CHAPTER 4

MODELING AND SIMULATION ANALYSIS OF SIR EPIDEMIC MODELS WITH IMMIGRATION USING NON-LINEAR INCIDENCE RATE

One of the primary reasons for studying infectious diseases is to control and ultimately eradicate the infection from the population. Models can be a powerful tool in this approach that allows us to optimize the use of limited resources or simply to target control measures more efficiently. It also helps us to understand the global dynamics of the spread of infectious diseases. The mathematical analysis of epidemiological modeling is often used for the assessment of the global asymptotic stability of both the disease free and endemic equilibrium.

4.1 INTRODUCTION

Mathematical models which describe the dynamics of infectious diseases have recently played a crucial role in the disease control in epidemiological aspect. Many authors [2, 3, 7, 13, 15, 36] have proposed various kind of epidemic models to understand the mechanism of disease transmission. Recently many research works are carried out on the global asymptotic stability of an endemic equilibrium of endemic models with a non-monotonic incidence rate. Xiao and Ruan [65] first proposed a non-monotonic incident rate \( \frac{\lambda}{1 + \alpha^2} \), where \( \lambda \) the infection force of the disease measures an \( \frac{1}{1 + \alpha^2} \) which describes the psychological or inhibitory effect from the behavioral change of the susceptible individuals when the number of infective individuals is very large. By applying Dulac function, Xiao and Ruan [65] established that the endemic equilibrium of an SIRS model with this non-monotonic incidence rate and no delay is globally asymptotically stable.

If individuals recover with permanent immunity, then the simplest model is an SIR model. If individuals recover with temporary immunity so that they eventually become susceptible again, then the simplest model is an
SIRS (S-Susceptible, I-Infective, R-Recovered or Removed, S-Susceptible again) model. If individuals do not recover, then the simplest model is an SI model. In general, SIR epidemic and endemic models are appropriate for viral agent diseases such as measles, mumps, and smallpox, while SIS models are appropriate for some bacterial agent diseases such as meningitis, plague, and sexually transmitted diseases, and for protozoan agent diseases such as malaria and sleeping sickness. Modeling and analysis of such infectious diseases have been done by many scientists [40, 56, 71]. Epidemiological models with latent or incubation period have been studied by many authors, because many diseases, such as influenza and tuberculosis, have a latent or incubation period, during which the individual is said to be infected but not infectious. Beretta et. al. [6] have studied global stability in an SIR epidemic model with distributed delay that describes the time which it takes for an individual to lose infectiousness. Zhou et. al. [76] analyzed the stability conditions of equilibria of non-linear matrix population models. Hyman and Li [39] introduced the effectiveness of isolation strategies in preventing standard epidemics.

Two mathematical models are constructed in this chapter. They are i) SIR epidemic model with immigration using non-linear incidence rate and ii) Modified SIR epidemic model with immigration using non-linear incidence rate. This chapter is organized as follows. In section 4.2, description of model I is given and the stability of the model is discussed. In this section, the numerical result displays the interpretation, inference, simulation and discussions. In section 4.3, description of model II and mathematical analysis are given related to this model. In the same section, the numerical results are illustrated with simulation and discussions. Conclusions are presented in section 4.4.

4.2 THE MODEL DESCRIPTION AND ANALYSIS FOR MODEL I

4.2.1 Model Description

Xiao and Ruan [65] proposed an epidemic model with non-monotonic incidence rate \( \frac{\lambda}{1 + \alpha Z} \). Using this non-monotonic incidence rate, then the model becomes
\[
\frac{dS}{dt} = -dS - \frac{\lambda SI}{1 + \alpha I^2} \\
\frac{dI}{dt} = \frac{\lambda SI}{1 + \alpha I^2} - (d + \beta)I \\
\frac{dR}{dt} = mI - (d + \beta)R
\]

Yuan and Bo Li [69] considered the non-linear incidence rate
\[\frac{\lambda I}{1 + \alpha I}\]

i.e., the infectious force takes the form
\[(\lambda I) = \frac{\lambda}{1 + \alpha + \alpha I} \]

Then the model becomes
\[
\frac{dS}{dt} = -\frac{\lambda I^2}{2 + \alpha I^2} + \frac{\lambda}{\alpha} \\
\frac{dI}{dt} = \frac{\lambda I^2}{2 + \alpha I^2} - \left(\frac{\lambda I}{\alpha}\right) \\
\frac{dR}{dt} = mI - \left(\frac{\lambda I}{\alpha}\right)
\]

In this chapter, this incidence rate has been considered with immigration rather than the non-monotonic incidence rate \[\frac{\lambda}{1 + \alpha^2}\].

4.2.2 Assumptions

- Consider Yuan and Bo Li [69] SIR epidemic model.
- Assume that the population consists of three types of individuals. They are susceptible, infective and recovered individuals.
- Let the non-linear incidence rate be \[\frac{\lambda I}{1 + \alpha} \]
- Assuming that the infectious force takes the form
  \[\frac{\lambda I}{1 + \alpha}\]
- Consider the susceptible rate with immigration.
- Let the immigration be constant.
**SIR epidemic model with immigration**: The non-linear incidence rate is considered.

