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STABILITY ANALYSIS OF THE SIQR MODEL OF DIPHTHERIA DISEASE SPREAD AND MIGRATION IMPACT

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ABSTRACT

Diphtheria is an acute disease that affects the upper respiratory tract caused by Corynebacterium diphtheriae, which can also affect the skin, eyes, and other organs. This article analyzes the stability of the SIQR model of diphtheria disease spread in Mandau District by considering the migration factor. The SIQR model is a development of the SIR model by incorporating the quarantine process as an alternative to reduce morbidity. The purpose of this study is to see the effect of migration on the spread of diphtheria disease in Mandau District through mathematical model simulation. We calculated the disease-free and endemic equilibrium points and the basic reproduction number (R_0) of the model. Model parameters were obtained using data from BPS Bengkalis Regency and UPTD Puskesmas Mandau. The calculation resulted in one disease-free equilibrium point and one endemic equilibrium point. If $R_0 < 1$, then the disease-free equilibrium point is asymptotically stable, and if $R_0 > 1$, then the endemic equilibrium point is also asymptotically stable. Based on the results of the data analysis, the value of $R_0 = 0.00224364$. This value is less than 1, so the equilibrium point obtained is a disease-free and asymptotically stable equilibrium point. This means that the population will be free from diphtheria and the level of migration affects the presence of diphtheria disease in Mandau District.

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1. INTRODUCTION

Diphtheria is an acute disease affecting the upper respiratory tract caused by Corynebacterium diphteriae. It also affects the skin, eyes, and other organs. Diphtheria shows a grayish-white membrane on the airway. Although it is rare, diphtheria sometimes occurs in developing countries [1],[2]. Prevention of diphtheria can be done through vaccination [3].

There have been many studies on diphtheria disease spread models, including [4] discussing mathematical modeling using the SIQR model with the influence of vaccination and quarantine. The result is that in order to prevent the spread of diphtheria, the vaccination rate must be greater than 0.884 and the cure rate must be greater than 0.049. As seen in [5] the stability analysis of modeling the spread of diphtheria using the MSEIR model with a saturated incidence rate. Furthermore, [6] presents a simple SIR model of diphtheria disease, which assumes that sick individuals do not receive specific treatments and rely on their immunity for recovery. The result is that the existence of diphtheria is determined by the magnitude of the cure rate and the transmission rate of the disease. Furthermore, [7] explored the SIRD model in relation to vaccines, concluding that a high vaccination rate could effectively curb the spread of diphtheria. According to [8] which explored the SEIR model of diphtheria in the context of quarantine, positing the possibility of re-infection among individuals who have recovered. The results showed that diphtheria is in a naturally endemic state. As demonstrated in [9] the SEIQR model of diphtheria disease resulted in the conclusion that the existence of diphtheria disease is determined by the vaccination rate. According to [10] which conducted a simulation where proper vaccination can reduce the basic reproduction rate of diphtheria spread. Furthermore, [11] discussed control measures for diphtheria disease, namely vaccination and treatment, and the simulation results show that both controls prevent diphtheria from becoming endemic.

Research [2]–[8] examine the spread of diphtheria by assuming a closed population, which means that there is no effect of migration. Population migration is the act of moving people from one place to another. The components that cause population migration include natural resources, socio-cultural environment, politics, economics, destination, and disease outbreaks. Several researchers confirmed that migration influences the dynamics of disease spread. [12] examined the SIRD model of Ebola spread with the influence of migration, where if the emigration rate is relatively large compared to the immigration rate, then Ebola will disappear. As seen in [13] the model of the spread of HIV/AIDS by considering the factors of therapy and migration, where the presence of migration also affects the existence of HIV/AIDS. Furthermore, [14] reviewed the population model of the number of smokers with the influence of migration, and it was concluded that the group of smokers will always exist in the population, but the number is determined by the size of the migration rate.

Therefore, the author is interested in developing a diphtheria disease spread model with the assumption of migration. This is because migration affects the population size in an area, as reviewed in articles [12]-[14]. This study investigates diphtheria cases in the Mandau sub-district. The reason is that the Mandau Sub-district is the most populous sub-district in Bengkalis Regency and also has a high number of population migration. The average population migration every month reaches 200 residents in the sub-district [15].

