International Journal of
Science and Engineering Investigations vol. 6, issue 64, May 2017
ISSN: 2251-8843

Mathematical Analysis of Quarantine on the Dynamical Transmission of Diphtheria Disease

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Abstract- Five (5) Compartmental model of (S, E, Q, I, R) were presented to have better understanding on the effect of quarantine of exposed individuals in the dynamical spread of Diphtheria disease in the population. The stability of the model was analyzed for the existence of disease free and endemic equilibrium points. Basic Reproduction Number (R_0) was obtained using next generation matrix method (NGM), and it is shown that the disease free equilibrium point is locally asymptotically stable whenever the basic reproduction number is less than unity i.e. (R_0<1) and unstable whenever the basic reproduction number is greater than unity (R_0>1).The basic reproduction number which is the number of new infected individual generated by a single infectious individual is a very important tool that helps in determining whether the disease persists and become endemic or dies out in the society. The model was solved numerically using the mathematical software (MAPLE) and the results were presented graphically. It was discovered that the higher the quarantine rate of exposed individual the lower the reproduction number and less is the infected individuals. Therefore, effort should be put in place in intensifying the quarantine rate of the disease so as to have the basic reproduction number not greater than unity, in order to prevent the endemic situation.

Keywords: *Diphtheria, Reproduction Number, Stability, Critical Point, Numerical Simulation*

I. INTRODUCTION

Diphtheria is an infectious disease caused by bacteria belonging to *Corynebacterium species* that generally produces exotoxins that injure human tissue. [15].Diphtheria disease has been infecting human population for centuries. The first documented description of diphtheria was produced by Hippocrates in the fifth century BC. The disease has been a leading cause of death in children for many years and this deadly disease continues to kill many children in industrialized and developing countries [14]. A large percentage of adults in many modern and developing countries are now vulnerable to diphtheria disease. Quite a lot of developed and developing countries where exposure has been very high for 5-10 years have reported diphtheria, even though the prevalent use of immunization. Diphtheria remains endemic in numerous regions [9] such as Brazil [6] the tropics and areas of South America [4], [12], also in Africa, India [14]. Since the beginning of 1990, diphtheria disease has re-emerged in the Russian Federation and spread across all Newly Independent States (NIS). Percentage of diphtheria cases in children greater or equal to 15 years old ranges from 64% to 82% annually. By the beginning of 1999, the diphtheria epidemic had caused over 157,000 cases and 5000 deaths. Adults between 40 and 49 years old had tremendously high occurrence, which accounted for almost half of all deaths in various countries. Older adults of over 50 years of age had fairly few cases [9]. Without difficulty, the organisms attack the tissue lining the throat, and at some stage in time, they produce exotoxins that damage the tissue and lead to the development of a pseudomembrane [2], [3]. The initial symptoms of diphtheria disease are flu-like but aggravate to include coughing, swallowing problems, hoarseness, fever, enlarged lymph nodes, and shortness of breath; some patients may have skin involvement, which may later produce skin ulcers. Poor health and depressed respiratory defense mechanisms contribute to the cause of diphtheria[7]. Mathematical epidemiology has greatly contributed to the understanding of the behavior of infectious diseases, its impacts and possible future predictions about its spreading. Mathematical models are used in comparing, evaluating, planning, implementing and optimizing various prevention, detection, control programs and therapy [17].

The term quarantine is often erroneously used to mean medical isolation, which is "to separate ill persons who have a communicable disease from those who are healthy whereas quarantine requires separation and restriction of movement of people who may have been exposed to a contagious illness,

but do not have symptoms to see if they become sick and these individuals may or may not be contagious [5].

In this paper, a mathematical model for the transmission dynamics for diphtheria is developed. This model demonstrates how quarantine of exposed individuals could be used to reduce the population of individuals infected with diphtheria disease in the community.