### 4.2.3 Notations

<table>
<thead>
<tr>
<th>Symbol</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>( S )</td>
<td>Number of susceptible</td>
</tr>
<tr>
<td>( I )</td>
<td>Number of infective</td>
</tr>
<tr>
<td>( R )</td>
<td>Number of removed or recovered individuals.</td>
</tr>
<tr>
<td>( \lambda )</td>
<td>Recruitment rate of the population</td>
</tr>
<tr>
<td>( \mu )</td>
<td>Natural death rate of the population</td>
</tr>
<tr>
<td>( \lambda )</td>
<td>The proportionality constant</td>
</tr>
<tr>
<td>( \alpha )</td>
<td>Natural recovery rate of the infective individuals</td>
</tr>
<tr>
<td>( \beta )</td>
<td>The rate at which recovered individuals lose immunity and return to susceptible class</td>
</tr>
<tr>
<td>( \alpha )</td>
<td>The parameter measures of the psychological or inhibitory effect</td>
</tr>
<tr>
<td>( \mu )</td>
<td>Increase of susceptible at a constant rate</td>
</tr>
<tr>
<td>( S_0 )</td>
<td>Disease-free equilibrium</td>
</tr>
<tr>
<td>( E )</td>
<td>Endemic equilibrium</td>
</tr>
<tr>
<td>( R_0 )</td>
<td>Basic Reproduction Number</td>
</tr>
<tr>
<td>( S^* )</td>
<td>The rate of susceptible at the endemic equilibrium</td>
</tr>
<tr>
<td>( R^* )</td>
<td>The rate of recovered or removed at the endemic equilibrium</td>
</tr>
<tr>
<td>( I^* )</td>
<td>The rate of infective at the endemic equilibrium</td>
</tr>
</tbody>
</table>

### 4.2.4 Mathematical Model I

Consider the SIR model with nonlinear incidence rate

\[
\begin{align*}
\frac{dS}{dt} &= \lambda - \mu S \left( \frac{I^2}{S^2 + \alpha^2 + \beta^2} \right) \\
\frac{dI}{dt} &= \lambda \frac{I^2}{S^2 + \alpha^2} - \left( \mu + \beta \right) I \\
\frac{dR}{dt} &= \beta I - \mu R
\end{align*}
\]  

(4.1)
Consider the following SIR model:

\[
\begin{align*}
\dot{S} &= \mu - \frac{\lambda}{\mu + \alpha + \beta} S^2 + \alpha S^2 + \beta S^2 \\
\dot{I} &= \frac{\lambda}{\mu + \alpha + \beta} S^2 - (\alpha + \beta) I - \beta I^2 \\
\dot{R} &= \beta I^2
\end{align*}
\] (4.2)

All the parameters are positive and have the similar biological meaning as in (4.1). Noting that the system (4.2) is not well defined at the origin \((0,0,0)\).

Now redefined that when \((S, I, R) = (0,0,0)\), then

\[
\begin{align*}
\dot{S} &= + \mu, \\
\dot{I} &= 0, \\
\dot{R} &= 0
\end{align*}
\] (4.3)

With this assumption, it is to easy that the first octant \(\mathbb{R}_+^3 = \{(S, I, R) \in \mathbb{R}_+^3 \mid S, I, R > 0\}\) is positively invariant for the systems (4.2) is continuous and satisfies the Lipschitz condition in \(\mathbb{R}_+^3\). The following result shows that the solutions of (4.2) is bounded, and hence, lie in a compact set and are continually for all positive time.

**Lemma: 4.2.1**

The plane \((S + I + R - \mu) = 0\) is an invariant manifold of system (4.2) is attracting in the first octant.

**Proof**

Summing up the three equations in (4.2) and denoting

\[
(S + I + R) = (S + I + R) - \mu
\] (4.4)

Then

\[
\begin{align*}
\dot{S} &= + \mu - \frac{\lambda}{\mu + \alpha + \beta} S^2 + \alpha S^2 + \beta S^2 \\
\dot{I} &= \frac{\lambda}{\mu + \alpha + \beta} S^2 - (\alpha + \beta) I - \beta I^2 \\
\dot{R} &= \beta I^2
\end{align*}
\] (4.5)

It is clear that \((S) = \frac{\mu}{\mu + \alpha + \beta}\) is a solution of (4.5) and for any \((S_0) \geq 0\), the general solution of (4.5) is
Now integrating, this implies

\[ \frac{-1}{\log[ + \mu - (\cdot)]} + \]

Put \( t = t_0 \)

\[ -\frac{1}{\log[ + \mu - (\cdot)]} + \]

\[ = -\frac{1}{\log[ + \mu - (\cdot)]} \]

\[ -\log\left(\frac{+ \mu - (\cdot)}{+ \mu - (\cdot)}\right) = (0 - ) \]

\[ \left(\frac{+ \mu - (\cdot)}{+ \mu - (\cdot)}\right)^{-d(t-t_0)} ( + \mu) - \]

\[ = \frac{1}{\left(\left( + \mu - (\cdot)\right)^{-d(t-t_0)}\right)^{d(t-t_0)}} \]

\[ \left( + \mu - (\cdot)\right)^{-d(t-t_0)} \]

\[ \lim_{t \to \infty} N(t) = \frac{a + \mu}{d} \]

In the following, consider the existence of equilibria of system (4.2). For any values of parameters, the model (4.2) always has a disease-free equilibrium

\[ _0^3 = (\frac{-\mu}{a}, 0, 0) \] and find the positive equilibria, set
Define the basic reproductive number as follows:

\[ R_o = \frac{\lambda}{d + m} \quad (4.8) \]

\[
\left[ \alpha - (\rho - 1) \left(1 + \frac{\rho}{\beta}\right)^2 \right]^2 + 2 \left(\rho - 1\right) \left(1 + \frac{\rho}{\beta}\right)^2 \]
i) If \( \rho < 1 \), then there is no positive equilibrium;

ii) If \( \rho > 1 \) then there is a unique positive equilibrium. \( \ast = (\ast, \ast, \ast, \ast) \)
called the endemic equilibrium and is given by

\[
\ast = \frac{\rho}{\sqrt{\beta - \lambda}}
\]

\[
\ast = \left(1 + \beta\right)^{-1}
\]

In the following section, the properties of these equilibria and the
global qualitative analysis of model (4.2) is obtained.