2. RESEARCH METHODS

This research will be conducted using the literature method. The steps used are as follows.

a. Determine the variables and parameters used in the model.
b. Adding the assumption of immigration and emigration to the Gina Puspita et al. model to form an SIQR model with migration.
    1) The number of births and deaths is assumed to be unequal. Newborn individuals belong to the susceptible class because newborn individuals are assumed to be healthy but susceptible to diphtheria.
    2) The population is assumed to be open therefore the process of migration, immigration, and emigration occurs in all classes.
c. Determine its equilibrium point.
d. Linearize the model using the Jacobian matrix at the equilibrium point.
e. Analyse the stability of the equilibrium point that has been determined, with the following conditions.

Equilibrium point, $\hat{x}$ with a system of nonlinear differential equations $\dot{x} = f(x)$,

1) The equilibrium point $\hat{x}$ is asymptotically stable if all eigenvalues of the Jacobian matrix $J(f(\hat{x}))$ have negative real.
2) The equilibrium point $\hat{x}$ is unstable if at least one eigenvalue of the Jacobian matrix $J(f(\hat{x}))$ has positive real.

Routh-Hurwitz Stability Criteria

Suppose $a_1, a_2, \dots, a_n$ is a natural number and $a_0 \neq 0$ and is given a polynomial equation

$$p(\lambda) = a_0\lambda^n + a_1\lambda^{n-1} + \cdots + a_n\lambda + a_n = 0$$

The roots of the polynomial equation have negative reals if and only if every determinant of the matrix M_n for every $k = 1,2, \dots, n$.

$$M_n = \begin{vmatrix} a_1 & a_3 & a_5 & \cdots & a_{2k-1} \\ a_0 & a_2 & a_4 & \cdots & a_{2k-2} \\ \vdots & \vdots & \vdots & \ddots & \vdots \\ 0 & 0 & 0 & \dots & a_k \end{vmatrix}$$

is positive.

f. Model simulation using maple 13.
g. Conclude the results of equilibrium point analysis and model simulation.
   1) If the basic reproduction number $R_0 < 1$ then the disease will disappear.
   2) If $R_0 > 1$ then the disease will become an outbreak.

3. RESULTS AND DISCUSSION

In this section, the results of the research are presented which include the process of model formation, analysis of the existence and stability of the equilibrium point, calculation of the basic reproduction number, and simulation to evaluate the dynamics of the system in accordance with the conditions in Mandau District, Bengkalis Regency.

3.1 SIQR Model Formation of Diphtheria Spread with the Effect of Migration

The SIQR model, with the effect of migration, causes the population to be open. The population is divided into four classes: suspect (S), infected (I), quarantine (Q), and recovery (R). Therefore, we introduce the variables and parameters of the SIQR model in **Table 1** and **Table 2**.

Table 1. List of Model Variables

Variable	Description	Condition
S	The total number of retired human population at the time t	$S(t) \geq 0$
I	The total infected human population at the time t	$I(t) \geq 0$
Q	The total number of humans under quarantine at the time t	$Q(t) \geq 0$
R	The total number of people cured at the time t	$R(t) \geq 0$
N	The total human population at the time t	$N(t) \geq 0$

Table 2. List of Model Parameters

Parameter	Description	Condition
p	proportion of vaccinations given to individuals	$0 \leq p \leq 1$
μ	natural mortality rate	$\mu > 1$
γ	recovery rate	$\gamma > 0$
β	odds of a susceptible individual having an infected individual	$\beta > 0$
α	The rate of individuals quarantined per unit of time is significant.	$\alpha > 0$
r	birth rate	$r > 0$
δ	death rate due to diphtheria disease	$\delta \geq 0$

Parameter	Description	Condition
m_1	the number of people who immigrate	$m_1 > 0$
m_2	the number of people who emigrate	$m_2 > 0$

Table 1 and **Table 2** present the variables and parameters used in this model, which form the SIQR model of diphtheria disease with migration.

$$\frac{dS}{dt} = (1-p)rN + m_1 S - \mu S - m_2 S - \beta \frac{S}{N} I \quad (1)$$

$$\frac{dI}{dt} = \beta \frac{S}{N} I + m_1 I - \delta I - m_2 I - \mu I - \alpha I \quad (2)$$

$$\frac{dQ}{dt} = \alpha I - \mu Q - \gamma Q \quad (3)$$

$$\frac{dR}{dt} = p\mu N + m_1 R + \gamma Q - m_2 R - \mu R \quad (4)$$

$$N = S + I + Q + R \quad (5)$$

To see the behavior of the SIQR model, first, determine the equilibrium point of the model and its stability.

