Covid 19 Seen by Differential Equations:Model II (Covid 19 Vu par des Equations Différentielles: Modèle II)

Mustapha Yebdri

University of Tlemcen, Algeria

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Hello (Salam) every one.

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In this lecture we are going to introduce the SIR model.

introduction

The spread of infectious disease is an important and interesting task not only from the statistical viewpoint of data analysis but also from the practical viewpoint of prevention. This lecture presents analyses based on dynamical models of infectious diseases in contrast to traditional approaches. In a typical traditional approach, data are phenomenologically analyzed applying a regression model consisting of merely observed variables, not deeply considering the mechanism lying behind. In contrast, in a dynamical model approach, we incorporate variables of the number of susceptible and infected individuals which are not available or at least very difficult to obtain.

introduction

Dynamical model approach is a kind of state-space approaches which treats system variables in addition to observed variables. By setting such substantial variables of the system, we ca easily consider preventive measure and calculate the effects of such measures. Dynamical system approach will provide new opportunities in the real of data analyses together with the use of highly developed computers.

One of the simplest mathematical models of disease spread splits the population into three basic categories according to disease status. People who have not yet had the disease are labelled "susceptibles". Everyone is assumed to be born susceptible and capable of being infected. Those who have contracted the disease and are capable of passing it to susceptibles are the "infectives". The third group are euphemistically referred to as the "removed" class. These are the people who have had the disease and recovered and are now immune, or those who have died. These "removed" individuals no longer contribute to the spread of the disease.

This is referred to as the SIR (susceptible-infected-removed) model. It was developed by Ronald Ross 1, William Hamer, and others in the early twentieth century [4], consists of a system of three coupled non-linear ordinary differential equations, which does not possess an explicit formula solution. However, simple tools from calculus allow us to extract a great deal of information about the solutions.

The Mathematical Model SIR

The SIR model is the following system of the three ordinary differential equation(ODEs):

$$\frac{dS}{dt} = -\beta SI \tag{1}$$

$$\frac{dI}{dt} = \beta SI - \nu I \tag{2}$$

$$\frac{dR}{dt} = \nu I. \tag{3}$$

The Mathematical Model SIR

Here, S is the number of susceptible individuals, I is the number of infected individuals, and R is one of the recovered or immune individuals in the host population at time t. The constante $\beta > 0$ is the disease transmission rate or the contact rate and $\nu > 0$ the recovery rate (or in other words, the duration of infection $D = \frac{1}{\nu}$). A mass-action term βSI is the number of new infected individuals per unit time.

The Mathematical Model SIR

This form of the term describing the rate of transmission of the disease is based on the assumption that the affected population is homogeneous mixing of the infected and susceptible classes. It is often used when the total total population size is constant. Thus the total population size should remain constant, and this easily follows from the SIR system: that the sum of the left hand sides of the three equations is the derivative of the total population size and the sum of the right hand sides is zero. We denote the total population size by N.