### 4.2.5 Mathematical Analysis

It is clear that limit of system is on the plane \( + + + = +\). Thus focus on the reduced system

\[
\begin{align*}
\frac{dI}{dt} &= \frac{\lambda \left(1 + \mu - \beta\right)}{\alpha^2 + \alpha^2} - \frac{I}{\gamma - \mu} - \frac{I}{\gamma} - (I, R) \\
\frac{dR}{dt} &= -\left(1 + \beta\right) - (, )
\end{align*}
\]

In order to study the disease free equilibrium \( \rho \) and the endemic
equilibrium \( \ast \), the system (4.10) is rescaled by

\[
\begin{align*}
\frac{dI}{dt} &= \frac{\lambda}{\beta + \mu \beta - \lambda} - \frac{I}{\gamma - \mu} - \frac{I}{\gamma} - (I, R) \\
\frac{dR}{dt} &= -\left(1 + \beta\right) - (, )
\end{align*}
\]
\[ 
\begin{align*}
\frac{dS}{dt} &= \lambda S\left(\frac{I}{S} + \frac{1}{\mu}\right) - \frac{\lambda I}{S} - \lambda \\
\frac{dI}{dt} &= \frac{\lambda I}{S} - \frac{\lambda I}{S}\left(\frac{I}{S} + \frac{1}{\mu}\right) - \mu I - \alpha I \\
\frac{dR}{dt} &= \mu I - \alpha I - \beta I - \alpha R
\end{align*}
\]

(4.11)

where

\[ 
\begin{align*}
\frac{\lambda I}{S} &= \alpha I \\
\frac{\lambda I}{S}\left(\frac{I}{S} + \frac{1}{\mu}\right) &= \frac{\lambda I}{S}\left(\frac{I}{S} + \frac{1}{\mu}\right) \\
\frac{\lambda I}{S}\left(\frac{I}{S} + \frac{1}{\mu}\right) &= \frac{\lambda I}{S}\left(\frac{I}{S} + \frac{1}{\mu}\right) \\
\frac{\lambda I}{S}\left(\frac{I}{S} + \frac{1}{\mu}\right) &= \frac{\lambda I}{S}\left(\frac{I}{S} + \frac{1}{\mu}\right)
\end{align*}
\]

(4.12)

This observation and simple calculation shows that \(0(0, 0)\) is the disease free equilibrium and the unique positive equilibrium \(\left(\cdot, \cdot\right)\) of the

**The Endemic Equilibrium \(\left(\cdot, \cdot\right)\)**

This observation and simple calculation shows that \(0(0, 0)\) is the disease free equilibrium and the unique positive equilibrium \(\left(\cdot, \cdot\right)\) of the
system (4.11)-(4.12) is the endemic equilibrium \( * \) of the system (4.2). It exists if \( - < 0 \) and \( * \) is a positive root of the equation

\[
\sqrt{2} + (1 + + 1) \cdot \sqrt{2} = 0
\]

\( * = * \)

Equation (4.13) gives,

\[
* = \frac{-(1 + + 1) + \sqrt{(1 + + 1)^2 - 4\cdot K}}{2}
\]

The Jacobian matrix for the equilibrium point \( 0(0,0) \) is

\[
0 = \begin{pmatrix} - & 0 \\ - & 1 \end{pmatrix}
\]

Therefore if \( ( - ) > 0 \) the point \( 0(0,0) \) is unstable saddle point, if \( ( - ) = 0 \) then \( 0(0,0) \) is saddle node and if \( ( - ) < 0 \) then \( 0(0,0) \) is stable node. The condition \( ( - ) > 0 \) is equivalent to \( 0 > 1 \) and the condition \( ( - ) < 0 \) is equivalent to \( 0 < 1 \). When \( * \) exists, \( E_0 \) is unstable.

Now when \( ( - ) > 0 \) or equivalently \( 0 > 1 \) discuss the stability at the point \( * \). The Jacobian matrix at \( *(0,0) \) is

\[
det(1) = \frac{\sqrt{2} + (1 + 2 \cdot *) - (1 + 2 \cdot *)}{2}
\]

The sign of the \( det(1) \) is the sign of the factor
\[ r_1 = -\frac{1}{2}(1 + \psi)^2 + (1 + 2\psi) + (1 + w) \]  

(4.16)

Using (4.14) and (4.15) in (4.16)

\[ r_1 = \Delta_1 \left( \frac{1}{2} \left( 1 + \frac{1}{2} \right) + \frac{2}{1 + \frac{1}{2}} \right) \]

Note that \[ \left( (1 + \frac{1}{2}) + \frac{2}{1 + \frac{1}{2}} \right)^2 - \Delta_1^2 > 0 \]

\[ \left( (1 + \frac{1}{2}) + \frac{2}{1 + \frac{1}{2}} - \Delta_1 \right) > 0 \]

which means that \( r_1 > 0 \) and hence \( \det(\Delta) \) is positive for any set of values of parameters. Now

\[ \begin{vmatrix} \star & (1 + \frac{1}{2})^2 + (1 + 2\psi) \star - (1 + 2\psi) \star \end{vmatrix} \]

Solving, one can see the sign of the \( r_1 \) is determined by the sign of

\[ -\frac{1}{2} \left( (1 + \frac{1}{2})\left( 1 + \frac{1}{2} \right) + (1 + 2\psi) \right) \leq 0 \]

Using again equation (4.15) in (4.16), this implies

\[ P_2 = P_3 x^* - P_4 \]

\[ P_3 = (1 + w + uv_1)((1 + w)^2 + u(1 + w)(1 + 2w + uv_1)) + 2uv_2K(1 + w) \]

\[ + u^2v_2K(1 + 2w) + 2u^2v_2(1 + w)(u - K) + u^3v_1v_2K \]

\[ P_4 = (K - u)((1 + w)^2 + u(1 + w)(1 + 2w + uv_1)) \]

\[ + uv_2((K - u)^2 + 2u(1 + K)(u - K) + u^2) \]

Therefore both \( P_2 \) and \( P_4 \) are positive in case \( K > u \). When the point \( (*, *, *) \) exists, it is locally stable if \( * < \frac{4}{3} \).
4.2.6 NUMERICAL RESULTS

ii) Simulation and Discussions of Model I

Let $\mu = 0.2$, $\lambda = 0.5$, $\rho = 0.3$

Hence the basic reproductive number $R_0 = 0.21 < 1$, there is no positive equilibrium $E^* = (x^*, y^*, z^*)$. In this case, the disease dies out.

