 0 \\ \vdots & \vdots & \ddots & \ddots & \vdots & \vdots \\ 0 & 0 & 0 & \delta_{n-2} & -\mu-\delta_{n-1} & 0 \\ 0 & 0 & 0 & \cdots & \delta_{n-1} & -\mu \end{bmatrix}$$

and

$$B = \begin{bmatrix} -r\beta_1+\alpha_1 & 0 & 0 & \cdots & 0 \\ 0 & -r\beta_2+\alpha_2 & 0 & \cdots & 0 \\ 0 & 0 & -r\beta_3+\alpha_3 & \cdots & 0 \\ \vdots & \vdots & \vdots & \ddots & \vdots \\ 0 & 0 & 0 & \cdots & -r\beta_n+\alpha_n \end{bmatrix}$$

and

$$C = \begin{bmatrix} r\beta_1-a_1 & 0 & 0 & \cdots & 0 & 0 \\ \epsilon_1 & r\beta_2-a_2 & 0 & \cdots & 0 & 0 \\ 0 & \epsilon_2 & r\beta_3-a_3 & \cdots & 0 & 0 \\ \vdots & \vdots & \ddots & \ddots & \vdots & \vdots \\ 0 & 0 & 0 & \epsilon_{n-2} & r\beta_{n-1}-a_{n-1} & 0 \\ 0 & 0 & 0 & \cdots & \epsilon_{n-1} & r\beta_n-a_n \end{bmatrix}$$

with $a_i = \mu+\alpha_i+\gamma_i+\epsilon_i$; $1 \le i < n$ and $a_n = \mu+\alpha_n+\gamma_n$.

The stability of the Jacobian matrix at the infection-free equilibrium is completely determined by the stability of C. Define matrices F and V as,

$$F = [A_1]_{1\times 1} \text{ and } V = [A_2]_{1\times 1}$$

where,

$$A_1 = \begin{bmatrix} r\beta_1 & 0 & 0 & \cdots & 0 & 0 \\ 0 & r\beta_2 & 0 & \cdots & 0 & 0 \\ 0 & 0 & r\beta_3 & \cdots & 0 & 0 \\ \vdots & \vdots & \vdots & \ddots & \vdots & \vdots \\ 0 & 0 & 0 & \cdots & r\beta_{n-1} & 0 \\ 0 & 0 & 0 & \cdots & 0 & r\beta_n \end{bmatrix}$$

and

$$A_2 = \begin{bmatrix} a_1 & 0 & 0 & \cdots & 0 & 0 \\ -\epsilon_1 & a_2 & 0 & \cdots & 0 & 0 \\ 0 & -\epsilon_2 & a_3 & \cdots & 0 & 0 \\ \vdots & \vdots & \ddots & \ddots & \vdots & \vdots \\ 0 & 0 & 0 & -\epsilon_{n-2} & a_{n-1} & 0 \\ 0 & 0 & 0 & \cdots & -\epsilon_{n-1} & a_n \end{bmatrix}$$

Then F is a nonnegative matrix and V is a nonsingular M-matrix. Hence the reproductive number, R_0, is equal to the spectral radius of the next generation operator FV^{-1} [15], $R_0 = \rho(FV^{-1})$. To determine the spectral radius of FV^{-1}, we first represent the inverse of V by the following lower triangular matrix, $V^{-1} = [A_3]_{1\times 1}$, where

$$A_3 = \begin{bmatrix} \frac{1}{a_1} & 0 & 0 & \cdots & 0 & 0 \\ m_{2,1} & \frac{1}{a_2} & 0 & \cdots & 0 & 0 \\ m_{3,1} & m_{3,2} & \frac{1}{a_3} & \cdots & 0 & 0 \\ \vdots & \vdots & \ddots & \ddots & \vdots & \vdots \\ m_{n-1,1} & m_{n-1,2} & m_{n-1,3} & \cdots & \frac{1}{a_{n-1}} & 0 \\ m_{n,1} & m_{n,2} & m_{n,3} & \cdots & m_{n,n-1} & \frac{1}{a_n} \end{bmatrix}$$

