Dynamical Analysis of Model for Cholera Disease Spread with Quarantine

Tyas Husadaningsih[1*], Wuryansari Muharini Kusumawinahyu[2], Moch. Aruman Imron[3]

[1]Master Program of Mathematics, Faculty of Mathematics and Natural Sciences, University of Brawijaya, Malang, Indonesia

[2]Department of Mathematics, Faculty of Mathematics and Natural Sciences, University of Brawijaya, Malang, Indonesia

Abstract

In this paper, the model of cholera disease spread with quarantine is discussed. It is assumed that the spread of cholera not only through direct contact between susceptible human populations with bacteria but also through direct contact between susceptible human populations with infected human populations and reduced bacterial populations not only die naturally but can also be done by means of extermination bacteria. Determination of equilibrium points, existence and local stability of equilibrium points are investigated. Numerical simulations are performed to illustrate the results of the analysis.

Keywords: Dynamical Analysis, Model of Spread Cholera, Runge-Kutta Method 4th order, Local Stability, Quarantine.

INTRODUCTION

Cholera disease is a disease caused by drinking water contaminated by poor sanitation or food contaminated by *Vibrio cholera* bacteria. Some symptoms of cholera are watery diarrhea, vomiting and leg cramps. Cholera diseases can be transmitted by direct contact between susceptible populations and the bacterial populations present in the environment [1]. In addition cholera disease can also be transmitted through direct contact between susceptible populations with infected individuals [2].

Cholera disease has spread globally in 1883. Outbreaks of cholera disease in Indonesia occurred since 1992. In 2008-2009 recorded 98,585 people infected with cholera and 4,287 deaths occurred [3]. Based on WHO (World Health Organization) data estimated at 3,000,000-5,000,000 people infected with cholera diseases annually and recorded about 100,000-120,000 cases of cholera suffering death annually [4]. The phenomenon shows that cholera disease poses a global threat to the world, especially in the areas of health, social and economic dynamics.

Based on the history of cholera disease, it is necessary to study the spread of cholera disease. The method used to determine the spread of disease is by using mathematical model of disease epidemic. The epidemic model known since 1927 is often referred to as the SIR type model proposed by Kermack and McKendrick [5]. The SIR model is divided into three compartments, namely S (Susceptible) which states the population is susceptible to disease, I (Infected) which states the population is infected with the disease, and R (Recovered) which states the population is cured of the disease. Furthermore, the model used to determine the spread of cholera disease is the SIRB model (Susceptible-Infected- Recovered -Bacterial) [2,6,7,8]. In the SIRB model [2], it modifies from the SIRB model [8] by adding vaccinations and bacterial eradication. The SIRB model was developed into the SIQRB model (Susceptible, Infected, Quarantine, Recovered, Bacteria) by adding class Q (Quarantine) [1].

In this paper, the cholera disease distribution model will be discussed using the SIQRB type model by modifying from model [1] by adding direct contact of susceptible and infected human populations and bacterial eradication in model [2]. Direct contact between susceptible human populations with infected human populations are added to know that transmission of cholera is not only transmitted through bacteria alone but can be transmitted through infected human populations. Meanwhile, the reduction of bacterial populations can affect the increase of very sharp bacteria. In the modified model, dynamic analysis is done by determining equilibrium point and existence condition, equilibrium point analysis on result of discussion. At the end, a numerical simulation is performed to illustrate the results of the analysis with Runge-Kutta Method 4th order.

* Correspondence address:
Tyas Husadaningsih
Email : tyashusada7@gmail.com
Address : Dept. Mathematics, Faculty of Mathematics and Natural Sciences, University of Brawijaya, Veteran Malang, Malang 65145.

ISSN. 2087-2852
E-ISSN. 2338-1655

MATERIALS AND METHODS

Model Formulation

In this research, we modified the SIQRB model (Susceptible, Infected, Quarantine, Recovered, Bacteria) [1] by adding direct contact of susceptible human populations to infected human populations and bacterial eradication in the SIRB model [2].

Determination of the Equilibrium Point

A dynamical system is a system whose condition in the future will be known if given conditions in the present or past [9]. In completing the dynamic analysis, the first step is to determine the equilibrium point in the mathematical model. The equilibrium point is obtained from equilibrium equations of the system of equations, that is when the population growth rate of SIQRB is zero or equal to zero [10]. From the completion of the equilibrium point that has been obtained it will get the existence of conditions from the point of equilibrium.

