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Stability and Numerical Simulation of SCIR Epidemic Model for COVID-19 Transmission

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Abstract

We present a SCIR epidemic model for the spread of COVID-19. The equilibrium points of the system are founded. The Stability of equilibrium points for the model is proved. Finally, a numerical simulation based on real data to predict the transmission of COVID-19 will be presented.

Keywords: COVID-19, Equilibrium point, Basic reproduction number, Numerical simulation
AMS Mathematical Subject Classification [2010]: 13D45, 39B42

1 Introduction

In late 2019, a new virus called coronavirus went viral at an unprecedented rate worldwide ([1]). Its origin was traced to the food market in Wuhan, China. The virus, officially known as SARS-CoV-2, has been responsible for more than 500 million hospitalized patients and the deaths of more than 6 million worldwide ([2]). The symptoms of this virus are various and appear with symptoms such as cough, shortness of breath, weakness, lethargy, fever, chills, fatigue, muscle aches, sore throat, etc ([3]). The virus is common between humans and animals. An infected person can transmit the virus to another person through inhaling particles ([4]). The disease is more common in the elderly and people with chronic diseases such as cancer, cardiovascular disease, kidney, lung, immune deficiency, and diabetes ([5, 6, 7, 8]). There is currently no definitive cure for the virus, and a variety of vaccines are used to reduce mortality and serious injury in patients and other non-infected individuals ([9, 10]). Complications of this disease can be acute respiratory distress syndrome (ARDS), blood clots, cardiac arrhythmias, heart shock, kidney damage or kidney failure, heart damage and eventually death ([11, 12, 13, 14, 15, 17]).

Epidemiological modeling of infectious disease using differential equations to investigate the transmission dynamics of epidemics is widely studied ([18, 19]). Thematic modeling of epidemic diseases shows that nonlinear dynamic equations can provide important insights into disease transmission dynamics or dynamic diffusion behaviors. The worldwide prevalence of Covid-19 has attracted the attention of those interested in mathematical modeling of this contagious disease by developing real nonlinear mathematical models that are driven by data to better understand the dynamics of epidemic transmission. (see, for example, [21, 22]).

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In viral epidemics, mathematical models are very important for predicting virus transmission by considering its behavior in different regions. Various mathematical models such as SIR, SEIAR, SIRS, SCIR, SIQR are used to study the prevalence of the diseases. According to the information published about COVID-19 by the World Health Organization, there are healthy people who are carriers and can transmit the disease microorganisms without any signs of infection. There are also people in this category who may get sick again after recovery. For this reason, we consider the following SCIR model of COVID-19 for $t > 0$ in which susceptible, carrier, symptomatic and recovered compartments are shown by S,C,I and R, respectively.

$$\begin{cases} \dot{S}(t) = \Lambda - \beta S(I + qC) - \mu S + \rho R, \\ \dot{C}(t) = \beta S(I + qC) - (\eta + \gamma + \mu)C, \\ \dot{I}(t) = \eta C - (\alpha + \mu + \delta)I, \\ \dot{R}(t) = \alpha I + \gamma C - (\mu + \rho)R, \end{cases} \tag{1}$$

where the initial conditions are $S(0) = S_0 > 0$, $C(0) = C_0 > 0$, $I(0) = I_0 > 0$, $R(0) = R_0 \geq 0$.

Parameters	The biological interpretation
Λ	the birth rate
μ	the death rate of people
β	the transmission rate of infection
γ	the recovery rate of the asymptomatic individuals
α	the rate of recovery of infected people
δ	the mortality rate due to the disease
η	the per capita rate of becoming infectious
ρ	improved susceptibility rate

This paper is organized as follows. In the next section, some basic results such as positivity, boundedness of solutions will be given. Section 3 deals with the existence of equilibrium points of the system and global stability of equilibria. Finally, numerical analysis of the model will be performed.

2 Basic Results

In this section, the positivity and boundedness of solutions of (1) will be established. Since model (1) represents the population dynamic, the individual numbers must remain positive and bounded. In the following the positivity and boundedness of population will be proven.