with

$$m_{i,j} = -\frac{\prod_{k=j}^{i-1} \epsilon_k}{\prod_{k=j}^{i} a_k}.$$

Now we are ready to derive an explicit formula for the reproductive number R_0. Then we have, $R_0 = \rho(A_4)$, where,

$$A_4 = \begin{bmatrix} r\beta_1\frac{1}{a_1} & 0 & 0 & \cdots & 0 & 0 \\ 0 & r\beta_2\frac{1}{a_2} & 0 & \cdots & 0 & 0 \\ 0 & 0 & r\beta_3\frac{1}{a_3} & \cdots & 0 & 0 \\ \vdots & \vdots & \vdots & \ddots & \vdots & \vdots \\ 0 & 0 & 0 & 0 & r\beta_{n-1}\frac{1}{a_{n-1}} & 0 \\ 0 & 0 & 0 & \cdots & 0 & r\beta_n\frac{1}{a_n} \end{bmatrix}$$

Therefore

$$R_0 = \max_{i=1,\ldots,n} \frac{r\beta_i}{a_i} = \max_{i=1,\ldots,n-1} \{\frac{r\beta_i}{\mu+\alpha_i+\gamma_i+\epsilon_i}, \frac{r\beta_n}{\mu+\alpha_n+\gamma_n}\}. \tag{3}$$

In summary, we have the following theorem:

2.1.1 Theorem

Define the reproductive number R_0 as

$$R_0 = \max_{i=1,...,n} \frac{r\beta_i}{a_i} = \max_{i=1,...,n-1} \{\frac{r\beta_i}{\mu + \alpha_i + \gamma_i + \epsilon_i}, \frac{r\beta_n}{\mu + \alpha_n + \gamma_n}\}. \quad (4)$$

If $R_0 < 1$ the infection-free equilibrium is locally asymptotically stable, and if $R_0 > 1$ the infection-free equilibrium is unstable.
For simple mathematical epidemiological models, the formula for R_0 can be interpreted as the product of the number of contacts per unit of time, the infectivity of infection, and the duration of infection. For the more complex model (1), the explicit formula (4) for the reproductive number R_0 can also be interpreted as the product of the mean number of contacts per unit of time, the total mean infectivity of infection, and total mean duration of infection. We define the mean duration of infection in each staged-progression-chain as, $\bar{\tau}_i = \frac{1}{a_i}, \quad i = 1, 2, ..., n$. Then, the total mean duration of infection for the model (1) is, $\bar{\tau} = \max_{i=1,...,n} \bar{\tau}_i$. Define the mean infectivity for each staged-progression-chain as, $\bar{\beta}_i = \frac{1}{\bar{\tau}_i}\frac{\beta_i}{a_i}$. Then, the total mean infectivity for the model (2.1) is, $\bar{\beta} = \frac{1}{\bar{\tau}} \max_{i=1,...,n} \bar{\beta}_i\bar{\tau}_i$. Therefore, the reproductive number R_0 can be written as, $R_0 = r\bar{\beta}\bar{\tau}$.

2.1.2 Corollary

Suppose we do not have travel from i patch to $i + 1$ patch or we do not have travel from I_i to I_{i+1}, then we have, $R_0 = \max_{i=1,...,n} \frac{r\beta_i}{\mu+\alpha_i+\gamma_i}$.

