Article

A Viral Disease That Damages the Immunity Conferred by Different Viral Diseases or Vaccination

James P. Braselton * and Martha L. Abell

Department of Mathematical Sciences, Georgia Southern University, P.O. Box 8093, Statesboro, GA 30458, USA; martha@georgiasouthern.edu

* Correspondence: jbraselton@georgiasouthern.edu

Abstract: In this paper we modify a standard SIR model used to study the spread of some diseases by incorporating a disease that destroys the immunity that is conferred by having one of the other diseases or being vaccinated against the disease. A specific biological example of this occurs with measles. Studies of recent measles' patients has shown that many patients have lost some (or all) of their immunity to other diseases from which they were previously protected. In the future, models like those developed here might be helpful in understanding how viruses that affect multiple organ systems can impact the effect the disease has on at risk populations.

Keywords: SIR; SIS; measles; immunity; herd immunity; basic reproductive ratio

Citation: Braselton, J.P.; Abell, M.L.

A Viral Disease That Damages the Immunity Conferred by Different Viral Diseases or Vaccination.

Mathematics **2021**, *9*, 808. <https://doi.org/10.3390/math9080808>

Academic Editor: Sergei Petrovskii

Received: 1 March 2021

Accepted: 5 April 2021

Published: 8 April 2021

Publisher's Note: MDPI stays neutral with regard to jurisdictional claims in published maps and institutional affiliations.

Copyright: © 2021 by the authors. Licensee MDPI, Basel, Switzerland. This article is an open access article distributed under the terms and conditions of the Creative Commons Attribution (CC BY) license (<https://creativecommons.org/licenses/by/4.0/>).

1. Introduction

Many viral diseases such as measles, chicken pox, mumps, smallpox, and so on confer immunity to the survivor of the disease. Unfortunately, diseases such as these can inflict serious damage on the infected individual, including death, as well as being spread to uninfected individuals who come in contact with infected ones. Consequently, it is a top priority of nearly all health organizations to vaccinate as many individuals as possible against diseases such as those mentioned here. For example, smallpox is a lethal (30% death rate) and highly contagious disease. Due to a well-documented global immunization campaign, the last documented case of smallpox occurred in Somalia in 1977 and, subsequently, smallpox was declared eradicated in 1980. As a consequence, individuals are no longer vaccinated against smallpox. (The interested reader may study the ramifications of this policy. Some have worried that the smallpox virus could be used as a biological weapon. As a consequence, it is theorized that many governments have stockpiled smallpox vaccines to prevent a global pandemic in the event that there was an attack using a virus such as smallpox as the weapon.) However, it is not known what percent of the population that was vaccinated against smallpox is still immune to smallpox. Thus, if a disease such as measles destroys immunity to existing diseases, if a person contracted measles and transmitted the infection to various individuals immune to smallpox, the measles infection might destroy their immunity to smallpox creating the possibility of a smallpox epidemic. The eradication of smallpox, which is frequently thought to be the only disease eradicated, is readily available. The Centers for Disease Control and Prevention provides a comprehensive overview of smallpox which you can access by pointing your browser to <https://www.cdc.gov/smallpox/index.html> (accessed on 7 April 2021).

For example, recently measles has seen outbreaks throughout the United States that have led to local epidemics that have been documented in scientific literature [1], as well as observed in popular media [2]. Additionally, recent research indicates that although surviving measles confers immunity to measles, having measles may damage and/or destroy the immunity to other diseases that was obtained by surviving infection or vaccination.

For a few examples, refer to articles by Mina et al. [3], Petrova et al. [4], Griffin [5], or Kelland [6].

The phrase as many individuals deserves special explanation. Mathematical models studying the spread of diseases are classified into a variety of different groups. A few such groups include

- Susceptible-infected-susceptible (SIS). After an individual has the disease and recovers from the disease, they are again susceptible to the disease. Many bacterial infections (such as strep throat and many sinus infections) are frequently included in this category.
- Susceptible-infected-recovered (SIR). After an individual has had the disease, they are no longer susceptible to the disease. Many viral infections (such as measles and chickenpox) are frequently included in this category because if an individual recovers from the disease, they are immune to subsequent occurrences of the disease.

This list is quite limited. Mathematical models take a variety of forms that take into consideration many variables such as including not taking births and deaths (without vital dynamics) or taking births and deaths (with vital dynamics) into consideration. In mathematical models such as these, the phrase as many individuals is quantified by a number, typically denoted as R_0 , which is called the basic reproductive ratio. The basic reproductive ratio, R_0 , is defined in different ways depending upon the context of the problem under consideration. We use Britton's [7], definition. In the context of a disease that may be spread through a population by an individual's contact with another, often R_0 is interpreted to mean the percentage of the population of individuals that need to be vaccinated so that an infected individual is not statistically likely to interact with a susceptible individual and, consequently, increase the spread of the disease. In situations such as this, the percentage that needs to be vaccinated to prevent the disease from being spread among the population is referred to as herd immunity and used interchangeably with basic reproductive ratio. Refer to introductory mathematical biology texts such as Britton [7], for a comprehensive introduction to mathematical biology and the vocabulary used here.

The value of R_0 to achieve herd immunity is *very* important. If the fraction vaccinated against a disease is less than its $1 - 1/R_0$ -value, the disease may become epidemic, a "widespread" occurrence of an infectious disease at a particular time, or endemic, regularly occurring or persistent, in the population. For many health-related issues there are reasons why some individuals cannot be vaccinated for various diseases. On the other hand, some individuals choose to not vaccinate for other reasons. Adding the two groups may result in the fraction of the population being vaccinated against a particular disease may result in the fraction of the population vaccinated less than its R_0 -value. Once the fraction of the population vaccinated is below its R_0 -value, epidemics and/or endemics can arise.

Many of the terms and concepts presented here were first introduced in the article that forms the foundations for the mathematical models of epidemics by Kermack and McKendrick [8], in 1927, which we summarize next.

