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Mathematical Modeling of SIQS Cholera Dynamics with Vaccination

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Abstract

Mathematics plays an important role in study of biological systems through mathematical models. Cholera is an acute intestinal infectious disease caused by the bacterium vibrio cholerae. In the present paper, a mathematical model for Susceptible-Infected-Quarantine-Susceptible cholera dynamics with vaccination is studied. Determine the equilibrium points of the model: disease-free and endemic .Also obtained basic reproduction number R_0 . Stability has been discussed for both equilibrium points using Routh–Hurwitz criteria ,Castillo-Chavez criteria and Dulac's criterion plus Poincare-Bendixson theorem respectively . Numerical simulations are also carried out to investigate the influence of certain parameters on the spread of disease, to support the analytical results of the model.
Keywords: Quarantine, stability, reproduction number, Routh–Hurwitz criteria ,Castillo-Chavez criteria and Dulac's criterion, Poincare-Bendixson theorem.

1. Introduction

Adebimpe O. et.al. studied an SIQS epidemic model with saturated incidence rate in [1]. They obtained two equilibrium points : disease-free and endemic equilibrium and discussed the global stability of the disease-free and endemic equilibrium is proved using Lyapunov functions and Poincare-Bendixson theorem plus Dulac's criterion respectively.Castillo-Chavez et. al. discussed reproductive number and stability for some epidemic models.Specially, they gave a theorem on globally analysis of equilibrium points known as Castillo-Chavez criterion[2] .Ezeagu et.al. proposed a SIQR cholera dynamical model with vaccination parameter as control strategy[3].In this paper, they discussed locally asymptotically stability of disease-free equilibrium and numerically results shown the effectiveness of quarantine and vaccination to control the disease contact rates and thus eliminates the spread of cholera.Mokati D. et.al. focused to the role of cyclic behavior of cholera disease with infectious individuals[4].They discussed the local stability of disease-free and endemic equilibria by Routh-Hurwitz criteria and graphically it is more clearly seen. Many mathematical models have been proposed by many researchers to investigate the complex epidemic and endemic behavior of cholera. The effects of vaccination on the transmission of cholera models are also studied by many authors.Nirwani N. et al. proposed a SIQR-B cholera epidemic model. They studied and analyzed the effects of quarantine and incidence on the spread of cholera disease[5].An SIQR compartment model has been discussed by Nirwani N. et al.[6]. Determined the equilibrium points of the model and stability analysed. They found that the equilibrium points are locally asymptotically stable under certain conditions . Wang et al. [7]presented and analyzed a cholera epidemiological model with control measures incorporated . Equilibrium analysis is conducted in the case with constant controls for both epidemic and endemic dynamics. Further , they applied optimal control theory to observe the

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cost-effective solution of multiple time-dependent intervention strategies against cholera outbreaks.

2. Model Formulation

We have referred Ezeagu et al.[3] and modified it by adding transmission rate αI .Considered an SIQS cholera epidemic model with quarantine and vaccination effect. In the model human population is divided into classes containing susceptible (S) , infectious (I) , quarantine (Q) and recovered (R) individuals at time t . The pathogen population at time t is given by $B(t)$ .Now consider the total number of population at time t is $S+I+Q+R=N$.

The flow of individual is depicted in the following transfer diagram(Figure 1)