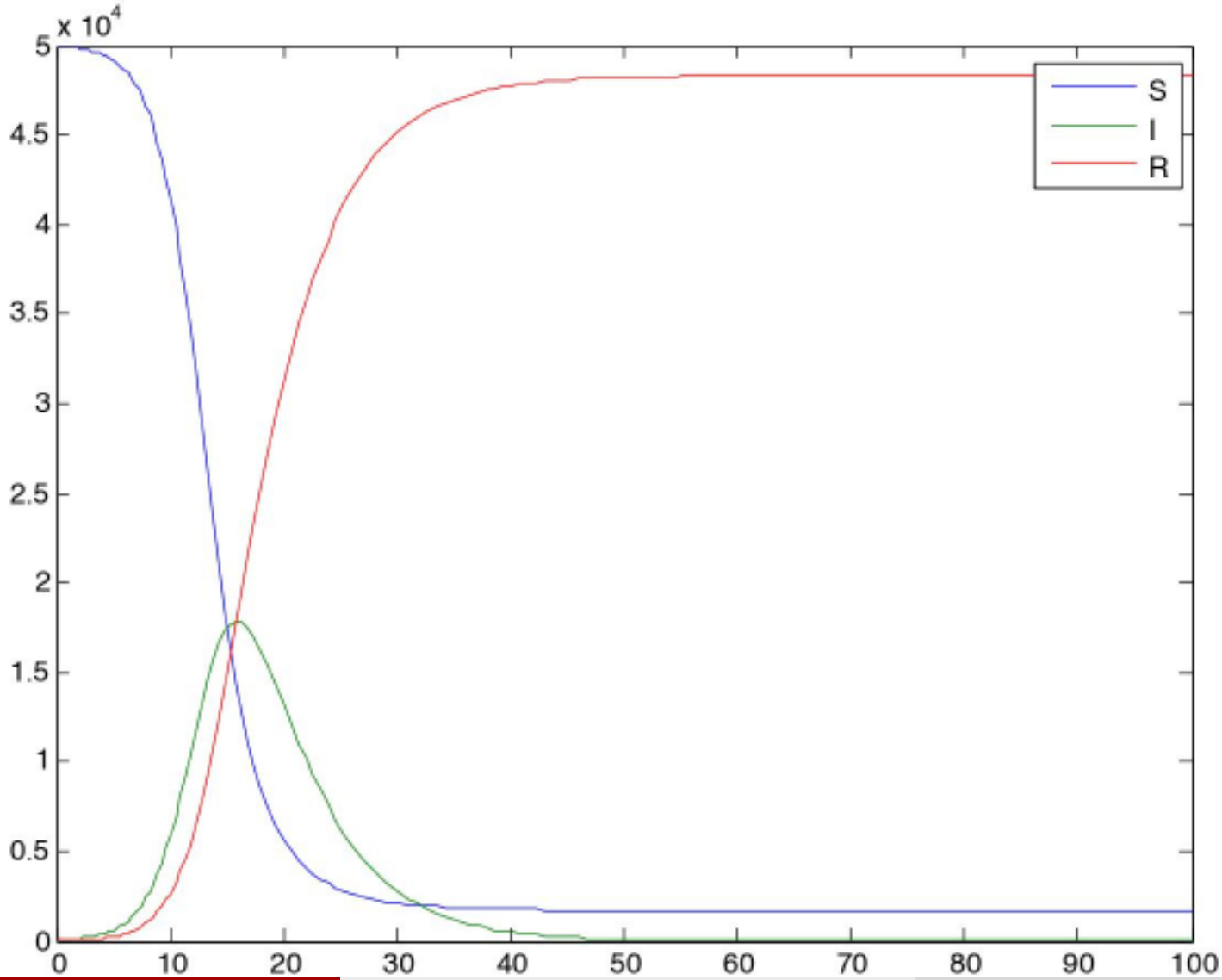
The Mathematical Model SIR

The infectives are assumed to cured at a rate νI at which point they enter the removed class. This implies that the average time of infectivity is $\frac{1}{\nu}$ because the probability of remaining infected for a time interval t is $\exp(-\nu t.)$ We note that the model is appropriate only if cases in which the epidemic is fast-acting so that the host population can be considered to be of constant size. In particular, births in the host population are not considered. Since $R(t) = N - S(t) - I(t)$, the system can be reduced to a system of two ODEs: (1) and (2).

The Mathematical Model SIR

Suppose that each infected individual has κ contacts (each sufficient for transmission) per unit time and κ is independent of the population size. Then $\kappa\frac{S}{N}$ of these contacts are with susceptible individuals. If the fraction τ of adequate contacts result in transmission, then each infected individual infects $\kappa\tau\frac{S}{N}$ susceptible individuals per unit time. Thus $\beta = \frac{b}{N}$ where $b = \kappa\tau$. The parameter τ is called the transmissibility of the infectious disease.

Analysis of the SIR Model



Analysis of the SIR Model

This graph is produced under the conditions, which will be discussed later, ensuring an epidemic Looking at the graphs one has the impression at first glance, that the model is well suited due to the behavior of the three classes. Indeed the number of susceptible people tends to decrease since every one is susceptible to be infected. the number of the recovered increases with respect of the evolution of the epidemic.Concerning the number of those infected will initially increase until a maximum, then it will decline until it vanishes.