2. Summary of the Basic SIR Model without Vital Dynamics

We summarize the case when the disease under consideration spreads and confers immunity, as is the case with many viral infections, such as chickenpox mentioned above, that was discussed by Kermack and McKendrick [8], for completeness purposes. In this situation, we have a susceptible (S), infected (I), and recovered (R) population where it is assumed that the R population is immune from contracting the disease again, such as is suspected with viral diseases such as measles. Without taking vital dynamics (such as births and deaths) into consideration, we assume that the population is closed with constant size N so that

$$S(t) + I(t) + R(t) = N.$$

Schematically we have

$$S \xrightarrow{\beta IS} I \xrightarrow{\gamma I} R$$

so the model takes the form

$$\begin{aligned}\frac{dS}{d\tau} &= -\beta IS \\ \frac{dI}{d\tau} &= \beta IS - \gamma I \\ \frac{dR}{d\tau} &= \gamma I.\end{aligned}\tag{1}$$

In this model, β represents the proportion of $I-S$ interactions that result in I infections, often referred to as the (pairwise) infectious contact rate, and γ represents the rate of recovery. In the subsequent discussion, the interpretations of the constants remain the same however we use subscripts to denote relationships between the S_i , I_j , and R_k classes of the population. Now we non-dimensionalize the equations by letting

$$u = \frac{1}{N}S, \quad v = \frac{1}{N}I, \quad w = \frac{1}{N}R, \quad \text{and} \quad t = \gamma\tau.$$

The equations become

$$\begin{aligned}\frac{du}{dt} &= -R_0uv \\ \frac{dv}{dt} &= (R_0u - 1)v \\ \frac{dw}{dt} &= v \\ u + v + w &= 1,\end{aligned}\tag{2}$$

where $R_0 = \frac{\beta N}{\gamma}$ is the basic reproductive ratio. Observe that if $R_0u - 1 < 0 \rightarrow R_0u < 1$, then $v \rightarrow 0$ as $t \rightarrow \infty$ so $u = 1$. On the other hand, if $R_0u - 1 > 0 \rightarrow R_0u > 1$, then $w \rightarrow 1$ as $t \rightarrow \infty$. For

$$\begin{aligned}\frac{du}{dt} &= -R_0uv \\ \frac{dv}{dt} &= (R_0u - 1)v\end{aligned}\tag{3}$$

we have two rest points $E_0 = (0, 0)$ and $E_u = (1, 0)$. The Jacobian for system (3) is

$$\mathbf{J} = \begin{pmatrix} -R_0v & -R_0u \\ R_0v & R_0u - 1 \end{pmatrix}.$$

Evaluated at E_0 , the Jacobian

$$\mathbf{J}(E_0) = \begin{pmatrix} 0 & 0 \\ 0 & -1 \end{pmatrix}$$

has eigenvalues $\lambda_1 = -1$ and $\lambda_2 = 0$. Thus, E_0 is stable, but not asymptotically stable. On the other hand, evaluated at E_u the Jacobian is

$$\mathbf{J}(E_u) = \begin{pmatrix} 0 & -R_0 \\ 0 & R_0 - 1 \end{pmatrix},$$

which has eigenvalues $\lambda_1 = R_0 - 1$ and $\lambda_2 = 0$. Once again, the equilibrium point is stable, but not asymptotically stable. The two situations are illustrated in Figure 1. In (a), $R_0 < 1$ while in (b) $R_0 > 1$.

Figure 1. (a) Trajectories for $R_0 < 1$ and (b) trajectories for $R_0 > 1$.

It is important to note that the scaling performed on system (1) cannot be performed if the population is not assumed to be constant, which would be the case if vital dynamics (such as births, deaths, immigration, emigration, and so on) were taken into consideration.

3. Summary of the Basic SIR Model with Vital Dynamics

An SIR model that takes basic vital dynamics (births and deaths) into consideration is

$$\begin{aligned}\frac{dS}{dt} &= B - \beta IS - dS \\ \frac{dI}{dt} &= \beta IS - \gamma I - cI - dI \\ \frac{dR}{dt} &= \gamma I - dR,\end{aligned}\tag{4}$$

where B is interpreted to be a constant birth rate, d is the natural death rate, c is the disease induced death rate, and $S + I + R = N$, where N represents the total population. Refer to texts like [7] or [9]. β and γ have the same interpretations as before. Adding the three equations in system (4) gives us

$$\frac{dN}{dt} = B - cI - dN.\tag{5}$$

Because $N = N(t)$ is not constant, it is not possible to perform the same scaling to dimensionless variables as with system (1).

Because of the equation $S + I + R = N$, we can analyze any three of the equations. We follow Britton's convention [7], and choose to analyze the (N, S, I) equations.

$$\begin{aligned}\frac{dN}{dt} &= B - cI - dN \\ \frac{dS}{dt} &= B - \beta IS - dS \\ \frac{dI}{dt} &= \beta IS - \gamma I - cI - dI.\end{aligned}\tag{6}$$

We first find the rest points (equilibrium points) of system (6) by solving

$$\begin{aligned} B - cI - dN &= 0 \\ B - \beta IS - dS &= 0 \\ \beta IS - \gamma I - cI - dI &= 0 \end{aligned} \quad (7)$$

resulting in

$$E_I = (N_I, S_I, I_I) = \left(\frac{B}{d}, \frac{B}{d}, 0 \right)$$

and

$$\begin{aligned} E^* = (N^*, S^*, I^*) &= \left(\frac{B(\gamma + d)}{d(c + \gamma + d)} + \frac{c}{\beta}, \frac{c + \gamma + d}{\beta}, \frac{B}{c + \gamma + d} - \frac{d}{\beta} \right) \\ &= \left(\frac{B - cI^*}{d}, \frac{B}{dR_0}, \frac{B - dS^*}{\beta S^*} \right), \end{aligned}$$

where $R_0 > 1$ (the basic reproductive ratio [7]) takes the form

$$R_0 = \frac{\beta B}{d(c + \gamma + d)} \longrightarrow \beta B = d(c + \gamma + d)R_0 \longrightarrow R_0 = \frac{B\beta}{d(c + \gamma + d)}.$$

to make infectious contacts and

$$S^* = \frac{c + \gamma + d}{\beta} \quad \text{and} \quad I^* = \frac{B}{c + \gamma + d} - \frac{d}{\beta} = \frac{B - dS^*}{\beta S^*}.$$

Comment: One interpretation of R_0 is that it is a number that guarantees that E_I will be unstable so that the diseases persists (i.e., is endemic) as shown in the following calculation.

The Jacobian of system (6) is

$$\mathbf{J} = \begin{pmatrix} -d & 0 & -c \\ 0 & 0 & \beta(-s) \\ 0 & 0 & -c - \gamma - d + \beta s \end{pmatrix}.$$

Evaluated at E_I , the Jacobian is

$$\mathbf{J}(E_I) = \begin{pmatrix} -d & 0 & -c \\ 0 & 0 & -\frac{B\beta}{d} \\ 0 & 0 & \frac{B\beta - d(c + \gamma + d)}{d} \end{pmatrix}$$

with eigenvalues $\lambda_1 = 0$, $\lambda_2 = -d$ and

$$\lambda_3 = \frac{B\beta - d(c + \gamma + d)}{d}.$$

To guarantee that E_I is unstable, we will further assume that

$$\begin{aligned} B\beta - d(c + \gamma + d) &> 0 \\ \frac{B\beta}{d(c + \gamma + d)} &> 1 \\ R_0 &> 1. \end{aligned}$$

On the other hand, evaluated at E^* (assuming that E^* exists) the Jacobian is

$$J(E^*) = \begin{pmatrix} -d & 0 & -c \\ 0 & 0 & -c - \gamma - d \\ 0 & 0 & 0 \end{pmatrix}$$

with eigenvalues $\lambda_{1,2} = 0$ and $\lambda_3 = -d$. E^* is stable when it exists. See Figure 2. In the figure, $N(t)$ (total population) is in black, $S(t)$ (the susceptible population) is in gray, and $I(t)$ (the infected population) is in dashed gray. Observe in (a) that the disease dies out so that $N(t) = S(t)$. On the other hand, in (b) the disease is endemic in the form of a stable equilibrium point. That is, the prevalence of each class is constant.

