Exploration of Basic Reproduction Number and Equilibrium Points in Epidemic Model

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Contents

1 Introduction

In this project, we mainly discuss about the concept of target reproduction number and its applications in ecology and epidemiology. More importantly, we take SIVS model as an example to analyze the stability of equilibrium points. Based on the previous work, we give the type of equilibrium points of SIVS model under different conditions. Numerical Simulation further verify our conclusion. Target Reproduction Number R_0 is an important threshold parameter in population model or disease model [Van den Driessche and Watmough [2002]]. It is usually used to determine the existence or demise of a subject, especially population persistence and control of infectious diseases. It is among the quantities most urgently estimated for emerging infectious diseases in outbreak situations, and its value provides insight when designing control interventions for established infections. In Epidemiology, R_0 is defined as the average number of new cases of an infection caused by one typical infected individual, in a population consisting of susceptibles only. In Ecology, R_0 has similar definition.

2 Significant Preliminaries

Compartmental models are the most frequently used type of epidemic model. In this class of models, individuals can be in a finite number of discrete states. Some of these states are simply labels that specify the various traits of individuals. Let $A = [a_{ij}] = B + C$ be a nonnegative irreducible $n \times n$ matrix, where the nonnegative target matrix $C = [c_{ij}]$ consists of all targeted entries, and the nonnegative residual matrix $B = [b_{ij}]$ consists of all entries not targeted. Note that each a_{ij} may be divided into two parts, one part b_{ij} unchanged, and one part c_{ij} subject to change, either a decrease or increase. Then, the population renewal equation can be written as $Ax_t = x_{t+1}$. To guide the effectiveness of practical measures considering the cost of different measures (here we consider control C), we have that $A_C(\tau) = B + \frac{1}{\tau}C$. τ is used to describe the effectiveness of the measure. Lewis et al. [2019] gives the following theorems which are important to our exploration and report.

- $T_c = \rho\left(C(I-B)^{-1}\right)$
- $\rho\left(A_C(\tau)\right) = 1 \Leftrightarrow \tau = T_c$
- $\rho(A) = 1 \Leftrightarrow Tc = 1$, $\rho(A)$ and T_c are on the same side of 1
- $\rho(B) < 1$ and $\rho(B^{'}) < 1$, if $C > C^{'}$, then $1 < T_c < T_{c^{'}}$ or $1 = T_c = T_{c^{'}}$ or $T_{c^{'}} < T_c < 1$
- In the case that rank(C)=1, $T_c = \frac{\Sigma_U(-1)^{1+c(U)}w(U)}{\Sigma_V(-1)^{c(V)}w(V)}$, where $c(U)$ is the number of cycle-union U in a subgraph. The weight $w(U)$ of a cycle-union U is the product of weights of arcs in U. Cycle-unions U and cycle-unions V of $D(B,C)$ that do and do not contain a target arc in C, respectively. $D(B,C)$ is the weighted multi-digraph associated with the residual matrix B and target matrix C

3 Applications

3.1 Applications to Ecology

In ecology, we mainly discuss about the net reproductive value. Assume that $x_{t+1} = Px_t$, P is called the population projection matrix.

$$P = T + F$$

where $T \geqslant 0$ contains the survivorship transitions and $F \geqslant 0$ contains the fecundities. $\lambda = \rho(P)$ is called the population growth rate. $\lambda > 1$ or $\lambda < 1$ determines the growth and extinction of the population.