3.2 Basic Reproduction Number

The R_0 is a threshold condition that determines whether a population is disease-free or disease-endemic. We will use **Equation (2)** to obtain R_0.

$$\frac{dI}{dt} = \beta \frac{S}{N} I + m_1 I - \delta I - m_2 I - \mu I - \alpha I$$

The R_0 will be found using the next-generation matrix.

$$I = \phi(S, Q, R), I) - \psi((S, Q, R), I)$$

$$\phi = \left[\beta \frac{S}{N} I + m_1 I\right]$$

$$\text{and } \psi = [\delta I + m_2 I + \mu I + \alpha I]$$

Next, the Jacobian matrix of ϕ and ψ is formed and then obtained.

$$F = \left[\frac{\partial \phi}{\partial I}\right] = \left[\beta \frac{S}{N} + m_1\right]$$

$$V = \left[\frac{\partial \psi}{\partial I}\right] = [\delta + m_2 + \mu + \alpha]$$

Next, insert the disease-free equilibrium point $E_0 = (S_0, I_0, Q_0, R_0)$ into the F and V matrices so that

$$F = \left[\beta \frac{S^*}{N} + m_2\right] = \left[\beta \frac{\frac{(1-P)rN}{m_2 + \mu - m_1}}{N} + m_2\right]$$

$$V = [\delta + m_2 + \mu + \alpha]$$

Then the next-generation matrix is obtained as follows:

$$FV^{-1} = \left[\beta \frac{\frac{(1-P)rN}{m_2 + \mu - m_1}}{N} + m_2\right] \left[\frac{1}{[\delta + m_2 + \mu + \alpha]}\right]$$

$$= \left[\frac{\beta(1-P)rN + m_2\big((m_2+\mu-m_1)N\big)}{(m_2+\mu-m_1)N}\right]\left[\frac{1}{[\delta+m_2+\mu+\alpha]}\right]$$

$$= \left[\frac{\beta(1-P)rN + m_2\big((m_2+\mu-m_1)N\big)}{N(m_2+\mu-m_1)(\delta+m_2+\mu+\alpha)}\right]$$

$$det(FV^{-1} - \lambda I) = \left(\left[\frac{\beta(1-P)rN + m_2\big((m_2+\mu-m_1)N\big)}{N(m_2+\mu-m_1)(\delta+m_2+\mu+\alpha)}\right] - \lambda\right)$$

The dominant eigenvalue of the matrix FV^{-}

$$\lambda = \left(\left[\frac{\beta(1-P)rN + m_2\big((m_2+\mu-m_1)N\big)}{N(m_2+\mu-m_1)(\delta+m_2+\mu+\alpha)}\right]\right)$$

Since R_0 is the dominant eigenvalue of the matrix FV^{-} then

$$R_0 = |\lambda| = \left[\frac{\beta(1-P)rN + m_2\big((m_2+\mu-m_1)N\big)}{N(m_2+\mu-m_1)(\delta+m_2+\mu+\alpha)}\right]$$

Thus, the basic reproduction number or R_0 is

$$R_0 = \left[\frac{\beta(1-P)rN + m_2\big((m_2+\mu-m_1)N\big)}{N(m_2+\mu-m_1)(\delta+m_2+\mu+\alpha)}\right] \tag{6}$$

3.3 Equilibrium Point

From **Equation (1)** to **Equation (5)**, first make the right-hand side of each equation equal to zero to find the equilibrium point. The model identifies two equilibrium points: the disease-free equilibrium point ($\hat{I} = 0$) and the disease-endemic equilibrium point ($I^* > 0$).