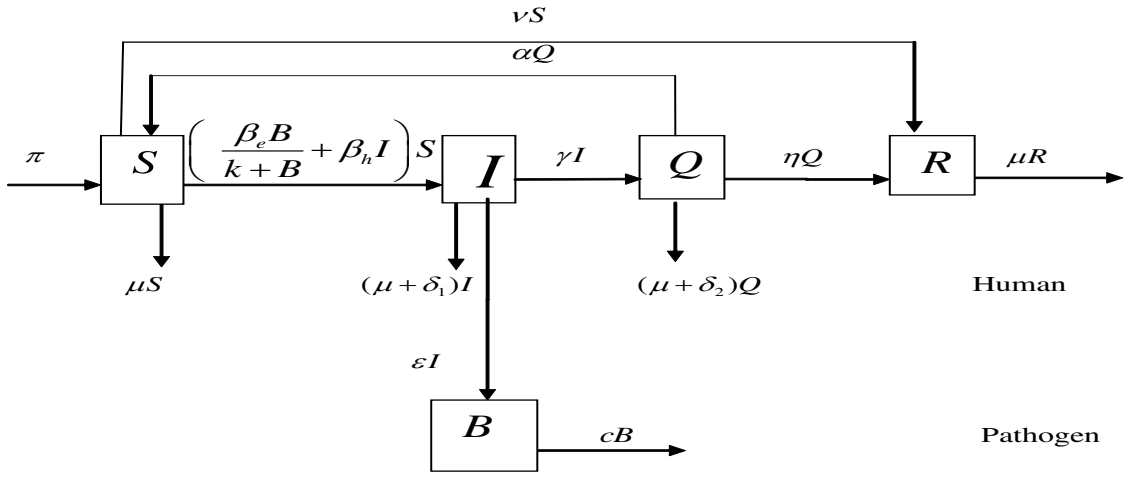

Figure 1 : Transfer diagram for SIQS cholera model

The symbols are used here stands for

π	Recruitment rate of population
β_h , β_e	Human-to-Human transmission rate, Environment–to-human transmission rate respectively
μ , ν	Natural death rate, Vaccination rate respectively
γ , η	Quarantine rate , Recovery rate respectively
k , α	Concentration rate, Rate at which individuals recover and return to Susceptible (S) from compartment Q respectively
ε , c	Sheding rate,Sanitation rate respectively
δ_1 , δ_2	Disease induced death rates(infected), Disease induced death rates(Quarantined)respectively

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All parameters are assumed nonnegative .

3. Mathematical Analysis

Basic Concepts

- **Dulac's Criterian**

  Consider the following general nonlinear autonomous system of differential equation

  $$x(t) = f(x),\ x \in E \qquad (*)$$

  Let $f = C^1(E)$ where E is a simple connected region in R^2. If the exists a function it $H \in C^1(E)$ such that $\nabla(H.f)$ is not identically zero and does not change sign in E, the system (*) has no close orbit lying entirely in E. if A is an annular region contained in E on which $\nabla(H.f)$ does not change sign, then there is at most one limit cycle of the system (*) in A.

- **Poincare-Bendixson Theorem :**Suppose that $f \in C^1(E)$ where E is an open subset of R^n and that the system (*) has a rejecting Γ contained in a compact subset f of E. Assume that the system (*) has only one unique equilibrium point x_0 in f, then one of the following possibilities holds.
  (a) $w(\Gamma)$ is the equilibrium point x_0 ,
  (b) $w(\Gamma)$ is a periodic orbit ,
  (c) $w(\Gamma)$ is a graphic .

The differential equations corresponding to the transfer diagram are

$$\left.\begin{aligned}
\frac{dS}{dt} &= \pi - \frac{B\beta_e S}{k+B} - \beta_h SI - (\mu+\nu)S + \alpha Q && (1.1)\\
\frac{dI}{dt} &= \frac{B\beta_e S}{k+B} + \beta_h SI - (\mu+\delta_1+\gamma)I && (1.2)\\
\frac{dQ}{dt} &= \gamma I - (\mu+\delta_2+\eta+\alpha)Q && (1.3)\\
\frac{dR}{dt} &= \nu S + \eta Q - \mu R && (1.4)\\
\frac{dB}{dt} &= \varepsilon I - cB && (1.5)\ .
\end{aligned}\right\} \quad (1)$$

The feasible region of human population D corresponding to the system (1) will be

$$D = \Omega_N \ X\ \Omega_B$$

where

$$\Omega_N = \{(S, I, Q, R) : S \geq 0, I \geq 0, Q \geq 0, R \geq 0, S + I + Q + R \leq (\pi/\mu)\}$$

and $\Omega_B = \{B : 0 \leq B(t) \leq (\varepsilon\pi/c\mu)\}$.

Thus, the proposed model is mathematically well posed and is epidemiologically reasonable, since all of the fractions remain between 0 and 1.