The net reproductive value R_0 is defined as the spectral radius of the next generation matrix $F(I-T)^{-1}$: $R_0 = \rho(F(I-T)^{-1}$. According to the previous definition, we have the conclusions that:

- The net reproductive value R_0 is the target reproduction number T_c as in for $A = P$ corresponding to the target matrix $C = F$.
- If $\rho(T) < 1$, then $1 < \lambda < R_0$ or $1 = \lambda = R_0$ or $R_0 < \lambda < 1$

We take Chamomile as an example (given by Lewis et al. [2019]). It is a perennial with three stages: seed bank (state 1), rosettes (state 2), and flowering plants (state 3). Biological transitions between three stages. Population projection matrix of this compartmental model is:

$$A = \begin{bmatrix} a_{11} & 0 & a_{13} \\ a_{21} & 0 & a_{23} \\ a_{31} & a_{32} & a_{33} \end{bmatrix}$$

where a_{ij} is the probability of transformation from state j to state i. The corresponding weighted digraph is as Figure 1 shows. We consider two controlling measure. First, control the offspring

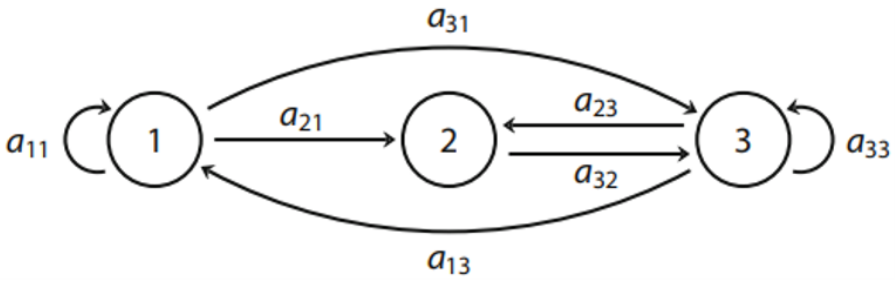


Figure 1: The weighted digraph of Chamomile

reproduction. Second, control the survival probability at the first stage.

3.1.1 Offspring Reproduction Controlling

Under this condition, the target matrix C has only nonzero entries $c_{i3} = a_{i3}$ for $1 \leqslant i \leqslant 3$, then the net reproductive value can be calculated easily by the graph of model.

$$\mathcal{T}_3 = \frac{a_{33} + a_{13}a_{31} + a_{23}a_{32} + a_{13}a_{32}a_{21} - a_{11}a_{33} - a_{11}a_{23}a_{32}}{1 - a_{11}}$$

3.1.2 First Stage Survival Probability Controlling

Under this condition, the target matrix C has only nonzero entries $c_{11} = a_{11}$. Similar, we can calculate the net reproductive value with the graph of model.

$$\mathcal{T}_{11} = \frac{a_{11}\left(1 - a_{33} - a_{23}a_{32}\right)}{1 - a_{33} - a_{13}a_{31} - a_{23}a_{32} - a_{13}a_{32}a_{21}}$$

3.2 Applications to Epidemiology

In Epidemiology, basic reproduction number R_0 is an important quantity, which is defined as the average number of secondary infections caused by a typical infectious individual introduced into a completely susceptible host population. Consider using a compartmental model. Let J

represents the linearization of disease dynamics of infected subgroups. Population is divided into N groups, then the shape of J is $N \times N$. Rewrite $J = T + \Sigma$, where T is the transmission part, describing the production of new infections. Σ is the transition part, describing changes in state (including removal by death or the acquisition of immunity). J_{ij} means transiting from group j to group i. Here we define $A = -T\Sigma^{-1}$ and $B = 0$ as Section 2 mentions. Then, target reproduction number is defined as

$$T = \rho(-T\Sigma^{-1})$$

Epidemiologically, target reproduction number is exactly the basic reproduction number! This is shocking because the former is defined in terms of an algebraic matrix, while the latter is derived from a system of differential equations.

