Analysis of SEIRS Model for Cholera Spreading with Vaccination and Treatment Factors

Syafruddin Side*, Sukarna, Gita Tri Asfarina, Muh. Isbar Pratama, and Usman Mulbar
Department of Mathematics, Universitas Negeri Makassar, Indonesia

*syafuddin@unm.ac.id

Abstract. In this study, the rate of vaccination and treatment than to see the effects on the spread of the disease. In this case, obtained the minimum vaccination and treatment level of the minimum needed for the disease can disappear from the population. For vaccination rates and treatment level above the minimum vaccination and minimum treatment, the greater the rate of vaccination and treatment levels cause the proportion of Susceptible individuals getting smaller, meaning that people with cholera gradually diminishing and the disease will disappear from the population and there is no endemic.

1. Introduction
Cholera is a disease that has long attacked humans and continues to be a problem for the health of the world community [1]. Cholera is an acute intestinal tract infection caused by Vibrio Cholera bacteria. These bacteria enter into a person's body through drinking water or eating foods contaminated with Vibrio Cholera bacteria. These bacteria produce Choleratoxin in the intestinal tract causing diarrhea with acute and severe vomiting. A person who within a few days will release a lot of body fluids that can cause dehydration [1]. This condition is an early symptom of acute diarrheal disease that can result in death if not treated quickly and appropriately. More children die from the disease, because they are more rapidly dehydrated than adults [2].

Cholera attracts global attention globally because of its potential epidemic and even pandemic (worldwide epidemic). The seventh pandemic or the last pandemic, started in Indonesia in 1961 and then spread to Asia, Africa, Europe, and Latin America until 2010 [3]. By 2014, WHO reports Africa is a continent with the most countries contracting the disease. According to the data obtained, there are about 3-5 million cases of cholera and 100-120 thousand of whom die each year. Since cases of cholera are continuously present every year, these infectious diseases can’t be underestimated and ignored [4].

Efforts that can be done to suppress the spread of cholera disease is to provide vaccinations and treatment for cholera sufferers. Vaccination is done by administering cholera vaccine, either a vaccine that has been switched off or an attenuated live vaccine. Cholera-CSL vaccine is derived from bacteria that have been killed by 0.5% phenol addition as preservative, may protect for several months (3-6 months). While the live attenuated vaccine can protect for 3 years. Treatment of cholera sufferers is early fluid and electrolytes that can prevent dehydration, when administered after dehydration, it is important to restore fluid balance and avoid death [5].
Mathematical studies on the spread of infectious diseases such as Tuberculosis, Dengue Fever, Hepatitis B and Cholera using the SIR or SEIR model have been done by [2,4,6,7,8,9,10]. [2] examined the mathematical model in cases of cholera epidemics with a constant population, [4] examined stability analysis for the spread of cholera disease based on the SIR model with vaccination. Both models are not considered treatment factors that may affect the spread of cholera disease. Therefore, this paper builds the SEIRS model of the spread of cholera disease by taking into account vaccination and treatment factors. Then do the analysis at the equilibrium point. The cholera disease distribution model with vaccination given to vulnerable sub-classes of the population, as well as the treatment factor given to the infected population sub-class so that once controlled the healing rate is increased, whereas the previous model did not show it.

2. Method
The research is a kind of pure research using SEIRS model that aims to analyze the stability around the equilibrium point. The steps taken to achieve the research objectives are as follows: Develop a mathematical model for the spread of cholera disease based on the SEIRS model with vaccination and treatment factor; Determine the equilibrium point of the model, the point of disease-free equilibrium and endemic; Analyze the stability around the equilibrium point of the model; and find the basic reproduction number, that is reproduction number of vaccination and reproduction number of treatment.