2.1.3 Corollary

Suppose we do not have travel from i patch to $i + 1$ patch and from I_i to S_i, then we have, $R_0 = \max_{i=1,...,n} \frac{r\beta_i}{\mu+\gamma_i}$

2.2 Example

In this Example for explain formula (4) we use the following model parameters, $n = 4$,$S_1^0 = 4000, S_2^0 = 3000, S_3^0 = 2000, S_4^0 = 1000, S_1(0) = 3500, S_2(0) = 3000, S_3(0) = 2500, S_4(0) = 2000, I_1(0) = 40, I_2(0) = 30, I_3(0) = 20, I_4(0) = 10$,$R_1(0) = R_2(0) = R_3(0) = R_4(0) = 0, \mu = 0.001, \alpha_1 = 0.04, \alpha_2 = 0.03, \alpha_3 = 0.02, \alpha_4 = 0.01, \delta_1 = 0.006, \delta_2 = 0.005, \delta_3 = 0.004$,$\gamma_1 = 0.03, \gamma_2 = 0.02, \gamma_3 = 0.01, \gamma_4 = 0.005, \epsilon_1 = 0.05, \epsilon_2 = 0.04, \epsilon_3 = 0.03$, and $\beta_1 = 0.0012, \beta_2 = 0.0009, \beta_3 = 0.0006, \beta_4 = 0.0006$, for $R_0 < 1$ and $\beta_1 = 0.014, \beta_2 = 0.0012, \beta_3 = 0.0008, \beta_4 = 0.0007$, for $R_0 > 1$.

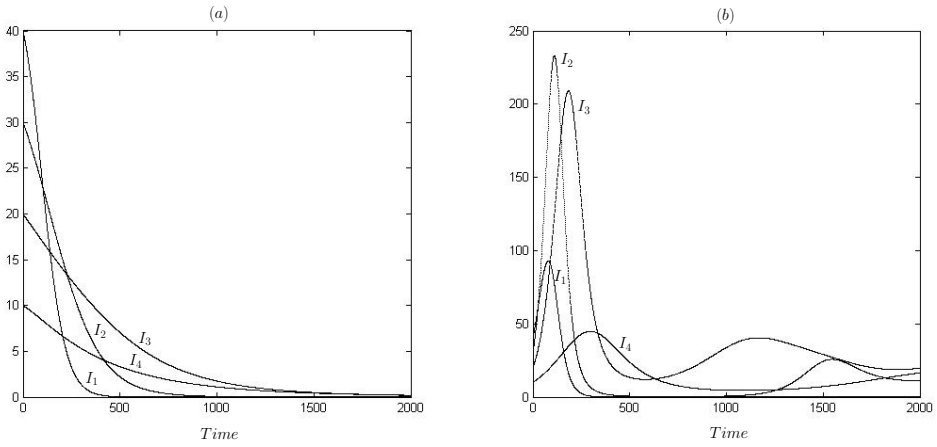

Figure 2: (a): $R_0 = \max\{0.9917, 0.9890, 0.9836, 0.9836\} = 0.9890 < 1$ and (b): $R_0 = \max\{1.1570, 1.3187, 1.3115, 1.1475\} = 1.5770 > 1$.

2.3 Example

Suppose in example (2.2) we have, $\epsilon_1 = \epsilon_2 = \epsilon_3 = 0$. We take, $\beta_1 = 0.0012, \beta_2 = 0.0009, \beta_3 = 0.0006, \beta_4 = 0.0006$, for $R_0 < 1$ and $\beta_1 = 0.0014, \beta_2 = 0.0012, \beta_3 = 0.0008, \beta_4 = 0.0007$, for $R_0 > 1$.

