Proceedings of Science and Mathematics
Faculty of Science, Universiti Teknologi Malaysia
Vol. 3, 2021, page 101-110

A Mathematical Model of Influenza using SITR Model Approach

Nurul Hidayah Usman [a], Fuaada Mohd Siam [b]*
[a,b]Department of Mathematical Sciences, Faculty of Science, Universiti Teknologi Malaysia
81310 Johor Bahru, Johor, Malaysia.
*Corresponding author: [2]fuaada@utm.my

Abstract
Influenza is one of the common infectious diseases that can affect people of all ages. A non-linear mathematical model is used to study the transmission dynamics of influenza using the Susceptible-Infected-Treatment-Recovered (SITR) model. The SITR model is developed based on the Ordinary Differential Equations (ODEs) system. The stability of the model is determined using the Routh-Hurwitz Criterion Method, and the equilibrium point is measured at a disease-free equilibrium point. To identify if the disease is extinct or widespread in the population, the basic reproduction number, R_0, is generated and analyzed using Next-Generation Matrix Method.
Keywords: Influenza; Disease-free equilibrium point; Basic reproduction number; SITR model; Routh-Hurwitz Criterion Method; Next-Generation Matrix Method.

1 Introduction

Influenza is an infectious disease that spreads within the population. Influenza is a respiratory infectious disease caused by the influenza virus, commonly known as flu [1]. It can spread from person to person through the air from the respiratory tract of an infected person when they talk, cough, or sneeze. Influenza symptoms include a high fever, muscle pain, fatigue, runny nose, sore throat, coughing, and nausea [2]. It can also be transmitted by touching a surface with respiratory droplets with influenza viruses and then touching the nose, mouth, or possibly eyes. Children under five years of age, adults over 65 years of age, pregnant mothers, people with chronic conditions such as asthma, heart disease, kidney disease, diabetes, and individual with weaker immune systems are at high risk for influenza [3]. However, most influenza-related deaths occur in the elderly (65 years of age and older) and in those with underlying cardiovascular and respiratory comorbidities. Although the influenza virus is commonly compared to a common cold, it can also result in more severe disease or death. During the 2018–2019 influenza season, the Centers for Disease Control and Prevention (CDC) estimated that influenza caused more than 35.5 million illnesses, 16.5 million medical visits, 490,600 hospitalizations, and 34,200 fatalities [4]. The Director-General of Health issued a press article on 21st January 2020 to inform the public of the ongoing management of influenza cases. It has been reported that 186 cases of influenza until 18th January 2020 in Malaysia compared to 11 cases recorded in the previous year [5]. There are many antiviral drugs on the market. Influenza can be prevented with the use of antiviral drugs. Suppose

the person is severely unwell and concurrently has another disease. If there is a risk factor, and antiviral medications are required, then it is advisable to consult a doctor for treatment.

Mathematical modelling plays an essential role in understanding the dynamics of infectious disease influenza and preventing the disease through treatment, vaccination, and isolation of infected population. Many mathematical models were developed and studied to spread contagious illness in people, and they were applied to specific cases. The history of mathematical modelling on contagious diseases has been shown a significant concern for humankind. Epidemiology models are useful in comparing the effects of prevention or control procedures. The majority of the influenza mathematical model uses the Ordinary Differential Equations (ODEs) inspired by the basic susceptible, infected and recovered (SIR) epidemic model. Susceptible-Infected-Recovered (SIR) model is the foundation in determining the dynamics of infectious disease. In this paper, an extended Susceptible-Infected-Recovered (SIR) model will be used to assess influenza transmission in a population. The new compartment, the proportion of the human population treated at time *t* (*T*), is added into the basic Susceptible-Infected-Recovered (SIR) model where it refers to the process of offering the influenza infected individual with medicine or vaccination.