3. Result and Discuss

3.1. SEIRS Model with Vaccine dan Treatment Factor
In this study discussed the formation of SEIRS model based on the assumptions made. Furthermore, the equilibrium point of the model is then analyzed, which is further interpreted in real life problems. In this case it is about the behavior of disease spread and its existence, the point of disease-free balance and the endemic balance point. The spread of disease in a population is assumed to have a constant amount and within a period of epidemic (t). The population divided into four classes, the Susceptible class (S) states the population of susceptible individuals affected by the disease, Exposed class (E) states the population of individuals detected by disease but not yet infected, Infected (I) class indicates the population of individuals who have been infected with the disease, and class Recovered (R) states the individual population who is cured of the disease, but has no immunity to the disease, meaning the individual will return to a vulnerable subpopulation.

Assumptions in SEIRS model with vaccination and treatment factor are:
1. The number of populations in each subpopulation within a time period is \( S(t), E(t), I(t), \) and \( R(t) \) by proportion \( S(t) + E(t) + I(t) + R(t) = N \).
2. Deaths that occur in each class Susceptible, Exposed, Infected, or Recovered only natural death.
3. The rate of birth and death are the same.
4. Susceptible individual class population infected with cholera disease, in case of contact through stool of infected individual class population
5. Individual detected will become infected.
6. Incubation period of cholera 1-4 days.
7. Treatment is given to individual classes Exposed.
8. Population of individuals recovering from cholera is again vulnerable.
9. Populations born in the Susceptible, Exposed, Infected, and Recovered classes will be susceptible to cholera diseases entering the Susceptible class.
10. Population of individuals infected with cholera can recover from illness with a rate of recovery \( \gamma \).
11. It is assumed that the vaccine is given after an outbreak, meaning that there is immediate control by vaccination. Vaccines are only given to the Susceptible individual class.
Based on the issue of the spread of cholera disease and assumptions given, can be described in the transfer chart as follows:

![Transfer Diagram of SEIRS Model with Vaccination and Treatment Factor](image)

**Fig 1.** Transfer Diagram of SEIRS Model with Vaccination and Treatment Factor

Based on Figure 1, obtained the SEIRS model with vaccination and treatment factor as follows:

\[
\begin{align*}
\frac{dS}{dt} &= bN + \sigma R - \beta S \frac{I}{N} - \nu S - \mu S \\
\frac{dE}{dt} &= \beta S \frac{N}{I} - \alpha E - \mu E \\
\frac{dI}{dt} &= \alpha E q I - \gamma I - \mu I \\
\frac{dR}{dt} &= \gamma I + \nu S - \sigma R - \mu R
\end{align*}
\]

(1)

(2)

(3)

(4)

with \( S(0) = S_0 \geq 0, E(0) = E_0 \geq 0, I(0) = I_0 \geq 0, R(0) = R_0 \geq 0 \), and \( S(t) + E(t) + I(t) + R(t) = N \)

and \( 0 \leq \nu \leq 0.9 \).

where:

- \( N \) : the total number of individuals in the population
- \( b \) : the rate of birth in the population
- \( \mu \) : the rate of death in the population
- \( \beta \) : the rate of transmission of the disease
- \( \alpha \) : the rate of disease infectivity
- \( \gamma \) : the rate of cure of disease
- \( \sigma \) : the rate of returning individuals vulnerable
- \( \nu \) : the ratio of the number of individuals who received the vaccine
- \( q \) : giving treatment

### 3.2. Equilibrium Point of SEIRS Model

The equilibrium point of the model found with equation (1), (2), (3), and (4) equals to zero as follows:

\[
\begin{align*}
bN + \sigma R - \beta S \frac{I}{N} - \nu S - \mu S &= 0 \\
\beta S \frac{N}{I} - \alpha E - \mu E &= 0 \\
\alpha E q I - \gamma I - \mu I &= 0
\end{align*}
\]

(5)

(6)

(7)
\[ \gamma I + \nu S - \sigma R - \mu R = 0 \]  
(8)

If \( I = 0 \), then the equations (5), (6), (7), and (8) as follows:

\[ S = \frac{bN + \sigma R}{(v + \mu)}, E = 0, R = \frac{\nu S}{(\sigma + \mu)} \]

The equilibrium point for free disease of Cholera is \( E_0 = \left( \frac{bN + \sigma R}{(v + \mu)}, 0, 0, \frac{\nu S}{(\sigma + \mu)} \right) \).