Stability of the Equilibrium Point

In this paper, a local equilibrium stability analysis is performed. The determination of local stability begins with a linearization model to be formed Jacobian matrix. From the Jacobian matrix, the roots of characteristic equations or eigen values in the linear system are determined. The stability point is stable locally if the real part of the characteristic roots is negative or equal to zero.

Numerical Simulation

Numerical simulation is done with MATLAB software by applying Runge-Kutta method 4th order. The initial steps taken by determining the value of parameters that fit the terms of existence and the stability requirements of the equilibrium point. Furthermore, in the last step is interpreting the results of numerical simulation in the form of phase portrait graph and the solution curve with time.

RESULT AND DISCUSSION

Model Formulation

In this model, the modifications [1] are made by adding direct contact of susceptible human populations and infected human populations as well as the eradication of bacteria in the model [2]. In the SIRB model and SIQRB model can be written as follows

SIRB Model Formulation [4]

$$\begin{aligned}
\frac{dS}{dt} &= \mu N - \left(\beta_e S\frac{B}{k+B} + \beta_h SI\right) - \mu S \\
&\quad -vS, \\
\frac{dI}{dt} &= \beta_e S\frac{B}{k+B} + \beta_h SI - (\gamma+\mu)I, \qquad (1)\\
\frac{dR}{dt} &= \gamma I - \mu R + vS, \\
\frac{dB}{dt} &= \xi I - \delta B - cB.
\end{aligned}$$

SIQRB Model Formulation [3]

$$\begin{aligned}
\frac{dS}{dt} &= \Lambda - \frac{\beta B}{k+B}S + \omega R - \mu S, \\
\frac{dI}{dt} &= \frac{\beta B}{k+B}S - (\delta+\alpha_1+\mu)I, \\
\frac{dQ}{dt} &= \delta I - (\varepsilon+\alpha_2+\mu)Q, \qquad (2)\\
\frac{dR}{dt} &= \varepsilon Q - (\omega+\mu)R, \\
\frac{dB}{dt} &= \eta I - dB.
\end{aligned}$$

Modified models of equations (1) and (2) become as follows

$$\begin{aligned}
\frac{dS}{dt} &= \Lambda - \frac{\beta_1 B}{k+B}S - \beta_2 SI + \omega R - \mu S, \\
\frac{dI}{dt} &= \frac{\beta_1 B}{k+B}S + \beta_2 SI - (\delta+\alpha_1+\mu)I, \\
\frac{dQ}{dt} &= \delta I - (\varepsilon+\alpha_2+\mu)Q, \qquad (3)\\
\frac{dR}{dt} &= \varepsilon Q - (\omega+\mu)R, \\
\frac{dB}{dt} &= \eta I - dB - cB.
\end{aligned}$$

Diagram of compartment model epidemic cholera of equation (3) can be seen in Figure 1. Description of model parameter of cholera disease can be seen in Table 1 as follows.

ISSN. 2087-2852
E-ISSN. 2338-1655

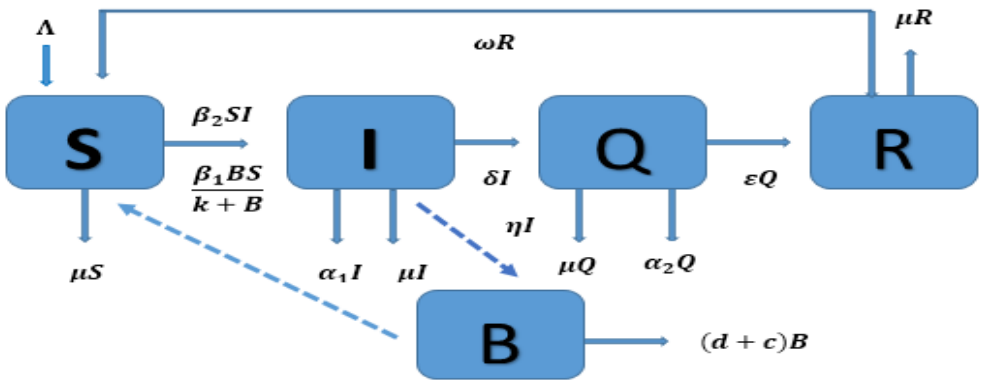


Figure 1. SIQRB Model Compartment Diagram

Table 1. Parameter values and initial conditions for the SIQRB

Parameter	Description
$S(0)$	Susceptible individuals at $t = 0$
$I(0)$	Infected individuals at $t = 0$
$Q(0)$	Quarantined individuals at $t = 0$
$R(0)$	Recovered individuals at $t = 0$
$B(0)$	Bacterial individuals at $t = 0$
Λ	Recruitment rate (birth and migration)
μ	Natural death rate
β_1	Environment-to-human transmission rate
β_2	Human-to-human transmission rate
k	Half saturation constant
ω	Immunity waning rate
δ	Quarantine rate
ε	Recovery rate
α_1	Death rate (infected)
α_2	Death rate (quarantined)
η	Shedding rate (infected)
d	Bacteria death rate
c	Disinfection rate