Analysis of the SIR Model

So we can state the following result

Theorem 1

1. The long term limits exist i.e.
   $S(\infty) = \lim_{t\to\infty} S(t)$, $R(\infty) = \lim_{t\to\infty} R(t)$, and
   $I(\infty) = \lim_{t\to\infty} I(t)$ exist.
2. The disease always dies out i.e. $I(\infty) = \lim_{t\to\infty} I(t) = 0$.
3. Epidemic threshold, let $R_e = \frac{S(0)}{N}\frac{b}{\nu}$ the effective reproductive number, than one has
   3.1. If $R_e \leq 1$, then $I(t)$ decreases monotonically to zero as $t \to \infty$.
   3.2. If $R_e > 1$, then $I(t)$ starts increasing, reaches its maximum, and then decreases to zero as $t \to \infty$. We call this scenario of increasing numbers of infected individuals an epidemic.

proof

1. **The existence of the long term limits.** Since the right hand side of (1) is negative and the right hand side of (3) is positive, this implies that $\frac{dS}{dt} \leq 0$ and $\frac{dR}{dt} \geq 0$. Since $0 \leq S(t) \leq S(0) \leq N$ and $0 \leq R(0) \leq R(t) \leq N$, this implies that the limits $S(\infty) = \lim_{t\to\infty} S(t), R(\infty) = \lim_{t\to\infty} R(t)$, and thus $I(\infty) = \lim_{t\to\infty} I(t) = N - S(\infty) - R(\infty)$ exist.
2. **The disease always dies out** It is also easy to prove that the disease always dies out, $I(\infty) = 0$ for all initial conditions, without having a formula for $I(t)$. If not, (3) implies that for t sufficiently large, $\frac{dR}{dt} > \nu\frac{I(\infty)}{2} > 0$, and this implies that $R(\infty) = \infty$, a contradiction.

proof

3. **Epidemic threshold theorem** We define the effective reproductive number $R_e = \frac{S(0)}{N}\frac{b}{\nu}$ and the basic reproductive number $R_0 = \frac{b}{\nu}$. If the entire population is initially susceptible, i.e., $S(0) = N - 1, I(0) = 1, R(0) = 0$, and large (recall this is a model assumption),then $R_e = (\frac{N-1}{N})\frac{b}{\nu}$ is approximately equal to R_0. Henceforth, to beautify formulas involving R_0, we will assume that the quantity $\frac{(N-1)}{N}$ is equal to 1. We now show that R_e is the threshold value or tipping point that determines whether an infectious disease will quickly die out or whether it will invade the population and cause an epidemic.

proof

3.1 From equation (2)one has
$\frac{dI}{dt} = (\beta S - \nu)I \leq (\beta S(0) - \nu)I = \nu(R_e - 1)I \leq 0$ for $R_e < 1$. This observation together with $I(\infty) = 0$ proves the first statement.

3.2 Equation(2) implies $\frac{dI}{dt}(0) = \nu(R_e - 1)I(0) > 0$ for $R_e > 1$. Thus $I(t)$ is increasing at $t = 0$. Equation (2) also implies that $I(t)$ has only one non-zero critical point. These observations, together with $I(\infty) = 0$ imply the second statement.

Remarks

- It follows that an infection can invade and cause an epidemic in an entirely susceptible population if $R_0 > 1$ or $b > \nu$.
- **We stress that the existence of a threshold for infection is far from obvious and was missed by many public health and infectious disease experts. The reason is that such a threshold can not be discerned from data; it requires a mathematical model to illuminate.** We understand from here, since R_e is expressed by β and ν in the model,that these two parameters are the only ones that need to be estimated in order to predict the behavior of the infection.

Above we observed that $\frac{dI}{dt}(0) = \nu(R_e - 1)I(0)$, which implies that the number of infected individuals initially starts growing/decreasing exponentially at rate $\nu(R_e - 1)$. The next section will provide strong

Public Health interpretation of R_e

We defined the effective reproductive number

$$R_e = \frac{S(0)\beta}{\nu} = \frac{S(0)b}{\nu N} = \frac{D\kappa\tau S(0)}{N} \tag{4}$$

which is the product of the duration of infection, the number of contacts an infected individual has with susceptible individuals per unit time, and the transmissibility (rate of transmission). Thus R_e is the number of new infections caused by each infected individual at the beginning of the outbreak. The parameter R_e is a measure of the fitness of the pathogen. With this interpretation, the first theorem is almost obvious: if at the beginning each infected individual infects three susceptible individuals, and each of these three infected individuals infects three additional susceptible individuals, then of course the number of infections starts growing exponentially. This is schematically illustrated in the Figure 2