If \( I \neq 0 \), by equation (7) found:

\[ E = \frac{(\gamma + \mu - q)I}{\alpha} \]  
(9)

If equation (9) substitute to (6), then found the equation (10) as follows:

\[ S = \frac{(\alpha + \mu)(\gamma + \mu - q)N}{\alpha \beta} \]  
(10)

If equation (10) substitute to (5), then found the equation (11) as follows:

\[ I = \frac{\alpha \beta (bN + \sigma R) - (v + \mu)(\alpha + \mu)(\gamma + \mu - q)N}{\beta(\alpha + \mu)(\gamma + \mu - q)} \]  
(11)

If equation (10) and (11) substitute to (6) and (8), found:

\[ E = \frac{\alpha \beta (bN + \sigma R) - (v + \mu)(\alpha + \mu)(\gamma + \mu - q)N}{\alpha \beta(\alpha + \mu)} \]  
(12)

\[ R = \left( \frac{(\gamma (\alpha \beta (bN + \sigma R) - (v + \mu)(\alpha + \mu)(\gamma + \mu - q)N))}{\beta(\alpha + \mu)(\gamma + \mu - q)(\sigma + \mu)} + \frac{\nu((\alpha + \mu)(\gamma + \mu - q)N)}{\alpha \beta(\sigma + \mu)} \right) \]  
(13)

The equilibrium point of endemic state for Cholera is \( E^* = (S^*, E^*, I^*, R^*) \) with

\[ S^* = \frac{(\alpha + \mu)(\gamma + \mu - q)N}{\alpha \beta}, E^* = \frac{\alpha \beta (bN + \sigma R) - (v + \mu)(\alpha + \mu)(\gamma + \mu - q)N}{\alpha \beta(\alpha + \mu)} \]

\[ I^* = \frac{\alpha \beta (bN + \sigma R) - (v + \mu)(\alpha + \mu)(\gamma + \mu - q)N}{\beta(\alpha + \mu)(\gamma + \mu - q)}, \text{ and} \]

\[ R^* = \left( \frac{(\gamma (\alpha \beta (bN + \sigma R) - (v + \mu)(\alpha + \mu)(\gamma + \mu - q)N))}{\beta(\alpha + \mu)(\gamma + \mu - q)(\sigma + \mu)} + \frac{\nu((\alpha + \mu)(\gamma + \mu - q)N)}{\alpha \beta(\sigma + \mu)} \right) \].

3.3. Stability Analysis of SEIRS Model for Free disease
The stability analysis is determined based on the eigenvalues and the Jacobian matrix obtained from the linearization method.
The Jacobian matrix in the neighborhood \( E_0 \) is:

\[
J_0 = \begin{bmatrix}
-v - \mu & 0 & -\beta (b + \sigma R) \\
0 & -\alpha - \mu & \beta (b + \sigma R) \\
0 & \alpha & q - \gamma - \mu \\
v & 0 & \gamma & -\sigma - \mu
\end{bmatrix}
\]

The characteristic equation is \( |J_0 - \lambda I| = 0 \):

\[
\begin{vmatrix}
-v - \mu & 0 & -\beta (b + \sigma R) \\
0 & -\alpha - \mu & \beta (b + \sigma R) \\
0 & \alpha & q - \gamma - \mu - \lambda \\
v & 0 & \gamma & -\sigma - \mu - \lambda
\end{vmatrix} = 0
\]

\[
\begin{vmatrix}
-v - \mu - \lambda & 0 & -\beta (b + \sigma R) \\
0 & -\alpha - \mu - \lambda & \beta (b + \sigma R) \\
0 & \alpha & q - \gamma - \mu - \lambda - \lambda \\
v & 0 & \gamma & -\sigma - \mu - \lambda - \lambda
\end{vmatrix} = 0
\]