2 Formulation of the Model

2.1 SITR Model

In this section, an extended Susceptible-Infected-Recovered (SIR) model of influenza transmission is introduced. The *T* (Treatment) compartment is added into the existing SIR model. The Susceptible-Infected-Treatment-Recovered (SITR) model consists of a system of four ordinary differential equations. The compartments are *S*(*t*) represents the number of susceptible individuals, *I*(*t*) represent the number of infected individuals, *T*(*t*) represents the number of treated individuals and *R*(*t*) represents number of recovered individuals. The total population at time *t, N*(*t*) is given by:

$$N(t) = S(t) + I(t) + T(t) + R(t) \tag{1}$$

The transfer diagram of the model is shown in Figure 1 below.

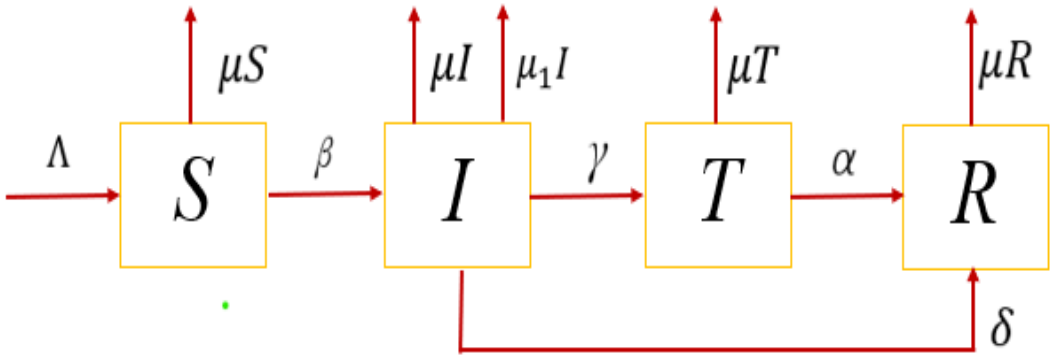

Figure 1: The schematic diagram of progression of transmission dynamics of

influenza with treatment [6].

According to Figure 1, we have following model [6]:

$$\frac{dS}{dt} = \Lambda - \beta SI - \mu S, \tag{2}$$

$$\frac{dI}{dt} = \beta SI - (\mu + \gamma + \delta + \mu_1)S, \tag{3}$$

$$\frac{dT}{dt} = \gamma I - (\alpha + \mu)T, \tag{4}$$

$$\frac{dR}{dt} = \alpha T + \delta I - \mu R. \tag{5}$$

There are several assumptions in the Susceptible-Infected-Treatment-Recovered (SITR) model. We assumed that the total population, $N(t)$, is not fixed, and due to contact of infectious individuals, all people are equally likely to be infected. It is believed that susceptible individuals becoming infected is the only way to exit the susceptible class, $S(t)$. The infected individuals can move to the treatment class, $T(t)$. After the infected individuals getting the treatment, the treated individuals move to the recovered class, $R(t)$, and recovered from the disease. It is also assumed that some infected people recovered without any treatment and gained immunity.

3 Analysis of the model

3.1 Disease-free equilibrium point (DFEP)

Disease-free equilibrium point (DFEP) of the Equation (2) – Equation (5) is assumed that there is no infection or disease. Therefore $I = 0$, and there is no individual treated, $T = 0$ and recovered, $R = 0$. The disease-free equilibrium point (DFEP) is denoted as E_0 and determine if the classes affected are either exposed or infectious. There is exactly one DFEP for systems and denoted by:

$$E_0\left(S_0, I_{0,} T_0, R_0\right) = \left(\frac{\Lambda}{\mu}, 0, 0, 0\right). \tag{6}$$

3.2 Existence of endemic equilibrium (EEP)

Endemic equilibrium point (EEP) denoted as $E_1 = (S^*, I^*, T^*, R^*)$ can be obtained when the disease cannot be eliminated, $I \neq 0$.