Proposition 2.1. *All solutions of system* (1) *with non-negative initial conditions exist for all* $t > 0$ *and remain bounded and non-negative.*

Proof. The right hand side functions of (1) are continuous, smooth and Lipschitz on $[0, T], T > 0$. Therefore, from Picard-Lindelöf theorem there is a unique solution to system (1) with the initial conditions.
To prove the positivity of solutions of (1) define

$$\mathbb{R}^4_+ = \{(S, C, I, R) \mid \ S \geq 0, \quad C \geq 0, \quad I \geq 0, \quad R \geq 0\}.$$

In fact, for any solution $(S(t), C(t), I(t), R(t)) \in \mathbb{R}^4_+$ we have

$$\dot{S} \mid_{S=0} = \lambda + \rho R > 0, \quad \dot{C} \mid_{C=0} = \beta SI \geq 0, \quad \dot{I} \mid_{I=0} = \eta C \geq 0, \quad \dot{R} \mid_{R=0} = \alpha I + \gamma C \geq 0.$$

Due to well known theorem by Nagumo [16], any solution $(S(t), C(t), I(t), R(t)) \in \mathbb{R}^4_+$ of (1), with initial point in $\mathbb{R}^4_+$, stays in $\mathbb{R}^4_+$. To prove the boundedness of solutions of (1) Let

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

Then,

$$\dot{N(t)} = \Lambda - \mu N(t) - \delta I(t) \leq \Lambda - \mu N(t).$$

Therefore

$$N(t) \leq \frac{\Lambda}{\mu} + e^{-\mu t}\left(N(0) - \frac{\Lambda}{\mu}\right),$$

where $N(0)$ is the initial population size. Thus, if $N(0) \leq \dfrac{\Lambda}{\mu}$, then $N(t) \leq \dfrac{\Lambda}{\mu}$ for $t > 0$. Consequently, the closed set $\Sigma = \{(S, C, I, R) \in \mathbb{R}^4_+ \mid N \leq \dfrac{\Lambda}{\mu}\}$ is positively invariant with respect to the model. □

3 Stability

In this section, the global stability of all steady states will be established by constructing some suitable Lyapunov functions and LaSalle's invariance principle. In the following, we consider the equilibria of (1) and introduce the basic reproduction number $\mathbf{R_0}$. In general (1) has two equilibrium points $\mathbf{E_0}$ and $\mathbf{E_1}$. In the absence of disease, there always exists an disease-free equilibrium $\mathbf{E_0} = (\mathbf{S_0}, 0, 0, 0) = (\frac{\Lambda}{\mu}, 0, 0, 0)$.

The procedures described in ([20]) is followed to calculate the basic reproduction number of the model. To find $\mathbf{R_0}$, first consider the system as follows:

$$\dot{\Psi}(t) = \mathcal{F}(\Psi(t)) - \mathcal{V}(\Psi(t)),$$

where

$$\mathcal{F}(\Psi(t)) = \begin{bmatrix} \beta S(t)(I(t) + qC) \\ \eta C \end{bmatrix}, \qquad \mathcal{V}(\Psi(t)) = \begin{bmatrix} (\eta + \gamma + \mu)C(t) \\ (\alpha + \mu + \delta)I(t) \end{bmatrix}.$$

At $\mathbf{E_0}$, the Jacobian matrices for $\mathcal{F}$ and $\mathcal{V}$ are obtained as follows:

$$F(\mathbf{E_0}) = \begin{bmatrix} \beta S q & \beta S \\ \eta & 0 \end{bmatrix}, \qquad V(\mathbf{E_0}) = \begin{bmatrix} (\eta + \gamma + \mu) & 0 \\ 0 & (\alpha + \mu + \delta) \end{bmatrix}.$$

The basic reproduction number is the spectral radius of matrix FV^{-1}, which is as

$$\mathbf{R_0} = \frac{\beta q \mathbf{S_0}}{(\eta + \gamma + \mu)} + \frac{\beta \eta \mathbf{S_0}}{(\eta + \gamma + \mu)(\alpha + \mu + \delta)} = \mathbf{R_{01}} + \mathbf{R_{02}},$$

and it is an epidemiologic metric used to describe the contagiousness or transmissibility of infectious agents.

