



Mathematical Modeling of Diphtheria: The Role of Antibiotics, Quarantine, and Healthcare Resource Allocation

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Abstract: Diphtheria remains a significant public health concern, especially in resource-limited settings. This study presents a mathematical model to investigate the dynamics of diphtheria transmission, incorporating factors such as quarantine, antibiotic treatment, and healthcare resource allocation. The model consists of compartments for susceptible, exposed, infectious, quarantined, under antibiotic treatment, and recovered individuals, and analyzes how various parameters affect disease dynamics. Numerical simulations reveal that increasing the rate of entry into quarantine effectively reduces the susceptible population and increases the quarantined population, demonstrating the importance of quarantine in controlling disease spread. Higher recovery rates, both from general recovery and specific treatments, significantly reduce the peak and overall number of infectious individuals while increasing the recovered population. The rate of entry into antibiotic treatment and access to healthcare resources also plays a crucial role in managing the outbreak. This analysis underscores the need for balanced resource allocation and effective intervention strategies to mitigate diphtheria's impact.

Keywords: Antibiotic treatment, Quarantine measures, Disease control, Recovery rates, Sensitivity analysis.

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1. Introduction

Diphtheria, an acute infectious disease caused by *Corynebacterium diphtheriae*, remains a public health concern, particularly in regions with low vaccination coverage. Despite advancements in vaccination and healthcare, periodic outbreaks continue to pose challenges to disease control. Mathematical modeling has emerged as a vital tool for understanding the transmission dynamics of infectious diseases, allowing for the evaluation of various intervention strategies (Hethcote, 2000). Several studies have focused on the mathematical modeling of diphtheria and other infectious diseases, highlighting the importance of factors such as vaccination, treatment, and quarantine in controlling outbreaks. For instance, Olayiwola and Alaje (2024) developed a mathematical model to analyze diphtheria transmission dynamics. Their model categorizes individuals based on susceptibility, vaccination status, infection, and recovery, providing a comprehensive analysis of disease spread. They emphasized the significance of periodic booster doses, treatment, and screening of asymptomatic carriers, and introduced a Caputo–Fabrizio fractional-order model for more nuanced analysis. Their findings underscore the need for periodic booster administration alongside treatment and screening to

significantly reduce disease spread. Fauzi et al. (2024) addressed the resurgence of diphtheria in West Java, Indonesia, following healthcare disruptions during the COVID-19 pandemic. They employed an SIR model incorporating DPT and booster vaccinations, calculating a basic reproduction number (R_0) of 1.17, signaling a high outbreak risk. Their spatial analysis identified hotspots requiring targeted interventions, and simulations suggested that increasing booster coverage could help control the rise in cases. Izzati et al. (2020) explored diphtheria transmission using an SEIQR model, focusing on optimizing control measures. Their study introduced an optimal control problem aimed at minimizing the disease spread through enhanced quarantine measures and targeted vaccination campaigns. The analytical and numerical results highlighted the effectiveness of these strategies in reducing both disease spread and associated costs.

Rahmi and Pratama (2023) developed a model incorporating factors like contact transmission, vaccination, quarantine, and hand-washing behavior. They demonstrated that the disease-free equilibrium is stable when the basic reproduction number (R_0) is less than one, but unstable otherwise. Their simulations revealed that comprehensive strategies, including vaccination, quarantine, and hand-washing, could significantly reduce both R_0 and the



number of infections, although vaccinating exposed individuals might increase both. Akponana et al. (2023) focused on the effects of waning immunity and antibiotics in diphtheria transmission. Their model highlighted the critical role of integrating vaccination, antibiotic treatment, and contact tracing in controlling outbreaks, particularly under scenarios involving waning immunity. Also, Akponana et al. (2024) presented a mathematical model specifically designed to evaluate the effects of vaccination and waning immunity on diphtheria transmission dynamics. Their model includes five compartments—Susceptible (S), Infected (I), Vaccinated (V), Vaccine-Induced Immunity (W), and Recovered (R)—and analyzes the conditions for disease control. Their numerical simulations emphasized the importance of combining vaccination with effective treatment and contact tracing to significantly reduce the spread of diphtheria.

In this study, we develop a mathematical model that incorporates these key factors—antibiotics, quarantine, and healthcare resource allocation—to explore their combined impact on diphtheria transmission dynamics. By analyzing the interplay between these factors, this model aims to provide insights into effective strategies for the prevention and control of diphtheria outbreaks.