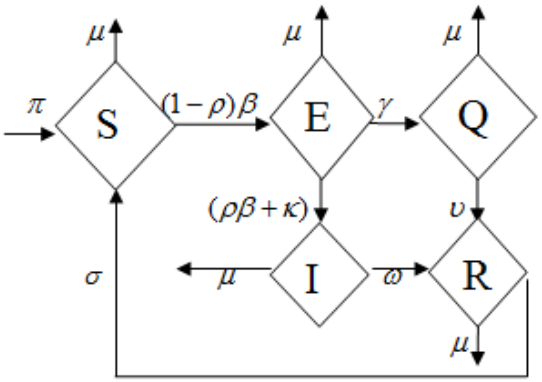

Figure 1. Schematic Diagram

II. MATHEMATICAL MODEL FORMULATION

The population size at time t denoted by N (t) is sub-divided into five (5) compartments of Susceptible individual S(t), Exposed individual E(t), Quarantine individual Q(t), Infected individual, $I(t)$ and Recovered individual R(t) so that

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

The susceptible population is increased by the recruitment of people (either by birth or immigration) into the population, all recruited individuals are assumed to be susceptible at a rate π, the population of Susceptible is further increased by the population of individual that are recovered at the rate (σ). Finally, the susceptible population decreases by infection which can be acquired following effective contact rate β and also by natural death at the rate (μ). Hence,

$$\frac{dS}{dt} = \pi - \beta SI - \mu S + \sigma R \tag{2}$$

A proportion $(1-\rho)$ of newly infected individuals that produce active diphtheria move to the exposed class E, while the remaining proportion ρ move to the infected class I. The population of exposed class is reduced by the natural death rate (μ), quarantine rate (γ) and the progression rate (κ). Hence,

$$\frac{dE}{dt} = (1-\rho)\beta SI - (\mu + \gamma + \kappa)E \tag{3}$$

The population of quarantine individual is increased by the quarantine of exposed individual at the rate (γ). The population later decreased by the natural death rate (μ) and the rate at which the quarantine individual recovered (υ). Hence,

$$\frac{dQ}{dt} = \gamma E - (\mu + \upsilon)Q \tag{4}$$

The population of Infected diphtheria individual is increased by the remaining proportion of individual that produce active diphtheria at the rate (ρ) and the progression of exposed diphtheria individual at the rate (κ). The population is decreased by the treatment of diphtheria infected individuals at the rate (ω), natural death of diphtheria infected individual at the rate (μ) and the disease induced death at the rate (δ). Hence,

$$\frac{dI}{dt} = \rho\beta SI + \kappa E - (\mu + \delta + \omega)I \tag{5}$$

The population of Recovered diphtheria individual is increased by the number of infected individuals that are treated at the rate (ω) and the exposed individual quarantined at the rate (υ). The population is decreased by the natural death rate of recovered individual at the rate (μ) and the recovered individual at the rate (σ). Hence,

$$\frac{dR}{dt} = \omega I + \upsilon Q - (\mu + \sigma)R \tag{6}$$

Thus in summary, the dynamics transmission model is given by the following system of non-linear differential equations.

$$\left.\begin{aligned}
\frac{dS}{dt} &= \pi - \beta SI - \mu S + \sigma R \\
\frac{dE}{dt} &= (1-\rho)\beta SI - K_1 E \\
\frac{dQ}{dt} &= \gamma E - K_2 Q \\
\frac{dI}{dt} &= \rho\beta SI + \kappa E - K_3 I \\
\frac{dR}{dt} &= \omega I + \upsilon Q - K_4 R
\end{aligned}\right\} \quad (7)$$

Where

$$K_1 = (\mu + \gamma + \kappa),\ K_2 = (\mu + \upsilon),$$
$$K_3 = (\mu + \delta + \omega),\ K_4 = (\mu + \sigma)$$

III. POSITIVITY OF SOLUTION

For this model it can be shown that the region

$$D^* = \{(S + E + Q + I + R) \in R^5_+ : N \le \pi / \mu\} \quad (8)$$

For Diphtheria model to epidemiological and mathematically well posed. We need to prove that all state variables are non-negative for all $t > 0$

Consider the biologically-feasible region D^*, defined above. The rate of change of the total population, obtained by adding all equations of the model (7), is given by

$$\frac{dN}{dt} = \pi - \mu N - \delta \quad (9)$$

In the absence of disease induce death,

$$\frac{dN}{dt} = \pi - \mu N$$

It follows that $\frac{dN}{dt} < 0$ whenever $N > \frac{\pi}{\mu}$. Furthermore,

Since $\frac{dN}{dt} \le \pi - \mu N$, it is clear that $N(t) \le \frac{\pi}{\mu}$ if $N(0) \le \frac{\pi}{\mu}$.