3.1 Equilibrium points and Reproduction number

3.1.1 Disease-free equilibrium (E^0)

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$$\left.\begin{aligned}
&\pi - \frac{B\beta_e S}{k+B} - \beta_h SI - (\mu+\nu)S + \alpha Q = 0 && (2.1)\\
&\frac{B\beta_e S}{k+B} + \beta_h SI - (\mu+\delta_1+\gamma)I = 0 && (2.2)\\
&\gamma I - (\mu+\delta_2+\eta+\alpha)Q = 0 && (2.3)\\
&\nu S + \eta Q - \mu R = 0 && (2.4)\\
&\varepsilon I - cB = 0 && (2.5)\ .
\end{aligned}\right\} \quad \textbf{(2)}$$

Assume that if the disease is not occur, then $I = 0$.
Now, from equations (2.3) to (2.5), we have

$$Q = 0, R = 0 \text{ and } B = 0 \ .$$

From equation (2.1), we get $S = \frac{\pi}{\mu+\nu}$.

Thus, the disease-free equilibrium is $E^0 = (\frac{\pi}{\mu+\nu}, 0, 0, 0, 0)$.

3.1.2 Endemic equilibrium (E^*)

$$\left.\begin{aligned}
&\pi - \frac{B^*\beta_e S^*}{k+B^*} - \beta_h S^* I^* - (\mu+\nu)S^* + \alpha Q^* = 0 && (3.1)\\
&\frac{B^*\beta_e S^*}{k+B^*} + \beta_h S^* I^* - (\mu+\delta_1+\gamma)I^* = 0 && (3.2)\\
&\gamma I^* - (\mu+\delta_2+\eta+\alpha)Q^* = 0 && (3.3)\\
&\nu S^* + \eta Q^* - \mu R^* = 0 && (3.4)\\
&\varepsilon I^* - cB^* = 0 && (3.5)\ .
\end{aligned}\right\} \quad \textbf{(3)}$$

By solving the equations of system (3), we obtain $E^* = (S^*, I^*, Q^*, R^*, B^*)$ such that

$$S^* = \frac{\pi - \left((\mu+\delta_1+\gamma) - \frac{\alpha\gamma}{(\mu+\delta_2+\eta+\alpha)}\right)I^*}{(\mu+\nu)}, \ I^* = \frac{\beta_e S^*}{(\mu+\delta_1+\gamma) - \beta_h S^*} - \frac{ck}{\varepsilon},$$

$$Q^* = \frac{\gamma I^*}{(\mu+\delta_2+\eta+\alpha)}, R^* = \frac{\nu S^* + \frac{\eta\gamma}{(\mu+\delta_2+\eta+\alpha)}I^*}{\mu}, B^* = \frac{\varepsilon I^*}{c}.$$

3.1.3 Reproduction Number

Using next generation matrix method, we calculate reproduction number R_0 for the cholera model given in system (1) as follows :

Let $X = (I, Q, B)^T$. System (1) can be written as

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$$\frac{dX}{dt} = F(\mathrm{X}) - V(\mathrm{X})$$

where

$$F(X) = \begin{bmatrix} \frac{B\beta_e S}{k+B} + \beta_h SI \\ 0 \\ 0 \end{bmatrix}, \quad V(X) = \begin{bmatrix} (\mu+\delta_1+\gamma)I \\ (\mu+\delta_2+\eta+\alpha)Q - \gamma I \\ cB - \varepsilon I \end{bmatrix}.$$

The Jacobian matrices of $F(X)$ and $V(X)$ at the disease free equilibrium E_0 are, respectively,

$$DF(E_0) = \begin{bmatrix} \beta_h S_0 & 0 & \frac{\beta_e S_0}{k} \\ 0 & 0 & 0 \\ 0 & 0 & 0 \end{bmatrix}, \; DV(E_0) = \begin{bmatrix} \mu+\delta_1+\gamma & 0 & 0 \\ -\gamma & \mu+\delta_2+\eta+\alpha & 0 \\ -\varepsilon & 0 & c \end{bmatrix}$$

Now ,

$$FV^{-1} = \begin{bmatrix} \frac{\beta_h \pi}{(\mu+v)(\mu+\delta_1+\gamma)} + \frac{\pi\beta_e\varepsilon}{ck(\mu+v)(\mu+\delta_1+\gamma)} & 0 & \frac{\pi\beta_e}{ck(\mu+v)} \\ 0 & 0 & 0 \\ 0 & 0 & 0 \end{bmatrix}$$

is the next generation matrix of system (1).