To determine the equilibrium points of system (1), we set the equations of the system equal to zero. By solving the algebraic equations, we obtain equilibrium points of system (1). The disease-free equilibrium

point is obtained as $\mathbf{E_0} = (\frac{\Lambda}{\mu}, 0, 0, 0)$. In addition, if $\mathbf{R_0} > 1$, then system (1) has a positive endemic equilibrium point $\mathbf{E_1} = (\mathbf{S_1}, \mathbf{C_1}, \mathbf{I_1}, \mathbf{R_1})$ so that

$$\begin{aligned}
\mathbf{S_1} &= \frac{(\alpha+\mu+\delta)(\eta+\gamma+\mu)}{\beta\eta+\beta q(\alpha+\mu+\delta)},\\
\mathbf{C_1} &= \frac{(\alpha+\mu+\delta)I}{\eta},\\
\mathbf{R_1} &= \frac{\alpha I}{(\mu+\rho)} + \frac{\gamma(\alpha+\mu+\delta)I}{(\mu+\rho)\eta},\\
\mathbf{I_1} &= \frac{\mu(\eta+\gamma+\mu)(\alpha+\mu+\delta)(\mu+\rho)\eta}{AB}[\mathbf{R0}-1],
\end{aligned}$$

where

$$\begin{aligned}
A &= [\eta\beta + \beta q(\alpha+\mu+\delta)],\\
B &= [(\eta+\gamma+\mu)(\alpha+\mu+\delta)(\mu+\rho) + \rho\alpha\eta + \rho\gamma(\alpha+\mu+\delta)].
\end{aligned}$$

The Jacobian matrix of system (1) is obtained as follows:

$$\mathbf{J} = \begin{bmatrix} -\beta(I+qC)-\mu & -\beta Sq & -\beta S & \rho \\ \beta(I+qC) & \beta Sq-(\eta+\gamma+\mu) & \beta S & 0 \\ 0 & \eta & -(\alpha+\mu+\delta) & 0 \\ 0 & \gamma & \alpha & -(\mu+\rho) \end{bmatrix}.$$

Therefore, the Jacobian matrix of system at $\mathbf{E_0}$ is as

$$\mathbf{J}(\mathbf{E_0}) = \begin{bmatrix} -\mu & -\beta\mathbf{S_0}q & -\beta\mathbf{S_0} & \rho \\ 0 & \beta\mathbf{S_0}q-(\eta+\gamma+\mu) & \beta\mathbf{S_0} & 0 \\ 0 & \eta & -(\alpha+\mu+\delta) & 0 \\ 0 & \gamma & \alpha & -(\mu+\rho) \end{bmatrix}.$$

where $\mathbf{S_0} = \frac{\Lambda}{\mu}$.

Theorem 3.1. *The equilibrium point* $\mathbf{E_0}$ *of system* (1) *is locally asymptotically stable if* $\mathbf{R_0} < 1$ *and* $\mathbf{E_0}$ *is unstable if* $\mathbf{R_0} > 1$.

Proof. Consider $|\mathbf{J}-\lambda I| = 0$ and expand it in terms of the first column. This will give an eigenvalue $\lambda_1 = -\mu$. Then, expanding the remaining matrix around the last column, will give an eigenvalue $\lambda_2 = -(\mu+\rho)$. The remaining two eigenvalues are the eigenvalues of the following matrix:

$$\mathbf{J_1} = \begin{bmatrix} \beta\mathbf{S_0}q-(\eta+\gamma+\mu) & \beta\mathbf{S_0} \\ \eta & -(\alpha+\mu+\delta) \end{bmatrix}.$$

Now we can apply the usual conditions that guarantee that the eigenvalues of $\mathbf{J_1}$ have negative real part. In particular, we want $\mathbf{TrJ_1} < 0$ and $\mathbf{DetJ_1} > 0$. The second inequality gives $-[\beta\mathbf{S_0}q-(\eta+\gamma+\mu)](\alpha+\mu+\delta) - \eta\beta\mathbf{S_0} > 0$. This condition gives a reproduction number in the form

$$\mathbf{R_0} = \frac{\beta\mathbf{S_0}q}{(\eta+\gamma+\mu)} + \frac{\eta\beta\mathbf{S_0}}{(\eta+\gamma+\mu)(\alpha+\mu+\delta)}.$$