TABLE I. DESCRIPTION OF VARIABLES

Variables	Definitions
S	Susceptible individual
E	Exposed individual
Q	Quarantine individual
I	Infected individual
R	Recovered individual

TABLE II. DESCRIPTION OF PARAMETERS

Parameters	Definitions
π	Recruitment rate into the population
ρ	Proportion of new infection that produce active diphtheria
υ	Rate at which quarantine individuals recovered.
ω	Treatment rate of infected individuals.
μ	Natural death rate
κ	Progression rate
σ	Loss of immunity
δ	Induced mortality rate
β	Effective contact rate
γ	Quarantine rate of exposed Individuals.

Therefore, all solutions of the model with initial conditions in D^* remain in D^* for all $t > 0$ (i.e., the ω-limits sets of the system (1) are contained in D^*). Thus, D^* is positively-invariant and attracting. In this region, the model can be considered as been epidemiologically and mathematically well posed.

A. Disease Free Equilibrium

For critical points, we set

$$\frac{dS}{dt}=\frac{dE}{dt}=\frac{dQ}{dt}=\frac{dI}{dt}=\frac{dR}{dt}=0 \tag{10}$$

At disease free equilibrium, it is assumed that there is no infection; Hence (DFE) is given as:

$$\varepsilon_0=(S,E,Q,I,R)=\left(\frac{\pi}{\mu},0,0,0,0\right)$$

B. Endemic Equilibrium

The endemic equilibrium of the model (7) is given below;

$$\left.\begin{aligned} S^* &= \frac{K_1K_3}{\beta C}\\ E^* &= \frac{B(\rho-1)K_2K_3K_4}{AC}\\ Q^* &= \frac{B(\rho-1)\gamma K_3K_4}{AC}\\ I^* &= \frac{BK_2K_4}{A}\\ R^* &= \frac{B(\gamma\upsilon K_3(\rho-1)+\omega K_2(\rho\kappa-\rho K_1-\kappa)}{A} \end{aligned}\right\} \tag{11}$$

Where

$$A=\beta(K_1K_2K_3K_4+K_3\gamma\sigma\upsilon(\rho-1)+\sigma\omega K_2(\kappa\rho-K_1-\kappa))$$
$$B=(\kappa\rho\pi\beta+\rho K_1\pi\beta+\kappa\pi\beta-\mu K_1K_3)$$
$$C=(\kappa+\rho K_1-\kappa\rho)$$

C. Basic Reproduction Number R_0

Basic reproduction number is an important notion in epidemiological models and is the usually denoted by R_0. This number can be defined as the expected average number of secondary infection generated by infected infectious individual in his/her infectious period in the susceptible population.

The basic reproduction number of the model (7) is calculated by using the next generation matrix [10]. Using the approach, we have,

$$\left.\begin{aligned} F &= \begin{pmatrix} (1-\rho)\beta\dfrac{\pi}{\mu}I\\ 0\\ \rho\beta\dfrac{\pi}{\mu}I\\ 0 \end{pmatrix}\\ V &= \begin{pmatrix} -K_1E\\ \gamma E-K_2Q\\ \kappa E-K_3I\\ \upsilon Q+\omega I-K_4R \end{pmatrix} \end{aligned}\right\} \tag{12}$$

After taking partial derivative F and V at the disease free equilibrium, we have:

$$F=\begin{pmatrix} 0 & 0 & \dfrac{(1-\rho)\beta\pi}{\mu} & 0\\ 0 & 0 & \dfrac{\rho\beta\pi}{\mu} & 0\\ 0 & 0 & 0 & 0\\ 0 & 0 & 0 & 0 \end{pmatrix} \tag{13}$$

$$V=\begin{pmatrix} K_1 & 0 & 0 & 0\\ -\gamma & K_2 & 0 & 0\\ -\kappa & 0 & K_3 & 0\\ 0 & -\upsilon & -\omega & K_4 \end{pmatrix} \tag{14}$$

Thus,

$$R_0=\frac{\beta\pi(\rho K_1+\kappa+\rho\kappa)}{\mu K_1K_3} \tag{15}$$

D. Local Stability of the Disease Free Equilibrium

Theorem 1: The disease free equilibrium is locally asymptotically stable if $R_o<1$ and unstable if $R_o>1$