2. Mathematical Model for Diphtheria Transmission Dynamics

The dynamics of diphtheria transmission can be described using a system of differential equations that captures the interactions between different compartments within the population. The compartments considered in this model include susceptible individuals (S), exposed individuals (E), infectious individuals (I), quarantined individuals (Q), individuals receiving antibiotic treatment (A), individuals with access to healthcare resources (H), and recovered individuals (R). Some assumptions made in the model includes:

1. Infectious individuals may receive antibiotic treatment at a rate (a), which leads to their transfer to the compartment (A). Treated individuals recover at rate γ_a .
2. Infectious individuals may receive enhanced care through healthcare resources at rate (h), leading to their transfer to the compartment (H). These individuals recover at rate γ_h .
3. Individuals who are susceptible may be quarantined at a rate (q), reducing their likelihood of becoming exposed. Quarantined individuals either recover or progress through the disease while isolated, with recovery rate γ_q and disease progression rate σ_q .
4. Infectious individuals who do not receive treatment or enhanced care recover naturally at rate γ or die due to the disease at rate α .

5. The population is assumed to mix homogeneously, meaning that each individual has an equal probability of coming into contact with an infectious person.

The schematic diagram illustrating the interactions between the various compartments is shown in the figure below.

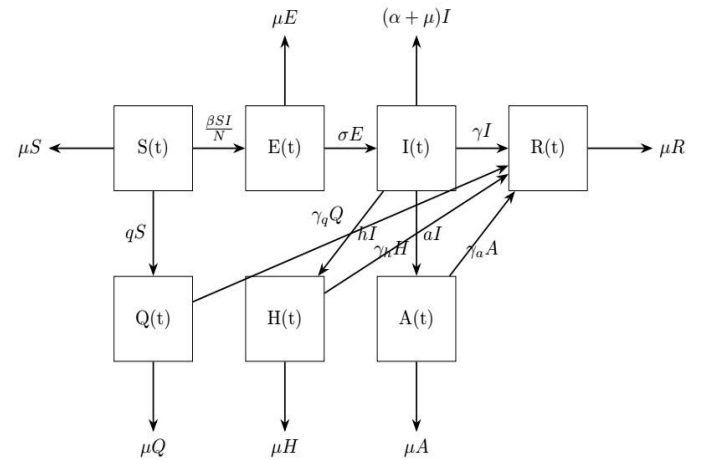


Figure 1: Schematic Diagram

The model is given by the following system of equations:

$$\frac{dS}{dt} = \Lambda - \frac{\beta SI}{N} - qS - \mu S \quad (1)$$

$$\frac{dE}{dt} = \frac{\beta SI}{N} - \sigma E - \mu E \quad (2)$$

$$\frac{dI}{dt} = \sigma E - (\gamma + a + h)I - (\alpha + \mu)I + \sigma_q Q \quad (3)$$

$$\frac{dQ}{dt} = qS - (\gamma_q + \sigma_q)Q - \mu Q \quad (4)$$

$$\frac{dA}{dt} = aI - \gamma_a A - \mu A \quad (5)$$

$$\frac{dH}{dt} = hI - \gamma_h H - \mu H \quad (6)$$

$$\frac{dR}{dt} = \gamma I + \gamma_q Q + \gamma_a A + \gamma_h H - \mu R \quad (7)$$

with $S(0) = 9000, E(0) = 100, I(0) = 50, Q(0) = 800, A(0) = 50, H(0) = 50, R(0) = 50$

The total population is given by $N(t) = S(t) + E(t) + I(t) + Q(t) + A(t) + H(t) + R(t)$ at any time t .