To verify the equivalence between the two concept, here we discuss SEI model with two latent categories (given by Diekmann et al. [2010]). Consider a system with the following states: S susceptible; $E1$ latently infected of category 1; $E2$ latently infected of category 2; I infectious; and R recovered/removed/immune. As usual, the letters for the states also indicate the size of the subpopulation in that state, where 'size' in our case is the number of individuals in that state. The idea behind this system might be that categories 1 and 2 represent individuals who, once infected, progress to infectiousness at different rates. We assume that there is a fixed ratio of the two categories in the population, $p : 1-p$, hence susceptibles enter the $E1$ and $E2$ states in that fixed ratio following exposure to infection. Let β be the transmission rate, μ the birth and death rates, v_1 and v_2 the rates of leaving the respective latency states, and γ the rate of leaving the infectious state. The equations are as follows.

$$\begin{aligned}
\dot{S} &= \mu N - \beta\frac{SI}{N} - \mu S \\
\dot{E}1 &= p\beta\frac{SI}{N} - (v_1 + \mu)E1 \\
\dot{E}2 &= (1-p)\beta\frac{SI}{N} - (v_2 + \mu)E2 \\
\dot{I} &= v_1 E1 + v_2 E2 - (\gamma + \mu)I \\
\dot{R} &= \gamma I - \mu R
\end{aligned} \tag{1}$$

with $N = S + E1 + E2 + I + R$. This system has three infected states, $E1$, $E2$, and I, and two uninfected states, S and R. Although there are five states in the model, it is four-dimensional as the total population size is constant. At the infection-free steady state $E1 = E2 = I = R = 0$, hence $S = N$. To simplify the equation, let's assume that S is equal to N, then we have the following linear system.

$$\begin{aligned}
\dot{E}1 &= p\beta I - (v_1 + \mu)E1 \\
\dot{E}2 &= (1-p)\beta I - (v_2 + \mu)E2 \\
\dot{I} &= v_1 E1 + v_2 E2 - (\gamma + \mu)I
\end{aligned} \tag{2}$$

We will refer to the ODEs 2 as the linearized infection subsystem, as it only describes the production of new infecteds and changes in the states of already existing infecteds. We set $x = (E1, E2, I)$, then we have the linearized infection subsystem in the form $\dot{x} = (T + \Sigma)x$. The matrix T corresponds to the transmissions and the matrix Σ to transitions. Hence, all epidemiological events that lead to new infections are incorporated in the model via T, and all other events via Σ. Progress to either death or immunity guarantees that Σ is invertible. If we refer to the infected states with indices i and j, with $i, j \in [1, 2, 3]$, then the entry T_{ij} is the rate at which individuals in infected state j give rise to individuals in infected state i. Therefore, we can derive T and Σ and calculate the target reproduction number as follows.

$$\mathbf{K} = -\mathbf{T}\Sigma^{-1} = \begin{pmatrix} 0 & 0 & p\beta \\ 0 & 0 & (1-p)\beta \\ 0 & 0 & 0 \end{pmatrix} \times \begin{pmatrix} \frac{1}{v_1+\mu} & 0 & 0 \\ 0 & \frac{1}{v_2+\mu} & 0 \\ \frac{v_1}{(v_1+\mu)(\gamma+\mu)} & \frac{v_2}{(v_2+\mu)(\gamma+\mu)} & \frac{1}{\gamma+\mu} \end{pmatrix} = \begin{pmatrix} \frac{p\beta v_1}{(v_1+\mu)(\gamma+\mu)} & \frac{p\beta v_2}{(v_2+\mu)(\gamma+\mu)} & \frac{p\beta}{\gamma+\mu} \\ \frac{(1-p)\beta v_1}{(v_1+\mu)(\gamma+\mu)} & \frac{(1-p)\beta v_2}{(v_2+\mu)(\gamma+\mu)} & \frac{(1-p)\beta}{\gamma+\mu} \\ 0 & 0 & 0 \end{pmatrix}.$$

Observe the matrix, we can see that $K_{11} = \frac{v_1}{v_1+\mu}\beta\frac{1}{\gamma+\mu}p$, which describes how many new cases of $E1$ it is expected to produce by an individual who has just entered state $E1$ for the remainder of its infectious life. The dominant eigenvalue of this matrix is equal to R_0, where

$$\mathcal{R}_0 = \left(\frac{pv_1}{v_1+\mu} + \frac{(1-p)\boldsymbol{v}_2}{\nu_2+\mu}\right)\frac{\beta}{\gamma+\mu}$$

If we look closely at this expression, we can see that it exactly satisfies the definition of the basic reproduction number, i.e. the average number of secondary infections caused by a typical infectious individual introduced into a completely susceptible host population!