Proof: The Jacobian matrix $J(E_o)$ of the model equation (7) evaluated at disease free equilibrium is given by;

$$J(E_o)=\begin{bmatrix} -\mu & 0 & 0 & \dfrac{-\beta\pi}{\mu} & \sigma\\ 0 & K_1 & 0 & \dfrac{(1-\rho)\beta\pi}{\mu} & 0\\ 0 & \gamma & -K_2 & 0 & 0\\ 0 & \kappa & 0 & \dfrac{\rho\beta\pi}{\mu}-K_3 & 0\\ 0 & 0 & \omega & 0 & -K_4 \end{bmatrix}$$

The eigenvalues of the Jacobian matrix are $\lambda s=-\mu,-K_4,-K_2$ and the remaining sub-matrix is given by $J_1(E_o)$ which is;

$$J_1(E_o)=\begin{pmatrix} -K_1 & \dfrac{(1-\rho)\beta\pi}{\mu}\\ \kappa & \dfrac{\rho\beta\pi}{\mu}-K_3 \end{pmatrix} \tag{16}$$

The characteristics polynomial of the above is;

$$A_2\lambda^2+A_1\lambda+A_0=0 \tag{17}$$

Where; $A_2=\mu$

$$A_1 = \mu K_1 + \mu K_3 - \pi\rho\beta$$

$$A_0 = (1 - R_o)\,\mu K_1 K_3$$

According to Routh Hurwitz criterion, the roots of the polynomial (17) will be negative if the coefficients A_i (for i=0, 1, 2) are all positive and that the Hurwitz matrices H are all greater than zero.

It can be seen clearly from the above that $A_2 > 0$, $A_1 > 0$ and that $A_0 > 0$ if $R_0 < 1$, Also, the Hurwitz matrices are as follow;

$$H_1 = A_1$$

$$H_2 = \begin{vmatrix} A_1 & \mu \\ 0 & A_0 \end{vmatrix}$$

From the above, the Hurwitz matrices for the polynomial are all positive, and then all the eigenvalues of the Jacobian matrix $J(E_O)$ are real and negative when $R_o < 1$, therefore the disease free equilibrium is locally asymptotically stable.

E. Global Stability of the Disease Free Equilibrium

Theorem 2: The disease free-equilibrium of the system (7) is globally asymptotically stable whenever $R_0 < 1$ and unstable if $R_0 > 1$.

Proof: It follows that $S = N^* - E - Q - I - R$ at steady state. The proof is based on using the comparison theorem [18]. The rate of change of the variables representing the infected component of the system can be written as follows.

$$\left.\begin{aligned} \frac{dE}{dt} &= (1-\rho)\beta I(N^* - E - Q - I - R) - K_1 E \\ \frac{dQ}{dt} &= \gamma E - K_2 Q \\ \frac{dI}{dt} &= \rho\beta SI + \kappa E - K_3 I \\ \frac{dR}{dt} &= \omega I + \upsilon Q - K_4 R \end{aligned}\right\} \tag{18}$$

For the model (7), the associated reproduction number is denoted by R_0, where

$$R_0 = \frac{\beta\pi(\rho K_1 + \kappa + \rho\kappa)}{\mu K_1 K_3}$$

The DFE of the model (7) is Globaly Asymptotically Stable in D^* if $R_0 < 1$.

Using comparison method, we have,

$$\begin{pmatrix} \frac{dE}{dt} \\ \frac{dQ}{dt} \\ \frac{dI}{dt} \\ \frac{dR}{dt} \end{pmatrix} = (F - V) \begin{pmatrix} E \\ Q \\ I \\ R \end{pmatrix} - Fi \begin{pmatrix} E \\ Q \\ I \\ R \end{pmatrix} \tag{19}$$

Then

$$\begin{pmatrix} \frac{dE}{dt} \\ \frac{dQ}{dt} \\ \frac{dI}{dt} \\ \frac{dR}{dt} \end{pmatrix} \le (F - V) \begin{pmatrix} E \\ Q \\ I \\ R \end{pmatrix} \tag{20}$$

Where

$$F = \begin{pmatrix} 0 & 0 & \frac{(1-\rho)\beta\pi}{\mu} & 0 \\ 0 & 0 & \frac{\rho\beta\pi}{\mu} & 0 \\ 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 \end{pmatrix} \tag{21}$$

$$V = \begin{pmatrix} K_1 & 0 & 0 & 0 \\ -\gamma & K_2 & 0 & 0 \\ -\kappa & 0 & K_3 & 0 \\ 0 & -\upsilon & -\omega & K_4 \end{pmatrix} \tag{22}$$

According to [17], all eigenvalues of the matrix F – V have negative real parts. It follows that the linearized differential inequality above is stable whenever $R_0 < 1$.