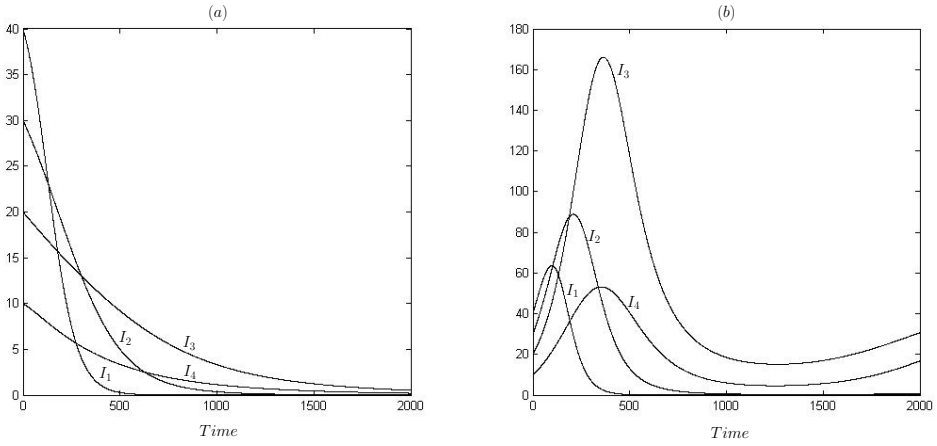

Figure 3: (a): $R_0 = \max\{0.9859, 0.9804, 0.9677, 0.9836\} = 0.9859 < 1$ and (b): $R_0 = \max\{1.1268, 1.1765, 1.2903, 1.1475\} = 1.2903 > 1$.

3 Conclusions

One of the fundamental questions of mathematical epidemiology is to find threshold conditions that determine whether an infectious disease will speared in a susceptible population when the disease is introduced into this population, and the threshold conditions are usually characterized by the reproductive number R_0. The reproductive number plays an important role in understanding transmission dynamics of epidemics and predicting epidemics spread. In this article we used the spectral radius of the next generation operator of infection in finding a formula for the reproductive number.

References

[1] R.M. Anderson and R.M. May. *Infectious Disease of Humans, dynamics and control*, Oxford Unuversity, Oxford (1991).

[2] N.G. Becker and K. Dietz, *The effects of the household distribution on transmission and control of highly infectious diseases*. Math. Biosci. **127** (1995), p.207.

[3] K. Dietz, J.A.P. Heesterbeek and D.W. Tudor, *The basic reproduction ratio for sexually transmitted disease, Part 2: effects of variable HIV infectivity*. Math. Biosci. **117** (1993), p. 35.

[4] M. G. M. Gomes, L. J. White and G. F. Medley, *Infection, reinfection, and vaccination under suboptimal immune protection: epidemiological perspectives*, Journal of Theoretical Biology **228** 2004, 539–549.

[5] J.A.P. Heesterbeek, R_0, *Thesis, Center for Mathematics and Computer science*, Amsterdam, 1991.

[6] J.A.P. Heesterbeek and K. Dietz, *The concept of R_0 in epidemic theory*. Statist. Neerlandica, **50** (1996), p. 89.

[7] H. W. Hethcote, *The Mathematics of Infectious Diseases,* SIAM REVIEW. **42** 2000, 599–653.

[8] J.M. Hyman and J. Li, *Disaese transmission models with biased partnership selection*. Appl. Numer. Math. **24** (1997), p. 379.

[9] J.M. Hyman, J. Li and E.A. Stanley, *Threshold conditions for the spread of the HIV infection in age-structured populations of homosexual men*. Theor. Biol. **166** (1994), p. 9.

[10] J.M. Hyman, J. Li and A.E. Stanley, *The differential infectivity and staged progression models for the transmission of HIV*. Math. Biosci. **155** (1999), p. 77.

[11] J.A. Jacquez, C.P. Simon, J. Koopman, L. Sattenspiel and T. perry, *Modeling and analyzing HIV transmission: the effect of contact patterns*. Math. Biosci. **92** (1988), p. 119.

[12] J.A. Jacquez, C.P. Simon and J. Koopman, *Core groups and the $R_0^i s$ for subgroups in heterogeneous SIS and SI models, in: D. Mollison (Ed.), Epidemic Models*: Their Structure and relation to Data Cambridge University, Cambridge, 1995, p. 279.

[13] X. Lin, *Qualitative analysis of an HIV transmission model*, Math. Biosci. **104** (1991), p. 111.

[14] R. Ross. *The Prevention of Malaria*, Murray, London (1909).

[15] P. van den Driessche and J. Watmough, *Reproduction numbers and subthresholdendemic equilibria for compartmental models of disease transmission*, Math. Biosci. **180** (2002), 29–48.

Received: August, 2011