4 Stability Analysis ——SIVS model

NOTE: This part refers to the SIVS model described in Yuliana et al. [2021]. On this basis, I independently completed the analysis of the existence and stability of the equilibrium points and the numerical experiment.

In this section, we discuss the SIVS model based on the introduction of vaccinated population, and analyze the equilibrium stability of the model. Vaccination is the act of getting a vaccine to help the immune system develop protection from a disease. However, vaccines do not necessarily provide perfect immunity to body because not all type of vaccines have 100% effectiveness. The following is assumption that used on SIVS epidemic model with vaccine ineffectiveness:

1. Vaccination is given to new individuals and susceptible individuals.
2. Not every new individual receive vaccine, then the new individuals who do not receive vaccine become susceptible.
3. Vaccination has temporary immunity that will lose as time pass, vaccinated individuals have potential to become susceptible again.
4. Vaccine is not 100% effective, consequently vaccinated individuals can get infected.

4.1 SIVS Model Setup

Based on previous assumption, the SIVS epidemic model with vaccine ineffectiveness can be formed as follows:

$$\begin{aligned} \dot{S} &= -\beta SI - \Phi S + \mu(b, I)I + \theta V \\ \dot{I} &= \beta SI + \sigma\beta VI - \mu(b, I)I \\ \dot{V} &= \Phi S - \sigma\beta VI - \theta V \end{aligned} \tag{3}$$

The meanings of variables and parameters are as follows.

Variable	Description
$S(t)$	Proportion of population of susceptible individuals at time t
$V(t)$	Proportion of population of vaccinated individuals at time t
$I(t)$	Proportion of population of infected individuals at time t
b	Medical effect
μ	Recovery rate
β	Rate of disease transmission
Φ	Rate of susceptible individuals who are vaccinated
θ	Rate of losing vaccine immunity
σ	Vaccine ineffectiveness

The recovery rate function is $\mu(b, I) = \mu_0 + (\mu_1 - \mu_0)\frac{b}{b+I}$. This function indicates that the more effective the medical treatment, the fewer infected people and the higher the recovery rate. To simplify the system, we replace $S = 1 - V - I$, then we get the following simplified equation,

$$\begin{aligned} \dot{I} &= \beta(1 - I - V)I + \sigma\beta VI - \mu(b, I)I \\ \dot{V} &= \Phi(1 - I - V) - \sigma\beta VI - \theta V \end{aligned} \tag{4}$$

As Yuliana et al. [2021] proved, the basic reproduction number of this system is $R_0 = \frac{\beta(\theta+\sigma\Phi)}{\mu_1(\Phi+\theta)}$

4.2 Existence of Equilibrium Point

By assuming $\frac{dI}{dt} = 0$, $\frac{dV}{dt} = 0$ and $\frac{dN}{dt} = 0$, the model contains two types of equilibrium points. Obviously, the model contains its disease free-equilibrium point $E_0(0, \frac{\Phi}{\Phi+\theta})$. The disease free-equilibrium point is normal. We mainly discuss about the existence of endemic equilibrium point $E^*(I^*, V^*)$. Substitute the equilibrium conditions, and get the following expression:

$$\begin{cases} \beta(1 - I - V)I + \sigma\beta VI - \mu(b, I)I = 0 \\ \phi(1 - I - V) - \sigma\beta VI - \theta V = 0 \end{cases} \Rightarrow \begin{cases} f(I) = \frac{\phi(1-I)}{\phi+\theta+\sigma\beta I} \\ g(I) = \frac{\beta(1-I)(b+I)-\mu_0 I-\mu_1 b}{\beta(1-\sigma)(b+I)} \end{cases}$$