Consequently $S = (E = Q = I = R = 0) \to (0,\ 0, 0,\ 0)$ *at* $t \to \infty$. Substituting $E = Q = I = R = 0$ in (R_0) gives $S(t) \to S(0)$ *as* $t \to \infty$. Hence, we have established that the disease free equilibrium is globally asymptotically stable whenever $R_0 < 1$.

F. Global Stability of Endemic-Equilibrium

Lemma: For $R_0 > 1$, the equation (7) is globally asymptotically stable if

$s = s^*$, $e = e^*$, $q = q^*$, $i = i^*$, $r = r^*$ and $M < N$ and unstable when $R_0 \le 1$.

Proof: Using the constructed lyapunov function, the global stability of the endemic equilibrium is proved by defining the lyapunov function as follows:

$$V = s^*,\ e^*, q^*, i^*,\ r^* \quad = \left(s - s^* - s^* \log \frac{s^*}{s} \right)$$
$$+ \left(e - e^* - e^* \log \frac{e^*}{e} \right) + \left(q - q^* - q^* \log \frac{q^*}{q} \right) +$$
$$\left(i - i^* - i^* \log \frac{i^*}{i} \right) + \left(r - r^* - r^* \log \frac{r^*}{r} \right) \tag{23}$$

By direct calculating, the derivative of V along the solution of equation (23), we have;

$$\frac{dV}{dt} = \left(\frac{s - s^*}{s} \right) \frac{ds}{dt} + \left(\frac{e - e^*}{e} \right) \frac{de}{dt}$$
$$+ \left(\frac{q - q^*}{q} \right) \frac{dq}{dt} + \left(\frac{i - i^*}{i} \right) \frac{di}{dt} + \left(\frac{r - r^*}{r} \right) \frac{dr}{dt} \tag{24}$$

$$\frac{dV}{dt} = \left(\frac{s - s^*}{s} \right) \left(\pi - \beta si - \mu s + \sigma r \right) +$$
$$\left(\frac{e - e^*}{e} \right) \left((1 - \rho)\beta si - (\mu + \gamma + \kappa)e \right) +$$
$$\left(\frac{q - q^*}{q} \right) \left(\gamma e - (\mu + \upsilon)q \right) + \left(\frac{i - i^*}{i} \right)$$
$$\left(\rho\beta si + \kappa e - (\mu + \delta + \omega)i \right)$$
$$+ \left(\frac{r - r^*}{r} \right) \left(\omega i + \upsilon q - (\mu + \sigma)r \right) \tag{25}$$

Substituting $s = s - s^*, e = e - e^*, q = q - q^*, i = i - i^*,\ r = r - r^*$ into equation (25) Collecting the like terms, we have:

$$\frac{dV}{dt} = \left(\frac{s - s^*}{s} \right) (\pi + \sigma(r - r^*)) - \left(\frac{(s - s^*)^2}{s} \right)$$
$$(\beta(i - i^*) + \mu) + \beta \left(\frac{e - e^*}{e} \right) (s - s^*)(i - i^*)(1 - \rho)$$
$$-(\mu + \gamma + \kappa) \left(\frac{(e - e^*)^2}{e} \right) + \gamma \left(\frac{q - q^*}{q} \right)$$
$$(e - e^*) - (\mu + \upsilon) \left(\frac{(q - q^*)^2}{q} \right) + \kappa \left(\frac{i - i^*}{i} \right) (e - e^*)$$
$$+ (\rho\beta(s - s^*)(i - i^*) - (\mu + \delta + \omega)$$
$$\left(\frac{(i - i^*)^2}{i} \right) + \left(\frac{r - r^*}{r} \right) (\omega(i - i^*) +$$
$$\upsilon(q - q^*)) - (\mu + \sigma) \left(\frac{(r - r^*)^2}{r} \right)$$