We obtain the disease-free equilibrium point E_0.

$$E_0 = (S_0, I_0, Q_0, R_0) = \left(\frac{(1-p)rN}{m_2+\mu-m_1}, 0, 0, \frac{prN}{m^2+\mu-m_1}\right)$$

and the endemic equilibrium point E_1 is

$$E_1 = (S^*, I^*, Q^*, R^*)$$

where,

$$S^* = \frac{(m_2+\delta-m_1+\mu+\alpha)N}{\beta}$$

$$I^* = \frac{\left(\frac{\big((1-p)rN\big)\beta}{(m_2+\delta-m_1+\mu+\alpha)N} + m_1 - m_2 - \mu\right)N}{\beta}$$

$$Q^* = \frac{aN\left(\frac{\big((1-p)rN\big)\beta}{(m_2+\delta-m_1+\mu+\alpha)N} + m_1 - m_2 - \mu\right)}{\beta(m_1+\mu+m_2+\gamma)}$$

$$R^* = \frac{prN + \gamma\left(\frac{aN\left(\frac{\big((1-p)rN\big)\beta}{(m_2+\delta-m_1+\mu+\alpha)N} + m_1 - m_2 - \mu\right)}{\beta(m_1+\mu+m_2+\gamma)}\right)}{m_1+m_2+\mu}$$

3.4 Analysis of Equilibrium Point Stability

The stability analysis is determined based on the eigenvalues obtained by first forming the matrix of the system of **Equation (1)** to **Equation (4)**, obtained

$$J=\begin{bmatrix} m_1-\mu-m_2-\frac{\beta}{N}I & \beta\frac{S}{N} & 0 & 0 \\ \frac{\beta}{N}I & \beta\frac{S}{N}+m_1-m_2-\mu-\alpha & 0 & 0 \\ 0 & \alpha & m_1-\mu-m_2-\gamma & 0 \\ 0 & 0 & \gamma & m_1-m_2-\mu \end{bmatrix}$$

3.4.1 Stability Analysis of Disease-Free Equilibrium Point

If $R_0<1$ and $m_1<m_2$ then the disease-free equilibrium point will be asymptotically stable. Substitute E_0 into the Jacobian matrix to obtain:

$$J(E_0)=\begin{bmatrix} m_1-\mu-m_2-\frac{\beta}{N}(0) & \frac{\beta\left(\frac{(1-P)rN}{m_2+\mu-m_1}\right)}{N} & 0 & 0 \\ \frac{\beta(0)}{N} & \frac{\beta\left(\frac{(1-P)rN}{m_2+\mu-m_1}\right)}{N}+m_1-m_2-\mu-\alpha & 0 & 0 \\ 0 & \alpha & m_1-\mu-m_2-\gamma & 0 \\ 0 & 0 & \gamma & m_1-m_2-\mu \end{bmatrix}$$

Then the eigenvalue of $J(E_0)$ is sought to obtain information on the disease-free state, so that the eigen polynomial is obtained:

$$(m_1-\mu-m_2-\lambda)\left(\frac{\beta\left(\frac{(1-P)rN}{m_2+\mu-m_1}\right)}{N}+m_1-\delta-m_2-\mu-\alpha-\lambda\right)(m_1-\mu-m_2-\gamma-\lambda)$$
$$\cdot(m_1-\mu-m_2-\lambda)=0$$

thus,

$$\lambda_1=m_1-\mu-m_2,$$
$$\lambda_2=\frac{B\left(\frac{(1-P)rN}{m_2+\mu-m_1}\right)}{N}+m_1-\delta-m_2-\mu-\alpha,$$
$$\lambda_3=m_1-\mu-m_2-\gamma,$$
$$\lambda_4=m_1-\mu-m_2$$

λ_1,λ_3, and λ_4 are all negative provided that $m_1<m_2$, while$\lambda_2<0$ is conditional

$$\lambda_2=\beta\left(\frac{(1-P)r}{m_2+\mu-m_1}\right)+m_1-\delta-m_2-\mu-\alpha<0$$
$$\Leftrightarrow\beta\frac{(1-P)r}{(m_2+\mu-m_1)(m_2+\mu+\alpha)}+\frac{m_1}{(m_2+\mu+\alpha)}-1<0$$
$$\Leftrightarrow\beta\frac{(1-P)r+m_1(m_2+\mu-m_1)}{(m_2+\mu-m_1)(m_2+\mu+\alpha)}-1<0\Leftrightarrow R_0<1$$