$$
\begin{aligned}
S^* &= \frac{\mu+\gamma+\delta+\mu_1}{\beta}, \\
I^* &= \frac{\beta\Lambda-\mu\left(\mu+\gamma+\delta+\mu_1\right)}{\beta\left(\mu+\gamma+\delta+\mu_1\right)}, \\
T^* &= \frac{\gamma I^*}{\alpha+\mu}, \\
R^* &= \frac{\alpha\gamma+\delta\left(\alpha+\mu\right)I^*}{\mu\left(\alpha+\mu\right)}.
\end{aligned} \tag{7}
$$

3.3 Basic Reproduction Number, R_0

Next, derivation of the basic reproduction number, R_0 for Equation 1 – Equation 4 is by using the Next-Generation Matrix Method. The disease-free equilibrium point (DFEP) is used to calculate the value of R_0. It tells us whether the population is at risk or save from the disease. When $R_0 > 1$, the occurrence of the disease will increase. When $R_0 < 1$, the occurrence of the disease will decrease, and the disease will eventually be eliminated. When $R_0 = 1$, the disease occurrence will remain constant [5]. The sub-model that are only consider diseases compartment are I and T.

At $E_0 = \left(\frac{\Lambda}{\mu}, 0, 0, 0\right)$, F and V are obtained as follows

$$
F = \begin{pmatrix} \beta S & 0 \\ 0 & 0 \end{pmatrix}, \tag{8}
$$

and

$$
V = \begin{pmatrix} \left(\mu+\gamma+\delta+\mu_1\right) & 0 \\ -\gamma & \left(\alpha+\mu\right) \end{pmatrix}. \tag{9}
$$

Next, inverse of V is computed.

$$
V^{-1} = \begin{pmatrix} \dfrac{1}{\left(\mu+\gamma+\delta+\mu_1\right)} & 0 \\ \dfrac{\gamma}{\left(\mu+\gamma+\delta+\mu_1\right)\left(\alpha+\mu\right)} & \dfrac{1}{\left(\alpha+\mu\right)} \end{pmatrix}. \tag{10}
$$

Consider the next generation matrix $G = FV^{-1}$,

$$G=\begin{pmatrix} \dfrac{\beta\Lambda}{\left(\mu+\gamma+\delta+\mu_1\right)\mu} & 0 \\ 0 & 0 \end{pmatrix}. \tag{11}$$

The basic reproduction number, R_0 is the largest eigenvalue of matrix G.
Therefore,

$$R_0=\frac{\beta\Lambda}{\left(\mu+\gamma+\delta+\mu_1\right)\mu}. \tag{12}$$

The disease-free equilibrium point (DFEP) is locally asymptotically stable if $R_0 < 1$ and unstable if $R_0 > 1$.

3.4 Stability analysis of the model at DFEP

Equation 1 – Equation 4 are a non-linear mathematical model. The system needs to be linearized by using the Jacobian matrix to determine the stability of the system at DFEP, E_0.

The Jacobian matrix of the reduced system is as follows:

$$J\left(E_0\right)=\begin{pmatrix} -\mu & -\beta\dfrac{\Lambda}{\mu} & 0 & 0 \\ 0 & \beta\dfrac{\Lambda}{\mu}-\left(\mu+\gamma+\delta+\mu_1\right) & 0 & 0 \\ 0 & \gamma & -\left(\alpha+\mu\right) & 0 \\ 0 & \delta & \alpha & -\mu \end{pmatrix}. \tag{13}$$

The eigenvalues determined are

$$\begin{aligned} \lambda_1&=-\mu, \\ \lambda_2&=\beta\frac{\Lambda}{\mu}-\left(\mu+\gamma+\delta+\mu_1\right), \\ \lambda_3&=-\left(\alpha+\mu\right), \\ \lambda_4&=-\mu. \end{aligned} \tag{14}$$