Stability of Equilibrium Points

The equilibrium point of model (3) is obtained when

$\frac{dS}{dt} = \frac{dI}{dt} = \frac{dQ}{dt} = \frac{dR}{dt} = \frac{dB}{dt} = 0$, that is,

$E_0^*\left(\frac{\Lambda}{\mu}, 0,0,0,0\right)$

$E_1^*(S_1^*, I_1^*, Q_1^*, R_1^*, B_1^*)$

where

$$k_1 = \delta + \alpha_1 + \mu, \qquad k_3 = \omega + \mu,$$

$$k_2 = \varepsilon + \alpha_2 + \mu, \qquad k_4 = d + c,$$

$$k_5 = \frac{\omega\varepsilon\delta - k_1 k_2 k_3}{\mu k_2 k_3} < 0,$$

$$A = \frac{\beta_2 \eta k_5}{k_4} < 0,$$

$$B = \left(\frac{\beta_1 \eta}{k_4} + \kappa\beta_2\right) k_5 + \frac{\eta}{k_4}\left(\frac{\beta_2 \Lambda}{\mu} - k_1\right),$$

$$C = \frac{\beta_1 \eta \Lambda}{k_4 \mu} + \kappa\left(\frac{\beta_2 \Lambda}{\mu} - k_1\right).$$

So that is obtained the value of endemic equilibrium point as follows.

$$S_1^* = \frac{\Lambda}{\mu} + k_5 I_1^*,$$

$$I_1^* = \frac{-B - \sqrt{B^2 - 4AC}}{2A}, \text{if } \frac{\beta_2 \Lambda}{\mu} > k_1$$

$$Q_1^* = \frac{\delta I_1^*}{k_2},$$

$$R_1^* = \frac{\varepsilon\delta I_1^*}{k_2 k_3},$$

$$B_1^* = \frac{\eta I_1^*}{k_4}.$$

The local stability analysis of the system equilibrium point (3) is determined by linearization. Jacobian matrix on model (3) is

$$J(E^*) = \begin{pmatrix} a_{11} & a_{12} & 0 & a_{14} & a_{15} \\ a_{21} & a_{22} & 0 & 0 & a_{25} \\ 0 & a_{32} & a_{33} & 0 & 0 \\ 0 & 0 & a_{34} & a_{44} & 0 \\ 0 & a_{52} & 0 & 0 & a_{55} \end{pmatrix}, \quad (5)$$

ISSN. 2087-2852
E-ISSN. 2338-1655

where

$a_{11} = -\frac{\beta_1 B}{\kappa+B} - \beta_2 I - \mu,\ a_{12} = -\beta_2 S,\ a_{14} = \omega,\ a_{15} = -\frac{\beta_1 S}{\kappa+B} + \frac{\beta_1 SB}{(\kappa+B)^2},\ a_{21} = \frac{\beta_1 B}{\kappa+B} + \beta_2 I,\ a_{22} = \beta_2 S - k_1,\ a_{25} = \frac{\beta_1 S}{\kappa+B} - \frac{\beta_1 SB}{(\kappa+B)^2},\ a_{32} = \delta,\ a_{33} = -k_2,\ a_{34} = \varepsilon,\ a_{44} = -k_3,\ a_{52} = \eta,\ a_{55} = -k_4.$

Theorem 1. The disease free equilibrium point E_0^* on system (3) is as follow.