3.4.2 Stability Analysis of Endemic Equilibrium Point

If $R_0 > 1$ then the equilibrium point of endemic disease is asymptotically stable. It will be proved that the endemic equilibrium point of the disease is asymptotically stable. First, substitute the endemic equilibrium point into the Jacobian matrix so that it is obtained:

$$J(E_1^*) = \begin{bmatrix} -\dfrac{\beta(1-p)r}{m_2 - m_1 + \mu + \alpha} & m_2 - m_1 + \mu + \alpha & 0 & 0 \\ \dfrac{\beta(1-p)r}{m_2 - m_1 + \mu + \alpha} + m_2 - m_1 + \mu + \alpha & 0 & 0 & 0 \\ 0 & \alpha & m_1 - \mu - m_2 - \gamma & 0 \\ 0 & 0 & \gamma & m_1 - m_2 - \mu \end{bmatrix}$$

The eigenvalue characteristic equation is obtained as follows:

$$(m_1 - m_2 - \mu - \lambda)(m_1 - \mu - m_2 - \gamma - \lambda)\left(\left(\frac{\beta(1-p)r}{m_2 - m_1 + \mu + \alpha} + \lambda\right)\lambda - \beta(1-p)r + \right.$$
$$\left.(m_1 - m_2 - \mu)(m_2 + \mu - m_1 + \alpha)\right) = 0$$

$\lambda_1 = m_1 - \mu - m_2 - \gamma < 0, \lambda_2 = m_1 - m_2 - \mu < 0$

While the other eigenvalues can be calculated by finding the root of the
$\left(\frac{\beta(1-p)r}{m_2 - m_1 + \mu + \alpha} + \lambda\right)\lambda - \beta(1-p)r + (m_1 - m_2 - \mu)(m_2 + \mu - m_1 + \alpha) = 0$

By manipulating algebraically, we get

$$(m_2 - m_1 + \mu + \alpha)\lambda^2 + \frac{R_0(m_2 + \mu - m_1)(m_2 + \mu + \alpha)}{(m_2 - m_1 + \mu + \alpha)}\lambda$$
$$+ (R_0 - 1)(m_2 + \mu - m_1)(m_2 + \mu + \alpha)(m_2 - m_1 + \mu + \alpha) = 0$$

Suppose,

$$a_0 = m_2 - m_1 + \mu + \alpha$$
$$a_1 = \frac{R_0(m_2 + \mu - m_1)(m_2 + \mu + \alpha)}{(m_2 - m_1 + \mu + \alpha)}$$
$$a_2 = (R_0 - 1)(m_2 + \mu - m_1)(m_2 + \mu + \alpha)(m_2 - m_1 + \mu + \alpha)$$

Based on the Routh-Hurtwiz criterion, the values of λ_3 and λ_4 are negative if $a_1 > 0, a_2 > 0$. The value of $a_1 > 0$ is because $m_1 < m_2$. While $a_2 > 0$ if $R_0 > 1$. It is proven that if $R_0 > 1$ then, the endemic equilibrium point will be asymptotically stable.

3.5 Case Study

Based on data from the Central Statistics Agency of Bengkalis Regency, Mandau District, in 2016, the number of births in Mandau District was 4,904 and the population in Mandau District was 242,927. From the data of UPTD Puskesmas Mandau Subdistrict, it is found that the number of individuals who have received diphtheria immunization is 3,261 while those who should get immunized should be 5,011, so there are still vulnerable individuals who have not received immunization. The sub-district has a human life expectancy of 70.63 years. So, the death rate parameter in the Mandau sub-district has a value of

$$\mu = \frac{1}{70.63\ year} = \frac{1}{847.56\ month} = \frac{0.001179}{month} \tag{7}$$

The birth rate in the Mandau sub-district is assumed to be the number of births divided by the population.

$$r = \frac{Birth\ rate}{N} = \frac{4{,}904}{242{,}927} = \frac{0.020187}{year} = \frac{0.0016822}{month} \tag{8}$$

The death rate δ due to disease in the Mandau sub-district is 0 because there are no deaths due to diphtheria. The infectivity period is the period in which the population in the infected class will move to the recovery class. The infectivity period is 28 days. The cure rate γ of diphtheria disease is assumed to be

$$\gamma = \frac{1}{\text{infectivity period}} = \frac{1}{0.93\ month} = \frac{1.075}{month} \tag{9}$$

