Analysis of the SIR Model with Vaccination: Bifurcation and Dynamics

Arij Qureshi

December 12, 2023

1 Introduction

The study of infectious diseases and their spread within populations is a critical aspect of public health management. One of the fundamental tools used in this field is the Susceptible-Infected-Recovered (SIR) model, a compartmental model in epidemiology that divides the population into three distinct groups: those susceptible to the infection (S), those currently infected (I), and those who have recovered from the infection (R). This model serves as a basis for understanding the dynamics of infectious diseases and for planning control strategies.

Incorporating vaccination strategies into the SIR model adds a vital dimension to its applicability, particularly in the context of ongoing global efforts to manage pandemics like COVID-19. Vaccination has a direct impact on the susceptible population, reducing the number of individuals who can be infected and thereby influencing the overall dynamics of disease spread.

This project focuses on a bifurcation analysis of a modified SIR model that includes vaccination, and logistic growth for the susceptible population. The model also includes birth and death rates(base rate and disease induced), rather than a constant value for total population. Bifurcation theory helps to understand how slight changes in system parameters can lead to qualitative changes in the model's dynamics. In particular, this analysis explores how vaccination impacts the spread of an infectious disease by studying changes in the basic reproduction number and the proportion of successfully vaccinated individuals.

The primary reference for this project is an article titled "SIR Model with Vaccination: Bifurcation Analysis," which provides a comprehensive analysis of how vaccination influences disease dynamics within the SIR framework. By examining the bifurcation phenomena in this context, this project aims to contribute to a deeper understanding of how vaccination strategies can be optimized to control the spread of infectious diseases.

2 The Equations

2.1 Base SIR Model

The basic SIR model is described by a set of ordinary differential equations (ODEs) that govern transitions between the different sets of population, depending on several factors such as the transmission rate and the recovery rate. Mathematically, it is expressed as:

$$\begin{aligned}\frac{dS}{dt} &= -\beta SI,\\ \frac{dI}{dt} &= \beta SI - gI,\\ \frac{dR}{dt} &= gI,\end{aligned}$$

where β is the transmission rate coefficient and g is the recovery rate coefficient.

2.2 Incorporating Logistic Growth and Death Rates

To make the model more realistic, we introduce logistic growth for the susceptible population and death rates for all compartments. Let A be the carrying capacity of S when $\beta = 0$. μ is the natural death rate of I and R, and d is the death rate of I from disease. The modified equations then are:

$$\frac{dS}{dt} = S(A - S) - \beta IS, \tag{1}$$

$$\frac{dI}{dt} = \beta IS - (\mu + d)I - gI, \tag{2}$$

$$\frac{dR}{dt} = gI - \mu R. \tag{3}$$

The logistic term $S(A - S)$ in the $\frac{dS}{dt}$ equation represents the logistic growth of the susceptible population, while $(\mu + d)I$ and μR in their respective equations account for the natural death rate and the additional death rate from the disease.

2.3 Final Modified SIR Model with Vaccination

To add the possibility of vaccination at birth, we add one more term to each of S and R. Let p be the proportion of S vaccinated at birth($0 \leq p \leq 1$), and m be the birth rate. The final equations come out to be:

$$\frac{dS}{dt} = S(A - S) - \beta IS - pm, \tag{4}$$

$$\frac{dI}{dt} = \beta IS - (\mu + d)I - gI, \tag{5}$$

$$\frac{dR}{dt} = pm + gI - \mu R. \tag{6}$$

The terms pm added in $\frac{dS}{dt}$ and $\frac{dR}{dt}$ account for the vaccinated population leaving S and joining R, the recovered population.

3 Analysis

3.1 Reduction

As $\frac{dS}{dt}$ and $\frac{dI}{dt}$ do not depend on R, we will only focus on those two equations. We let $\sigma = \mu + d$ for simplicity's sake henceforth.

3.2 Vaccination Requirements

To calculate whether vaccination should be considered, we calculate the *base reproduction rate*, R_0 interpreted as the number of secondary infections caused by one infected person.

$$R_0 = \frac{A\beta}{g + \sigma} \geq 0 \tag{7}$$

Vaccination should only be considered when $R_0 \geq 1$(*i.e.* $p > 0$), otherwise the disease would diminish on its own.