The exponential growth at the outbreak of an epidemic

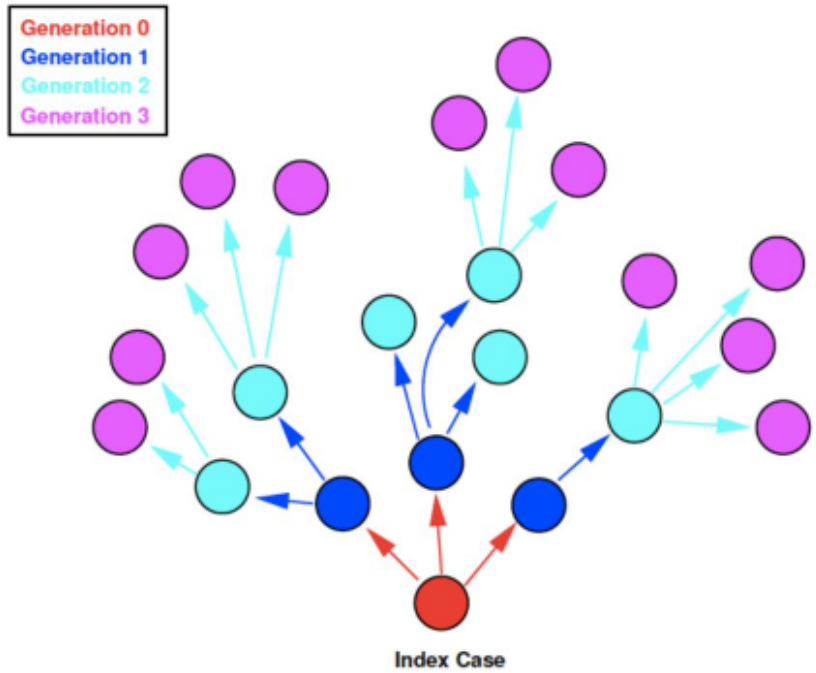


Figure: The exponential growth at the outbreak of an epidemic

The theoretical foundation of public health interventions

Theorem 1 and equation (4) provide strategies for public health experts to prevent an epidemic by reducing R_e to less than one. For example, for the flu:

1. Reduce the duration of infection D with antivirals;
2. Reduce the contact rate κ by self-isolation of susceptible individuals (request that they stay at home and skip school or work etc$\cdots$);
3. Reduce $S(0)$ by offering flu vaccines;
4. Reduce the transmissibility τ by encouraging frequent hand washing and, in some cultures, distributing face masks.

These strategies provide a theoretical underpinning for public health interventions.

Vaccination and heard immunity

Vaccinating susceptible individuals removes them from the susceptible class. Even if a vaccine is 100% effective (during a year when the flu vaccine matches the circulating strains well, the annual flu vaccine is estimated to be about 60% effective), vaccinating an entire population is very expensive, and not everybody can take the vaccine. Some individuals, such as those with compromised immune systems or severe allergies, the vaccine may be worse than the disease. We ask the question, can an epidemic be prevented by vaccinating only a fraction of the susceptible class?

It easily follows from our analysis of the SIR model that the answer is yes, and the phenomenon is called herd immunity.

Vaccination and heard immunity

Recall, to prevent an epidemic, we require that $R_e \leq 1$. Let ρ denote the fraction of the susceptible individuals who gets vaccinated (assuming that the vaccine is 100% effective). These $\rho S(0)$ vaccinated individuals have moved from the susceptible class to the removed class, and thus the size of the susceptible class becomes $(1-\rho)S(0)$. To prevent an epidemic, we require that $(1-\rho)S(0)\frac{\beta}{\nu} = (1-\rho)R_e \leq 1$. This will occur when $\rho \geq \rho_c$, where $\rho_c = 1 - \frac{1}{R_e}$ denotes the critical vaccination threshold. Thus vaccination against a disease can be completely effective without making everyone immune.

Vaccination and heard immunity

The existence of a herd immunity threshold is also far from obvious and was missed by many public health experts. A significant number of experts thought that such a threshold did not exist and thus believed that mass vaccination programs were bound to fail. The reason it was missed is that it can not be discerned from data; it requires again a mathematical model to illuminate. Assuming a completely susceptible population, to prevent a flu outbreak with $R_0 = 1.3$, one must vaccinate "only" 23% of the population to prevent an epidemic. If the vaccine is only 60% effective then it is easy to verify that one must vaccinate at least $\frac{23\%}{0.6} \approx 39\%$ of the population to prevent an epidemic.

Vaccination and heard immunity

To prevent a smallpox epidemic with $R_0 = 5$, one must vaccinate 80% of the population. Based in part on this finding, along with the belief that humans are the only natural hosts of the smallpox virus, in 1967 the World Health Organization (WHO) mounted a successful worldwide smallpox eradication program. Smallpox is one of only a very small number of human infectious diseases that has been almost completely irradiated around the world. Even if a malaria vaccine that is 100% effective, since $R_0 > 100$, it would be necessary to vaccinate 99% of the population to prevent epidemics.