Table 1. Biological description of model parameters

Parameters	Biological significance	Values
Λ	recruitment rate	0.2
β	transmission rate	0.2
μ	mortality rate	0.001
q	rate of entry into quarantine	0.1
σ	rate of progression from exposed to infectious	0.2
γ	recovery rate	0.1
a	rate of entry into antibiotic treatment	0.05
h	rate of access to healthcare resources	0.05
α	disease induced death rate	0.008
σ_q	rate of progression from quarantined to infectious	0.05
γ_q	rate of recovery from quarantine	0.1
γ_a	rate of recovery with antibiotic treatment	0.15
γ_h	rate of recovery with healthcare resources	0.15

The values of $\Lambda, \beta, \mu, \gamma$ and α are gotten from Akponana et al. (2024) while the rest are assumed

3. Analysis of Model Dynamics

In this section, we look into the mathematical analysis of the model by identifying the equilibrium points, which represent the steady states of the system where the population dynamics remain constant over time. We then derive the basic reproduction number, R_0 , a critical threshold parameter that determines whether the disease will spread or die out in the population. The stability of these equilibrium points is assessed using analytical techniques to determine their behavior under small perturbations, providing insight into the long-term outcomes of the disease in different scenarios. Additionally, sensitivity analysis is conducted to evaluate the impact of various model parameters on R_0 and the stability of the system, thereby highlighting key factors that influence the effectiveness of intervention strategies. This analysis is crucial for understanding the conditions under which diphtheria can be controlled or eradicated and for informing public health policies and resource allocation.

3.1. Positivity of the Model

To ensure the epidemiological relevance of the $SEIQAHR$ model, it is crucial to establish the positivity of its state variables. In other words, we need to verify that the model's solutions remain non-negative for all time, which is a fundamental requirement for any compartmental epidemiological model. In this section, the conditions under which the model's state variables S, E, I, Q, A, H and R remain positive will be derived thereby guaranteeing the model's biological feasibility.

Proof of Positivity

From equation (1) we have

$$\frac{dS}{dt} = \Lambda - \frac{\beta SI}{N} - qS - \mu S$$

Setting $S = 0$, we get

$$\frac{dS}{dt} = \Lambda$$

Since Λ represents the recruitment rate it is inherently non-negative.

However, to ensure that S remains positive over time, we also need to ensure that:

$$\Lambda \geq \left(\frac{\beta I}{N} + q + \mu \right) S$$

This condition ensures that the susceptible compartment remains positive over time.

From equation (2) we have

$$\frac{dE}{dt} = \frac{\beta SI}{N} - \sigma E - \mu E$$

Setting $E = 0$, we get

$$\frac{dE}{dt} = \frac{\beta SI}{N}$$

Since β, S, I and N are non-negative, $\frac{dE}{dt} \geq 0$ when $E = 0$.

However, to ensure that E remains positive over time, we also need to ensure that:

$$\frac{\beta SI}{N} \geq (\sigma + \mu) E$$

This condition ensures that the exposed compartment remains positive over time.

From equation (3) we have

$$\frac{dI}{dt} = \sigma E - (\gamma + a + h) I - (\alpha + \mu) I + \sigma_q Q$$

Setting $I = 0$, we get

$$\frac{dI}{dt} = \sigma E + \sigma_q Q$$

Since σ, E, σ_q and Q are non-negative, $\frac{dI}{dt} \geq 0$ when $I = 0$.

However, to ensure that I remains positive over time, we also need to ensure that:

$$\sigma E + \sigma_q Q \geq (\gamma + a + h + \alpha + \mu)I$$

This condition ensures that the infectious compartment remains positive over time.

From equation (4) we have

$$\frac{dQ}{dt} = qS - (\gamma_q + \sigma_q)Q - \mu Q$$

Setting $Q = 0$, we get

$$\frac{dQ}{dt} = qS$$

Since q and S are non-negative, $\frac{dQ}{dt} \geq 0$ when $Q = 0$.

However, to ensure that Q remains positive over time, we also need to ensure that:

$$qS \geq (\gamma_q + \sigma_q + \mu)Q$$

This condition ensures that the quarantined compartment remains positive over time.

From equation (5) we have

$$\frac{dA}{dt} = aI - \gamma_a A - \mu A$$

Setting $A = 0$, we get

$$\frac{dA}{dt} = aI$$

Since a and I are non-negative, $\frac{dA}{dt} \geq 0$ when $A = 0$.

However, to ensure that A remains positive over time, we also need to ensure that:

$$aI \geq (\gamma_a + \mu)A$$

This condition ensures that the antibiotic treatment compartment remains positive over time.

From equation (6) we have

$$\frac{dH}{dt} = hI - \gamma_h H - \mu H$$

Setting $H = 0$, we get

$$\frac{dH}{dt} = hI$$

Since h and I are non-negative, $\frac{dH}{dt} \geq 0$ when $H = 0$.