Figure 2. (a) The disease dies out. (b) The disease is endemic in the population at a constant rate. (In the figure S is in black, I is in gray, and R is dashed).

4. Two Infectious SIR Diseases Where One Disease Destroys Immunity to the Other Endemic to the Population

To consider two infectious SIR diseases, we first rewrite system (4) as two systems, using the subscripts one and two, respectively, to separate the two diseases. The birth rates and natural death rates (B and d) are assumed to be the same for each disease. The notation is the same as that used previously: S_i denotes the portion of the population susceptible to disease i , I_i denotes the portion of the population infected by disease i , and R_i denotes the portion of the population recovered from disease i .

$$\begin{aligned} \frac{dS_1}{dt} &= B - \beta_1 I_1 S_1 - dS_1 & \frac{dS_2}{dt} &= B - \beta_2 I_2 S_2 - dS_2 \\ \frac{dI_1}{dt} &= \beta_1 I_1 S_1 - \gamma_1 I_1 - c_1 I_1 - dI_1 & \frac{dI_2}{dt} &= \beta_2 I_2 S_2 - \gamma_2 I_2 - c_2 I_2 - dI_2 \\ \frac{dR_1}{dt} &= \gamma_1 I_1 - dR_1 & \frac{dR_2}{dt} &= \gamma_2 I_2 - dR_2. \end{aligned} \quad (8)$$

We will assume that the second disease destroys immunity to the first. To form the model, we introduce three additional variables, S_3 , I_3 , and R_3 . The interpretations of the nine dependent variables change slightly

- The $S_1 I_1 R_1$ Equations.
 - S_1 represents the portion of the population that is susceptible to disease one but not disease two. The S_1 population increases as those in the R_2 and the R_3 populations recover.
 - I_1 represents the portion of the population that were initially in the S_1 group but are now infected.

- R_1 represents the portion of the population that were initially in the I_1 group but are now recovered.
- The $S_2I_2R_2$ Equations.
 - S_2 represents the portion of the population that is susceptible to disease two but not disease one.
 - I_2 represents the portion of the population that were initially in the S_2 group but are now infected.
 - R_2 represents the portion of the population that were initially in the I_2 group but are now recovered.
- The $S_3I_3R_3$ Equations.
 - S_3 represents the portion of the population that is susceptible to diseases one and two. The growth rate of S_3 is assumed to be constant, B , but those in the S_3 class move to the I_1 and S_2 classes, I_2 and S_1 classes, or I_3 class.
 - I_3 represents the portion of the population that were initially in the S_3 group but are now infected by both diseases. Those in the I_3 class who survive the disease move to the R_3 class.
 - R_3 represents the portion of the population that were initially in the I_3 group but are now recovered from both diseases. Those in the R_3 class move to the S_1 class, which models the destruction of immunity to the first disease by the second disease.

With the above in mind, we start by forming the S_3 equation using the standard equations, (8) as a guide. The interpretations of the constants remain the same.

All are born into the S_3 class. The susceptibles are born into the class and then removed to class I_1 and S_2 , I_2 and S_1 , or I_3 so the S_3 equation takes the form

$$\frac{dS_3}{dt} = B - \beta_{13}I_1S_3 - \beta_{23}I_2S_3 - \beta_{33}I_3S_3 - dS_3, \quad (9)$$

where the constants have the same interpretation as discussed previously. The equations for the infected and recovered portions of the population are nearly the same, other than the growth rates might differ with this model.

The I_3 equation takes into consideration the infectives to both the first and second diseases. An individual can become a member of the I_3 class by an I_3S_3 interaction. Once an individual recovers from both diseases they move to the R_3 class and the S_1 class because the second diseases destroys immunity to the first disease.

$$\begin{aligned} \frac{dI_3}{dt} &= \beta_{33}I_3S_3 - \gamma_3I_3 - c_3I_3 - dI_3 \\ \frac{dR_3}{dt} &= \gamma_3I_3 - dR_3. \end{aligned} \quad (10)$$

Observe that an I_3S_3 interaction could result in an I_1 or I_2 infection, as well. Similarly, it is possible that an I_1S_3 and I_2S_3 simultaneously could occur that would result in an I_3 infection. For now, we will assume that the number of I_1 , I_2 , and I_3 infections as a result of such interactions is small enough to be ignored but will be revisited in a later study.

If an individual moves into the I_1 class then they move into the S_2 class and if an individual moves into the I_2 class they move into the S_1 class. Thus,

$$\begin{aligned}\frac{dI_1}{dt} &= \beta_{11}I_1S_1 + \beta_{13}I_1S_3 - \gamma_1I_1 - c_1I_1 - dI_1, \\ \frac{dR_1}{dt} &= \gamma_1I_1 - dR_1, \\ \frac{dS_2}{dt} &= \beta_{13}I_1S_3 - \beta_{22}I_2S_2 - dS_2, \\ \frac{dI_2}{dt} &= \beta_{22}I_2S_2 + \beta_{23}I_2S_3 - \gamma_2I_2 - c_2I_2 - dI_2, \quad \text{and} \\ \frac{dR_2}{dt} &= \gamma_2I_2 - dR_2.\end{aligned}\tag{11}$$

We now turn our attention to the S_1 equation: the individuals susceptible to the first disease. These are individuals who have contracted the second disease but not the first so moved to class I_2 . However, because we are assuming that the second disease destroys immunity to the first, the S_1 class also includes the survivors of the second disease which are included in the R_2 class. Thus, the S_1 equation takes the form

$$\frac{dS_1}{dt} = \beta_{23}I_2S_3 + \gamma_2I_2 - \beta_{11}I_1S_1 - dS_1.\tag{12}$$

Combining Equations (9)–(12) yields the system of interest.