\[
\begin{vmatrix}
-v - \mu - \lambda & 0 & -\beta (b + \sigma R) \\
0 & -\alpha - \mu - \lambda & \beta (b + \sigma R) \\
0 & \alpha & q - \gamma - \mu - \lambda - \lambda \\
v & 0 & \gamma & -\sigma - \mu - \lambda - \lambda
\end{vmatrix} = 0
\]

\[
\begin{vmatrix}
-v - \mu - \lambda & \alpha & 0 \\
0 & -\alpha - \mu - \lambda & 0 \\
0 & \alpha & q - \gamma - \mu - \lambda - \lambda \\
v & 0 & \gamma & -\sigma - \mu - \lambda - \lambda
\end{vmatrix} = 0
\]

\[
\begin{vmatrix}
-v - \mu - \lambda & \alpha & 0 \\
0 & -\alpha - \mu - \lambda & 0 \\
0 & \alpha & q - \gamma - \mu - \lambda - \lambda \\
v & 0 & \gamma & -\sigma - \mu - \lambda - \lambda
\end{vmatrix} = 0
\]

\[
\begin{vmatrix}
-v - \mu - \lambda & 0 & -\beta (b + \sigma R) \\
0 & -\alpha - \mu - \lambda & \beta (b + \sigma R) \\
0 & \alpha & q - \gamma - \mu - \lambda - \lambda \\
v & 0 & \gamma & -\sigma - \mu - \lambda - \lambda
\end{vmatrix} = 0
\]

\[
\begin{vmatrix}
-v - \mu - \lambda & 0 & -\beta (b + \sigma R) \\
0 & -\alpha - \mu - \lambda & \beta (b + \sigma R) \\
0 & \alpha & q - \gamma - \mu - \lambda - \lambda \\
v & 0 & \gamma & -\sigma - \mu - \lambda - \lambda
\end{vmatrix} = 0
\]

\[
\begin{vmatrix}
-v - \mu - \lambda & 0 & -\beta (b + \sigma R) \\
0 & -\alpha - \mu - \lambda & \beta (b + \sigma R) \\
0 & \alpha & q - \gamma - \mu - \lambda - \lambda \\
v & 0 & \gamma & -\sigma - \mu - \lambda - \lambda
\end{vmatrix} = 0
\]

\[
\begin{vmatrix}
-v - \mu - \lambda & 0 & -\beta (b + \sigma R) \\
0 & -\alpha - \mu - \lambda & \beta (b + \sigma R) \\
0 & \alpha & q - \gamma - \mu - \lambda - \lambda \\
v & 0 & \gamma & -\sigma - \mu - \lambda - \lambda
\end{vmatrix} = 0
\]

\[
\begin{vmatrix}
-v - \mu - \lambda & 0 & -\beta (b + \sigma R) \\
0 & -\alpha - \mu - \lambda & \beta (b + \sigma R) \\
0 & \alpha & q - \gamma - \mu - \lambda - \lambda \\
v & 0 & \gamma & -\sigma - \mu - \lambda - \lambda
\end{vmatrix} = 0
\]

\[
\begin{vmatrix}
-v - \mu - \lambda & 0 & -\beta (b + \sigma R) \\
0 & -\alpha - \mu - \lambda & \beta (b + \sigma R) \\
0 & \alpha & q - \gamma - \mu - \lambda - \lambda \\
v & 0 & \gamma & -\sigma - \mu - \lambda - \lambda
\end{vmatrix} = 0
\]

\[
\begin{vmatrix}
-v - \mu - \lambda & 0 & -\beta (b + \sigma R) \\
0 & -\alpha - \mu - \lambda & \beta (b + \sigma R) \\
0 & \alpha & q - \gamma - \mu - \lambda - \lambda \\
v & 0 & \gamma & -\sigma - \mu - \lambda - \lambda
\end{vmatrix} = 0
\]
Thus, there are two possibilities for determining the eigenvalues:
1. \((−v−μ−\lambda)(−\sigma−μ−\lambda)−(v+\sigma+\mu)=0\)