However, to ensure that H remains positive over time, we also need to ensure that:

$$hI \geq (\gamma_h + \mu)H$$

This condition ensures that the healthcare resources compartment remains positive over time.

From equation (7) we have

$$\frac{dR}{dt} = \gamma I + \gamma_q Q + \gamma_a A + \gamma_h H - \mu R$$

Setting $R = 0$, we get

$$\frac{dR}{dt} = \gamma I + \gamma_q Q + \gamma_a A + \gamma_h H$$

Since $\gamma, I, \gamma_q, Q, \gamma_a, A, \gamma_h$ and H are non-negative, $\frac{dR}{dt} \geq 0$ when $R = 0$.

However, to ensure that A remains positive over time, we also need to ensure that:

$$\gamma I + \gamma_q Q + \gamma_a A + \gamma_h H \geq \mu R$$

This condition ensures that the recovered compartment remains positive over time.

3.2. Boundedness of the Model

To ensure that the model remains within biologically reasonable limits, it is necessary to demonstrate that the solutions to the system are bounded for all time $t \geq 0$.

Proof of Boundedness

To prove boundedness, we consider the total population $N(t)$ defined as:

$$N(t) = S(t) + E(t) + I(t) + Q(t) + A(t) + H(t) + R(t)$$

Summing the equations, we have:

$$\frac{dN}{dt} = \frac{dS}{dt} + \frac{dE}{dt} + \frac{dI}{dt} + \frac{dQ}{dt} + \frac{dA}{dt} + \frac{dH}{dt} + \frac{dR}{dt}$$

Substituting the respective equations:

$$\begin{aligned} \frac{dN}{dt} = & \Lambda - \mu(S + E + I + Q + A + H + R) - \alpha I - \gamma I - \gamma_q Q \\ & - \gamma_a A - \gamma_h H \end{aligned}$$

Given that the death rates μ and α , along with the recovery rates $\gamma, \gamma_q, \gamma_a, \gamma_h$, are non-negative, the equation simplifies to:

$$\frac{dN}{dt} \leq \Lambda - \mu N$$

Solving this differential inequality, we obtain:

$$N(t) \leq \frac{\Lambda}{\mu} + \left(N(0) - \frac{\Lambda}{\mu} \right) e^{-\mu t}$$

As t increases, the exponential term $e^{-\mu t}$ tends to zero, leading to:

$$N(t) \leq \frac{\Lambda}{\mu}$$

Thus, the total population $N(t)$ is bounded above by $\frac{\Lambda}{\mu}$. Since each compartment $S(t), E(t), I(t), Q(t), A(t), H(t), R(t)$ is a non-negative part of the total population, each of these variables is also bounded by $\frac{\Lambda}{\mu}$.

3.3. Equilibrium Points

In the study of infectious disease models, equilibrium points play a crucial role in understanding the long-term behavior of the disease within a population. An equilibrium point, also known as a steady-

state solution, occurs when the rates of change of all the compartments in the system are equal to zero. At these points, the population remains in a steady state, meaning that the number of individuals in each compartment (e.g., susceptible, infected, recovered) does not change over time. Analyzing these equilibrium points allows us to determine whether a disease will die out, persist, or grow within the population. There are typically two primary types of equilibrium points considered in epidemiological models: the Disease-Free Equilibrium (DFE) and the endemic equilibrium.

3.3.1. The Disease-Free Equilibrium Point (DFEP)

The Disease-Free Equilibrium (DFE) is a critical concept in the analysis of infectious disease models. The DFE represents the scenario where the disease has been eradicated or has not yet invaded the population. At this equilibrium, the number of infected individuals is zero, meaning there is no ongoing transmission of the disease. The DFE is essential for public health planning, as it indicates the baseline state that public health interventions aim to achieve. The DFE occurs when there are no infections in the population, meaning ($I = 0$), the system can then be solved and we get the following values:

$$S = \frac{\Lambda}{\mu + q}, E = 0, I = 0, Q = 0, A = 0, H = 0, R = 0$$

Therefore, the disease-free equilibrium is given by,

$$(S, E, I, Q, A, H, R) = \left(\frac{\Lambda}{\mu + q}, 0, 0, 0, 0, 0, 0 \right)$$