Since three eigenvalues obtained are negative where $-\mu, -(\alpha+\mu)$ and $-\mu$, the other root will be negative if $\beta\frac{\Lambda}{\mu} < (\mu+\gamma+\delta+\mu_1)$ and it will be positive if $\beta\frac{\Lambda}{\mu} > (\mu+\gamma+\delta+\mu_1)$.
Considering $\lambda_2 < 0$,

$$\begin{aligned} \beta\frac{\Lambda}{\mu} &< \left(\mu+\gamma+\delta+\mu_1\right), \\ \frac{\beta\Lambda}{\left(\mu+\gamma+\delta+\mu_1\right)\mu} &< 1, \\ R_0 &< 1. \end{aligned} \tag{15}$$

$R_0 < 1$implies that the disease dies out at disease-free equilibrium point (DFEP) is true. Therefore, we can conclude that the Equation 1 – Equation 4 at disease-free equilibrium point (DFEP) is stable.

3.5 Stability analysis of the model at EEP

The endemic equilibrium point (EEP), $E_1 = (S^*, I^*, T^*, R^*)$, is locally asymptotically stable if $R_0 > 1$ and unstable if $R_0 < 1$. The Jacobian matrix is computed to understand the stability of the system at EEP.

The Jacobian matrix of the systems of Equation 1 – Equation 4 at $E_1 = (S^*, I^*, T^*, R^*)$ is given by

$$J\left(E_1\right) = \begin{pmatrix} -\mu-\beta I^* & -\beta S^* & 0 & 0 \\ \beta I^* & \beta S^* - \left(\mu+\gamma+\delta+\mu_1\right) & 0 & 0 \\ 0 & \gamma & -\left(\alpha+\mu\right) & 0 \\ 0 & \delta & \alpha & -\mu \end{pmatrix}. \tag{16}$$

The characteristic polynomials are obtained as follows

$$\begin{aligned} L(\lambda) = {} & \lambda^4 + \left(3\mu + \left(\mu+\gamma+\delta+\mu_1\right) + \alpha + \beta\left(I^* - S^*\right)\right)\lambda^3 \\ & + \begin{pmatrix} \mu\left(1+3\mu+\alpha\right) + \beta I^*\left(\alpha+2\mu\right) - \beta S^*\left(-3\mu-\alpha\right) - \beta^2 S^* I^* \\ +\left(3\mu+\beta I^*+\alpha\right)\left(\mu+\gamma+\delta+\mu_1\right) \end{pmatrix}\lambda^2 \\ & + \begin{pmatrix} \mu\left(1+\mu\left(\alpha+\mu\right)+\left(\alpha+\mu\right)\beta I^*\right) + \beta^2 S^* I^*\left(-\alpha-2\mu\right) \\ +\left(2\alpha\mu+2\mu^2+\left(\alpha+2\mu\right)\beta I^*\right) - \beta S^*\left(-2\alpha\mu-3\mu^2\right) \end{pmatrix}\lambda^1 \\ & + \left(\alpha\mu^2+\mu^3+\beta I^*\left(\alpha\mu+\mu^2\right)\right)\left(\mu+\gamma+\delta+\mu_1\right) - \beta S^*\left(-\alpha\mu-\mu^3\right) \\ & - \beta^2 S^* I^*\left(-\alpha\mu-\mu^2\right) \end{aligned} \tag{17}$$

where

$$
\begin{aligned}
a_0 &= 1,\\
a_1 &= 3\mu + \left(\mu+\gamma+\delta+\mu_1\right)+\alpha+\beta\left(I^*-S^*\right),\\
a_2 &= \mu\left(1+3\mu+\alpha\right)+\beta I^*\left(\alpha+2\mu\right)-\beta S^*\left(-3\mu-\alpha\right)-\beta^2 S^* I^*\\
&\quad +\left(3\mu+\beta I^*+\alpha\right)\left(\mu+\gamma+\delta+\mu_1\right),\\
a_3 &= \mu\left(1+\mu\left(\alpha+\mu\right)+\left(\alpha+\mu\right)\beta I^*\right)+\beta^2 S^* I^*\left(-\alpha-2\mu\right)\\
&\quad +\left(2\alpha\mu+2\mu^2+\left(\alpha+2\mu\right)\beta I^*\right)-\beta S^*\left(-2\alpha\mu-3\mu^2\right),\\
a_4 &= \left(\alpha\mu^2+\mu^3+\beta I^*\left(\alpha\mu+\mu^2\right)\right)\left(\mu+\gamma+\delta+\mu_1\right)-\beta S^*\left(-\alpha\mu-\mu^3\right)\\
&\quad -\beta^2 S^* I^*\left(-\alpha\mu-\mu^2\right).
\end{aligned}
$$