Given the characteristic equation
\[\lambda^2+(2\mu+\sigma+v)\lambda+\mu(v+\sigma+\mu)=0\]
Suppose \(\lambda^2+A\lambda+B=0\)

Based on the characteristic equation (14), then it is obtained:
\[A=2\mu+\sigma+v\]
\[B=\mu(v+\sigma+\mu)\]

Because \(\mu, \sigma, v > 0\), then \(2\mu+\sigma+v=A>0\) and \(\mu(v+\sigma+\mu)=B>0\).

Based on the coefficient value of equation \(Q(\lambda)\) obtained: \(h_0=1, h_1=A, h_2=B\)
formed the following Hurwitz matrix:
\[
H = \begin{bmatrix}
    h_1 & h_3 \\
    h_0 & h_2
\end{bmatrix}
= \begin{bmatrix}
    A & 0 \\
    1 & B
\end{bmatrix}
\]

Based on the above Hurwitz matrix, the determinants of Hurwitz are obtained:
\[\Delta_1 = |h_1| = |A| = A\]
\[\Delta_2 = \begin{vmatrix}
    h_1 & h_3 \\
    h_0 & h_2
\end{vmatrix}
= \begin{vmatrix}
    A & 0 \\
    1 & B
\end{vmatrix}
= AB\]

of the value \(A\) and \(B\), it can be seen that:
\(A>0 \Rightarrow \Delta_1 = A>0\)
\(A>0, B>0\), maka \(AB>0 \Rightarrow \Delta_2 = AB>0\)

2. \((−\alpha−\mu−\lambda)(q−\gamma−\mu−\lambda)−\beta\left(\frac{b+\sigma R}{v+\mu}\right)(\alpha)=0\)

Given the characteristic equation
\[\lambda^2+(2\mu+\alpha+\gamma-q)\lambda+(\mu+\alpha)\left(\mu+\gamma-q−\frac{\beta(b+\sigma R)}{v+\mu}\right)=0\]
Suppose \(\lambda^2+A\lambda+B=0\)

Based on the characteristic equation (15), then it is obtained:
\[A=(2\mu+\alpha+\gamma-q)\]
\[B=(\mu+\alpha)\left(\mu+\gamma-q−\frac{\beta(b+\sigma R)}{v+\mu}\right)\]

Because \(\mu, \alpha, \gamma, q, \beta, b, \sigma, v > 0\), then \(2\mu+\alpha+\gamma-q=A>0\)
and \((\mu+\alpha)\left(\mu+\gamma-q−\frac{\beta(b+\sigma R)}{v+\mu}\right)=B>0\).
Based on the coefficient value of equation $Q(\lambda)$ obtained:

$h_0 = 1, h_1 = A, h_2 = B$

formed the following Hurwitz matrix:

$$H = \begin{bmatrix} h_1 & h_2 \\ h_0 & h_2 \end{bmatrix} = \begin{bmatrix} A & 0 \\ 1 & B \end{bmatrix}$$

Based on the above Hurwitz matrix, the determinants of Hurwitz are obtained:

$$\Delta_3 = |h_1| = |A| = A$$

$$\Delta_4 = \begin{vmatrix} h_1 & h_2 \\ h_0 & h_2 \end{vmatrix} = \begin{vmatrix} A & 0 \\ 1 & B \end{vmatrix} = AB$$

of the value $A$ and $B$, it can be seen that:

$A > 0 \Rightarrow \Delta_3 = A > 0$

$A > 0, B > 0$, maka $AB > 0 \Rightarrow \Delta_4 = AB > 0$

Because of the values $\Delta_1 > 0, \Delta_2 > 0, \Delta_3 > 0$, and $\Delta_4 > 0$ then the polynomial $Q(\lambda)$ has a zero-maker whose real part is negative. Thus, all real numbers of eigenvalues in the matrix $J_0$ are negative. Based on the Routh-Hurwitz Criteria, if the determinant of Hurwitz is positive, then all the roots of the polynomial equation $Q(\lambda)$ are negative or have a negative real part. In other words, the eigenvalues have a negative real part. So it can be concluded that the system around the equilibrium point of the disease $E_0$ is stable asymptotically local. This suggests that over long periods of time, individuals in the population go to the point $E_0$ or no individual is infected with the disease.