Open the brackets of (26)

$$\frac{dV}{dt} = \pi - \pi \frac{s^*}{s} + \sigma r \left(\frac{s - s^*}{s} \right) -$$
$$\sigma r^* \left(\frac{s - s^*}{s} \right) - \beta i \left(\frac{(s - s^*)^2}{s} \right) +$$
$$\left(\frac{(s - s^*)^2}{s} \right) (\beta i^* + \mu) + \beta si - \beta si^* - \beta s^* i +$$
$$\beta s^* i^* - \beta \frac{e^*}{e} si + \beta \frac{e^*}{e} si^* + \beta \frac{e^*}{e} s^* i -$$
$$\beta \frac{e^*}{e} s^* i^* - \beta\rho si + \beta\rho si^* + \beta\rho s^* i - \beta\rho s^* i^* +$$
$$\beta\rho \frac{e^*}{e} si - \beta\rho \frac{e^*}{e} si^* - \beta\rho \frac{e^*}{e} s^* i + \beta\rho \frac{e^*}{e} s^* i^*$$
$$- \left(\frac{(e - e^*)^2}{e} \right) (\mu + \gamma + \kappa) + \gamma e - \gamma e^* - \gamma q^* \frac{e}{q}$$
$$+ \gamma e^* \frac{q^*}{q} - (\mu + \upsilon) \frac{(q - q^*)^2}{q} + \rho\beta s \left(\frac{(i - i^*)^2}{i} \right) \tag{27}$$
$$-(\rho\beta s^* + (\mu + \delta + \omega)) \left(\frac{(i - i^*)^2}{i} \right) + \kappa e - \kappa e^*$$
$$- \frac{i^*}{i} \kappa e + \frac{i^*}{i} \kappa e^* + \omega i - \omega i^* - \frac{r^*}{r} \omega i + \frac{r^* \omega i^*}{r} +$$
$$\upsilon q - \frac{r^* \upsilon q}{r} - \upsilon q^* + \frac{r^* \upsilon q^*}{r} - \left(\frac{(r - r^*)^2}{r} \right) (\mu + \sigma)$$

Re-arranging the positive and negative terms

Where $\frac{dV}{dt} = M - N$

$$M = \pi + \sigma r \left(\frac{s - s^*}{s} \right) + \left(\frac{(s - s^*)^2}{s} \right) (\beta i^* + \mu)$$
$$+ \beta si - \beta si^* - \beta s^* i + \beta s^* i^* + \beta \frac{e^*}{e} si^* + \beta \frac{e^*}{e} s^* i$$
$$+ \beta\rho \frac{e^*}{e} si + \beta\rho si^\bullet + \beta\rho s^* i + \beta\rho \frac{e^*}{e} s^* i^* +$$
$$\rho\beta s \left(\frac{(i - i^*)^2}{i} \right) + \kappa e + \frac{i^*}{i} \kappa e^* + \omega i + \frac{r^* \omega i^*}{r} +$$
$$\upsilon q + \frac{r^* \upsilon q^*}{r} + \gamma e + \frac{\gamma e^* q^*}{q}$$

$$N = \pi\frac{s^*}{s} + \sigma r^*\left(\frac{s-s^*}{s}\right) + \beta i\left(\frac{(s-s^*)^2}{s}\right)$$
$$+\beta\frac{e^*}{e}si + \beta\frac{e^*}{e}s^*i^* + \beta\rho si + \beta\rho s^*i^* +$$
$$\beta\rho\frac{e^*}{e}si^* + \beta\rho\frac{e^*}{e}s^*i + \left(\frac{(e-e^*)^2}{e}\right)(\mu+\gamma+\kappa)$$
$$+(\rho\beta s^* + (\mu+\delta+\omega))\left(\frac{(i-i^*)^2}{i}\right) + \kappa e^* + \frac{i^*}{i}\kappa e$$
$$+\omega i^* + \frac{r^*}{r}\omega i + \frac{r^*\upsilon q}{r} + \upsilon q^* + \left(\frac{(r-r^*)^2}{r}\right)$$
$$(\mu+\sigma) + \gamma e^* + \frac{\gamma q^* e}{q} + (\mu+\upsilon)\frac{(q-q^*)^2}{q}$$

Hence, if $M < N$, then we obtain $\frac{dV}{dt} \le 0$. Noting that $\frac{dV}{dt} = 0$ if and only if $s = s^*$, $e = e^*$, $q = q^*, i = i^*$, $r = r^*$, therefore, the largest compact invariant set:

$\left\{(s^*, e^*, q^*, i^*, r^*) \in \Gamma : \frac{dV}{dt} = 0\right\}$ Is the singleton $\{E^*\}$

where E^* is the endemic equilibrium. Hence, by La Salle's principle, it implies that E^* is globally asymptotically stable in Γ if $M < N$.