Now, $\left|FV^{-1} - \lambda I\right| = 0$

$$\begin{vmatrix} \frac{\beta_h \pi}{(\mu+v)(\mu+\delta_1+\gamma)} + \frac{\pi\beta_e\varepsilon}{ck(\mu+v)(\mu+\delta_1+\gamma)} - \lambda & 0 & \frac{\pi\beta_e}{ck(\mu+v)} \\ 0 & -\lambda & 0 \\ 0 & 0 & -\lambda \end{vmatrix} = 0 .$$

This means that either $\lambda_1 = 0, \lambda_2 = 0$ or

$$\lambda = \frac{\beta_h \pi}{(\mu+v)(\mu+\delta_1+\gamma)} + \frac{\pi\beta_e\varepsilon}{ck(\mu+v)(\mu+\delta_1+\gamma)} \approx R_0 .$$

Hence , the spectral radius of FV^{-1} which is denoted by basic reproduction number, is

$$R_0 = \rho(FV^{-1}) = \frac{\beta_h \pi}{(\mu+v)(\mu+\delta_1+\gamma)} + \frac{\pi\beta_e\varepsilon}{ck(\mu+v)(\mu+\delta_1+\gamma)} .$$

Or $R_0 = R_h + R_e$

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where , $R_h = \frac{\beta_h \pi}{(\mu+\nu)(\mu+\delta_1+\gamma)}$ (strands for the continuation of infectios individuals from human to human interaction) and $R_e = \frac{\pi\beta_e\varepsilon}{ck(\mu+\nu)(\mu+\delta_1+\gamma)}$ (strand from the environment to human interaction).

4. Stability Analysis

4.1 Local and Global Stability of disease-free equilibrium

Theorem 1. If $R_h < 1$, then the disease-free equilibrium of system (1) is locally asymptotically stable.

Proof. At disease-free equilibrium points, the matrix will be

$$J(E^0) = \begin{bmatrix} -\mu-\nu & -\beta_h S_0 & \alpha & 0 & \frac{-\beta_e S_0}{k} \\ 0 & \beta_h S_0 - (\mu+\delta_1+\gamma) & 0 & 0 & 0 \\ 0 & \gamma & -(\mu+\delta_2+\eta+\alpha) & 0 & 0 \\ \nu & 0 & \eta & -\mu & 0 \\ 0 & \varepsilon & 0 & 0 & -c \end{bmatrix}$$

Now,

$$\left|J(E^0) - zI\right| = 0$$

$$\begin{vmatrix} -(\mu+\nu+z) & -\beta_h S_0 & \alpha & 0 & \frac{-\beta_e S_0}{k} \\ 0 & \beta_h S_0 - (\mu+\delta_1+\gamma+z) & 0 & 0 & 0 \\ 0 & \gamma & -(\mu+\delta_2+\eta+\alpha+z) & 0 & 0 \\ \nu & 0 & \eta & -(\mu+z) & 0 \\ 0 & \varepsilon & 0 & 0 & -(c+z) \end{vmatrix} = 0$$

or $(\mu+\nu+z)\left(\frac{\beta_h \pi}{(\mu+\nu)} - (\mu+\delta_1+\gamma+z)\right)(\mu+\delta_2+\eta+\alpha)(\mu+z)(c+z) = 0$

or $z = -(\mu+\nu)$, $z = -(\mu+\delta_2+\eta+\alpha)$, $z = -\mu$, $z = -c$ and $z = \frac{\beta_h \pi}{(\mu+\nu)} - (\mu+\delta_1+\gamma) < 0 \Leftrightarrow \frac{\beta_h \pi}{(\mu+\nu)} < (\mu+\delta_1+\gamma)$

.