3.4. Stability Analysis of SEIRS Model for Endemic disease

The Jacobian matrix $E_*$ in the neighborhood is:

$$J_1 = \begin{bmatrix} -\beta I^* - v - \mu & 0 & -\beta S^* / N & \sigma \\ \beta I^* / N & -\alpha - \mu & \beta S^* / N & 0 \\ 0 & \alpha & q - \gamma - \mu & 0 \\ v & 0 & \gamma & -\sigma - \mu \end{bmatrix}$$

The characteristic equation is $|J_0 - \lambda I| = 0$

$$\Rightarrow \begin{bmatrix} -\beta I^* - v - \mu & 0 & -\beta S^* / N & \sigma \\ \beta I^* / N & -\alpha - \mu & \beta S^* / N & 0 \\ 0 & \alpha & q - \gamma - \mu & 0 \\ v & 0 & \gamma & -\sigma - \mu \end{bmatrix} \begin{bmatrix} \lambda & 0 & 0 & 0 \\ 0 & \lambda & 0 & 0 \\ 0 & 0 & \lambda & 0 \\ 0 & 0 & 0 & \lambda \end{bmatrix} = 0$$
The characteristic equation is
\[
\lambda^4 + A\lambda^3 + B\lambda^2 + C\lambda + D = 0
\]
(16)

Suppose:
\[
\lambda^4 + A\lambda^3 + B\lambda^2 + C\lambda + D = 0
\]
With
\[
A = \left(1 + 4\mu + \sigma + \gamma + v + \alpha + \beta \frac{I^*}{N} - q\right) > 0
\]
Based on the polynomial value $Q(\lambda)$, obtained:

$h_0=1,h_1=A,h_2=B,h_3=C,h_4=D$

formed the following Hurwitz matrix:

$$H = \begin{bmatrix} h_1 & h_2 & 0 & 0 \\ h_3 & h_4 & h_5 & h_6 \\ h_7 & h_8 & h_9 & h_{10} \end{bmatrix} = \begin{bmatrix} A & 1 & 0 & 0 \\ C & B & A & 1 \\ 0 & D & C & B \\ 0 & 0 & 0 & D \end{bmatrix}$$
Based on the above Hurwitz matrix, Hurwitz's determinant is obtained:
\[ \Delta_1 = |J_1| = |A| = A \]
\[ \Delta_2 = \begin{vmatrix} h_1 & h_2 \\ h_3 & h_4 \end{vmatrix} = AB - C \]
\[ \Delta_3 = \begin{vmatrix} h_1 & h_2 & h_3 \\ h_4 & h_5 & h_6 \end{vmatrix} = AB(C - DA^2 - C^2) \]
\[ \Delta_4 = \begin{vmatrix} h_1 & h_0 & 0 \\ h_4 & h_5 & h_6 \\ h_7 & h_8 & h_9 \end{vmatrix} = ABCD(D^2A) - C(CD) \]

By the values of \( A, B, C, \) and \( D \) then, we have:
\[ A > 0 \Rightarrow \Delta_1 = A > 0 \]
\[ A > 0, B > 0, C > 0, A > B > C, \text{then } AB > C \Rightarrow \Delta_2 = AB - C > 0 \]
\[ A > 0, B > 0, C > 0, D > 0, A > B > C > D, \text{then } ABC > D \Rightarrow \Delta_3 = ABC - (DA^2 + C^2) > 0 \]
\[ A > 0, B > 0, C > 0, D > 0, A > B > C > D \Rightarrow \Delta_4 = ABCD - D^2A - C(CD) > 0 \]