The probability of an individual being susceptible to diphtheria β in Mandau sub-district is assumed to be

$$\beta = \frac{\text{the number of infected individuals}}{Nx\text{infectivity period}} = \frac{10}{242{,}927(0.93)} = 0.000044263 \tag{10}$$

The proportion of vaccination p given is assumed to be people who received DPT immunization in Mandau sub-district in 2016, which was 78.63%. So, the vaccination proportion is

$$p = 78.63\% = 0.7863 \tag{11}$$

The recommended quarantine rate α for diphtheria is 5 days, so the quarantine rate is assumed to be

$$\alpha = \frac{1}{0.17\ month} = \frac{5.88}{month} \tag{12}$$

Immigration that occurred in the Mandau sub-district in 2016 was 15,567.6871. The immigration rate that occurs in the Mandau sub-district is assumed to be

$$m_1 = \frac{\text{the number of individuals who immigrate}}{N} = \frac{15{,}567.6871}{242{,}927} = \frac{0.0640838}{year} = \frac{0.0053365}{month} \tag{13}$$

The emigration rate that occurred in Mandau sub-district in 2016 was 16,756.9374. The immigration rate that occurs in the Mandau sub-district is assumed to be

$$m_2 = \frac{\text{the number of individuals who emmigrate}}{N} = \frac{16{,}756.9374}{242{,}927} = \frac{0.0689793}{year} = \frac{0.0057482}{month} \tag{14}$$

The initial values for this model are given as follows

$$N(t) = 242{,}927;\ S(0) = 242{,}927$$
$$I(0) = 10;\ Q(0) = 10;\ R(0) = 10$$

With these parameter values obtained,

$$\frac{dS}{dt} = (1 - 0.7863)(0.0016822)(0.00179)N + (0.053363)S - (0.00179)S - (0.0057482)S - (0.00044263)\frac{S}{N}I$$
$$\frac{dI}{dt} = (0.000044263)\frac{S}{N}I + (0.0053363)I - (0)I - (0.0057482)I - (0.00179)I - (5.88)I$$
$$\frac{dQ}{dt} = (5.88)I + (0053363)Q - (0.00179)Q - (0.0057482)Q - (1.075)Q$$
$$\frac{dR}{dt} = (0.7863)(0.00179)N + (0.005363)R + (1.075)Q - (0.0057482)R - (0.00179)R$$

The simulation results can be seen in the figure below.

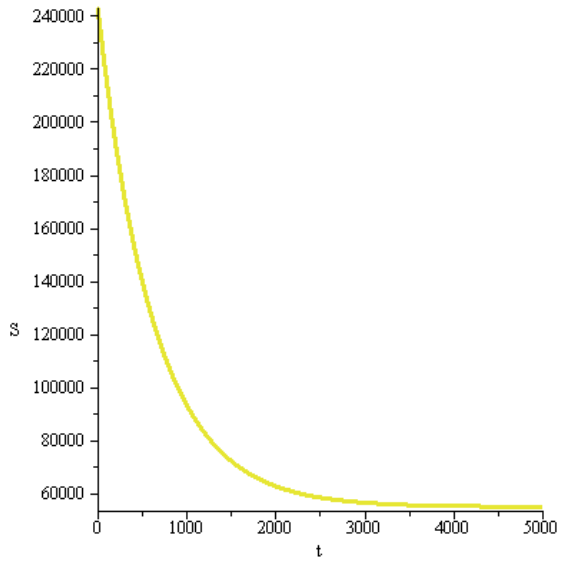

Figure 1. A Graph of S(t) Against t

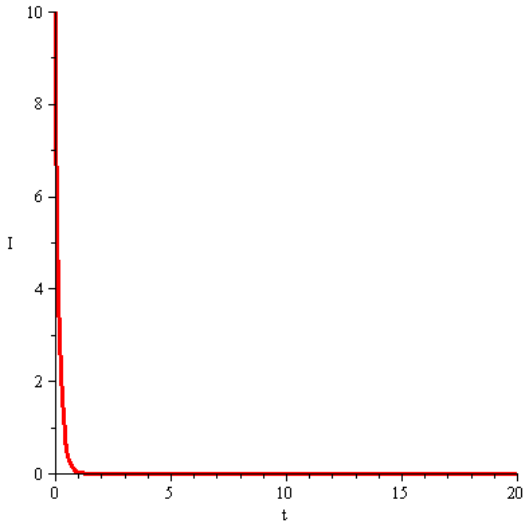

Figure 2. A Graph of $I(t)$ Against t

In **Figure 1**, it can be seen that the graph tends to decrease, which indicates that individuals who are susceptible to diphtheria will decrease over time t. In **Figure 2**, it can be seen that individuals infected with diphtheria will decrease to zero. This means that there will be no more individuals infected with diphtheria disease at the time t.