Since $a_1 > 0, a_2 > 0, a_3 > 0, a_4 > 0$ and $a_1 a_2 - a_3 > 0$, so it meets the Routh-Hurwitz Criterion method. Hence, EEP is asymptotically stable.

4 Numerical Simulation

In this section, numerical results of the Susceptible-Infected-Treatment-Recovered (SITR) model are presented. The system is simulated with the initial conditions are assumed as $S(0) = 415$, $I(0) = 180$, $T(0) = 110$, $R(0) = 50$. We consider all the parameters are in per day. The time constraints is assumed as $0 \leq t \leq 1000$ in days. Table 1 shows the estimated parameters for Susceptible-Infected-Treatment-Recovered (SITR) model [6].

Table 1: Description and estimation of parameters [6]

Parameters	Description	Values
Λ	Recruitment rate of $S(t)$ class	15
β	Transmission rate of $S(t)$ class	0.0005
γ	Treatment rate of $I(t)$ class	0.1
α	Recovery rate of $T(t)$ class	0.003
δ	Recovery rate of $I(t)$ class without treatment	0.006
μ_1	Death rate due to infection	0.042
μ	Natural death rate	0.04

The value of γ will be adjusted to investigate the effect of treatment for influenza-infected individuals. For the first simulation, we choose $\gamma = 0.1$.

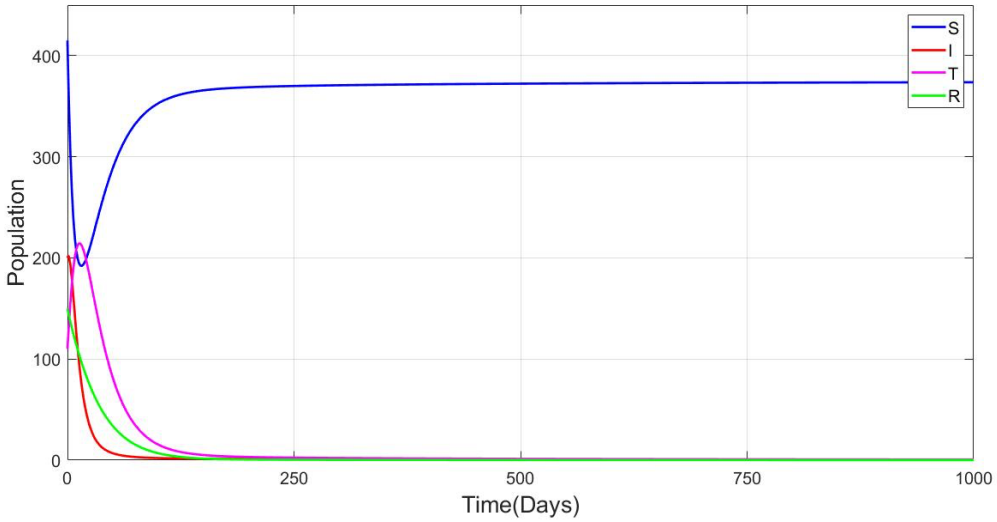

Figure 2: Graph of Individual Population Dynamics for Treatment Rate of Infected Individuals, $\gamma = 0.1$.

From Figure 2, the number of infected individuals decreases due to receiving the treatment. Individuals who received the treatment is increasing but after some time decreases. The basic reproduction number, R_0, obtained for $\gamma = 0.1$ is 0.9973 less than 1. Therefore, the disease-free equilibrium point (DFEP) is locally asymptotically stable and there is a decline in the number of cases.