3.3 Fixed Points, Stability

The system of equations for $\frac{dS}{dt}$ and $\frac{dI}{dt}$ have three possible fixed points. Two are disease free(*i.e.* $I^* = 0$). The disease free equilibria are:

$$X_0^* = (S_0^*, I_0^*) = \left(\frac{A - \sqrt{A^2 - 4pm}}{2}, 0\right) \tag{8}$$

$$X_1^* = (S_1^*, I_1^*) = \left(\frac{A + \sqrt{A^2 - 4pm}}{2}, 0\right) \tag{9}$$

when $0 < p \leq \frac{A^2}{4m}$. These equilibria only exist for p small enough. The endemic equilibrium(*i.e.* where the infection stabilizes) is:

$$X_2^* = (S_2^*, I_2^*) = \left(\frac{\sigma + g}{\beta}, \frac{-pm\beta^2 + A(\sigma+g)\beta - (\sigma+g)^2}{\beta^2(\sigma+g)} \right). \tag{10}$$

The stability of X_0^* and X_1^* can be calculated by linearizing the problem about these fixed points. The Jacobian of the system is:

$$J = \begin{pmatrix} A - 2S - \beta I & -\beta S \\ \beta I & \beta S - (\sigma + g) \end{pmatrix} \tag{11}$$

Evaluated at X_0^*:

$$J = \begin{pmatrix} \sqrt{A^2 - 4pm} & \frac{-A\beta + \beta\sqrt{A^2-4pm}}{2} \\ 0 & \frac{A\beta - \beta\sqrt{A^2-4pm}}{2} - (\sigma + g) \end{pmatrix} \tag{12}$$

Giving eigenvalues

$$\lambda_1 = \sqrt{A^2 - 4pm} > 0 \tag{13}$$

$$\lambda_2 = \frac{\beta}{2}(A - \sqrt{A^2 - 4pm}) - (\sigma + g) \tag{14}$$

Therefore, if $A\beta \geq \beta\sqrt{A^2 - 4pm} + 2(\sigma + g)$, X_0^* is an unstable node. Otherwise, it is a saddle node. A similar evaluation of the Jacobian at X_1^* leads to showing that if $A\beta \geq \beta\sqrt{A^2 - 4pm} + 2(\sigma + g)$, X_1^* is a saddle, otherwise it is a stable node. Analyzing the stability of X_2^* would be a similar task, but the Jacobian gets very complicated for arbitrary values. We will use values of R_0 later to examine the stability of the endemic equilibrium without vaccination.

3.4 Saddle Node Bifurcation

We can study the bifurcations of this problem using the parameter p. Noticing that (S_0^*, I_0^*) and (S_1^*, I_1^*) only exist for $p < \frac{A^2}{4m}$. Therefore, at $p = \frac{A^2}{4m}$ there is a saddle node bifurcation. Using MATLAB, attached is a plot to show the saddle node bifurcation within this problem.

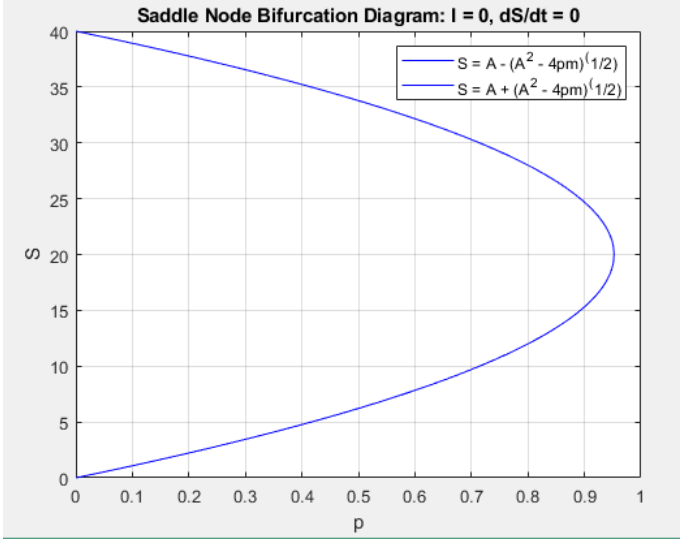

Figure 1: A Bifurcation plot in the Sp plane, where $I = 0$. The figure shows a bifurcation at $p = \frac{A^2}{4m}$, for the specific values used for the plot.