Analyze the above equations, we get

$$\begin{aligned} &f(1) = 0, \qquad f(0) = \tfrac{\phi}{\phi+\theta} && g(0) = \tfrac{(b\mu_1-b\beta)}{b\beta(\sigma-1)}, \qquad g(1) = \tfrac{b\mu_1+\mu_0}{(b+1)\beta(\sigma-1)} \\ &f'(I) = -\tfrac{\phi(\beta\sigma+\phi+\theta)}{(\beta\sigma I+\phi+\theta)^2} < 0. && g'(I) = \tfrac{\beta I^2+2b\beta I+b^2\beta+b\mu_0-b\mu_1}{(b+I)^2\beta(\sigma-1)} \\ &f''(I) = \tfrac{2\beta\sigma\phi(\beta\sigma+\phi+\theta)}{(\beta\sigma I+\phi+\theta)^3} > 0 && g''(I) < 0 \end{aligned}$$

$g'(0) = \frac{\beta b+\mu_0-\mu_1}{\beta(\sigma-1)}$, then if $\beta b < \mu_1 - \mu_0$, $g(I)$ first increase and then decrease; if $\beta b \geqslant \mu_1 - \mu_0$, $g(I)$ is monotone decreasing. Let's discuss it by case:

When $R_0 > 1$, $f(0) < g(0)$ and $f(1) > g(1)$. According to the monotony of the function, $g(I)$ and $f(I)$ have only one intersection point in the interval (0,1), that is, the system has a unique endemic equilibrium point.

When $R_0 < 1$, $f(0) > g(0)$, if $f^{'}(0) \geqslant g^{'}(0)$, $g(I)$ and $f(I)$ must not intersect on the interval (0,1); if $f^{'}(0) < g^{'}(0)$, there exists one point $\hat{I}$ such that $f^{'}(\hat{I}) = g^{'}(\hat{I})$

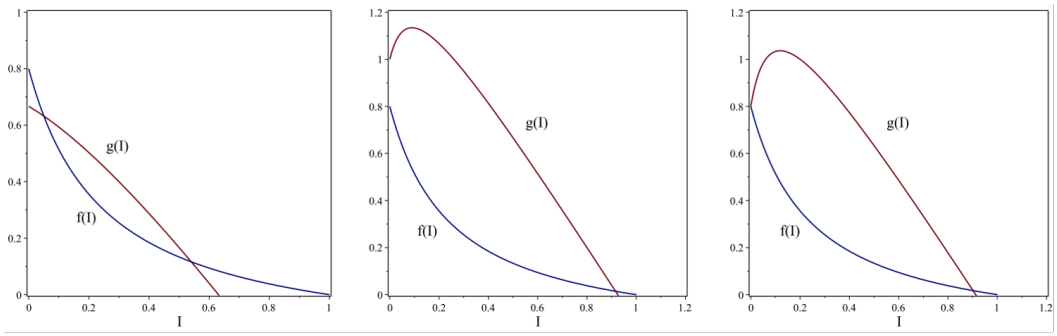
- if $f(\hat{I}) < g(\hat{I})$, $g(I)$ and $f(I)$ intersect at I_1^* and I_2^*. Assume $I_1^* < I_2^*$, then there exists two endemic equilibrium points, denote to $E_1^*(I_1^*, V_1^*)$ and $E_2^*(I_2^*, V_2^*)$
- if $f(\hat{I}) = g(\hat{I})$, then $g(I)$ is tangent to $f(I)$ on the interval (0,1), that is, the system has a endemic equilibrium point.

- if $f(\hat{I}) > g(\hat{I})$, then $g(I)$ and $f(I)$ do not intersect on the interval (0,1), that is, system does not have a endemic equilibrium points.