3.3.2. The Endemic Equilibrium (EE)

The endemic equilibrium represents a state where the disease persists in the population at a stable, constant level over time. Unlike the Disease-Free Equilibrium (DFE), where the infection is absent, the endemic equilibrium occurs when the infection continues to circulate, resulting in a steady number of infected individuals. At this equilibrium, the rates of new infections and recoveries balance out, leading to no overall change in the population's health status. The endemic equilibrium is significant because it helps us understand the conditions under which a disease remains present in the population and what factors influence its persistence. Solving the entire system of equations, we obtain the EE as follows:

$$S_e = -\frac{1}{2} \frac{Na_1b_1c_1d_1 + \Lambda\beta\sigma d_1 \pm \sqrt{N^2a_1^2b_1^2c_1^2d_1^2 + 4\Lambda N\beta qb_1^2c_1d_1\sigma_q - 2\Lambda N\beta\sigma a_1b_1c_1d_1^2 + \Lambda^2\beta^2\sigma^2d_1^2}}{\beta(qb_1\sigma_q - \sigma a_1d_1)}$$

$$E_e = \frac{S_e + \Lambda}{b_1} \quad I_e = \frac{-Na_1S_e + N\Lambda}{\beta S_e} \quad Q_e = \frac{qS_e}{d_1}$$

$$A_e = \frac{aN(S_e a_1 + \Lambda)}{\beta S_e e_1} \quad H_e = \frac{hN(S_e a_1 + \Lambda)}{\beta S_e f_1}$$

$$R_e = \frac{\left(\left((-a_1d_1\gamma\sigma + b_1q(\gamma\sigma_q + c_1\gamma_q))f_1 - \gamma_h h(-qb_1\sigma_q + \sigma a_1d_1) \right) e_1 - a\gamma_a f_1 (-qb_1\sigma_q + \sigma a_1d_1) \right) S_e + ((\gamma f_1 + h\gamma_h)e_1 + a\gamma_a f_1)\Lambda d_1 \sigma}{c_1 b_1 e_1 f_1 \mu d_1}$$

$$\text{where } a_1 = (q + \mu), b_1 = (\sigma + \mu), c_1 = (\gamma + a + h + \alpha + \mu), d_1 = (\gamma_q + \sigma_q + \mu),$$

$$e_1 = (\gamma_a + \mu), f_1 = (\gamma_h + \mu)$$

3.4. Stability Analysis

In this section, we investigate the stability of the *SEIQAHR* model using the Lyapunov function method. The Lyapunov function is a powerful tool for analyzing the stability of nonlinear systems, providing a way to determine the asymptotic behaviour of the system. By constructing a suitable Lyapunov function, we can establish the stability of the system and gain insights into its behaviour.

Let's define a Lyapunov function in terms of the infected compartments (E, I, Q, A, H)

$$V(E, I, Q, A, H) = bE + cI + dQ + eA + fH$$

Where b, c, d, e and f are positive constants.

To analyze the stability of the system, we compute the derivative of the Lyapunov function V along the trajectories of the system:

$$\frac{dV}{dt} = b \left(\frac{dE}{dt} \right) + c \left(\frac{dI}{dt} \right) + d \left(\frac{dQ}{dt} \right) + e \left(\frac{dA}{dt} \right) + f \left(\frac{dH}{dt} \right)$$

Substituting the expressions for $\frac{dE}{dt}, \frac{dI}{dt}, \frac{dQ}{dt}, \frac{dA}{dt}$ and $\frac{dH}{dt}$ from the model, we get:

$$\frac{dV}{dt} = b \left(\frac{\beta SI}{N} - \sigma E - \mu E \right) + c(\sigma E - (\gamma + a + h)I - (\alpha + \mu)I + \sigma_q Q)$$

$$+d(qS - (\gamma_q + \sigma_q)Q - \mu Q) + e(aI - \gamma_a A - \mu A) + f(hI - \gamma_h H - \mu H)$$

Simplifying the expression, we get:

$$\frac{dV}{dt} = b \frac{\beta SI}{N} - b(\sigma + \mu)E + c\sigma E - c(\gamma + a + h + \alpha + \mu)I + c\sigma_q Q + dqS + d(\gamma_q + \sigma_q - \mu)Q$$

$$+eal - e(\gamma_a + \mu)A + fhI - f(\gamma_h + \mu)H$$

To determine the stability of the system, we need to analyze the sign of $\frac{dV}{dt}$.