We notice that the condition $\mathbf{R_0} < 1$ implies both $\mathbf{TrJ_1} < 0$ and $\mathbf{DetJ_1} > 0$. Therefore, if $\mathbf{R_0} < 1$, then the disease-free equilibrium is locally asymptotically stable. If $\mathbf{R_0} > 1$, then the disease-free is unstable. □

Theorem 3.2. *The equilibrium point* $\mathbf{E_1}$ *of system* (1) *is always asymptotically stable.*

Proof. Consider $|\mathbf{J} - \lambda I| = 0$ and expand it in terms of the first column. This will give an eigenvalue $\lambda_1 = -(\mu + \rho)$. Then, we can expand the remaining matrix around the last column which will give another eigenvalue $\lambda_2 = -(\alpha + \mu + \delta)$. The remaining two eigenvalues are the eigenvalues of the following matrix:

$$\mathbf{J_2} = \begin{bmatrix} -\beta(\mathbf{I_1} + q\mathbf{C_1}) - \mu & -\beta\mathbf{S_1}q \\ \beta(\mathbf{I_1} + q\mathbf{C_1}) & \beta\mathbf{S_1}q - (\eta + \gamma + \mu) \end{bmatrix}.$$

In particular, we want $\mathbf{TrJ_2} < 0$ and $\mathbf{DetJ_2} > 0$. For matrix $\mathbf{J_2}$, it can be obtained that

$$\begin{aligned} \mathbf{DetJ_2} &= (\beta\mathbf{I_1} + \mu)(\eta + \gamma + \mu) > 0, \\ \mathbf{TrJ_2} &= -\beta\mathbf{I_1}\left(1 + \frac{\mathbf{S_1}}{\mathbf{C_1}}\right) - \mu < 0. \end{aligned}$$

Therefore, it can be concluded that the endemic equilibrium point $\mathbf{E_1}$ of system (1) is always asymptotically stable. □

In the following, the global stability of disease-free equilibrium $\mathbf{E_0}$ will be shown.

Theorem 3.3. *The equilibrium point* $\mathbf{E_0}$ *of system* (1) *is globally asymptotically stable if* $\mathbf{R_{01}} < \frac{1}{2}$ *and* $\mathbf{R_{02}} < \frac{1}{2}$.

Proof. Consider the following Lyapunov function:

$$\mathbf{V_0}(S, C, I, R) = S - \mathbf{S_0} - \mathbf{S_0} \ln\left(\frac{S}{\mathbf{S_0}}\right) + C + \mathbf{A_1}I + \mathbf{A_2}R,$$

where,

$$\begin{aligned} \mathbf{A_1} &= \frac{2\beta\mathbf{S_0} + (\alpha + \delta + \mu)(\eta + \gamma + \mu)}{\eta(\eta + \alpha + \mu + \delta)}, \\ \mathbf{A_2} &= \frac{(\alpha + \delta + \mu)(\eta + \gamma + \mu)[1 - 2\mathbf{R_{02}}]}{2\gamma(\eta + \alpha + \mu + \delta)}. \end{aligned}$$

By computing the time derivative of $\mathbf{V_0}$ along the solution of (1) and using equilibrium conditions, we have:

$$\begin{aligned} \dot{\mathbf{V}}_\mathbf{0} &= \left(1 - \frac{\mathbf{S_0}}{S}\right)\dot{S} + \dot{C} + \mathbf{A_1}\dot{I} + \mathbf{A_2}\dot{R} \\ &= \left(1 - \frac{\mathbf{S_0}}{S}\right)[\Lambda - \beta S(I + qC) - \mu S + \rho R] + \beta S(I + qC) - (\eta + \gamma + \mu)C \\ &\quad + \mathbf{A_1}[\eta C - (\alpha + \mu + \delta)I] + \mathbf{A_2}[\alpha I + \gamma C - (\mu + \rho)R] \\ &= \Lambda\left(2 - \frac{\mathbf{S_0}}{S} - \frac{S}{\mathbf{S_0}}\right) + \rho\left(\frac{S - \mathbf{S_0}}{S}\right) + I\left[\frac{\beta\eta\mathbf{S_0}}{(\alpha + \delta + \mu)(\eta + \gamma + \mu)} - \frac{1}{2}\right] + C\left[\frac{2\beta q\mathbf{S_0}}{\eta + \gamma + \mu} - 1\right] \\ &= \Lambda\left(2 - \frac{\mathbf{S_0}}{S} - \frac{S}{\mathbf{S_0}}\right) + \rho\left(\frac{S - \mathbf{S_0}}{S}\right) + I\left[\mathbf{R_{01}} - \frac{1}{2}\right] + C\left[2\mathbf{R_{02}} - 1\right] \end{aligned}$$