IV. NUMERICAL SIMULATION

Numerical Simulation of the model was performed by the help of MAPLE 17 software using Runge-kutta method of order four (4). The set of parameters used are given in table 3.

TABLE III. PARAMETERS AND VALUES

Parameters	Values	Source
π	500	Assumed
β	0.2	Assumed
ω	0.2	Assumed
κ	0.002	Assumed
μ	0.5	Assumed
δ	0.9	Assumed
ρ	0.01	Assumed
γ	0.2	Assumed
υ	0.2	Assumed
σ	0.2	Assumed

V. DISCUSSION OF RESULTS AND CONCLUSION

A Five (5) Compartmental model was formulated to have insight into the effect of Quarantine on the exposed individuals and basic reproduction number in the dynamical spread of Diphtheria. The positivity of solution shows that the model is mathematically and epidemiologically well posed. Basic reproduction number R_0 which is the average number of new secondary infection generated by a single infected person during his/her infectious period determines whether diphtheria dies out whenever (i.e when $R_0 < 1$) or spreads (i.e when $R_0 > 1$). The global stability of endemic equilibrium was analyzed using Lyapunov function.

Numerical simulation of the model was carried out by MAPLE 17 software using the Runge-kutta method of order four. Figures 1 shows the effect of quarantine rate on the exposed individuals, it shows that as quarantine rate of exposed individual increases, the exposed individual decreases. At the initial stage, the population of the exposed class increases, with no changes when different quarantine rates are being applied but later decreases, i.e the exposed class reaches its peak over a short period before the positive effect of the quarantine manifested. This is because quarantine involves monitoring and treatment of selected infectious/infected individuals, in which they will move out of the class when they are cleared off of the disease. Figure 2 shows that as quarantine rate increases, the quarantine class increases. Figures 3 shows the effect of quarantine rate on the basic reproduction number. The result shows that as the quarantine rate increases, the basic reproduction number decreases, which means that increase in quarantine rate will reduce the spread of diphtheria disease in the community. Figures 4-7 show the effect of quarantine rate on the basic reproduction number. The result shows that as the quarantine rate increases, the basic reproduction number decreases which make it easier to reduce the spread of diphtheria disease in the community. Conclusively, the quarantine of exposed individual should be given priority by policy health makers in order to have efficient control of Diphtheria disease in the community.