By using the above values, then it gives $x = 1.04$, $y = 0.34$ and rescaling the system implies that $-\sigma < 0$. In this case, the disease free equilibrium $(0, 0)$ is a stable node.

Therefore if $-\sigma > 0$ the point $E_0(0, 0)$ is unstable saddle point, if $-\sigma < 0$ then $E_0(0, 0)$ is stable node. The condition $-\sigma > 0$ is equivalent to $R_0 > 1$ and the condition $-\sigma < 0$ is equivalent to $R_0 < 1$. Let

$a = 3$, $\mu = 0.2$, $\lambda = 0.5$, $\rho = 0.4$, $\beta = 0.3$, $\alpha_1 = 0.3$, $\alpha_2 = 0.4$

Then $x^* = 0.17$, $y^* = 0.03$, $p_3 = 48.76$, $p_4 = 33.22$ and $\frac{p_4}{p_3} = 0.6813$

This implies that $x^* < \frac{p_4}{p_3}$. Therefore the point $(x^*, y^*)$ exists and it is stable.
ii) Numerical Table for Model I

Table 4.2:1

(Effects of $\mu$ on $S^*$, $I^*$ and $R^*$)

$\alpha = 2, \quad \gamma = 1, \quad \delta = 0.5, \quad \lambda = 2, \quad \beta = 0.5$

$\mu$ varies from 0.1 to 1.0

<table>
<thead>
<tr>
<th>$\mu$</th>
<th>$S^*$</th>
<th>$I^*$</th>
<th>$R^*$</th>
</tr>
</thead>
<tbody>
<tr>
<td>0.1</td>
<td>2.9997</td>
<td>0.8981</td>
<td>0.2994</td>
</tr>
<tr>
<td>0.2</td>
<td>4.9999</td>
<td>1.7146</td>
<td>0.5715</td>
</tr>
<tr>
<td>0.3</td>
<td>6.1999</td>
<td>2.5311</td>
<td>0.8437</td>
</tr>
<tr>
<td>0.4</td>
<td>8.1999</td>
<td>3.3476</td>
<td>1.1160</td>
</tr>
<tr>
<td>0.5</td>
<td>10.1999</td>
<td>4.1464</td>
<td>1.3880</td>
</tr>
<tr>
<td>0.6</td>
<td>12.1998</td>
<td>4.9806</td>
<td>1.6602</td>
</tr>
<tr>
<td>0.7</td>
<td>14.1998</td>
<td>5.7971</td>
<td>1.9324</td>
</tr>
<tr>
<td>0.8</td>
<td>16.1998</td>
<td>6.6135</td>
<td>2.2045</td>
</tr>
<tr>
<td>0.9</td>
<td>18.1998</td>
<td>7.4300</td>
<td>2.4767</td>
</tr>
<tr>
<td>1.0</td>
<td>20.1997</td>
<td>8.2465</td>
<td>2.4749</td>
</tr>
</tbody>
</table>

Interpretation:

From table 4.2:1, the following is found.

1. When the immigration $\mu$ increases, $S^*$, $I^*$ and $R^*$ also increases at the endemic equilibrium.

2. The recovered rate gradually increases for the increasing values of $\mu$.

Inference:

From this table, it is noted that if the susceptible rate increases, then the disease will spread into the population. But the recovered rate increases gradually.
4.3 THE MODEL DESCRIPTION AND ANALYSIS FOR MODEL II

4.3.1 Model Description

Xiao and Ruan [65] used a non-monotonic incidence rate \( \frac{\lambda}{1 + \alpha^2} \) instead of the general incidence rate \( \lambda \). Then the model becomes

\[
\begin{align*}
\frac{dS}{dt} &= a - dS - \frac{\lambda SI}{1 + \alpha^2} + \beta R \\
\frac{dI}{dt} &= \frac{\lambda IS}{1 + \alpha^2} - (d + m)I \\
\frac{dR}{dt} &= mI - (d + \beta)R
\end{align*}
\]

Gajendra Ujjainkar [28] introduced a modified non-monotonic incidence rate \( \frac{\lambda}{1 + \alpha_1 + \alpha_2^2} \) in place of the incidence rate \( \frac{\lambda}{1 + \alpha^2} \). This incidence rate contains two parametric measures \( \alpha_1 \) and \( \alpha_2 \). In this section, the model 4.2 is considered with modified nonlinear incidence rate

\[
\left( _, _ \right) = \frac{\lambda( _, _ )}{1 + \alpha_1( _, _ ) + \alpha_2( _, _ S )}
\]

Here the infectious force is \( \left( _, _ \right) = \left( _, _ \right) = \frac{\lambda}{1 + \alpha_1 + \alpha_2} \)

4.3.2 Assumptions

- Consider Yuan and Bo Li [69] SIR epidemic model.
- Assume that the population consists of three types of individuals. They are susceptible, infective and recovered individuals.
- Let the non-linear incidence rate be \( \left( _, _ \right) = \frac{\lambda( _, _ )}{1 + \alpha_1( _, _ ) + \alpha_2( _, _ S )} \)
- Assuming that the infectious force takes the form

\[
\left( _, _ \right) = \left( _, _ \right) = \frac{\lambda}{1 + \alpha_1 + \alpha_2}
\]
**Modified SIR epidemic model with immigration:** The non-linear incidence rate is considered with immigration.