Because of the values \( \Delta_1 > 0, \Delta_2 > 0, \Delta_3 > 0, \) and \( \Delta_4 > 0 \) then the polynomial \( Q(\lambda) \) has a zero-maker whose real part is negative. Thus, all real numbers of eigenvalues in the matrix \( J_1 \) are negative. Based on the Routh-Hurwitz Criteria, if the determinant of Hurwitz is positive, then all the roots of the polynomial equation \( Q(\lambda) \) are negative or have a negative real part. So it can be concluded that the system around the equilibrium point \( E_\ast = (S^\ast, E^\ast, I^\ast, R^\ast) \) is stable asymptotically local endemic. This suggests that over long periods of time, individuals in the population are on the point \( E_\ast \) or there are individuals who are infected with cholera.

### 3.5. Basic Reproduction Number

To know the extent of the spread of a disease required a parameter. The parameter commonly used in disease-related problems is the reproduction number. The reproduction numbers used in this study are vaccination reproduction number and reproduction treatment number. The reproduction vaccination and treatment reproduction numbers are obtained by using a constant number in the characteristic equation of the stability of the disease-free equilibrium point.

\[ \Rightarrow (\mu + \sigma + \mu)\left[ \mu + \alpha \right] \left[ \mu + \gamma - q \right] - \left( \frac{\beta(b + \sigma R)}{v + \mu} \right) > 0 \]

\[ \Rightarrow \frac{(\mu + \gamma - q)(v + \mu)}{\beta(b + \sigma R)} < 1 \]

\[ \Rightarrow \frac{\mu + \gamma - q}{\beta(b + \sigma R)} < 1 \] (17)
Based on equation (4.17), the ratio of vaccine reproduction and treatment numbers is as follows:

\[
R_0 = \frac{(\mu + \gamma - q)(v + \mu)}{\beta(b + \sigma R)} \tag{18}
\]

If \( R_0 < 1 \) it means, the disease will disappear from the population and if \( R_0 > 1 \) it means, the infection will go unlimited.

If \( R_0 = 1 \) obtain the minimum vaccination level and minimum treatment level, namely:

\[
v_m = \mu - \frac{\beta(b + \sigma R)}{(\mu + \gamma - q)}
\]

\[
q_m = \mu + \gamma - \frac{\beta(b + \sigma R)}{(v + \mu)} \tag{19}
\]

If the vaccination rate is given more than the minimum vaccination rate, \( v_m \) then:

\[
\frac{(\mu + \gamma - q)(v + \mu)}{\beta(b + \sigma R)} < \frac{(\mu + \gamma - q)(v_m + \mu)}{\beta(b + \sigma R)} \tag{21}
\]

\( R_0(v) < R_0(v_m) = 1 \)

If the given vaccination rate is less than the minimum vaccination level \( v_m \), then:

\[
\frac{(\mu + \gamma - q)(v + \mu)}{\beta(b + \sigma R)} > \frac{(\mu + \gamma - q)(v_m + \mu)}{\beta(b + \sigma R)} \tag{22}
\]

\( R_0(v) > R_0(v_m) = 1 \)

If the treatment level is given more than the minimum treatment level \( q_m \), then:

\[
\frac{(\mu + \gamma - q)(v + \mu)}{\beta(b + \sigma R)} < \frac{(\mu + \gamma - q_m)(v + \mu)}{\beta(b + \sigma R)} \tag{23}
\]

\( R_0(q) < R_0(q_m) = 1 \)

If the treatment level is less than the minimum treatment level \( q_m \), then:

\[
\frac{(\mu + \gamma - q)(v + \mu)}{\beta(b + \sigma R)} > \frac{(\mu + \gamma - q_m)(v + \mu)}{\beta(b + \sigma R)} \tag{24}
\]

\( R_0(q) > R_0(q_m) = 1 \)