After classification discussion, we can get the number of endemic equilibrium points under different conditions:

- if basic reproduction number $R_0 > 1$, then there exists only one endemic equilibrium point if basic reproduction number $R_0 = 1$, then if $f^{'}(0) \geqslant g^{'}(0)$, there exists no endemic equilibrium point; if $f^{'}(0) < g^{'}(0)$, there exists only one endemic equilibrium point.
- if basic reproduction number $R_0 < 1$, and there exists I_1, $0 < I < 1$, satisfying that $f^{'}(I_1) = g^{'}(I_1)$, then if $f(I_1) < g(I_1)$, there exists two one endemic equilibrium points; if $f(I_1) = g(I_1)$, there exists only one endemic equilibrium point; if $f(I_1) > g(I_1)$, there exists no endemic equilibrium point.

Different parameter combinations are selected to verify the correctness of the above conclusion. Three pictures in Figure 2 correspond $R_0 < 1$, $R_0 > 1$, $R_0 = 1$ in turn, and the numerical



μ_1=3, b=0.9, R_0=0.87 μ_1=2, b=0.1, R_0=1.3 μ_1=2.6, b=0.1, R_0=1

Figure 2: Numerical Simulation of Endemic Equilibrium Point

results satisfy the conclusions 4.2.

4.3 Stability of Equilibrium Point

In this part, we discuss about the stability of equilibrium points. Since the equation is a nonlinear system, we consider the local linear approximation at the disease-free equilibrium point. The system has Jacobi Matrix as follows at $E_0(0, \frac{\Phi}{\Phi+\theta})$:

$$\begin{pmatrix} \frac{\beta}{\phi+\theta}(\theta+\sigma\phi) - \mu_1 & 0 \\ -\phi - \frac{\beta\sigma\phi}{\phi+\theta} & -(\phi+\theta) \end{pmatrix}$$

According Vieta theorem, we have $tr(J) = -\mu_1(1-R_0) - (\Phi+\theta) = \lambda_1 + \lambda_2$ and $det(J) = \mu_1(\Phi+\theta)(1-R_0) = \lambda_1\lambda_2$. If $R_0 < 1$, then all the eigenvalue have negative real parts, that is, the disease-free equilibrium is locally asymptotically stable and it is a stable node. If $R_0 > 1$, the disease-free equilibrium $E_0 is unstable and it is an unstable saddle point.$

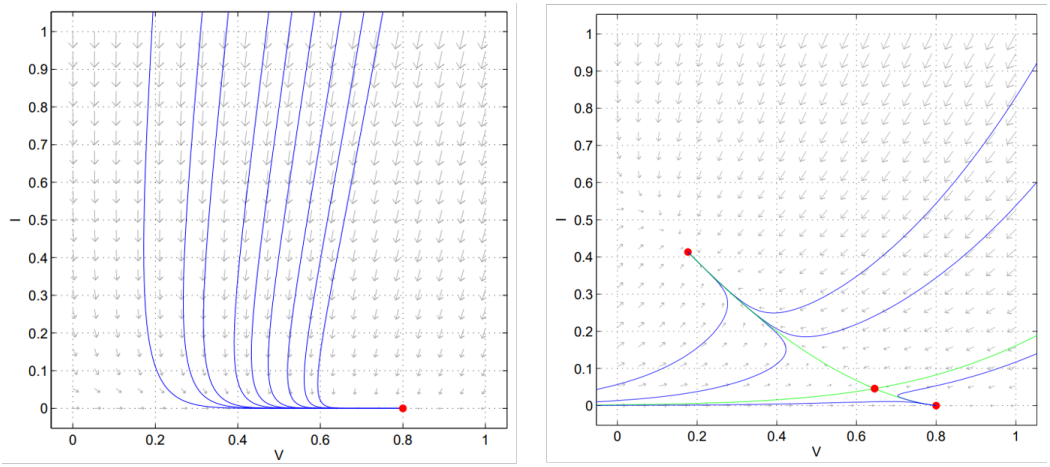
As for the endemic equilibrium point, the Jacobi Matrix at endemic equilibrium point $E^*(I^*, V^*)$ is as follows:

$$\begin{pmatrix} -\beta I^* + (\mu_1 - \mu_0)\frac{bI^*}{(b+I^*)^2} & \beta I^*(\sigma - 1) \\ -\phi - \beta\sigma V^* & -(\Phi+\theta) - \sigma\beta I^* \end{pmatrix}$$