We have $S - \mathbf{S_0} \leq 0$, because $S \leq \mathbf{S_0}$. On the other hand, since the arithmetic mean is greater than or equal to the geometric mean, it is easy to check that

$$2 - \frac{\mathbf{S_0}}{S} - \frac{S}{\mathbf{S_0}} \leq 0.$$

Since $\mathbf{R_{01}} < \frac{1}{2}$ and $\mathbf{R_{02}} < \frac{1}{2}$, it can be concluded that $\dot{\mathbf{V}}_\mathbf{0} \leq 0$ for all $S, C, I, R > 0$. Hence, the disease-free equilibrium $\mathbf{E_0}$ is stable. On the other hand, $\dot{\mathbf{V}}_\mathbf{0} = 0$ if and only if $S = \mathbf{S_0}$, $C = 0$, $I = 0$ and $R = 0$. Let Ω_0 be the largest invariant set in

$$\Psi_0 = \{(S, C, I, R) \mid \dot{\mathbf{V}}_\mathbf{0} = 0\} = \{\mathbf{E_0}\}.$$

We have that $\Omega_0 = \{\mathbf{E_0}\}$. The global asymptotic stability of $\mathbf{E_0}$ follows from LaSalle's invariance principle. □

4 Numerical Simulation

In this section by using real data and FDE12 method in MATLAB, numerical simulation of system (1) will be given. For simulation, the value of the parameters should be first determined. The birth rate for the world in 2022 was 17.668 births per 1000 individuals, and the death rate was 7.678 per 1000 individuals. The worlds population on 15 June was $N = 7914981120$, so $\Lambda = \frac{n \times N}{365} = 383128.455$ and $\mu = \frac{7.678}{365 \times 1000}$. Since $N(0) = S(0) + C(0) + I(0) + R(0)$ and on 15 June $I(0) = 15315220$, then we can suppose $C(0) = 45000000$, $R(0) = 0$ and $S(0) = 7869665900$. In addition, we consider the existent infection cases in the world in the period of time , 15 June to 4 August 2022, so that any part is three day. The parameters values of model are available in Table 1. In this simulation, the equilibrium point is

$$\mathbf{E_1} = (7.1606 \times 10^9, 2.1214 \times 10^7, 6.6886 \times 10^6, 2.7472 \times 10^8).$$

The real data for infected cases, as well as the results of model (1) can be seen in Fig. 1. Also, in Figures 2,3,4 and 5, it is predicted how each of the classes S, C, I and R will change.

Table 1: Parameter Values used for simulation

Parameter	Value	Ref
Λ	384409.48	Estimated
μ	2.10356×10^{-5}	Estimated
β	9.08×10^{-11}	Fitted
q	0.1	Fitted
ρ	0.02	Fitted
η	0.14	Fitted
γ	0.13	Fitted
α	0.41	Fitted
δ	0.034	[19]