$$\begin{aligned}\frac{dS_1}{dt} &= \beta_{23}I_2S_3 + \gamma_2I_2 - \beta_{11}I_1S_1 - dS_1 \\ \frac{dI_1}{dt} &= \beta_{11}I_1S_1 + \beta_{13}I_1S_3 - \gamma_1I_1 - c_1I_1 - dI_1 \\ \frac{dR_1}{dt} &= \gamma_1I_1 - dR_1 \\ \frac{dS_2}{dt} &= \beta_{13}I_1S_3 - \beta_{22}I_2S_2 - dS_2 \\ \frac{dI_2}{dt} &= \beta_{22}I_2S_2 + \beta_{23}I_2S_3 - \gamma_2I_2 - c_2I_2 - dI_2 \\ \frac{dR_2}{dt} &= \gamma_2I_2 - dR_2 \\ \frac{dS_3}{dt} &= B - \beta_{13}I_1S_3 - \beta_{23}I_2S_3 - \beta_{33}I_3S_3 - dS_3 \\ \frac{dI_3}{dt} &= \beta_{33}I_3S_3 - \gamma_3I_3 - c_3I_3 - dI_3 \\ \frac{dR_3}{dt} &= \gamma_3I_3 - dR_3,\end{aligned}\tag{13}$$

where all the initial conditions are nonnegative and at least one initial condition is positive. The β_{ij} , γ_i , c_i , and d terms have the same interpretation as discussed previously. Because the second disease destroys immunity to the first we consider it to be the more “dangerous” disease.

A diagram of the model is shown in Figure 3.

Figure 3. A diagram of the dynamics modeled by system (13).

5. The Boundary Rest Points

Observe that if $B > 0$, then it is not possible for $S_3 = 0$ to be a rest point. Boundary rest points of interest occur if $S_2 = 0$ and $I_2 = 0$ or if $S_1 = 0$, $I_1 = 0$, $S_2 = 0$ and $I_2 = 0$. Note that if $S_1 = 0$ and $I_1 = 0$ then $S_2 = 0$ and $I_2 = 0$.

$$S_1 = 0, I_1 = 0; S_2 = 0, I_2 = 0$$

If $S_1 = 0$ and $I_1 = 0$ (and/or $S_2 = 0$ and $I_2 = 0$), solving

$$\begin{aligned}
\beta_{23}I_2S_3 + \gamma_2I_2 - \beta_{11}I_1S_1 - dS_1 &= 0 \\
\beta_{11}I_1S_1 + \beta_{13}I_1S_3 - \gamma_1I_1 - c_1I_1 - dI_1 &= 0 \\
\gamma_1I_1 - dR_1 &= 0 \\
\beta_{13}I_1S_3 - \beta_{22}I_2S_2 - dS_2 &= 0 \\
\beta_{22}I_2S_2 + \beta_{23}I_2S_3 - \gamma_2I_2 - c_2I_2 - dI_2 &= 0 \\
\gamma_2I_2 - dR_2 &= 0 \\
B - \beta_{13}I_1S_3 - \beta_{23}I_2S_3 - \beta_{33}I_3S_3 - dS_3 &= 0 \\
\beta_{33}I_3S_3 - \gamma_3I_3 - c_3I_3 - dI_3 &= 0 \\
\gamma_3I_3 - dR_3 &= 0
\end{aligned} \tag{14}$$

results in $S_2 = 0$, $I_2 = 0$ (and/or $S_1 = 0$, $I_1 = 0$), $S_3 = B/d$, and $R_3 = 0$, which we will denote as

$$E_0 = (S_1, I_1, R_1, S_2, I_2, R_2, S_3, I_3, R_3) = (0, 0, 0, 0, 0, 0, B/d, 0, 0).$$

We define $D_i = c_i + d + \gamma_i$. A second equilibrium point is

$$E_1 = (S_1, I_1, R_1, S_2, I_2, R_2, S_3, I_3, R_3) = \left(0, 0, 0, 0, 0, 0, \frac{D_3}{\beta_{33}}, \frac{B}{D_3} - \frac{d}{\beta_{33}}, \frac{b\gamma_3}{d}D_3 - \frac{\gamma_3}{\beta_{33}}\right).$$

The Jacobian of system (13) evaluated at E_0 is

$$\mathbf{J}(E_0) = \begin{pmatrix} -d & 0 & 0 & 0 & \frac{B}{d}\beta_{23} + \gamma_2 & 0 & 0 & 0 & 0 \\ \frac{1}{d}(B\beta_{13} - dD_1) & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 \\ 0 & \gamma_1 & -d & 0 & 0 & 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & -d & -\frac{B}{d}\beta_{23} & 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 & \frac{1}{d}(B\beta_{23} - dD_2) & 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 & \gamma_2 & -d & 0 & 0 & 0 \\ 0 & -\frac{B}{d}\beta_{13} & 0 & 0 & -\frac{B}{d}\beta_{23} & 0 & -d & -\frac{B}{d}\beta_{33} & 0 \\ 0 & 0 & 0 & 0 & 0 & 0 & 0 & \frac{1}{d}(B\beta_{33} - dD_3) & 0 \\ 0 & 0 & 0 & 0 & 0 & 0 & 0 & \gamma_3 & -d \end{pmatrix}$$

with eigenvalues

$$\lambda_i = \frac{1}{d}(B\beta_{i3} - d(c_i + \gamma_i + d)) = \frac{1}{d}(B\beta_{i3} - dD_i)$$

for $i = 1, 2$, and 3 and then $\lambda_{4,5,6,7,8,9} = -d$. Thus, E_0 will be stable when

$$\begin{aligned}
R_0 &= \max\{B\beta_{13} - dD_1, B\beta_{23} - dD_2, B\beta_{33} - dD_3\} \\
&= \max\left\{D_1\left(\frac{\beta_{13}}{D_1} - d\right), D_2\left(\frac{\beta_{23}}{D_2} - d\right), D_3\left(\frac{\beta_{33}}{D_3} - d\right)\right\} < 0.
\end{aligned} \tag{15}$$

B (the constant birth rate) and d (the natural death rate) are constant for all three populations. The disease induced death rates, c_j , are assumed to be different as well as the recovery rates, γ_j . The transmission coefficients for moving from the S_3 class to the I_j class are given by β_{j3} . In (15), we assume that $\frac{\beta_{33}}{D_3} - d$ is the largest of these three numbers: being susceptible to both diseases is more risky than being susceptible to only one of them.

With the interpretation of the variables in mind, we solve for when

$$B\beta_{j3} - d(c_j + \gamma_j + d) = \beta_{j3}B - dD_j < 0 : \tag{16}$$

as follows.

$$\begin{aligned}
 B\beta_{j3} - d(c_j + \gamma_j + d) &< 0 \\
 \beta_{j3}B - dD_j &< 0 \\
 \beta_{j3}B &< dD_j \\
 \frac{B}{dD_j} &< \frac{1}{\beta_{j3}} \quad \text{or} \quad \frac{B}{D_j} - \frac{d}{\beta_{j3}} < 0.
 \end{aligned} \tag{17}$$

The results coincide with what most would predict: the diseases are eliminated when the transmission coefficients (contact rates) are sufficiently small.