Proof. The Jacobian matrix at point E_0^* is obtained by substituting the equilibrium point E_0^* in the matrix $J(E^*)$ is obtained.

$$J(E_0^*) = \begin{pmatrix} b_{11} & b_{12} & 0 & b_{14} & b_{15} \\ 0 & b_{22} & 0 & 0 & b_{25} \\ 0 & b_{32} & b_{33} & 0 & 0 \\ 0 & 0 & b_{34} & b_{44} & 0 \\ 0 & b_{52} & 0 & 0 & b_{55} \end{pmatrix},$$

where

$b_{11} = -\mu,\ b_{12} = \frac{-\beta_2 \Lambda}{\mu},\ b_{14} = \omega,\ b_{15} = \frac{-\beta_1 \Lambda}{\mu\kappa},\ b_{22} = \frac{\beta_2 \Lambda}{\mu} - k_1,\ b_{25} = \frac{\beta_1 \Lambda}{\mu\kappa},\ b_{32} = \delta,\ b_{33} = -k_2,\ b_{34} = \varepsilon,\ b_{44} = -k_3,\ b_{52} = \eta,\ b_{55} = -k_4.$

The eigen value of $J(E_0^*)$ is obtained by solving . The characteristic equation $|J(E_0^*) - \lambda I| = 0$

$$-(\mu+\lambda)(k_3+\lambda)(k_2+\lambda)\begin{pmatrix} \frac{\beta_2\Lambda}{\mu} - k_1 - \lambda & \frac{\beta_1\Lambda}{\mu\kappa} \\ \eta & -k_4 - \lambda \end{pmatrix} = 0,$$

Then generated three roots equation of negative characteristic is $\lambda_1 = -\mu, \lambda_2 = -k_3$, and $\lambda_3 = -k_2$ while the other eigen value is the eigen values of the matrix

$$X = \begin{pmatrix} \frac{\beta_2\Lambda}{\mu} - k_1 & \frac{\beta_1\Lambda}{\mu\kappa} \\ \eta & -k_4 \end{pmatrix}.$$

It is seen that the matrix X has a value

$$\det(X) = k_4\left(k_1 - \frac{\beta_2\Lambda}{\mu}\right) - \frac{\eta\beta_1\Lambda}{\mu\kappa}$$

and $trace\,(X) = \frac{\beta_2\Lambda}{\mu} - k_1 - k_4$

Based on [9], the equilibrium point E_0^* is asymptotically stable when the value

$$\det(X) = k_4\left(k_1 - \frac{\beta_2\Lambda}{\mu}\right) - \frac{\eta\beta_1\Lambda}{\mu\kappa} > 0$$

and $trace\,(X) = \frac{\beta_2\Lambda}{\mu} - k_1 - k_4 < 0$. Stability require-ments E_0^* causing existence condition E_1^* is not fulfilled

Theorem 2. The endemic Equilibrium point E_1^* on system (3) is as follow.

Proof. The Jacobi matrix at point E_1^* is obtained by substituting the equilibrium point E_1^* in matrix $J(E^*)$ is obtained

$$J(E_1^*) = \begin{pmatrix} c_{11} & c_{12} & 0 & \omega & c_{15} \\ c_{21} & c_{22} & 0 & 0 & c_{25} \\ 0 & d & -k_2 & 0 & 0 \\ 0 & 0 & \varepsilon & -k_3 & 0 \\ 0 & \eta & 0 & 0 & -k_4 \end{pmatrix}.$$

where

$c_{11} = -\frac{\beta_1 B^*}{\kappa+B^*} - \beta_2 I^* - \mu,\ c_{21} = \frac{\beta_1 B^*}{\kappa+B^*} + \beta_2 I^*,\ c_{12} = -\beta_2 S^*,\ c_{22} = \beta_2 S^* - k_1,\ c_{15} = -\frac{\beta_1 S^*}{\kappa+B^*} + \frac{\beta_1 S^* B^*}{(\kappa+B^*)^2},\ c_{25} = \frac{\beta_1 S^*}{\kappa+B^*} - \frac{\beta_1 S^* B^*}{(\kappa+B^*)^2}.$

The eigen value of $J(E_1^*)$ is obtained by solving $|J(E_1^*) - \lambda I| = 0$, that is

$$\lambda^5 + A_1\lambda^4 + A_2\lambda^3 + A_3\lambda^2 + A_4\lambda + A_5 = 0$$