Thus , by the Routh-Hurwitz criteria the disease-free equilibrium is locally asymptotically stable if $R_h < 1$.

Theorem 2. The disease-free equilibrium is globally asymptotically stable if $R_h < 1$.

Proof . Using method of Castillo-Chavez we will prove that the disease-free equilibrium is globally asymptotically.

We group equation(1) into two compartments , that is , uninfected and infected individuals, given by $a_1 : \frac{dX}{dt} = F(X,Z)$ and $a_2 : \frac{dZ}{dt} = G(X,Z), G(X,0) = 0$.

Where , $X = (S,R) \in R_+^2$, $Z = (I,Q,B) \in R_+^3$.

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Let $E^0 = (N_0, 0), N_0 = (\frac{\pi}{\mu+\nu})$. **(4)**

Then $E^0 = (N_0, 0)$ is globally asymptotically stable equilibrium of (4) if the following conditions are satisfied :

b_1: E^0 is globally asymptotically stable for $\frac{dX}{dt} = F(X,0)$, $b_2 : \hat{G}(X,Z) \geq 0, (X,Z) \in D$,

Where $G(X,Z) = AZ - \hat{G}(X,Z)$, $A = D_z G(N_0, 0)$ is a Metzier matrix.

Then we can write $A = F - V$ and D is given by (4). Then we have

$$\frac{dX}{dt} = F(X,Z) = \begin{bmatrix} \pi - \frac{B\beta_e S}{k+B} - \beta_h SI - (\mu+\nu)S + \alpha Q \\ \nu S + \eta Q - \mu R \end{bmatrix} \text{ and } b_1 : \frac{dX}{dt} = F(X,0) = \begin{bmatrix} \pi - (\mu+\nu)S \\ \nu S \end{bmatrix}$$

$$\text{and } \frac{dZ}{dt} = G(X,Z) = \begin{bmatrix} \frac{B\beta_e S}{k+B} + \beta_h SI - (\mu+\delta_1+\gamma)I \\ \gamma I - (\mu+\delta_2+\eta+\alpha)Q \\ \varepsilon I - cB \end{bmatrix}, G(X,0) = 0.$$

Hence, b_1: E^0 is globally asymptotically stable for $\frac{dX}{dt} = F(X,0)$.

Now for b_2, $A = F - V = \begin{bmatrix} \frac{\beta_h \pi}{\mu+\nu} - (\mu+\delta_1+\gamma) & 0 & \frac{\beta_e \pi}{\mu+\nu} \\ \gamma & -(\mu+\delta_2+\eta+\alpha) & 0 \\ \varepsilon & 0 & -c \end{bmatrix}$ and

$$AZ = \begin{bmatrix} \frac{\beta_h \pi}{\mu+\nu} - (\mu+\delta_1+\gamma) & 0 & \frac{\beta_e \pi}{\mu+\nu} \\ \gamma & -(\mu+\delta_2+\eta+\alpha) & 0 \\ \varepsilon & 0 & -c \end{bmatrix} \begin{bmatrix} I \\ Q \\ B \end{bmatrix} = \begin{bmatrix} \frac{\beta_h \pi I}{\mu+\nu} - (\mu+\delta_1+\gamma)I + \frac{\beta_e \pi}{\mu+\nu} \\ \gamma I - (\mu+\delta_2+\eta+\alpha)Q \\ \varepsilon I - cB \end{bmatrix}$$

Thus, $\hat{G}(X,Z) = AZ - G(X,Z) = \begin{bmatrix} 0 \\ 0 \\ 0 \end{bmatrix} = \begin{bmatrix} \hat{G}(X,Z)_1 \\ \hat{G}(X,Z)_2 \\ \hat{G}(X,Z)_3 \end{bmatrix}$. Hence, $b_2 : \hat{G}(X,Z) \geq 0, (X,Z) \in D$.

Therefore, The disease-free equilibrium is globally asymptotically stable if $R_h < 1$.