If E_0 is stable, both diseases are eliminated from the population. Observe that E_1 exists if E_0 is unstable (otherwise, the I_3 -component is negative). If E_1 exists, the Jacobian of system (13) evaluated at E_1 is

$$J(E_1) = \begin{pmatrix} -d & 0 & 0 & 0 & \gamma_2 + \frac{\beta_{23}}{\beta_{33}}D_3 & 0 & 0 & 0 & 0 \\ 0 & \frac{\beta_{13}}{\beta_{33}}D_3 - D_1 & 0 & 0 & 0 & 0 & 0 & 0 & 0 \\ 0 & \gamma_1 & -d & 0 & 0 & 0 & 0 & 0 & 0 \\ 0 & \frac{\beta_{13}}{\beta_{33}}D_3 & 0 & -d & 0 & 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 & \frac{\beta_{23}}{\beta_{33}}D_3 - D_2 & 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 & \gamma_2 & -d & 0 & 0 & 0 \\ 0 & -\frac{\beta_{13}}{\beta_{33}}D_3 & 0 & 0 & -\frac{\beta_{23}}{\beta_{33}}D_3 & 0 & -\beta_{33}\frac{B}{D_3} & -D_3 & 0 \\ 0 & 0 & 0 & 0 & 0 & 0 & \beta_{33}\frac{B}{D_3} - d & 0 & 0 \\ 0 & 0 & 0 & 0 & 0 & 0 & 0 & \gamma_3 & -d \end{pmatrix}$$

with eigenvalues $\lambda_i = \frac{1}{\beta_{33}}(\beta_{i3}D_3 - \beta_{33}D_i)$ for $i = 1, 2$, $\lambda_{3,4,5,6,7} = -d$ and

$$\lambda_{8,9} = \frac{1}{2D_3} \times \left(-\beta_{33}B \pm \sqrt{4c_3D_3(dD_3 - \beta_{33}B) + (\beta_{33}B - 2dD_3)^2 + 4\gamma_3(dD_3 - \beta_{33}B)D_3} \right).$$

In the numerical examples, we have chosen parameter values that illustrate the variety of situations and outcomes that we observed. Because the variables are dimensionless, we cannot use real data here.

Example 1. Our first example illustrates a scenario with $B = 1$, $\beta_{11} = \beta_{13} = 0.02$, $\beta_{22} = \beta_{23} = 5$, $\beta_{33} = 10$, $\gamma_1 = \gamma_2 = \gamma_3 = 10$, $d = 0.5$, $c_1 = c_2 = c_3 = 1$. Figure 4 indicates that in the case when individuals are susceptible, infected, and recovered from both diseases persist while the cases when individuals are susceptible, infected, and recovered from one disease are eliminated.

Figure 4. (a) S_j , (b) I_j , and (c) R_j . The first disease is represented in blue, the second in orange and those susceptible/infected/recovered by diseases in green.

Example 2. Our second example illustrates a scenario with $B = 1$, $\beta_{11} = \beta_{13} = 0.2$, $\beta_{23} = 0.8$, $\beta_{33} = 0.4$, $\gamma_1 = 0.1$, $\gamma_2 = 0.2$, $\gamma_3 = 0.3$, $d = 0.05$, $c_1 = c_2 = 0.4$, $c_3 = 1$. Figure 5 indicates that in the case when individuals are susceptible, infected, and recovered from one of the diseases persist while the cases when individuals are susceptible, infected, and recovered from both diseases are eliminated.

Figure 5. (a) S_j , (b) I_j , and (c) R_j . The first disease is represented in blue, the second in orange and those susceptible/infected/recovered by diseases in green.

The two examples reveal the extremes possible as well as some of the limitations of the model.

6. Simple Vaccination

System (13) does not take vaccination against the disease into consideration. We will assume that vaccination of an individual in the S_i class moves the individual to the R_i class. Let v_i denote the vaccination rate of the population S_i . For example, v_3 denotes the vaccination rate of the the population S_3 against both diseases. Then, system (13) becomes

$$\begin{aligned}
 \frac{dS_1}{dt} &= \beta_{23}I_2S_3 + \gamma_2I_2 - \beta_{11}I_1S_1 - dS_1 - v_1S_1 \\
 \frac{dI_1}{dt} &= \beta_{11}I_1S_1 + \beta_{13}I_1S_3 - \gamma_1I_1 - c_1I_1 - dI_1 \\
 \frac{dR_1}{dt} &= \gamma_1I_1 - dR_1 + v_1S_1 \\
 \frac{dS_2}{dt} &= \beta_{13}I_1S_3 - \beta_{22}I_2S_2 - dS_2 - v_2S_2 \\
 \frac{dI_2}{dt} &= \beta_{22}I_2S_2 + \beta_{23}I_2S_3 - \gamma_2I_2 - c_2I_2 - dI_2 \\
 \frac{dR_2}{dt} &= \gamma_2I_2 - dR_2 + v_2S_2 \\
 \frac{dS_3}{dt} &= B - \beta_{13}I_1S_3 - \beta_{23}I_2S_3 - \beta_{33}I_3S_3 - dS_3 - v_3S_3 \\
 \frac{dI_3}{dt} &= \beta_{33}I_3S_3 - \gamma_3I_3 - c_3I_3 - dI_3 \\
 \frac{dR_3}{dt} &= \gamma_3I_3 - dR_3 + v_3S_3,
 \end{aligned} \tag{18}$$

where all the initial conditions are nonnegative and at least one initial condition is positive. The β_{ij} , γ_i , c_i , and d terms have the same interpretation as discussed previously.

The most desirable outcome is that $I_1 = I_2 = I_3 = 0$. It is not possible for $I_1 = I_2 = 0$ but $I_3 \neq 0$, $I_1 = I_3 = 0$ but $I_2 \neq 0$, $I_2 = I_3 = 0$ but $I_1 \neq 0$ or that exactly one of I_1 , I_2 , or $I_3 = 0$ but the other two infection rates do not. In any of these situations, the only rest points have at least one negative component, which is not meaningful in the context of the discussion as we are discussing populations sizes which must be greater than or equal to zero.