where

$$\begin{aligned} A_1 &= -c_{11} + k_2 + k_3 + k_4 - c_{22}, \\ A_2 &= -k_3c_{22} + c_{11}c_{22} - k_2c_{22} - \eta c_{25} - c_{11}k_2 + k_3k_4 + k_2k_4 - c_{11}k_3 + k_2k_3 - \\ &\quad - c_{22}k_4 - c_{21}c_{12}, \\ A_3 &= -c_{11}k_2k_3 + c_{11}c_{22}k_3 - c_{11}k_3k_4 + c_{11}c_{22}k_2 - c_{11}k_2k_4 + c_{11}c_{22}k_4 + \eta c_{11}c_{25} - c_{22}k_2k_3 \\ &\quad + k_2k_3k_4 - k_3k_4c_{22} - \eta k_3c_{25} - k_2k_4c_{22} - \eta k_2c_{25} - \eta c_{21}c_{15} - c_{21}c_{12}k_4 \\ &\quad - c_{21}c_{12}k_2 - c_{21}c_{12}k_3, \\ A_4 &= -c_{21}d\varepsilon\omega + c_{11}c_{22}k_2k_3 - c_{11}k_3k_4k_2 + c_{11}c_{22}k_3k_4 + \eta c_{11}c_{25}k_3 + c_{11}c_{22}k_2k_4 \\ &\quad + \eta c_{11}c_{25}k_2 - c_{22}k_2k_3k_4 - \eta c_{25}k_2k_3 - \eta c_{21}c_{15}k_3 - \eta c_{21}c_{15}k_2 \\ &\quad - c_{21}c_{12}k_2k_4 - c_{21}c_{12}k_3k_4 - c_{21}c_{12}k_2k_3, \\ A_5 &= -c_{21}d\varepsilon\omega + c_{11}k_2k_3k_4c_{22} + c_{11}k_2k_3\eta c_{25} - c_{21}c_{15}\eta k_3k_4 - c_{21}c_{12}k_2k_3k_4. \end{aligned}$$

The values of the characteristic equations are solved using the Routh-Hurwitz criterion [11]. The root of the characteristic equation has a

ISSN. 2087-2852
E-ISSN. 2338-1655

negative real part if it qualifies several of the following criteria :

1. Requirements for $A_1 > 0$,
2. Requirements for $A_5 > 0$,
3. Terms for $A_1A_2 - A_3 > 0$,
4. Terms for $(A_1A_2 - A_3)A_3 - {A_1}^2A_4 > 0$,
5. Terms for $(A_1A_4 - A_5)(A_1A_2A_3 - A_3^2 - A_1^2A_4) - A_5(A_1A_2 - A_3)^2 - A_1A_5^2 > 0$.

Numerical Method and Simulations

The numerical method of epidemic model of spreading cholera disease of SIQRB is solved using MATLAB R 2010a software with Runge-Kutta method of order 4. The simulation is done in order to illustrated the result of analysis result so that the behavior of system solution (3) can be depicted graphically. There are two simulated cases that are numerical simulations showing the stability of the equilibrium point $E_0^*\left(\frac{\Lambda}{\mu}, 0,0,0,0\right)$ and numerical simulations showing the stability of the equilibrium point $E_1^*(S_1^*, I_1^*, Q_1^*, R_1^*, B_1^*)$.

The first parameter is chosen to simulate the first equilibrium point is

$\Lambda = 0.009,\ \mu = 0.0002,\ \beta_1 = 0.8,\ \beta_2 = 0.00001,\ \kappa = 10^6,\ \omega = 0.02,\ \delta = 0.05,\ \varepsilon = 0.2,\ \alpha_1 = 0.015,\ \alpha_2 = 0.001,\ \eta = 5,\ d = 0.03,\ c = 1.$

The condition is indicated by modifying various initial values

$NA_1 = (15, 20, 15, 0, 0),\ NA_2 = (22, 10, 5, 10, 5),\ NA_3 = (26, 5, 5, 10, 5),$

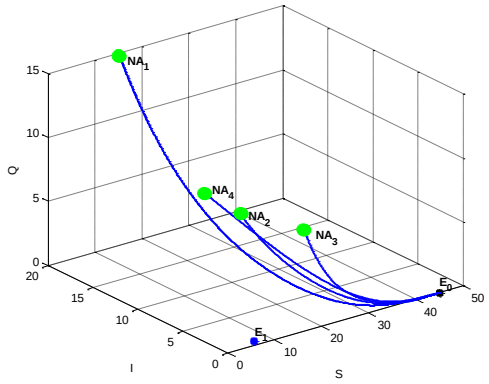
and $NA_4 = (24, 15, 5, 5, 10)$

as shown in Figure 1 and Figure 2. Figure 2 illustrates the subpopulation change between by using 4 initial values. It appears that the number of susceptible human populations can survive while the human population is infected, the human population is quarantined, the human population recovered. While the bacterial population is extinct. This condition can be said that the bacteria of *V. cholera* and infected population did not successfully infect the vulnerable population.