3.5 The case with no vaccination: $p = 0$

To continue studying the SIR problem, and view how R_0 is a critical parameter in the decision of whether or not a diseased population will grow in size, we will now consider the model without vaccination:

$$\frac{dS}{dt} = S(A - S) - \beta IS, \tag{15}$$

$$\frac{dI}{dt} = \beta IS - (\sigma + g)I, \tag{16}$$

$$\tag{17}$$

The equilibria are now

$$X_0^* = (0, 0),$$

$$X_1^* = (A, 0),$$

$$X_2^* = \left(\frac{\sigma + g}{\beta}, \frac{A\beta - (\sigma + g)}{\beta^2}\right) \overset{(7)}{=} \left(\frac{A}{R_0}, \frac{A}{\beta}\left(1 - \frac{1}{R_0}\right)\right).$$

Since we only consider $S, I > 0$, the endemic equilibrium X_2^* only exists is in the first quadrant when $R_0 > 1$. The Jacobian for this system is the same as before (12). Evaluating at the fixed points, we can prove the following:
The system exhibits:

1. Two disease free fixed points at X_0^* and X_1^* where
   (a) X_0^* is a saddle $\forall R_0 \in \mathbb{R}$
   (b) X_1^* has undergoes a transcritical bifurcation at $R_0 = 1$
   (c) X_1^* is a stable node for $R_0 < 1$, and a saddle otherwise.
2. an endemic equilibrium X_2^* such that
   (a) $1 < R_0 < 1 + \frac{1}{4\beta} \implies X_2^*$ is a stable node,
   (b) $R_0 > 1 + \frac{1}{4\beta} \implies X_2^*$ is a stable spiral,
   (c) at $R_0 = 1 + \frac{1}{4\beta}$, X_2^* undergoes a Belyakov transition.

To prove the previous statements, we can evaluate the Jacobian at each fixed point. The eigenvalues of $J(X_0^*)$ are $A > 0, -(\sigma + g) < 0$, implying a saddle point. The eigenvalues of $J(X_1^*)$ are $A\beta - (\sigma + g)$ and $-A < 0$, proving 1b and 1c. If $A\beta - (\sigma + g) > 0 \leftrightarrow \frac{A\beta}{\sigma + g} > 1 \leftrightarrow R_0 > 1$, X_1^* is a saddle, otherwise a stable node. Proving 2 is a more involved process which will not be included for the length of this paper.

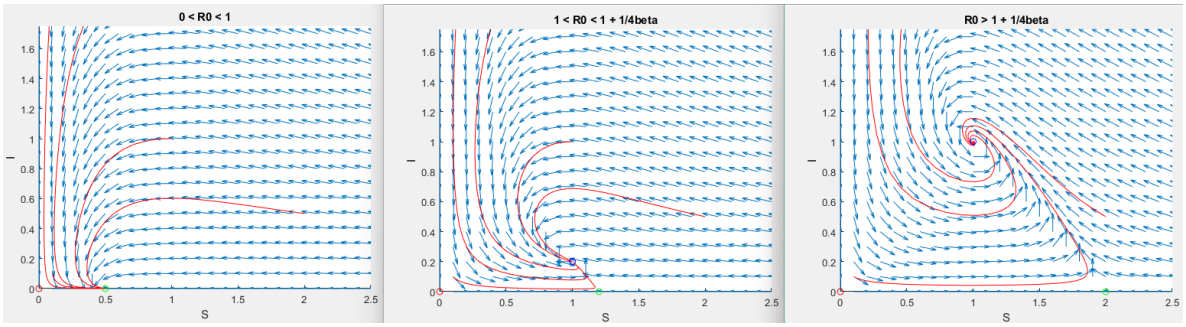

Figure 2: Phase Planes and Trajectories for different R_0 values. The image on the left shows that X_2^* is not in the positive quadrant, and that X_0^* is a saddle and X_1^* is a stable node. The middle image shows the appearance of X_2^* in the positive quadrant and the transcritical bifurcation for X_1^*, becoming a saddle. The image on the right then shows X_2^* going through the Belyakov transition from a stable node to a stable spiral.

4 Conclusion

The SIR Model with Vaccination has interesting behavior that can be observed to predict the behavior of various diseases and epidemics, such as COVID-19. The parameter R_0 is commonly used to discuss whether or not a disease will turn into an epidemic, or if could settle down on its own. This is exactly what the transcritical bifurcation at $R_0 = 1$ tells us. When $R_0 < 1$, the diseased population, I, will always reach 0, no matter the initial conditions. When $R_0 > 1$, we see that all trajectories will always approach a point with a constant diseased population, which is not ideal. This is why we consider vaccination for $R_0 > 1$ (*i.e.* $p > 0$). The introduction of vaccination allows us as humans to alter the trajectory of the epidemic, creating fixed points with $I = 0$ for sufficient p values. Due to the complexity of the problem, many more complex bifurcations were not included in this paper, that can be viewed within the referenced paper. This study emphasizes the essential role of vaccination in controlling infectious diseases, as shown through the SIR model.