The Jacobian of system (18) is

$$J = \begin{pmatrix} -E_1 & -\beta_{11}S_1 & 0 & 0 & \gamma_2 + \beta_{23}S_3 & 0 & \beta_{23}I_2 & 0 & 0 \\ \beta_{11}I_1 & \beta_{11}S_1 + \beta_{13}S_3 - D_1 & 0 & 0 & 0 & 0 & \beta_{13}I_1 & 0 & 0 \\ v_1 & \gamma_1 & -d & 0 & 0 & 0 & 0 & 0 & 0 \\ 0 & \beta_{13}S_3 & 0 & -E_2 & -\beta_{22}S_2 - \beta_{23}S_3 & 0 & \beta_{13}I_1 & 0 & 0 \\ 0 & 0 & 0 & \beta_{22}I_2 & \beta_{22}S_2 + \beta_{23}S_3 - D_2 & 0 & \beta_{23}I_2 & 0 & 0 \\ 0 & 0 & 0 & v_2 & \gamma_2 & -d & 0 & 0 & 0 \\ 0 & -\beta_{13}S_3 & 0 & 0 & -\beta_{23}S_3 & 0 & -\beta_{13}I_1 - \beta_{23}I_2 - E_3 & -\beta_{33}S_3 & 0 \\ 0 & 0 & 0 & 0 & 0 & 0 & \beta_{33}I_3 & \beta_{33}S_3 - D_3 & 0 \\ 0 & 0 & 0 & 0 & 0 & 0 & v_3 & \gamma_3 & -d \end{pmatrix},$$

where $D_i = c_i + \gamma_i + d$ and $E_i = d + \beta_{ii}I_i + v_i$.

$$I_1 = I_2 = I_3 = 0$$

The most desirable outcome is that both diseases are eliminated. In the case that $I_1 = I_2 = I_3 = 0$, system (18) has a single rest point

$$E_0 = (S_1, I_1, R_1, S_2, I_2, R_2, S_3, I_3, R_3) = \left(0, 0, 0, 0, 0, 0, \frac{B}{d + v_3}, 0, \frac{Bv_3}{d(d + v_3)}\right).$$

Evaluated at E_0 , $J(E_0)$ is

$$J(E_0) = \begin{pmatrix} -d - v_1 & 0 & 0 & 0 & \frac{\beta_{23}B}{d + v_3} + \gamma_2 & 0 & 0 & 0 & 0 \\ 0 & \frac{\beta_{13}B - (d + v_3)D_1}{d + v_3} & 0 & 0 & 0 & 0 & 0 & 0 & 0 \\ v_1 & \gamma_1 & -d & 0 & 0 & 0 & 0 & 0 & 0 \\ 0 & \frac{\beta_{13}B}{d + v_3} & 0 & -d - v_2 & -\frac{\beta_{23}B}{d + v_3} & 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 & \frac{\beta_{23}B - (d + v_3)D_2}{d + v_3} & 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & v_2 & \gamma_2 & -d & 0 & 0 & 0 \\ 0 & -\frac{\beta_{13}B}{d + v_3} & 0 & 0 & -\frac{\beta_{23}B}{d + v_3} & 0 & -d - v_3 & -\frac{\beta_{33}B}{d + v_3} & 0 \\ 0 & 0 & 0 & 0 & 0 & 0 & 0 & \frac{\beta_{33}B - (d + v_3)D_3}{d + v_3} & 0 \\ 0 & 0 & 0 & 0 & 0 & 0 & v_3 & \gamma_3 & -d \end{pmatrix}$$

with eigenvalues $\lambda_{1,2,3} = -d$, $\lambda_4 = -d - v_1$, $\lambda_5 = -d - v_2$, $\lambda_6 = -d - v_3$, $\lambda_7 = \frac{1}{d + v_3}(\beta_{13}B - (d + v_3)D_1)$, $\lambda_8 = \frac{1}{d + v_3}(\beta_{23}B - (d + v_3)D_2)$, and $\lambda_9 = \frac{1}{d + v_3}(\beta_{33}B - (d + v_3)D_3)$.

Observe that E_0 will be stable when $\lambda_{7,8,9}$ are all negative, which occurs if

$$v_3 > \max \left\{ \frac{\beta_{13}}{D_1}B - d, \frac{\beta_{23}}{D_2}B - d, \frac{\beta_{33}}{D_3}B - d \right\}. \quad (19)$$

In the same manner as in Equation (15), in inequality (19), we assume that $\frac{\beta_{33}}{D_3}B - d$ is the largest of these three numbers because being susceptible to both diseases creates more risk than only be susceptible to one of them. We are assuming that the transmission rate is greater for those susceptible to both diseases rather than those susceptible to only one. (Thus, we are fundamentally assuming that a single vaccination against both diseases is more desirable than multiple vaccinations against several.)

Example 3. The first example uses the parameter values $B = 1$, $\beta_{11} = \beta_{13} = 0.02$, $\beta_{22} = \beta_{23} = 5$, $\beta_{33} = 10$, $\gamma_1 = \gamma_2 = \gamma_3 = 10$, $d = 0.5$, $c_1 = c_2 = c_3 = 1$, $v_1 = 0$, $v_2 = 0$, $v_3 = 0.7$. Figure 6 indicates the dramatic difference of how vaccination changes the outcome. With this scenario, we see that individuals infected with one of the diseases persist while those infected with both are not.

On the other hand, using the same parameter values without vaccination we saw that the infectives with both diseases persisted.

Figure 6. (a) S_j , (b) I_j , and (c) R_j . The first disease is represented in blue, the second in orange and those susceptible/infected/recovered by diseases in green.

Example 4. Next we use the parameter values $B = 1$, $\beta_{11} = \beta_{13} = 0.02$, $\beta_{22} = \beta_{23} = 5$, $\beta_{33} = 10$, $\gamma_1 = \gamma_2 = 10$, $\gamma_3 = 0.5$, $d = 1$, $c_1 = c_2 = c_3 = 1$, $v_1 = 0.5$, $v_2 = 0.5$, $v_3 = 0$. Figure 7 indicates the dramatic difference of how vaccination changes the outcome. With this scenario, we see that individuals infected with both of the diseases persist while infected with one are not, even with very high vaccination rates for both the S_1 and S_2 populations.

Figure 7. (a) S_j , (b) I_j , and (c) R_j . The first disease is represented in blue, the second in orange and those susceptible/infected/recovered by diseases in green.

Example 5. Finally, we illustrate a desired solution that comes with a “cost.” We illustrate with the parameter values $B = 1$, $\beta_{11} = \beta_{13} = 0.02$, $\beta_{22} = \beta_{23} = 5$, $\beta_{33} = 10$, $\gamma_1 = \gamma_2 = 10$, $\gamma_3 = 0.5$, $d = 1$, $c_1 = c_2 = c_3 = 1$, $v_1 = 0.0$, $v_2 = 0.0$, $v_3 = 0.4$. Observe that the “cost” is the portion of vaccinations of to the S_3 group to achieve elimination of both diseases. Figure 8 illustrates that if the S_3 population is illustrated at a very high rate, both diseases can be eradicated from the population.

Figure 8. (a) S_j , (b) I_j , and (c) R_j . The first disease is represented in blue, the second in orange and those with susceptible/infected/recovered by diseases in green.

7. Selective Vaccination

One of the main limitations of the model represented by system (18) is that v_i is the vaccination rate of the S_i population class and moves them from the S_i class to the R_i class. We propose a different vaccination scheme that might be more realistic in many situations as follows.