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4.2 Local and global Stability of endemic equilibrium

Theorem 3. If $R_h > 1$, then the endemic equilibrium is locally asymptotically stable.

Proof. The variational matrix will be

$$J(E^*)=\begin{bmatrix} -\frac{B^*\beta_e}{k+B^*}-\beta_h I^*-(\mu+\nu) & -\beta_h S^* & \alpha & 0 & \frac{-\beta_e k S^*}{(k+B^*)^2} \\ \frac{B^*\beta_e}{k+B^*}+\beta_h I^* & \beta_h S^*-(\mu+\delta_1+\gamma) & 0 & 0 & \frac{\beta_e k S^*}{(k+B^*)^2} \\ 0 & \gamma & -(\mu+\delta_2+\eta+\alpha) & 0 & 0 \\ \nu & 0 & \eta & -\mu & 0 \\ 0 & \varepsilon & 0 & 0 & -c \end{bmatrix}.$$

Now, $Trace(J(E^*))=-\frac{B^*\beta_e}{k+B^*}-\beta_h I^*+\beta_h S^*-(4\mu+\nu+\delta_1+\gamma+\delta_2+\eta+\alpha+c)<0$

and

$$\det(J(E^*))=-\mu\left\{-\left(\frac{B^*\beta_e}{k+B^*}+\beta_h I^*+(\mu+\nu)\right)\left[(\beta_h S^*-(\mu+\delta_1+\gamma))c(\mu+\delta_2+\eta+\alpha)+\frac{\beta_e k S^*\varepsilon(\mu+\delta_2+\eta+\alpha)}{(k+B^*)^2}\right]-\left(\frac{B^*\beta_e}{k+B^*}+\beta_h I^*\right)(\alpha c\gamma)\right\}>0$$

only if $R_h > 1$.

Hence ,the endemic equilibrium is locally asymptotically stable if $R_h > 1$.

Theorem 4. The endemic equilibrium is globally asymptotically stable if $R_h > 1$.

Proof . Assume

$$F_1=\pi-\frac{B\beta_e S}{k+B}-\beta_h SI-(\mu+\nu)S+\alpha Q$$

$$F_2=\frac{B\beta_e S}{k+B}+\beta_h SI-(\mu+\delta_1+\gamma)I$$

$$F_3=\gamma I-(\mu+\delta_2+\eta+\alpha)Q$$

$$F_4=\nu S+\eta Q-\mu R$$

To prove the result , we use Dulac plus Poincare Bendixson theorem as follows

Consider , $H(S,I,Q,R,B)=\frac{1}{SIQRB}$ where $S>0, I>0, Q>0, R>0, B>0$.

Then , $\nabla(HF)=\frac{\partial}{\partial S}(H.F_1)+\frac{\partial}{\partial I}(H.F_2)+\frac{\partial}{\partial Q}(H.F_3)+\frac{\partial}{\partial R}(H.F_4)+\frac{\partial}{\partial B}(H.F_5)$

$$\Rightarrow \nabla(HF)=\frac{-\pi}{S^2IQRB}-\frac{\alpha}{S^2IRB}-\frac{\beta_e}{I^2QR(k+B)}-\frac{\gamma}{SQ^2RB}-\frac{\nu}{IQR^2B}-\frac{\eta}{SIR^2B}-\frac{\varepsilon}{SQRB^2}<0.$$

Hence,by Dulac's criterian , there is no closed orbit in the first quadrant.
Therefore, the endemic equilibrium is globally asymptotically stable.