Acknowledgment

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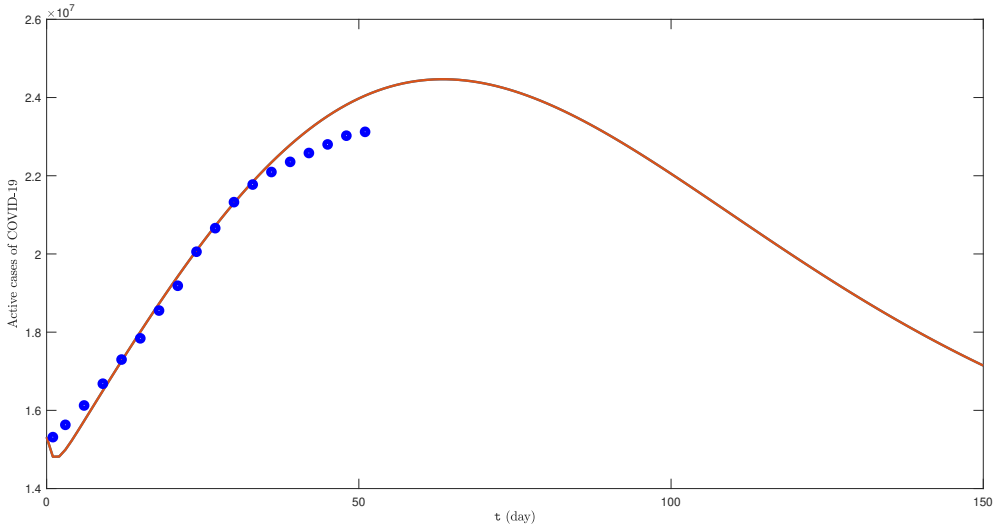

Figure 1: Active cases of COVID-19 on periode

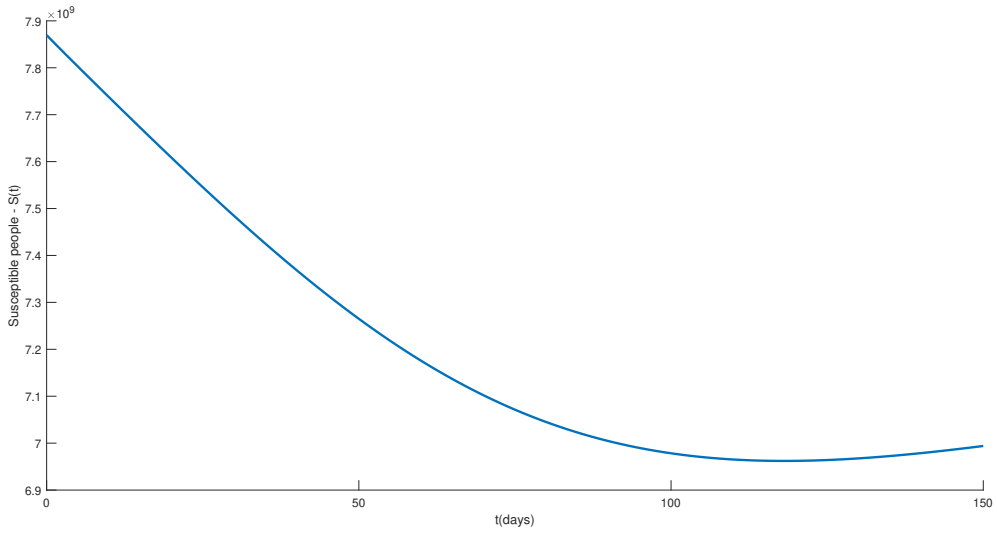

Figure 2: Dynamics of Susceptible People

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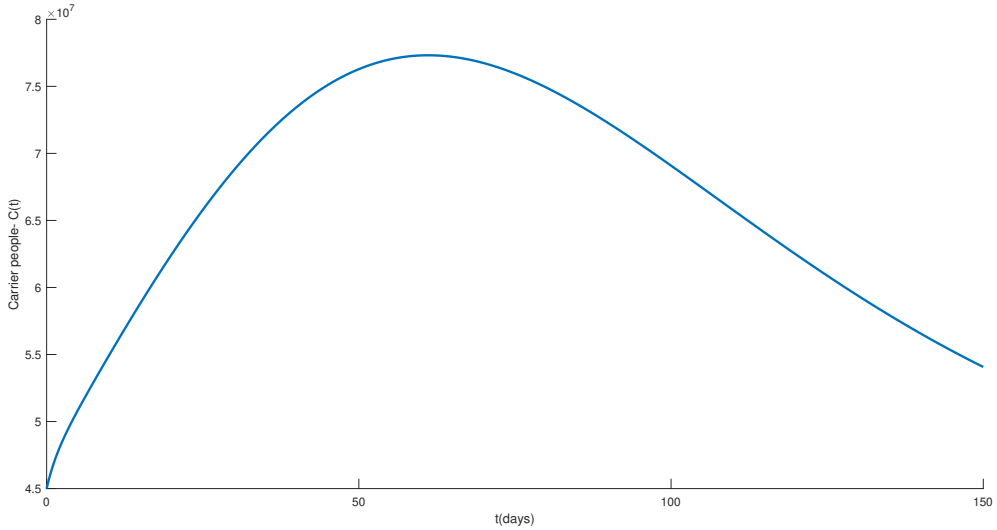