### 4.3.3 Notations

- $r$: Recruitment rate of the population
- $d$: Natural death rate of the population
- $\lambda$: The proportionality constant
- $\gamma$: Natural recovery rate of the infective individuals
- $\beta$: The rate at which recovered individuals lose immunity and return to the susceptible class
- $\alpha_1, \alpha_2$: The parameter measures of the psychological or inhibitory effect
- $\mu$: Increase of susceptible at a constant rate
- $E_0$: Disease-free equilibrium
- $T_0$: Capacity of the treatment

All other assumptions and notations in this section are as in model I of section 4.2

### 4.3.4 Mathematical Model II

The model is of the form

\[ \begin{align*}
\frac{dS}{dt} &= r - \mu S - \frac{\lambda S^2 + \alpha_1 S^2 + \alpha_2 S^2 + \beta S^2}{2 + \alpha_1 + \alpha_2} \\
\frac{dI}{dt} &= \frac{\lambda S^2 + \alpha_1 S^2 + \alpha_2 S^2 + \beta S^2}{2 + \alpha_1 + \alpha_2} - (\gamma + \beta) I \\
\frac{dR}{dt} &= -\gamma (E_0 + \beta) R
\end{align*} \]  

(4.17)

To find the endemic equilibria, set

\[ \begin{align*}
\frac{dS}{dt} &= 0 \\
\frac{dI}{dt} &= 0 \\
\frac{dR}{dt} &= 0
\end{align*} \]  

(4.18)
All the parameters are positive and have the similar biological meaning as in (4.17). Noticing that the system (4.18) is not well defined at the origin (0,0,0). It is redefined that when (, ,) = (0,0,0).

\[ - = + \mu, \quad (4.19) \]

With this assumption, it is easy that the first octant \[ R^+ = \{(S, I, R) / S, I, R \geq 0\} \] is positively invariant for system (4.18) is continuous and satisfies the condition in \( \mathbb{R}^+ \). The following result shows that the solutions of (4.18) is bounded, and hence, lie in a compact set and are continually for all positive time.

**Lemma: 4.3.1**

The plane \[ \mu \] in an invariant manifold of system (4.20), (4.17) is acting in the first octant.

**Proof**

Summing up the three equations in (4.20), (4.21) and (4.22) and denoting

\[ ( ) = ( ) + ( ) + ( ) \quad (4.20) \]

Then

\[ - = ( + \mu) - \quad (4.21) \]

It is clear that \[ ( ) = \frac{+ \mu}{\mu} \] is a solution of (4.20) and for any \( (0) \geq 0 \) the general solution of (4.21) is

\[ \frac{dN(t)}{dt} = (a + \mu) - dN(t) \]

\[ \frac{dN}{(a + \mu) - dN(t)} = dt \]

Now integrating this,
\[-\frac{1}{d}\log((a + \mu) - (x)) = 0\]

Put \( \frac{1}{d}\log(a + \mu - dN(t_0)) = t_0 + c \)

\[-\frac{1}{d}\log[a + \mu - dN(t_0)] - t_0 = c \]

\[-\frac{1}{d}\log[a + \mu - dN(t_0)] = t - \frac{1}{d}\log[a + \mu - dN(t_0)] - t_0 \]

\[-\frac{1}{d}\log[a + \mu - dN(t)] + \frac{1}{d}\log[a + \mu - dN(t_0)] = t - t_0 \]

\[\frac{1}{d}\log\left(\frac{a + \mu - dN(t)}{a + \mu - dN(t_0)}\right) = t_0 - t \]

\[\log\left(\frac{a + \mu - dN(t)}{a + \mu - dN(t_0)}\right) = d(t_0 - t) \]

\[\left(\frac{a + \mu - dN(t)}{a + \mu - dN(t_0)}\right) = [a + \mu - dN(t_0)]e^{-d(t - t_0)} \]

\[N(t) = \frac{1}{d}\left\{(a + \mu) - [a + \mu - dN(t_0)]e^{-d(t - t_0)}\right\} \quad (4.22) \]

\[N(t) = \frac{\frac{a + \mu}{d} - [a + \mu - dN(t_0)]e^{-d(t - t_0)}}{d} \]

\[\lim_{t \to \infty} N(t) = \frac{a + \mu}{d} \quad (4.23) \]

In the following, the existence of equilibria of system (4.18) is considered. For any values of parameters, these equations always have a disease-free equilibrium \( \mathbf{0} = (0, 0, 0) \). To find the positive equilibria, from the system (4.18) implies

\[= \left(\frac{\mu}{\theta} + \beta\right) \]
From equation (4.21)

\[ \lambda S^2 - (d + m)(S^2 + \alpha I S + \alpha I^2) = 0 \]

\[ S^2(\lambda - d - m) - \alpha_1 I(d + m) S - \alpha_2 I(d + m) = 0 \]

\[ \Rightarrow S = \frac{\alpha_1 I + I \sqrt{\alpha_1^2 + 4\alpha_2(d + m)} - \lambda}{2(d + m)} \]

Substituting \( R \) and \( S \) in (4.20), it gives

\[ (a + \mu) - d \left[ \frac{\alpha_1 I + I \sqrt{\alpha_1^2 + 4\alpha_2(d + m)} - \lambda}{2(d + m)} \right] - (d + m)I + \frac{\beta m}{d + \beta} I = 0 \]

\[ a + \mu - I \left[ \frac{d[\alpha_1 + \sqrt{\alpha_1^2 + 4\alpha_2(R_0 - 1)} - \lambda]}{2(R_0 - 1)} - (d + m) + \frac{\beta m}{d + \beta} \right] = 0 \]

\[ I = \frac{a + \mu}{d[\alpha_1 + \sqrt{\alpha_1^2 + 4\alpha_2(R_0 - 1)} - \lambda]} \left[ 2(R_0 - 1) - (d + m) + \frac{\beta m}{d + \beta} \right] \]

Define the basic reproductive number as follows:

\[ R_0 = \frac{\lambda}{\alpha_0} \quad (4.24) \]

i) If \( R_0 \leq 1 \), then there is no positive equilibrium;

ii) If \( R_0 > 1 \), then there is a unique positive equilibrium.

\[ I^* = \left( \frac{\alpha_1}{\alpha_0}, \frac{\lambda}{\alpha_0}, \ldots, \frac{\lambda}{\alpha_0} \right) \]

is called the endemic equilibrium and is given by

\[ I^* = \frac{\alpha_1 + \sqrt{\alpha_1^2 + 4\alpha_2(- \lambda)} - \lambda}{2(- \lambda - 1)} \]
In the following section, the properties of these equilibria and the global qualitative analysis of the equations (4.18) is discussed.