Then, for the second simulation, the value of $\gamma = 0.1$ is changed to $\gamma = 0.02$.

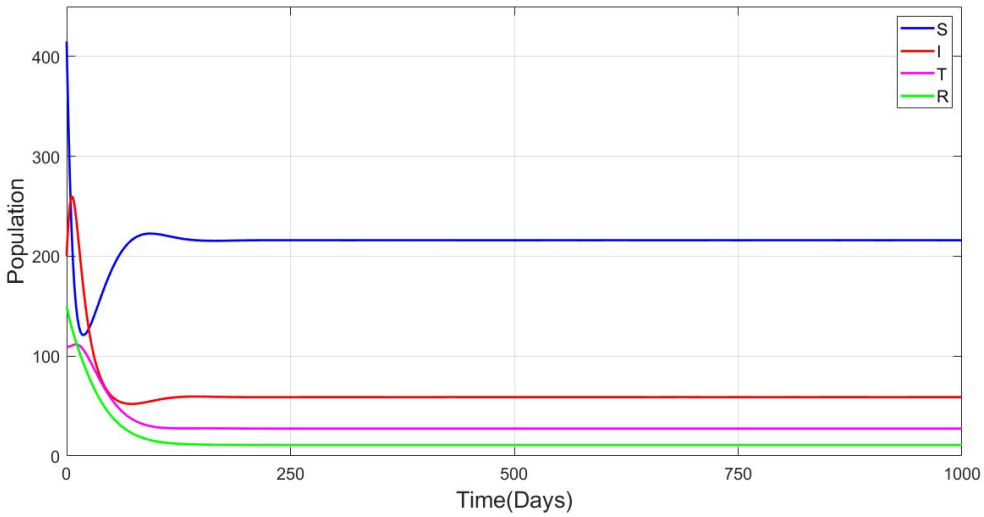

Figure 3: Graph of Individual Population Dynamics for Treatment Rate of Infected Individuals, $\gamma = 0.02$.

Based on Figure 3, the disease-free equilibrium point (DFEP) is unstable since the value of

$R_0 = 1.7361 > 1$. The graph in Figure 3 shows that the number of infected individuals slightly increases but drastically decreases as the number of susceptible individuals increases. Thus, the number of cases will increase, such as at the start of an epidemic.

Next, for the third simulation, the value of γ is changed to $\gamma = 0.3$.

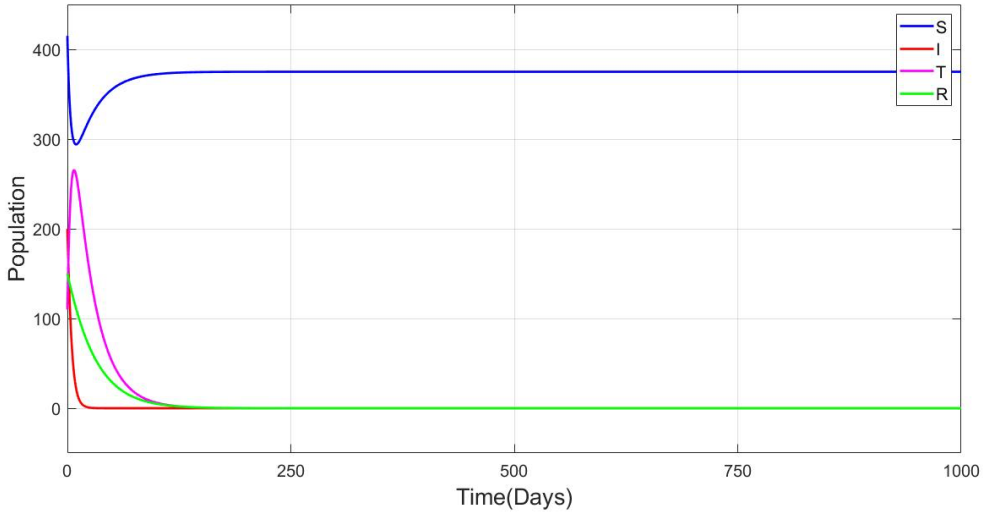

Figure 4: Graph of Individual Population Dynamics for Treatment Rate of Infected Individuals, $\gamma = 0.3$.