3.6. Discussion

Reny (2009) had found the mathematical model in cases of cholera epidemics with a constant population [2] and Hidayati (2015) examined stability analysis for the spread of cholera disease based on the SIR model with vaccination [4]. Both models are not considered treatment factors that may affect the spread of cholera disease. Therefore, this paper found the SEIRS model for transmission of cholera disease by taking into account vaccination and treatment factors then done the analysis at the equilibrium point. The cholera disease distribution model with vaccination given to vulnerable sub-classes of the population, as well as the treatment factor given to the infected population sub-class so that once controlled the healing rate is increased, whereas the previous model did not show it.
4. Conclusion
According to the result, we found the SEIRS model for transmission of Cholera disease, with vaccine and treatment factor. The SEIRS model have two equilibrium points are obtained, namely the disease-free equilibrium point and the endemic equilibrium point are free disease and endemic disease. Based on the Routh-Hurwitz Criteria, the disease-free equilibrium point and the endemic equilibrium point are local asymptotic stabilized. The number of reproductive vaccinations, if $R_0 < 1$ then the number of cholera patients gradually decreases so that the disease will disappear from the population and do not occur endemic. If $R_0 > 1$ then the number of patients with cholera disease gradually increasing so that the disease extends and becomes endemic. In order for the number of cholera patients to be suppressed as small as possible and the disease may disappear from the population, the vaccination rate should be more than the minimum vaccination rate. Based on the number of reproductive treatments, if $R_t < 1$ the number of cholera patients will gradually heal and decrease so that the disease will disappear from the population and do not occur endemic. If $R_t > 1$ then the number of patients with cholera disease gradually increasing so that the disease extends and becomes endemic. In order for the cure rate of cholera patients to increase and the disease may disappear from the population, the treatment level should be more than the minimum treatment level.

References
[1]. Fitrianah, Andi. 2015. *Vibrio Cholerae*. Medan: Departemen Mikrobiologi Fakultas Kedokteran Universitas Sumatera Utara.
[2]. Renny. 2009. *Jurnal: Model Matematika dalam Kasus Epidemik Kolera dengan Populasi Konstan*. Purwokerto: Program Studi Matematika Fakultas Matematika dan Ilmu Pengetahuan Alam Universitas Jenderal Sudirman.
[3]. Fitriyah, Aini. 2015. *Tesis: Suatu Analisis dari Model Matematika Penyakit Kolera*. Yogyakarta: Program Studi Matematika Fakultas Matematika dan Ilmu Pengetahuan Alam Universitas Gajah Mada.
[4]. Hidayati, Noer, dkk. 2015. *Analisis Kestabilan untuk Penyebaran Penyakit Kolera Berdasarkan Model SIR dengan Vaksinasi*. Yogyakarta:Universitas Negeri Yogyakarta.
[5]. Lesmana, Murad. 2004. *Jurnal: Perkembangan Mutakhir Infeksi Kolera*. Jakarta: Fakultas Kedokteran Universitas Trisakti.
[6]. YM Rangkuti, MS Sinaga, F Marpaung, S Side, 2014. A VSEIR model for transmission of Tuberculosis (TB) disease in North Sumatera, Indonesia. *AIP Conference Proceedings* 1635 (1), 201-208
[7]. S Side, W Sanusi, MK Aidid, S Sidjara, 2016. Global stability of SIR and SEIR model for Tuberculosis disease transmission with Lyapunov function method.*Asian. J. Appl. Sci* 9, 87-96
[8]. S Syafruddin, MSM Noorani, 2013. Lyapunov function of SIR and SEIR model for transmission of dengue fever disease. *International Journal of Simulation and Process Modelling* 8 (2-3), 177-184
[9]. YM Rangkuti, S Side, MSM Noorani, 2014. Numerical analytic solution of SIR model of dengue fever disease in south Sulawesi using homotopy perturbation method and variational iteration method. *Journal of Mathematical and Fundamental Sciences* 46 (1), 91-105
[10]. S Side, Irwan, U Mulbar, W Sanusi, 2017. SEIR model simulation for Hepatitis B. *AIP Conference Proceedings* 1885 (1), 020198