**4.3.5 Mathematical Analysis**

It is clear that limit of system is on the plane \( + + \frac{a + \mu}{d} \). Thus the reduced system is

\[
\frac{dI}{dt} = \frac{\lambda IS^2}{S^2 + \alpha IS + \alpha I^2}
\left( \frac{a + \mu}{d} - I - R \right) - (d + m)I \equiv P(I, R)
\]

\[
\frac{dR}{dt} = mI - (d + \beta)R \equiv Q(I, R)
\]

In order to study the disease free equilibrium \( \ast \) and the endemic \( \ast \), rescale the system (4.26) by

\[
\frac{\lambda}{d + \beta} = \frac{\lambda}{d + \beta} \equiv \left( \frac{d + \beta}{d + \beta} \right)
\]

\[
\frac{\lambda}{d + \beta} = \frac{\lambda}{d + \beta}
\]

\[
\frac{\lambda}{d + \beta} = \frac{\lambda}{d + \beta}
\]

\[
\frac{dI}{dz} = \frac{\lambda I}{S^2 + \alpha IS + \alpha I^2}
\left( \frac{\lambda(a + \mu)}{d(d + \beta)} - \frac{\lambda I}{d + \beta} - \frac{\lambda R}{d + \beta}\right) - \frac{\lambda I}{d + \beta} \left( \frac{d + m}{d + \beta} \right)
\]

\[
\frac{dx}{dz} = \frac{x}{1 + v_1x + v_2x^2}(K - x - y) - ux
\]

\[
\frac{dy}{dt} = \frac{\lambda}{d + \beta} \frac{dR}{dt}
\]
\[
\begin{align*}
\frac{dz}{dt} &= d + \beta \\
\frac{dy}{dz} &= \frac{\lambda}{d + \beta} (m I - (d + \beta) R) \\
&= \frac{\lambda I}{d + \beta} \left( \frac{m}{d + \beta} \right) - \frac{\lambda R}{d + \beta} \left( \frac{d + \beta}{d + \beta} \right)
\end{align*}
\]

\( (4.28) \)

where \( K = \frac{\lambda (a + \mu)}{d(d + \beta)}, \ u = \frac{d + m}{d + \beta}, \ v_1 = \frac{\alpha_1 (d + \beta)}{\lambda}, \)

\( v_2 = \frac{\alpha_2 (d + \beta)^2}{\lambda^2}, \ w = \frac{m}{d + \beta}. \)

**The Endemic Equilibrium** \( E^* = (\cdot, \cdot, \cdot). \)

An observation and simple calculation shows that \( E_0(0,0) \) is the disease free equilibrium and the unique positive equilibrium \( (\cdot, \cdot, \cdot) \) of the equation (4.31)-(4.32) is the endemic equilibrium \( E^* \) of the model system (4.21)-(4.22). It exists if \( \mu_2 < 0 \) and \( \lambda \) is a positive root of the equation

\[
\mu_2 + (1 + + 1) \lambda + ( - - K) = 0
\]

\( (4.29) \)

and \( \lambda = \lambda^* \)

\( (4.30) \)

Equation (4.33) gives,

\[
\lambda = - (1 + + 1) + \sqrt{(1 + + 1)^2 - 4(2K)}
\]

\( (4.31) \)

The Jacobian matrix for the equilibrium point \( E_0(0,0) \) is

\[
\begin{pmatrix}
- \mu_2 & 0 \\
0 & -1
\end{pmatrix}
\]

Therefore if \( \mu_2 > 0 \) the point \( E_0(0,0) \) is unstable saddle point, if \( \mu_2 = 0 \) then \( E_0(0,0) \) is **saddle node** and if \( \mu_2 < 0 \) the \( E_0(0,0) \) is
**stable node.** The condition \(- > 0\) is equivalent to \(R_0 > 1\) and the condition \(- < 0\) is equivalent to \(R_0 < 1\). When \(\ast \) exists, \(R_0 \) is **unstable**.

Now when \(- > 0\) or equivalently \(R_0 > 1\). To discuss the stability at the point \(E^\ast\).

The Jacobian matrix at \(E^\ast(\ast, \ast)\) is

\[
J_{1} = \begin{bmatrix}
\ast \left\{ \begin{array}{c}
\ast \ast^2 + \left( 1 + 2 \ast \ast \right) \ast - \left( 1 + 2 \ast \ast \right) - 1
\end{array} \right.

\end{bmatrix}
\]

\[
det(J_{1}) = -\ast \left\{ \begin{array}{c}
\ast \ast^2 + \left( 1 + 2 \ast \ast \right) \ast - \left( 1 + 2 \ast \ast \right) - 1
\end{array} \right.
\]

The sign of the \(\det(M_1)\) is the sign of the factor

\[
P_1 = -v_2(1 + w)x^\ast + K(v_1 + 2v_2x^\ast) + (1 + w)
\]

Using (4.30) and (4.31) in (4.33)

\[
J_{1} = \frac{\Delta_1(1 + \frac{1}{2})}{2} \left\{ \begin{array}{c}
(1 + \frac{1}{2}) + \frac{\Delta_1(1 + \frac{1}{2})}{2}
\end{array} \right.
\]