- (1) We assume that the first disease (modeled with the $S_1 I_1 R_1$ equations) is well understood and that the population is vaccinated at a high enough rate to achieve herd immunity. Thus the S_3 population class is vaccinated against the first disease so a portion of the S_3 class moves to the R_1 class and the S_2 class. This is represented by a $-u_1 S_3$ term in the S_3 population that is then added to the R_1 and S_2 equations in system (20).
- (2) The second disease (modeled with the $S_2 I_2 R_2$ equations) is not well understood but is considered to be more harmful than the first disease. Some ways it might be more harmful are listed as follows,
 - The second disease may have a higher death rate than the first disease.
 - The second disease may destroy the immunity conferred by either having the first disease or being vaccinated against the first disease.
- (3) Once the second disease is understood, those in the S_2 class are vaccinated against the second disease and those in the S_3 class are vaccinated against both the first and second diseases. In system (20), this is represented by the $-v_2 S_2$ term in the S_2 equation that is then added to the R_2 equation in the same way as in (18). The $v_3 S_3$ term now has the same interpretation as it did in system (18).

These assumptions are taken into consideration with

$$\begin{aligned}
 \frac{dS_1}{dt} &= \beta_{23} I_2 S_3 + \gamma_2 I_2 - \beta_{11} I_1 S_1 - dS_1 - v_1 S_1 \\
 \frac{dI_1}{dt} &= \beta_{11} I_1 S_1 + \beta_{13} I_1 S_3 - \gamma_1 I_1 - c_1 I_1 - dI_1 \\
 \frac{dR_1}{dt} &= \gamma_1 I_1 - dR_1 + v_1 S_1 + u_1 S_3 \\
 \frac{dS_2}{dt} &= \beta_{13} I_1 S_3 + u_1 S_3 - \beta_{22} I_2 S_2 - dS_2 - v_2 S_2 \\
 \frac{dI_2}{dt} &= \beta_{22} I_2 S_2 + \beta_{23} I_2 S_3 - \gamma_2 I_2 - c_2 I_2 - dI_2 \\
 \frac{dR_2}{dt} &= \gamma_2 I_2 - dR_2 + v_2 S_2 \\
 \frac{dS_3}{dt} &= B - \beta_{13} I_1 S_3 - \beta_{23} I_2 S_3 - \beta_{33} I_3 S_3 - dS_3 - v_3 S_3 - u_1 S_3 \\
 \frac{dI_3}{dt} &= \beta_{33} I_3 S_3 - \gamma_3 I_3 - c_3 I_3 - dI_3 \\
 \frac{dR_3}{dt} &= \gamma_3 I_3 - dR_3 + v_3 S_3,
 \end{aligned} \tag{20}$$

where all the initial conditions are nonnegative and at least one initial condition is positive. The β_{ij} , γ_i , c_i , and d terms have the same interpretation as discussed previously.

The Jacobian of system (20) is

$$J = \begin{pmatrix} -E_1 & -\beta_{11}S_1 & 0 & 0 & \gamma_2 + \beta_{23}S_3 & 0 & \beta_{23}I_2 & 0 & 0 \\ \beta_{11}I_1 & \beta_{11}S_1 + \beta_{13}S_3 - D_1 & 0 & 0 & 0 & 0 & \beta_{13}I_1 & 0 & 0 \\ v_1 & \gamma_1 & -d & 0 & 0 & 0 & u_1 & 0 & 0 \\ 0 & \beta_{13}S_3 & 0 & -E_2 & -\beta_{22}S_2 - \beta_{23}S_3 & 0 & u_1 + \beta_{13}I_1 & 0 & 0 \\ 0 & 0 & 0 & \beta_{22}I_2 & \beta_{22}S_2 + \beta_{23}S_3 - D_2 & 0 & \beta_{23}I_2 & 0 & 0 \\ 0 & 0 & 0 & v_2 & \gamma_2 & -d & 0 & 0 & 0 \\ 0 & -\beta_{13}S_3 & 0 & 0 & -\beta_{23}S_3 & 0 & -\beta_{13}I_1 - \beta_{23}I_2 - E_3 - u_1 & -\beta_{33}S_3 & 0 \\ 0 & 0 & 0 & 0 & 0 & 0 & \beta_{33}I_3 & \beta_{33}S_3 - D_3 & 0 \\ 0 & 0 & 0 & 0 & 0 & 0 & v_3 & \gamma_3 & -d \end{pmatrix},$$

where $D_i = c_i + \gamma_i + d$ and $E_i = d + \beta_{ii}I_i + v_i$.

$$I_1 = I_2 = I_3 = 0.$$

If $I_1 = I_2 = I_3 = 0$ we obtain the rest point

$$E_0 = (S_1, I_1, R_1, S_2, I_2, R_2, S_3, I_3, R_3) \\ = \left(0, 0, \frac{u_1 B}{d(d+u_1+v_3)}, \frac{u_1 B}{(d+v_2)(d+u_1+v_3)}, 0, \frac{u_1 v_2 B}{d(d+v_2)(d+u_1+v_3)}, \frac{B}{d+u_1+v_3}, 0, \frac{v_3 B}{d(d+u_1+v_3)} \right).$$

We now abbreviate $d + u_1 + v_3$ with $D = d + u_1 + v_3$. Evaluated at E_0 , $J(E_0)$ is

$$J(E_0) = \begin{pmatrix} -d - v_1 & 0 & 0 & 0 & \frac{\beta_{23}B}{D} + \gamma_2 & 0 & 0 & 0 & 0 \\ 0 & \frac{\beta_{13}B - DD_1}{D} & 0 & 0 & 0 & 0 & 0 & 0 & 0 \\ v_1 & \gamma_1 & -d & 0 & 0 & 0 & u_1 & 0 & 0 \\ 0 & \frac{\beta_{13}B}{D} & 0 & -d - v_2 & -\frac{\beta_{23}B}{D} & 0 & u_1 & 0 & 0 \\ 0 & 0 & 0 & 0 & \frac{(\beta_{22}u_1 + (d+v_2)\beta_{23})B}{D(d+v_2)} - D_2 & 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & v_2 & \gamma_2 & -d & 0 & 0 & 0 \\ 0 & -\frac{\beta_{13}B}{D} & 0 & 0 & -\frac{\beta_{23}B}{D} & 0 & -D & -\frac{\beta_{33}B}{D} & 0 \\ 0 & 0 & 0 & 0 & 0 & 0 & 0 & \frac{\beta_{33}B - DD_3}{D} & 0 \\ 0 & 0 & 0 & 0 & 0 & 0 & v_3 & \gamma_3 & -d \end{pmatrix}$$

with eigenvalues $\lambda_{1,2,3} = -d$, $\lambda_4 = -d - v_1$, $\lambda_5 = -d - v_2$, $\lambda_6 = -d - u_1 - v_3$, $\lambda_7 = \frac{\beta_{13}B}{d+u_1+v_3} - D$, $\lambda_8 = \frac{\beta_{33}B}{d+u_1+v_3} - D$, and

$$\lambda_9 = -\frac{1}{(d+v_2)(d+u_1+v_3)} \left[d(-\beta_{23}B + \gamma_2(u_1 + v_2 + v_3) + v_2(u_1 + v_3)) - (\beta_{22}u_1 + \beta_{23}v_2)B + c_2(d+v_2)(d+u_1+v_3) + d^3 + d^2(\gamma_2 + u_1 + v_2 + v_3) + \gamma_2 v_2(u_1 + v_3) \right].$$

Finding reasonable conditions for which all the eigenvalues, particular $\lambda_{7,8,9}$ are negative so that E_0 is stable is difficult. Nevertheless, examples can indicate some of the possible outcomes.