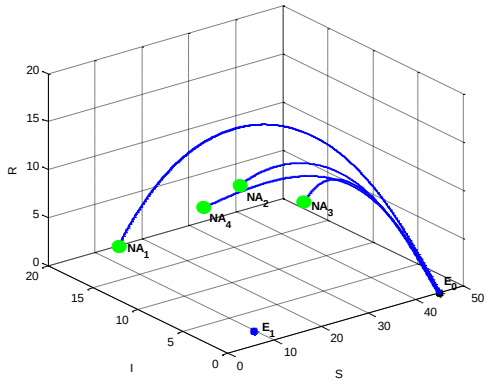
Based on the parameter values, the stability condition of the equilibrium point E_0^* is

$det = 0.0644425 > 0$ and
$trace = -1.09475 < 0$

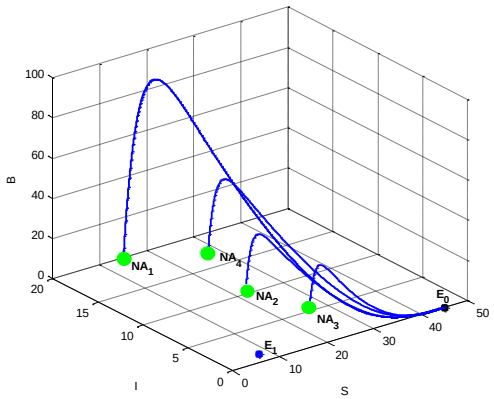
then the number of each subpopulation will go to equilibrium-free equilibrium point $E_0^* = (45, 0, 0, 0, 0)$. Therefore E_0^* is stable asymptotically local.



(a) Point phase SIQ



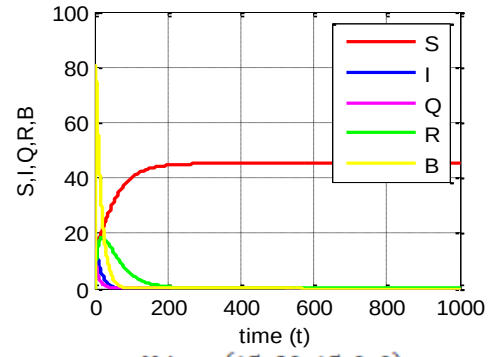
(b) Point phase SIR



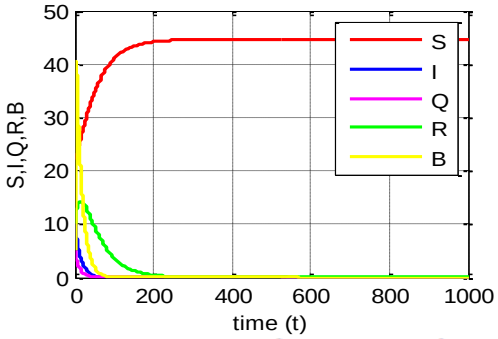
(c) Point phase SIB

Figure 1. Stability the disease free equilibrium E_0^* for NA_1, NA_2, NA_3 and NA_4