Note that

\[
\left\{ \begin{array}{c}
(1 + \frac{1}{2}) + \frac{\Delta_1(1 + \frac{1}{2})}{2}
\end{array} \right. - \Delta_1^2 > 0
\]

\[
\left\{ \begin{array}{c}
(1 + \frac{1}{2}) + \frac{\Delta_1(1 + \frac{1}{2})}{2} - \Delta_1
\end{array} \right. > 0
\]

It means \(P_1 > 0\), and hence \(\det(M_1)\) is positive for any set of values of parameters. Now

\[
\text{Trace}(M_1) = \frac{x^\ast \left\{ v_2x^2 + \left( v_1 + 2v_2x^\ast \right)wx^\ast - K \left( v_1 + 2v_2x^\ast \right) - 1 \right\}}{(1 + v_1x^\ast + v_2x^2)^2} - 1
\]

Solving this, the sign of the \(\text{trace}(M_1)\) is determined by the sign of
Using again equation (4.29) in (4.33), it gives
\[ P_2 = P_3 x^* - P_4 \]
\[ P_3 = (1 + w + uv_1)[(1 + w)^2 + u(1 + w)(1 + 2w + uv_1)] + 2uv_2K(1 + w) \]
\[ + u^2v_2K(1 + 2w) + 2u^2v_2(1 + w)(u - K) + u^3v_1v_2K \]
\[ P_4 = (u - K)[(1 + w)^2 + u(1 + w)(1 + 2w + uv_1)] \]
\[ + uv_2[(u - K)^2 + 2u(1 + K)(u - K) + u^2} \]

Therefore both \( P_3 \) and \( P_4 \) are positive in case \( K > u \). When the point \((\_*, \_*, \_*)\) exists, it is locally stable if \( \_* < \frac{4}{3} \).

### 4.3.8 NUMERICAL RESULTS

i) **Simulation and Discussions of Model II**

Let \( \lambda = 3, \mu = 0.3, \beta = 0.2, \gamma = -1, \sigma = 1.5, \beta = 0.5, \alpha_1 = 2, \alpha_2 = 3 \)

Hence the basic reproductive number \( R_0 = 0.26 < 1 \), there is no positive equilibrium \( \_* = (\_*, \_*, \_*) \). In this case, the disease dies out and the only disease free equilibrium \((0,0)\) is a saddle node.

Using the above values, then \( \lambda = 1.67, \mu = 0.44 \). By rescaling the system it implies that \( \_* < 0 \) when \( \_* \) exists and \( \_\_ \) is unstable.

Let \( \lambda = 2, \mu = 0.3, \beta = 5, \gamma = 2, \sigma = 0.5, \beta = 0.3 \)

Then \( \_\_ = 2 > 1 \), then there is a unique positive equilibrium. In this case, the disease invades the population.

Using the above values, then \( \lambda = 1.08, \mu = 2.5 \). By rescaling the system it implies that \( \_* > 0 \). In this case, the disease free equilibrium \((0,0)\) is an unstable saddle point. Consider

\[ \lambda = 2, \mu = 0.3, \beta = 5, \gamma = 2, \sigma = 0.5, \beta = 0.3, \alpha_1 = 0.2, \alpha_2 = 0.4 \]
By rescaling the system, it gives \( u - K < 1 \) hence there exists unique positive equilibrium \( * = -1.17 \) and \( * = -0.25 \). Using the above parameters \( \frac{P_1}{P_3} = 0.65 \) and therefore the sufficient condition for stability \( \frac{4}{3} \) is satisfied. Hence the point is locally stable.

**ii) Numerical Table for Model II**

<table>
<thead>
<tr>
<th>( \mu )</th>
<th>( a + \mu )</th>
<th>( S^* )</th>
<th>( I^* )</th>
<th>( R^* )</th>
</tr>
</thead>
<tbody>
<tr>
<td>0.1</td>
<td>1.1</td>
<td>10.1800</td>
<td>1.1096</td>
<td>0.0792</td>
</tr>
<tr>
<td>0.2</td>
<td>1.2</td>
<td>10.2140</td>
<td>1.1121</td>
<td>0.1568</td>
</tr>
<tr>
<td>0.3</td>
<td>1.3</td>
<td>10.2522</td>
<td>1.1149</td>
<td>0.2333</td>
</tr>
<tr>
<td>0.4</td>
<td>1.4</td>
<td>10.2946</td>
<td>1.1180</td>
<td>0.3088</td>
</tr>
<tr>
<td>0.5</td>
<td>1.5</td>
<td>10.3398</td>
<td>1.1213</td>
<td>0.3835</td>
</tr>
<tr>
<td>0.6</td>
<td>1.6</td>
<td>10.3892</td>
<td>1.1249</td>
<td>0.4576</td>
</tr>
<tr>
<td>0.7</td>
<td>1.7</td>
<td>10.4457</td>
<td>1.1290</td>
<td>0.5313</td>
</tr>
<tr>
<td>0.8</td>
<td>1.8</td>
<td>10.5078</td>
<td>1.1335</td>
<td>0.6045</td>
</tr>
<tr>
<td>0.9</td>
<td>1.9</td>
<td>10.5771</td>
<td>1.1385</td>
<td>0.6774</td>
</tr>
<tr>
<td>1.0</td>
<td>2.0</td>
<td>10.6564</td>
<td>1.1442</td>
<td>0.7499</td>
</tr>
<tr>
<td>1.1</td>
<td>2.1</td>
<td>10.7459</td>
<td>1.1506</td>
<td>0.8222</td>
</tr>
<tr>
<td>1.2</td>
<td>2.2</td>
<td>10.8498</td>
<td>1.1580</td>
<td>0.8944</td>
</tr>
<tr>
<td>1.3</td>
<td>2.3</td>
<td>10.9698</td>
<td>1.1665</td>
<td>0.9662</td>
</tr>
<tr>
<td>1.4</td>
<td>2.4</td>
<td>11.1105</td>
<td>1.1764</td>
<td>1.0379</td>
</tr>
<tr>
<td>1.5</td>
<td>2.5</td>
<td>11.2795</td>
<td>1.1882</td>
<td>1.1096</td>
</tr>
</tbody>
</table>

**Interpretation:**

From table 4.3:1, it is found that when \( \alpha_1 \) and \( \alpha_2 \) kept constant and \( \mu \) varies from 0.1 to 1.5, the endemic equilibrium \( * = ( * , * , * ) \) monotonically increases for the increasing value of \( \mu \).
Inference:

When the immigration increases i.e., the susceptible rate increases, then the disease will be in the endemic stage. At this stage, treatment rate should be kept constant to increase the recovered rate.