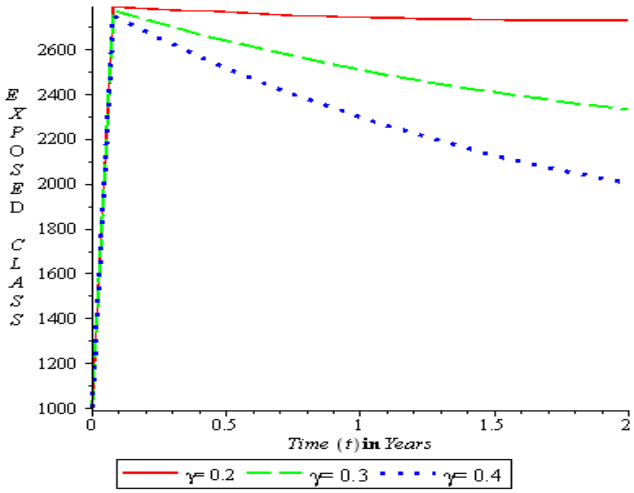

Figure 2. Effect of quarantine rate on the exposed individuals

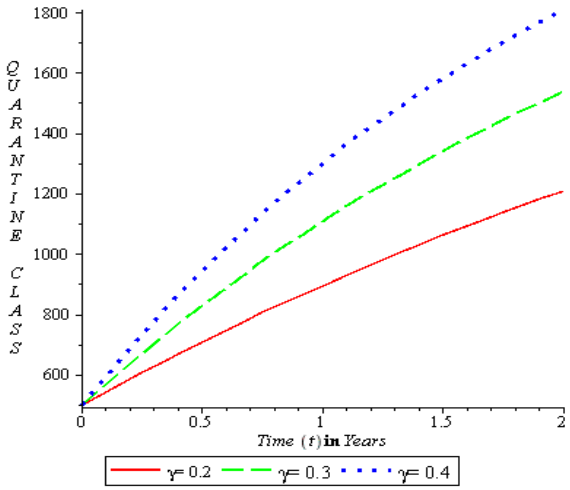

Figure 3. Rate at which the quarantine class increases

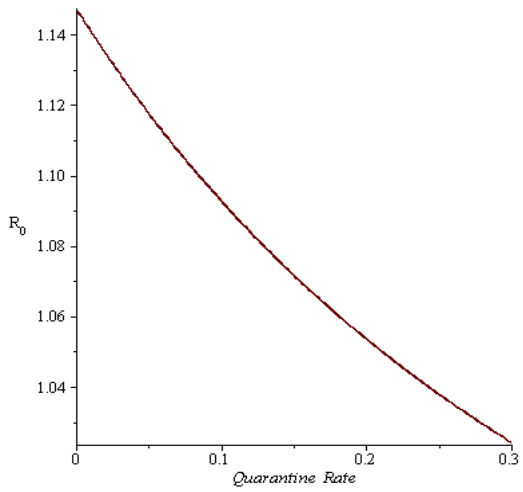

Figure 4. Effect of quarantine rate on the basic reproduction number

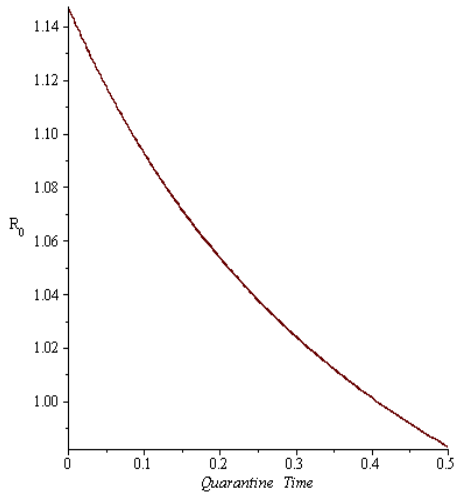

Figure 5. Effect of quarantine rate on the basic reproduction number

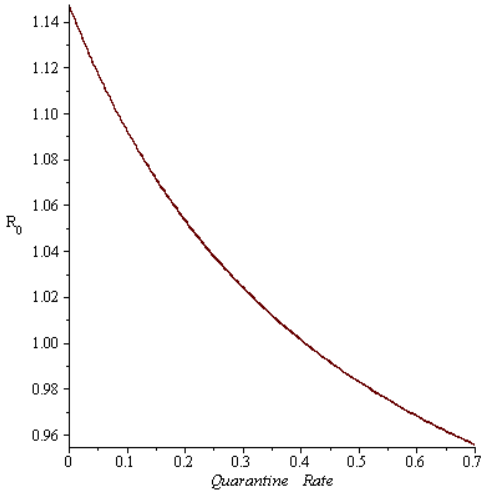

Figure 6. Effect of quarantine rate on the basic reproduction number

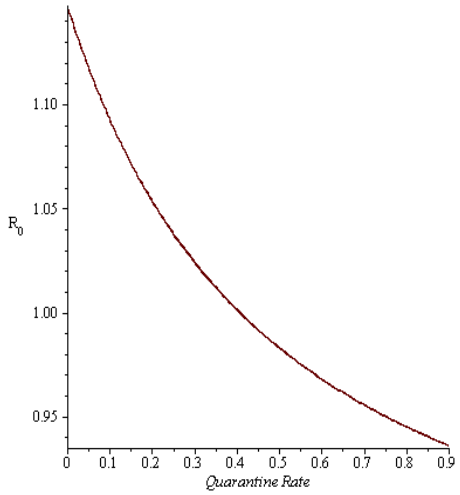

Figure 7. Effect of quarantine rate on the basic reproduction number

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