Similarly, we discuss the determinant and trace of the matrix. The conclusion is that if the system has two endemic equilibrium points (whose derivatives are opposite), the smaller endemic equilibrium point is the unstable saddle point, and the larger equilibrium point is not the saddle point, and its behavior varies with the parameters.

4.4 Numerical Simulation of Equilibrium Points

Under different parameter combinations, we draw the orbit distribution to observe its equilibrium state. For Figure 3, under the parameters in the left figure, the system only has a

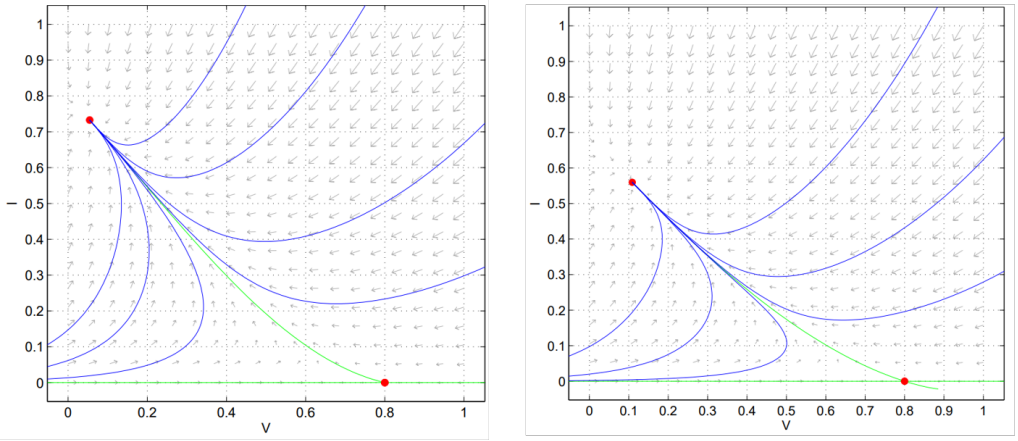


Left: $\beta = 5, \mu 0 = 0.2, \mu 1 = 10, b = 10, \theta = 0.1, \sigma = 0.4, \phi = 0.4,\ R_0 = 0.26$

Right: $\beta = 5, \mu 0 = 0.2, \mu 1 = 3, b = 2, \theta = 0.1, \sigma = 0.4, \phi = 0.4,\ R_0 = 0.86$

Figure 3: Numerical Simulation of Orbit Distribution

disease-free equilibrium point and is globally asymptotically stable. In the figure on the right, the system presents two endemic equilibrium points and one disease-free point, the smaller endemic equilibrium point is unstable, and the larger endemic equilibrium point and disease-free point are stable. The equilibrium point is also locally asymptotically stable.



Left: $\beta = 5, \mu 0 = 0.2, \mu 1 = 2.6, b = 0.5, \theta = 0.1, \sigma = 0.4, \phi = 0.4,\ R_0 = 1.00$

Right: $\beta = 5, \mu 0 = 0.2, \mu 1 = 2.5, b = 2, \theta = 0.1, \sigma = 0.4, \phi = 0.4,\ R_0 = 1.04$

Figure 4: Numerical Simulation of Orbit Distribution

For the figure on the left in Figure 4, the system has an endemic equilibrium and is locally asymptotically stable, while the disease-free equilibrium is unstable. In the right part, $R_0 > 1$, the number of equilibrium points and their stability are consistent with the figure on the left.