Table 4.3:2

(Effects of $\alpha_1$ and $\alpha_2$ on $S^*, I^*, R^*$)

\[ a = 1, d = 1, \lambda = 2, \beta = 0.5, m = 0.5, R_0 = 2.0 \]

$\alpha_1$ varies from 0.1 to 15 and $\alpha_2$ varies from 1 to 15

<table>
<thead>
<tr>
<th>$\alpha_1$</th>
<th>$\alpha_2$</th>
<th>$S^*$</th>
<th>$I^*$</th>
<th>$R^*$</th>
</tr>
</thead>
<tbody>
<tr>
<td>0.1</td>
<td>1.0</td>
<td>1.0905</td>
<td>0.2998</td>
<td>0.0993</td>
</tr>
<tr>
<td>0.5</td>
<td>1.5</td>
<td>1.2978</td>
<td>0.3319</td>
<td>0.1106</td>
</tr>
<tr>
<td>1.0</td>
<td>2.0</td>
<td>1.6121</td>
<td>0.3739</td>
<td>0.1246</td>
</tr>
<tr>
<td>1.5</td>
<td>2.5</td>
<td>1.9470</td>
<td>0.3991</td>
<td>0.1330</td>
</tr>
<tr>
<td>2.0</td>
<td>2.5</td>
<td>2.5555</td>
<td>0.4991</td>
<td>0.1664</td>
</tr>
<tr>
<td>2.5</td>
<td>3.5</td>
<td>2.6430</td>
<td>0.4279</td>
<td>0.1426</td>
</tr>
<tr>
<td>3.5</td>
<td>4.0</td>
<td>3.6522</td>
<td>0.4994</td>
<td>0.1665</td>
</tr>
<tr>
<td>4.0</td>
<td>5.0</td>
<td>3.7135</td>
<td>0.4496</td>
<td>0.1499</td>
</tr>
<tr>
<td>5.0</td>
<td>6.0</td>
<td>4.4345</td>
<td>0.4580</td>
<td>0.1527</td>
</tr>
<tr>
<td>6.0</td>
<td>8.0</td>
<td>4.6355</td>
<td>0.4660</td>
<td>0.1353</td>
</tr>
<tr>
<td>10.0</td>
<td>10.5</td>
<td>8.4051</td>
<td>0.4998</td>
<td>0.1666</td>
</tr>
<tr>
<td>11.0</td>
<td>12.0</td>
<td>8.7963</td>
<td>0.4790</td>
<td>0.1597</td>
</tr>
<tr>
<td>12.5</td>
<td>13.5</td>
<td>9.6904</td>
<td>0.4813</td>
<td>0.1604</td>
</tr>
<tr>
<td>13.0</td>
<td>14.0</td>
<td>10.2552</td>
<td>0.4820</td>
<td>0.1607</td>
</tr>
<tr>
<td>14.0</td>
<td>14.5</td>
<td>11.3301</td>
<td>0.4998</td>
<td>0.1666</td>
</tr>
<tr>
<td>15.0</td>
<td>15.0</td>
<td>12.4309</td>
<td>0.5165</td>
<td>0.1722</td>
</tr>
</tbody>
</table>

Interpretation:

From table 4.3:2, the following is obtained.

1) When the parametric measures $\alpha_1$ and $\alpha_2$ increases, the susceptible rate $S^*$ will also increase.
2) The infective rate and the removal rate both increases when the parametric measures $\alpha_1$ and $\alpha_2$ increases.

**Inference:**

It means that when the parametric measures $\alpha_1$ and $\alpha_2$ increases, the disease will grow or invade the population. So that the infective rate and the removal rate both are increased.

### 4.4 CONCLUSION

This chapter is constructed with two epidemic models, they are i) SIR epidemic model with immigration using nonlinear incidence rate and ii) Modified SIR epidemic model with immigration using nonlinear incidence rate. In these models, the basic reproductive number $R_0$ is used to analyze the stability point of the disease. If $R_0 \leq 1$, then the disease eventually dies out from the population. Because each infected cannot guarantee transmission of the infectious agent to one susceptible. Therefore the disease-free equilibrium is asymptotically stable and the population cannot be invaded by the disease. On the other hand if $R_0 > 1$, then each infected individual produces the population. Therefore the disease-free equilibrium is unstable and invasion is always possible.

In model I, the disease cannot grow when the basic reproduction number $R_0 \leq 1$. Then there exists no positive equilibrium and the disease free equilibrium is globally stable. The disease can invade the population when the reproduction number $R_0 > 1$ and the unique endemic equilibrium are globally stable. The local and global stability analysis of the disease-free and the endemic equilibrium have been carried out using different assumptions and contact rates. From the numerical table 4.2:1, it is noted that $\star, \star, \star$ increases when the immigration increases. The equilibrium points $(\star, \star)$ exists and it is locally stable since $\star < \frac{4}{3}$.
Model II is analyzed through new incidence rate with two parametric measures $\alpha_1$ and $\alpha_2$. In this model, the table 4.3:1 predicts that when $\alpha_1$ and $\alpha_2$ kept constant and $\mu$ increases, the endemic equilibrium $\ast = (\ast, \ast, \ast)$ monotonically increases for the increasing value of $\mu$. From table 4.3:2, it infer that the susceptible rate, infective rate and the removal rate increases when the parametric measures $\alpha_1$ and $\alpha_2$ increases.