Figure 4 shows that the number of influenza-infected individuals decreases as the number of treated individuals increases at the initial time but then gradually decreases. The numerical simulation in Figure 4 gives $R_0 = 0.4832 < 1$. Therefore, the disease-free equilibrium point (DFEP) is locally asymptotically stable since the basic reproduction number, R_0 is less than 1.

Based on these three figures, there are significant differences that can be seen for each class. From Figure 2, it can be observed that the susceptible individuals decreased gradually but started to increase at $t = 20$. These are those individuals who are not infected. However, they could become infected. The number of infected individuals reduced due to receiving the treatment.

In Figure 3, for the susceptible class, when the γ value is reduced near to zero, the number of susceptible individuals drop drastically. In contrast, the number of infected individuals is relatively higher than in Figure 2 and Figure 4. The number of treated individuals in Figure 3 is steadily decreasing is due to the value of γ, which is the treatment rate of infected individuals is reduced, causing that the number of infected individuals does not get the treatment.

In Figure 4, when the γ value increases, the number of susceptible individuals is slightly higher and remains stable. The graph in Figure 4 also shows that the number of infected individuals decreases and, over time, can be decreased near to zero. The number of infected individuals who received the treatment is relatively higher and also declining because fewer infected individuals need the treatment and cured of the disease then entered the recovered class.

Table 2 shows the values of the basic reproduction number, R_0, for $\gamma = 0.1$, $\gamma = 0.02$ and $\gamma = 0.3$.

Table 2: The value of R_0

Value of γ	R_0
0.1	0.9973

0.02	1.7361
0.3	0.4832

It can be observed that whenever the value of γ is increases, the basic reproduction number, R_0, decreases. Hence, the number of infected individuals also decreases since the number of influenza-infected individuals getting the treatment is increases.

5 Conclusion

In this paper, an extended Susceptible-Infected-Recovered (SIR) model for an influenza epidemic model is constructed. We incorporate the new compartment, the individuals who received the treatment, $T(t)$, in the model. The Susceptible-Infected-Treatment-Recovered (SITR) model stability is tested by using the Routh Hurwitz Criterion method. With the aid of the following generation method, the primary reproduction number is obtained, and the dynamics of the model is derived. The outbreak of the disease is expected to continue if $R_0 > 1$. But when $R_0 < 1.$, the occurrence of the disease will decrease, and the disease will successfully be eradicated in the population. When $R_0 = 1$, the condition will remain constant. Numerical simulations are also conducted to test the analysis of the system. The results show that the effect of treatment on infected-influenza individuals, such as medication or vaccination, can help to reduce the number of infected individuals.

6 References

[1] History.com Editors. (2020) *Influenza.* History.

[2] Centers for Disease Control and Prevention (CDC). (2020) *Flu Symptoms and Complications.* Seasonal Influenza.

[3] Mayo Clinic. (2020) *Influenza (Flu).* https://www.mayoclinic.org/.

[4] Centers for Disease Control and Prevention (CDC). (2013) *Estimated Influenza Illnesses, Medical Visits, Hospitalizations, and Deaths in the United States – 2012-2013 Influenza Season..* MMWR Morb Mortal Wkly Rep. 62(49): 997–1000.

[5] Ketua Pengarah Kesihatan Malaysia. (2020) *Situasi Terkini Jangkitan Influenza di Malaysia* [*Press Release*]. https://kpkesihatan.com/. 2020.

[6] Goswami, N.K and Shanmukha, B. (2016) A Mathematical Model of Influenza: Stability and Treatment. Conference: International Conference on Mathematical Modeling and Simulation (ICMMS-16).