5 Source Code

Listing 1: Bifurcation Plotting with parameter p

```
% Parameters
A = 20;     % Carrying capacity
m = 105;    % Birth rate

% bifurcation point
p_center = A^2 / (4 * m);
p_values = linspace(0, p_center, 1000);

% Bifurcation diagram for dS/dt = 0 with I = 0
% dS/dt = S * (A - S) - p * m = 0
% S = (A +- sqrt(A^2 - 4pm))/2

% Initialize vectors to store S values for each branch of the bifurcation
S_branch1 =  A - (A^2 - 4*p_values * m).^(1/2);
S_branch2 = A + (A^2 - 4*p_values * m).^(1/2);

% Plotting the bifurcation diagram
figure;
plot(p_values, S_branch1, 'b-', 'DisplayName', 'S = A - (A^2 - 4pm)^(1/2)');
hold on;
plot(p_values, S_branch2, 'b-', 'DisplayName', sprintf('S = A + (A^2 - 4pm)^(1/2)'));
xlabel('p');
xlim([0,1]);
ylabel('S');
title('Saddle Node Bifurcation Diagram: I = 0, dS/dt = 0');
legend;
grid on;
```

Listing 2: Phase Portrait Plotting with Parameter R0

```
% Parameters common to all cases - set to make calculation of R0 easy
beta = 1;
sigma = 0.5;
g = 0.5;

% Case 1: 0 < R0 < 1
A1 = 0.5;
R0_1 = A1 * beta / (sigma + g);

% Case 2: 1 < R0 < 1 + 1/(4*beta)
A2 = 1.2;
R0_2 = A2 * beta / (sigma + g);

% Case 3: R0 > 1 + 1/(4*beta)
A3 = 2;
R0_3 = A3 * beta / (sigma + g);


% Define grid for vector field
[S_grid, I_grid] = meshgrid(0:0.1:4, 0:0.1:4);

% Set of initial conditions
initial_conditions_set = [0.1, 0.1; 1, 1; 2, 0.5; 0.5, 2; 3, 3];
```

```
% Plot phase portraits for each R0
R0_values = [R0_1, R0_2, R0_3];
A_values = [A1, A2, A3];
c = 1;
for i = 1:length(R0_values)
    R0 = R0_values(i);
    A = A_values(i);
    tspan = [0, 20];

    % Vector field calculations
    dS = S_grid .* (A - S_grid) - beta .* S_grid .* I_grid;
    dI = beta .* S_grid .* I_grid - (sigma + g) .* I_grid;
    % Normalize vectors for plotting
    speeds = sqrt(dS.^2 + dI.^2);
    dS_normalized = dS ./ (2.5 * speeds);
    dI_normalized = dI ./ (2.5 * speeds);

    % Plotting
    figure;
    hold on;
    quiver(S_grid, I_grid, dS_normalized, dI_normalized); % Plot vector field

    % Plot trajectories for each initial condition
    for j = 1:size(initial_conditions_set, 1)
        initial_conditions = initial_conditions_set(j, :);
        [t, X] = ode45(@(t, X) systemEquations(X(1), X(2), A, beta, sigma, g), tspan, in
        plot(X(:,1), X(:,2), 'r');
    end

    % Mark fixed points
    plot(0, 0, 'ro'); % X0*
    plot(A, 0, 'go'); % X1*
    if R0 > 1
        plot(A/R0, A/beta * (1 - 1/R0), 'bo'); % X2* if it exists
    end
    if c == 1
        title('0<R0<1')
    elseif c == 2
        title('1<R0<1+1/4beta')
    else
        title('R0>1+1/4beta')
    end
    xlabel('S');
    ylabel('I');
    axis([0 2.5 0 1.75]);
    hold off;
    c = c + 1;
end

% Define the system of equations
function dXdt = systemEquations(S, I, A, beta, sigma, g)
    dSdt = S * (A - S) - beta * S * I;
    dIdt = beta * S * I - (sigma + g) * I;
    dXdt = [dSdt; dIdt];
end
```

6 References

1. Maurício de Carvalho, João P., and Alexandre A. Rodrigues. "Sir model with vaccination: Bifurcation analysis." *Qualitative Theory of Dynamical Systems*, vol. 22, no. 3, 2023, https://doi.org/10.1007/s12346-023-00802-2.