Figure 3: Dynamics of Carrier People

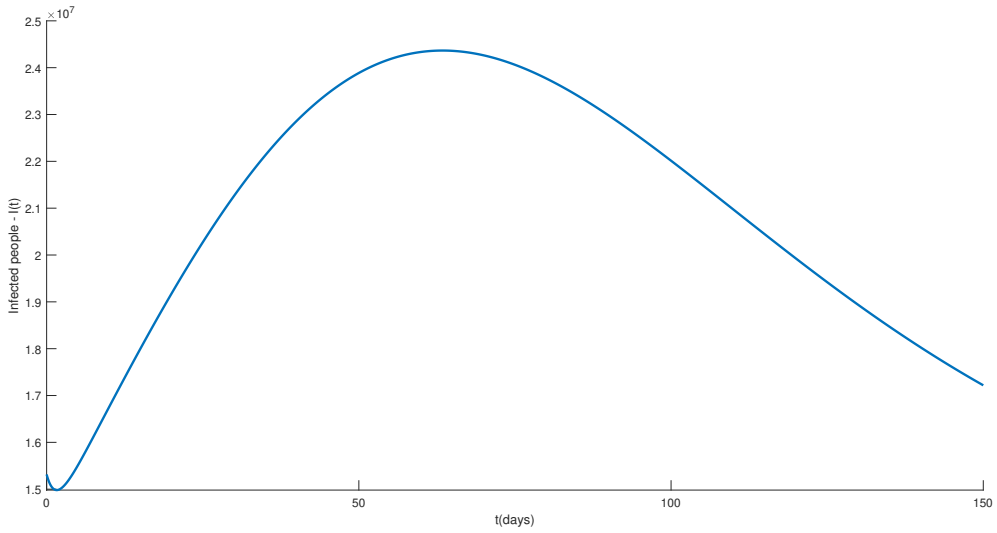

Figure 4: Dynamic of Infected People

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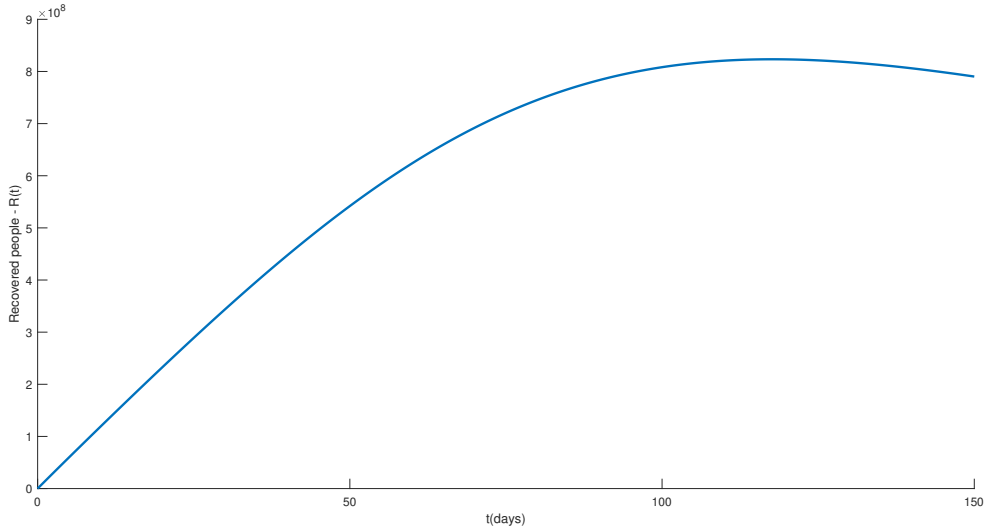

Figure 5: Dynamic of Recovered People

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