The maximum number of infected individuals

We now show that although we can not explicitly solve the SIR system of ODEs, we can still obtain a formula solution for I_{max}. Dividing (1) by (2) yields the ODE

$$\frac{dS}{dI} = \frac{-\beta SI}{\beta SI - \nu I}$$

This ODE is separable, since for $I > 0$ it can be written as

$$\int \frac{\beta S - \nu}{\beta S} dS = \int -dI$$

Hence, $-I - S0 + \frac{\nu}{\beta} \ln S = C$. In other words, for every $t \geq 0$,

$$I(t) + S(t) - \frac{\nu}{\beta} \ln S(t) = I(0) + S(0) - \frac{\nu}{\beta} \ln S(0). \tag{5}$$

I_{max} occurs when $\frac{dI}{dt} = 0$ which from (2) yields occurs when $S = \frac{\nu}{\beta}$.

The maximum number of infected individuals

Applying (5) yields $I_{max} + \frac{\nu}{\beta} - \frac{\nu}{\beta} \ln \frac{\nu}{\beta} = I(0) + S(0) - \frac{\nu}{\beta} \ln S(0)$ or $I_{max} = I(0) + S(0) - \frac{\nu}{\beta} \ln S(0) - \frac{\nu}{\beta} + \frac{\nu}{\beta} \ln \frac{\nu}{\beta}$.

by an easy calculation we can show that for an initially fully susceptible population, the maximum fraction of infected individuals is solely a function of R_0 : $\frac{I_{max}}{N} = 1 - \frac{1}{R_0}(1 + \ln R_0)$. Expression (5) has another useful application. It states that the solutions $(S(t), I(t))$ viewed in the $S - I$ plane (orbits) are contained in the level curves of the function $F(S, I) = S + I - \frac{\nu}{\beta} \ln S$. The level curves of this function are shown in Figure 3.

The maximum number of infected individuals

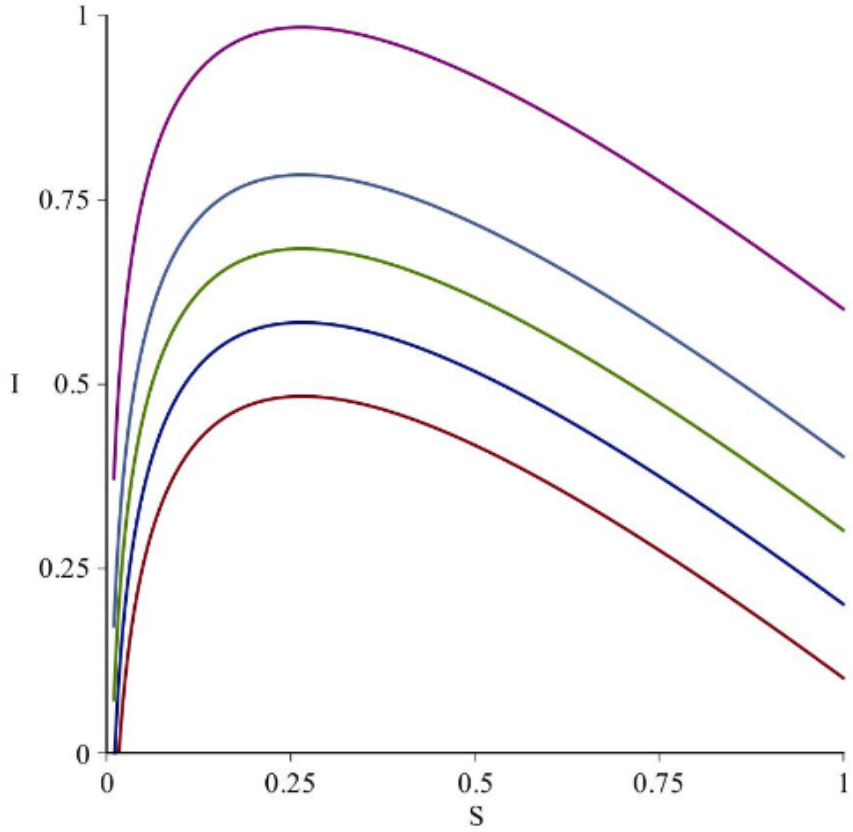


Figure: The level curves of $F(S, I)$ for $\beta = 1.66$ and $\nu = 0.44$

Why do epidemics end?