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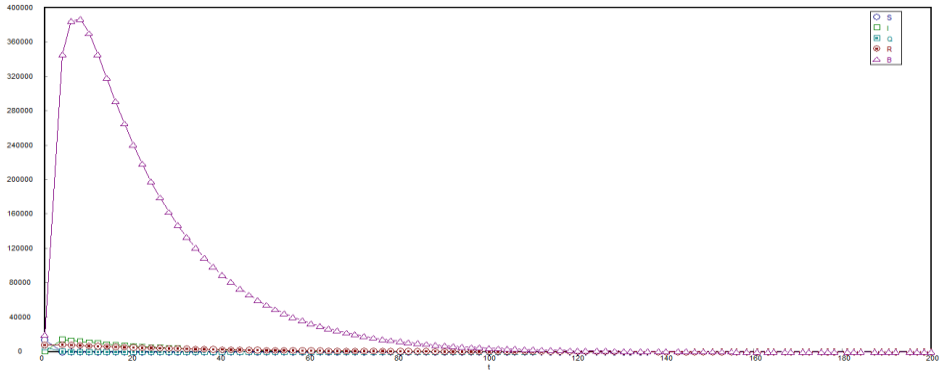
5. Numerical Results

In this section ,we have analyzed the model numerically and graphically by considering the set of parameters values . From practical point of view, numerical solutions are very important beside analytical system.

Case I

$S(0)=14000(persons), I(0)=1000(persons), Q(0)=5000(persons), R(0)=8000(persons), B(0)=20*10^{3}(cell\,ml^{-1}),$
$\pi=9.13*10^{-5}(day^{-1}), \beta_h=0.02(day^{-1}), \beta_e=0.214(day^{-1}), \mu=0.033(day^{-1}), \nu=0.07(day^{-1}), \gamma=0.005(day^{-1}), \delta_1=0.015(day^{-1}),$
$\delta_2=0.0001(day^{-1}), \eta=0.2(day^{-1}), k=10^{6}(cell.ml^{-1}), \varepsilon=10(cell.ml^{-1}day^{-1}person^{-1}), c=0.33(day^{-1}), \alpha=0.4(day^{-1}), R_h=0.00033<1$



Time t

Figure 2. SIQS cholera model with vaccination effect when $R_h<1$

Figure 2 shows that *S(t)* and *R(t)*approaches to its steady state value while *I(t)*, *Q(t)* and *B(t)* approaches zero as time progresses, the disease dies out .

Case II

$S(0)=14000(persons), I(0)=1000(persons), Q(0)=5000(persons), R(0)=8000(persons), B(0)=20*10^{3}(cell\,ml^{-1}),$
$\pi=0.9(day^{-1}), \beta_h=0.8(day^{-1}), \beta_e=0.5(day^{-1}), \mu=0.5(day^{-1}), \nu=0.07(day^{-1}), \gamma=0.005(day^{-1}), \delta_1=0.02(day^{-1}),$
$\delta_2=0.0001(day^{-1}), \eta=0.2(day^{-1}), k=10^{6}(cell.ml^{-1}), \varepsilon=10(cell.ml^{-1}day^{-1}person^{-1}), c=0.33(day^{-1}), \alpha=0.9(day^{-1}), R_h=2.4>1$

Time t

Figure 3. SIQS cholera model with vaccination effect when $R_h>1$

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Figure 3 shows that *S(t)* and *R(t)*approaches to its steady state value while *I(t)*, Q(t) and *B(t)* approaches at a value as time progresses, the disease becomes endemic.

6. Conclusion

Cholera was prevalent in the U.S. in the 1800s, before modern water and sewage treatment systems eliminated its spread by contaminated water. Cholera outbreaks are still a serious problem in other parts of the world. At least 150,000 cases are reported to the World Health Organization each year. Cholera was first spread in Russia in 1817, after few years in Europe, and from Europe to North America and the rest of the world. In this paper, we have considered an SIQR cholera epidemic model of Ezeagu N.J. et al.[3] and converted into SIQS cholera epidemic model with quarantine and vaccination effect which is a generalized form.

I have found disease-free and endemic equilibria for the model and analyzed the stability criteria for the both equilibria. I have seen that the disease-free equilibria and endemic equilibria are locally asymptotically stable if reproduction number is less than and greater than unity respectively .It plays an important role in controlling the disease.Also, numerical simulations are carried out for the model with graphical representation and found that if reproduction number is less than unity, the disease dies out and if reproduction number is greater than unity , the disease becomes endemic .The results shows that the effectivity of quarantine and vaccination and proper sanitation to reduce the disease contact rates and to control the disease.

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