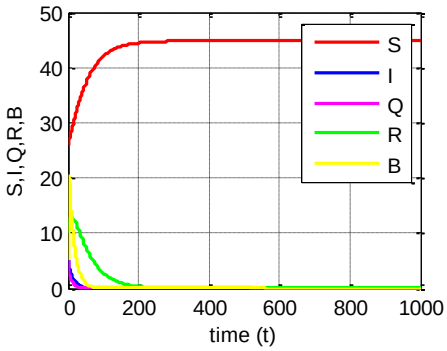
ISSN. 2087-2852
E-ISSN. 2338-1655



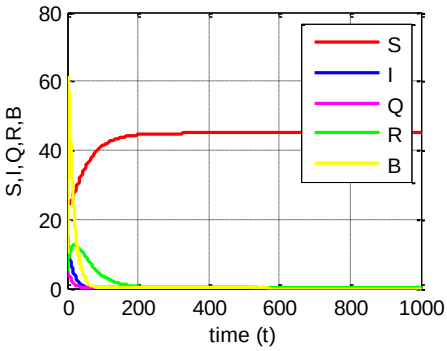
(a) $NA_1 = (15, 20, 15, 0, 0)$



(b) $NA_2 = (22, 10, 5, 10, 5)$



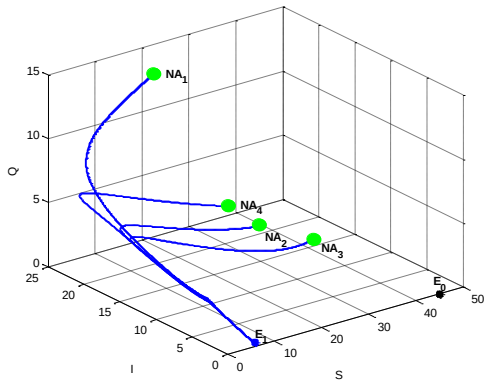
(c) $NA_3 = (26, 5, 5, 10, 5)$



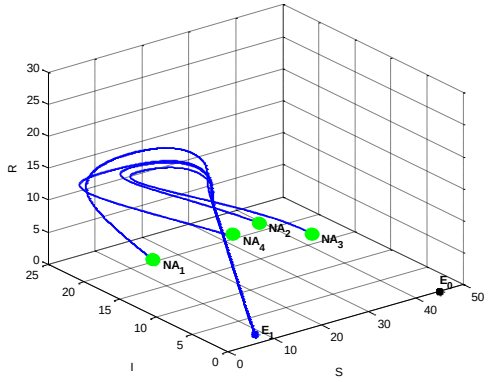
(d) $NA_4 = (24, 15, 5, 5, 10)$

Figure 2. The solution curve of endemic equilibrium point to time $0 \leq t \leq 1000$

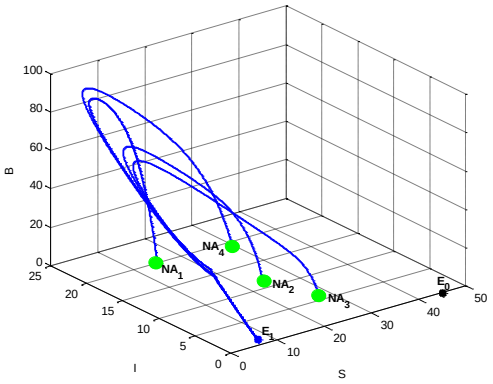
Select the parameter value endemic E_1^* by changing the parameter value $\beta_2 = 0.01$ while the other parameter values are the same as the first parameter value, then the stability condition of equilibrium point E_0^* is not fulfilled. While the conditions of existence and stability E_1^* are qualify that is the local asymptotic stable. The condition is shown by using various initial values $NA_1 = (15, 20, 15, 0, 0)$, $NA_2 = (22, 10, 5, 10, 5)$, $NA_3 = (26, 5, 5, 10, 5)$, and $NA_4 = (24, 15, 5, 5, 10)$. As shown on figure 3 and figure 4.