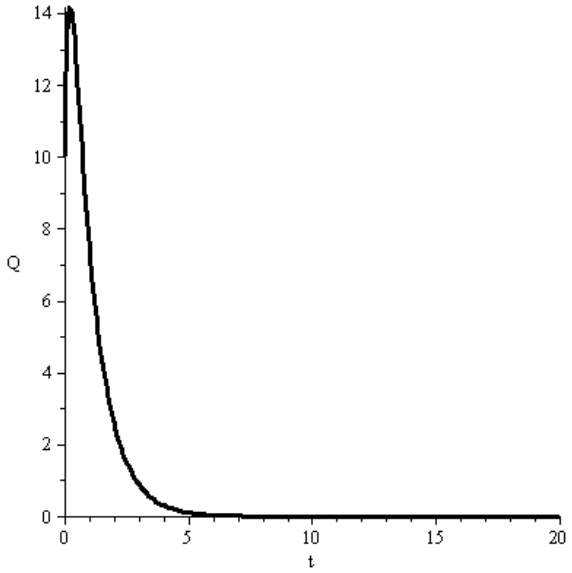

Figure 3. A Graph of $Q(t)$ Against t

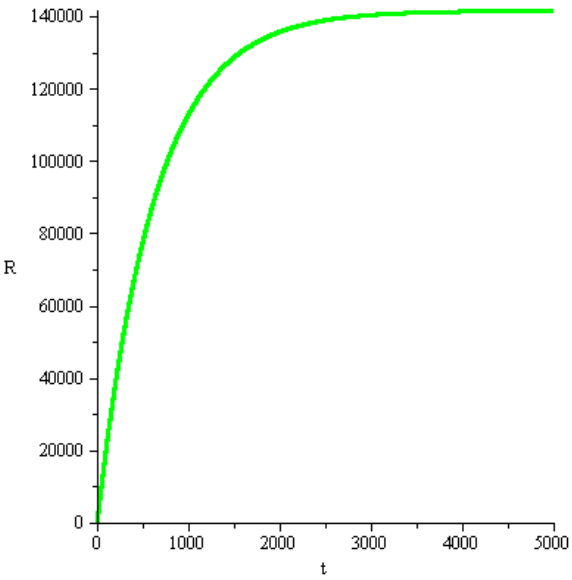

Figure 4. A Graph of R(t) Against t

Figure 3 shows a decrease in the quarantine graph, indicating a decrease in the number of infected individuals over time. Then, in **Figure 4**, it can be seen that the recovery graph has a very significant increase over time.

Substituting the parameter values in **Equation (7)** to **Equation (14)** and the given initial values into the following formula yields the basic reproduction number:

$$R_0 = \left[\frac{\beta(1-P)rN + m_2\big((m_2+\mu-m_1)N\big)}{N(m_2+\mu-m_1)(\delta+m_2+\mu+\alpha)}\right] = 0.00224364 < 1$$

.

Because of $R_0 < 1$, diphtheria in the Mandau Subdistrict will one day be extinct from the population, so the equilibrium point obtained is a disease-free equilibrium point.

4. CONCLUSIONS

The SIQR model of diphtheria disease spread was applied to a case study in Mandau District using data from UPTD Puskesmas Duri Kota in 2016. From a total population of 242,927 people, there were 10 individuals infected with diphtheria. From the research conducted, the results show that the probability of a person getting diphtheria disease is 0.000044263 which is the basic reproductive number $\boldsymbol{R_0 = 0.00224364 < 1}$. This value is smaller than one, which means that diphtheria disease will disappear in Mandau District in a long time and its equilibrium point is called an asymptotically stable disease-free equilibrium point.

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