From the model we see that the epidemics are dying out. What's the cause? Do they end because there are no longer susceptible individuals in the population and there is no one left to infect? This question perplexed public health experts for many years. If so, then it would be the case that $S(\infty) = 0$. We now show this is not true.

Proposition

The limiting number of susceptible individuals

$S(\infty) \geq S(0)\exp(-R_0) > 0.$

proof

Dividing (1) by(3) yields the ODE

$$\frac{dS}{dR} = \frac{-\beta SI}{\nu I} = \frac{-\beta S}{\nu}$$

This ODE is separable, since for$S > 0$ it can be rewritten as Integrating both sides yields

$$\int \frac{1}{S} dS = \int \frac{-\beta}{\nu} dR$$

Integrating both sides yields

$$S(t) = S(0) \exp(\frac{-\beta}{\nu}(R(t) - R(0))), \tag{6}$$

Since $0 \leq R(t) - R(0) \leq N$ it follows that $S(t) \geq S(0) \exp(\frac{-\beta N}{\nu})$ and thus $S(\infty) \geq S(0) \exp(\frac{-\beta N}{\nu}) = S(0) \exp(-R_0) > 0$.

Remark

As an epidemic proceeds, the number of susceptible individuals decreases and so the rate at which new infections arise also decreases. Eventually, $S(t)$ drops below $\frac{\nu}{\beta}$, and the rate at which individuals recover exceeds the rate at which new infections occur. Thus, I(t) starts decreasing. The epidemic ends because of the lack of new infected individuals and not because of the lack of susceptible individuals.

This is still another fundament fact can not be discerned from data; it requires a mathematical model to illuminate.

The size of an epidemic?

Equation (6) easily yields a transcendental equation for $S(\infty)$, which when $R(0) = 0$, reduces to

$$\frac{S(\infty)}{N} = \frac{S(0)}{N} \exp\left(\frac{-b\frac{R(\infty)}{N}}{\nu}\right) = \frac{S(0)}{N} \exp\left(\frac{-b(1 - \frac{S(\infty)}{N})}{\nu}\right) \qquad (7)$$

(recall from Theorem 1 that $I(\infty) = 0$). If the entire population is initially susceptible(7) has the following simple, but transcendental form solely in terms of R_0 :

$$\ln\left(\frac{S(\infty)}{N}\right) = R_0\left(\frac{S(\infty)}{N} - 1\right)$$

We numerically solve this equation, and Figure 4 contains a plot of $\frac{S(\infty)}{N}$ verses R_0. It also follows in this case that the attack rate, the total fraction in individuals who get infected, is $1 - \frac{S(\infty)}{N}$.

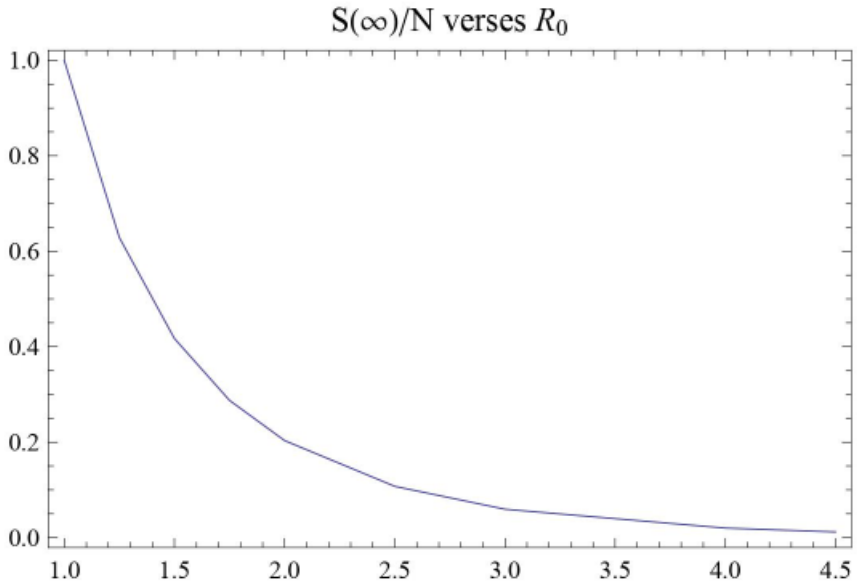


Figure: $\frac{S(\infty)}{N}$ verses R_0.