(a) Point phase SIQ



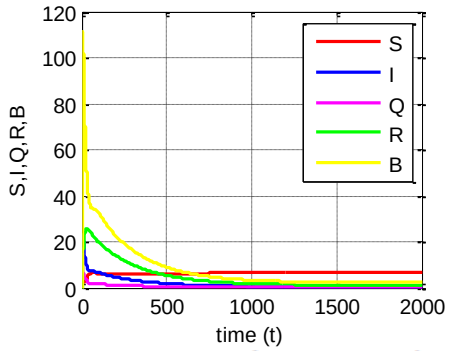
(b) Point phase SIR



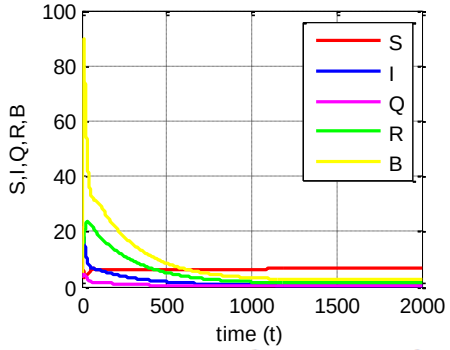
(c) Point phase SIB

Figure 3. Stability the endemic equilibrium E_1^* for NA_1, NA_2, NA_3 and NA_4

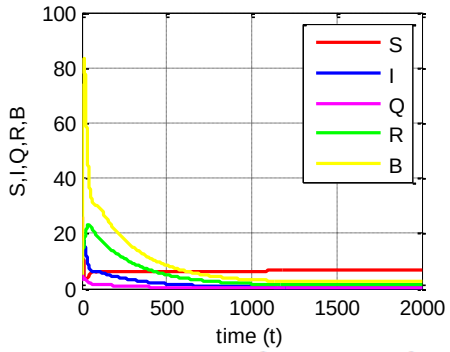
ISSN. 2087-2852
E-ISSN. 2338-1655



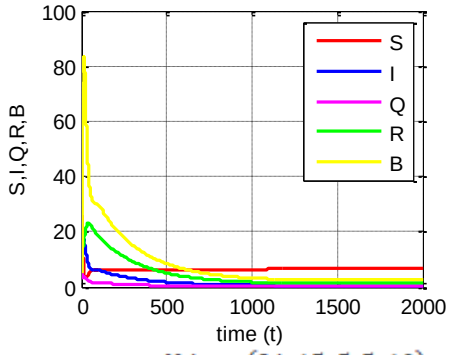
(a) $NA_1 = (15, 20, 15, 0, 0)$



(b) $NA_2 = (22, 10, 5, 10, 5)$



(c) $NA_3 = (26, 5, 5, 10, 5)$



(d) $NA_4 = (24, 15, 5, 5, 10)$

Figure 4. The solution curve of endemic equilibrium point to time $0 \leq t \leq 2000$

Figure 4 illustrates the subpopulation change between $0 \leq t \leq 2000$ by using 4 initial values.

It appears that the human population is susceptible (S), the human population is infected (I), the human population is quarantined (Q), the human population recovered (R), and the bacterial population (B) can survive. This condition can be said that the bacteria vibrio cholera and infected population have been infected the vulnerable population.

Based on the parameter values, the stability condition of the equilibrium point E_1^* is

$$A_1 = 1.256443742 > 0,\ A_5 = 0.0000007190869874 > 0,\ A_1A_2 - A_3 = 0.2941765335 > 0,\ (A_1A_2 - A_3)A_3 - A_1{}^2A_4 = 0.001542449551 > 0,\ (A_1A_4 - A_5)(A_1A_2A_3 - A_3^2 - A_1^2A_4) - A_5(A_1A_2 - A_3)^2 - A_1A_5^2 = 0.0000001174750234 > 0$$

then the number of each subpopulation will go to the equilibrium point of endemic disease

$$E_1^* = (6.51746895,\ 0.4813232099,\ 0.11961131237,\ 1.184288354,\ 2.336520436)$$

Therefore E_1^* is the local asymptotic stable.

CONCLUSION

The SIQRB model is a modification of the model [1] by adding direct contact of susceptible human populations to infected human population and bacterial eradication in model [2]. SIQRB model obtained 2 equilibrium point value that is equilibrium point of disease E_0^* and endemic point of disease E_1^*. Equilibrium points E_0^* and E_1^* are asymptotically stable locally on terms already discussed in the previous discussion. The equilibrium point results are investigated using numerical simulations according to the analysis.

REFERENCES

[1] Lemos-Paiao, A.P., C.J. Silva., D.F.M. Torres. 2017. An epidemic model for cholera with optimal control treatment. *J. Comput. Appl. Math.* 318. 168-180.

[2] Sun, G., J. Xie, S. Huang, Z. Jin, M. Li, L. Liu. 2017. Transmission dynamics of cholera: Mathematical modeling and control strategis. *J. Commun. Nonlinear. Sci. Numer. Simulat. Elsevier B. V.* 45.b235-244.

[3] Mukandavire Z., S. Liao, J. Wang, H. Gaff, D.L. Smith, J.G. Morris. 2011. Estimating the reproductive numbers for the 2008-2009

cholera outbreaks in Zimbabwe. DOI: 10.1073/pnas.1019712108.

[4] World Health Organization (WHO). 2011. Cholera Fact Sheet. Geneva: World Health Organization. Available at: http://www.who.int/mediacentre/factsheets/fs107/en/index.html.

[5] Shuai, Z., J.H. Tien. 2012. Cholera models with hyperinfectivity and temporary immunity. *Bull. Math. Biol.* 74. 2423-2445.

[6] Cheng, Y., J. Wang, X. Yang. 2012. On the global stability of a generalized cholera epidemiological model. *J. Biol. Dynamics.* 6(2). 1088-1104.

[7] Khan, M.A., A. Ali, L.C.C. Dennis, T. Gui. 2015. Dynamical behavior of cholera epidemic model with non-linear incidence rate. *Appl. Math. Sci.* 9(20). 989-1002.

[8] Wang, J., C. Modnak. 2011. Modeling cholera dynamics with controls. *Canadian Appl. Math. Quarterly.* 19(3), 255-273.

[9] Panfilov, A. 2004. Qualitative of differential equation. Utrect University. Utrecht.

[10] Boyce, W.E., R.C. Diprima 2012. Elementary differential equation and boundary value problems, 9th Ed., John Willey and Sons, Inc. United State of America.

[11] Murray, J.D. 2002. Mathematical biology: an introduction, 3rd Ed. Springer-Verlg, Inc. Berlin.

ISSN. 2087-2852
E-ISSN. 2338-1655