We fix the parameters and draw the figure to show the change of I as R_0 changes. When R_0 is less than 1, there are two endemic equilibrium points, the larger endemic equilibrium point being locally stable and the smaller endemic equilibrium point is unstable, where there exists backward bifurcation as Figure 5 shows.

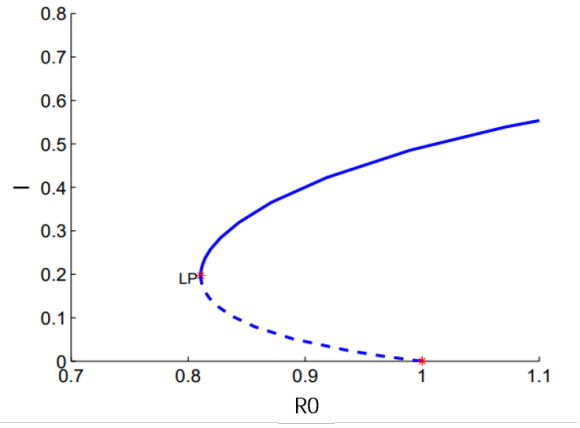


Figure 5: Fixed parameter $\beta = 5, \mu_0 = 0.2, b = 2, \theta = 0.1, \sigma = 0.4, \Phi = 0.4$, I along with R_0

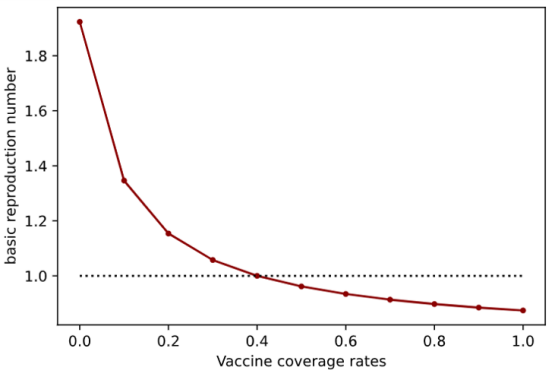


Figure 6: Basic Reproduction Number as a function of vaccination rate

4.5 Vaccine Coverage Rate and Basic Reproduction Number

Increasing the vaccination rate will bring the basic reproduction number below 1, but it will not eliminate the infection. At the beginning of the disease in order to prevent an epidemic outbreaks, large coverage rate of vaccination can keep the basic reproduction number within a small range. In general, the basic reproduction number is the threshold that determines the prevalence of disease. If basic reproduction number is less than 1, the disease is eliminated. If it is greater than one, the disease spreads. Because the population has different infectious rates, non-linear incidence rate and age structure. Backward bifurcation is a very important phenomenon in infectious disease models. The presence of backward bifurcation suggests that the basic reproduction number alone does not describe or determine the prevalence of disease. In this situation, the prevalence of the disease depends on the initial population value.

We plotted the relationship between the basic reproduction number and the vaccination rate under the given parameters ($\beta = 5, \mu_0 = 0.2, \mu_1 = 2.6, b = 0.5, \theta = 0.1, \sigma = 0.4$) as Figure 6 shows. The basic reproduction number decreased with the increase of vaccine coverage rate. There is a threshold at which the basic reproduction number is 1. In the given case, the threshold is 0.4. This threshold has great meaning of guidance for vaccination efforts.

5 Conclusion

This project is mainly divided into two parts. Firstly, we discuss the applications of target reproduction number in ecology and epidemiology. The consistency between the target reproduction number and the basic reproduction number in epidemiology is verified by the SEI model. In the second part, we emphatically discuss the existence and stability of the equilibrium points of SIVS model. Under different parameter combinations, the model has different behaviors. We perform numerical simulation to verify this. Finally, we discuss the relationship between vaccination coverage rate and basic reproduction number, and give the important threshold of vaccination rate.

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