Example 6. We choose parameter values similar to those used in the previous examples. Here, $B = 1$, $\beta_{11} = \beta_{13} = 0.2$, $\beta_{22} = 0.8$, $\beta_{23} = 0.5$, $\beta_{33} = 0.4$, $\gamma_1 = 0.1$, $\gamma_2 = 0.2$, $\gamma_3 = 0.3$, $d = 0.05$, $c_1 = c_2 = 0.5$, $c_3 = 1$, $v_1 = v_2 = v_3 = 0$, and $u_1 = 0.7$. These parameter values are interpreted to mean that a large portion of the S_3 population is vaccinated against the first disease. As seen in Figure 9, the results are interesting. Even with the high vaccination rate against the

first disease, both the first and second diseases continue to persist in the population, although the individuals infected by both are effectively removed.

Figure 9. (a) S_j , (b) I_j , and (c) R_j . The first disease is represented in blue, the second in orange and those susceptible/infected/recovered by diseases in green.

Example 7. We slightly vary the parameter values from the previous example. In this example, we choose $B = 1$, $\beta_{11} = \beta_{13} = 0.2$, $\beta_{22} = 0.8$, $\beta_{23} = 0.5$, $\beta_{33} = 0.4$, $\gamma_1 = 0.1$, $\gamma_2 = 0.2$, $\gamma_3 = 0.3$, $d = 0.05$, $c_1 = c_2 = 0.5$, $c_3 = 1$, $v_1 = 0$, $v_2 = v_3 = 0.8$, and $u_1 = 0.7$. These parameter values are interpreted to mean that a large portion of the S_3 population is vaccinated against the first disease as well as a large portion of the population vaccinated against the second disease. As seen in Figure 10, the results indicate that vaccinating appropriately and at high enough levels to achieve herd immunity can (theoretically) combat the endemic.

Figure 10. (a) S_j , (b) I_j , and (c) R_j . The first disease is represented in blue, the second in orange and those susceptible/infected/recovered by diseases in green.

8. Conclusions

We have developed a basic model of two interacting diseases where we assume that one is detrimental to the immunity conferred by the other. Recovering from or being vaccinated against a viral disease often confers immunity. Here, we have assumed that the second disease, assumed to be the more lethal disease, destroys any immunity conferred by having the first disease or being immunized against it.

These are very simple assumptions yet the relatively simple mathematical model developed here results in complicated calculations.

For example, to list a few of the limitations of this introductory model, we did not consider the possibility that an I_3S_3 interaction could result in an I_1 , I_2 , I_3 or no infections. We hope to investigate these situations in future studies as well as SIS dynamics as well as a combination of SIS and SIR dynamics.

Nevertheless, the calculations do indicate that strategic vaccination of diseases will help control their infection rates.

We suspect that these results agree with observed data. We hope that this introductory model will help motivate the study of more comprehensive models that study the effects of emerging diseases and how they interact with and affect the populations that are affected by them.

Author Contributions: The authors contribution in this work are equal. J.P.B. and M.L.A. contributed to the writing and numerical simulations in this paper. All authors have read and agreed to the published version of the manuscript.

Funding: This research received no external funding.

Institutional Review Board Statement: Not applicable.

Informed Consent Statement: Not applicable.

Data Availability Statement: Not applicable.

Conflicts of Interest: The authors declare no conflict of interest.

Computational Notes: The graphics and computations in this paper were carried out with *Mathematica* 12.0 [10]. You can receive a copy of the *Mathematica* notebooks used here by sending a request to jbraselton@georgiasouthern.edu.

References

1. CDC. Measles Cases and Outbreaks. 2019. Available online: <https://www.cdc.gov/measles/cases-outbreaks.html/> (accessed on 31 December 2019).
2. Rivera, L.S. Measles Outbreaks 2019: This Is Why We Get Vaccinated. 2019. Available online: <https://blog.uvahealth.com/2019/05/10/measles-outbreaks/> (accessed on 31 December 2019).
3. Mina, M.J.; Kula, T.; Leng, Y.; Li, M.; de Vries, R.D.; Knip, M.; Siljander, H.; Rewers, M.; Choy, D.F.; Wilson, M.S.; et al. Measles virus infection diminishes preexisting antibodies that offer protection from other pathogens. *Science* **2019**, *366*, 599–606. [CrossRef] [PubMed]
4. Petrova, V.N.; Sawatsky, B.; Han, A.X.; Laksono, B.M.; Walz, L.; Parker, E.; Pieper, K.; Anderson, C.A.; de Vries, R.D.; Lanzavecchia, A.; et al. Incomplete genetic reconstitution of B cell pools contributes to prolonged immunosuppression after measles. *Sci. Immunol.* **2019**, *4*. [CrossRef] [PubMed]
5. Griffin, A.H. Measles and Immune Amnesia. 2019. Available online: <https://asm.org/Articles/2019/May/Measles-and-Immune-Amnesia> (accessed on 31 December 2019).
6. Kelland, K. Infection Amnesia: Measles ‘Destroys Immune System Memory’. 2019. Available online: <https://www.reuters.com/article/us-health-measles-immunity-idUSKBN1XA2E4> (accessed on 31 December 2019).
7. Britton, N.F. *Essential Mathematical Biology*; Springer: London, UK, 2003.
8. Kermack, W.O.; McKendrick, A.G. A Contribution to the Mathematical Theory of Epidemics. *Proc. R. Soc. Lond. Ser. Contain. Pap. Math. Phys. Character* **1927**, *115*, 700–721.
9. Murray, J.D. *Mathematical Biology I: An Introduction*; Interdisciplinary Applied Mathematics; Springer: New York, NY, USA, 2002; Volume 17. [CrossRef]
10. Research, W. *Mathematica 12.0*; Champaign: Illinois, IL, USA, 2019.