If $\frac{dV}{dt} \leq 0$, the system is asymptotically stable.

If $\frac{dV}{dt} \geq 0$, the system is unstable.

By choosing appropriate values for the constants a, b, c, d, and e, we can ensure that $\frac{dV}{dt} \leq 0$, indicating asymptotic stability.

3.5. The Basic Reproduction Number

where:

$$\mathcal{F}(t) = \begin{pmatrix} 0 & \frac{\beta SI}{N} & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 & 0 \end{pmatrix} \text{ and } \mathcal{V}(t) = \begin{pmatrix} -(\sigma + \mu) & 0 & 0 & 0 & 0 \\ \sigma & -(\gamma + a + h + \alpha + \mu) & \sigma_q & 0 & 0 \\ 0 & 0 & -(\gamma_q + \sigma_q + \mu) & 0 & 0 \\ 0 & a & 0 & -(\gamma_a - \mu) & 0 \\ 0 & h & 0 & 0 & -(\gamma_h + \mu) \end{pmatrix}$$

Evaluating the derivatives of F and V at the disease-free equilibrium point obtained above, yields FV^{-1} as seen below:

$$FV^{-1} = \begin{pmatrix} -\frac{\beta S\sigma}{Nb_1c_1} & -\frac{\beta S}{Nc_1} & -\frac{\beta S\sigma_q}{Nd_1c_1} & 0 & 0 \\ 0 & 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 & 0 \end{pmatrix}$$

where $b_1 = (\sigma + \mu)$, $c_1 = (\gamma + a + h + \alpha + \mu)$, $d_1 = (\gamma_q + \sigma_q + \mu)$

By solving the dominant eigenvalue of the next generation matrix FV^{-1} , we get the basic reproduction number to be

$$R_0 = -\frac{\beta S\sigma}{N(\sigma + \mu)(\gamma + a + h + \alpha + \mu)}$$

Recall that

$$S = \frac{\Lambda}{\mu + q}$$

Therefore, the basic reproduction number of the given system becomes:

$$R_0 = -\frac{\beta \Lambda \sigma}{N(\mu + q)(\sigma + \mu)(\gamma + a + h + \alpha + \mu)}$$

The basic reproduction number, denoted as R_0 , is a key metric in epidemiology that quantifies the average number of secondary infections produced by a single infected individual in a completely susceptible population. Understanding R_0 is critical for assessing the potential spread of a disease and determining the necessary level of intervention to prevent an outbreak. If R_0 is greater than one, each infected individual, on average, causes more than one new infection, leading to the possibility of a disease outbreak and persistence in the population. Conversely, if R_0 is less than one, the infection will likely die out over time, as each infected individual generates fewer than one new case on average.

To calculate R_0 for our model, we will use the next-generation matrix method, a mathematical approach that allows for the systematic computation of the reproduction number based on the structure of the model. This method involves constructing matrices that represent the rate of new infections and the transfer of individuals between different states of infection. Let $X(t) = (E, I, Q, A, H)$ to accurately represent the transmission dynamics within the population.

$$X'(t) = \mathcal{F}(t) - \mathcal{V}(t)$$

3.6. Sensitivity Analysis

Sensitivity analysis is a critical tool for understanding how changes in model parameters impact key outcomes, such as the reproduction number R_0 and the stability of equilibrium points. This analysis helps identify which parameters have the most significant influence on the dynamics of disease transmission and

can guide the design of effective control strategies. In this subsection, we will perform a sensitivity analysis using the approach developed by Chitnis et al. (2008). This method allows us to systematically assess the relative importance of different parameters in the model by calculating sensitivity indices. These indices measure how variations in each parameter affect the reproduction number and other model outputs.

The sensitivity index for a parameter, say Λ is defined as

$$\xi_{\Lambda}^{R_0} = \frac{\partial R_0}{\partial \Lambda} \times \frac{\Lambda}{R_0}$$

Computing the sensitivity indices of each parameter we get the results below:

$$\begin{aligned} \xi_{\beta}^{R_0} &= 1 > 0 & \xi_{\Lambda}^{R_0} &= 1 > 0 & \xi_{\sigma}^{R_0} &= \frac{\mu}{\sigma + \mu} > 0 \\ \xi_{\mu}^{R_0} &= -\frac{\mu(3\mu^2 + (2a + 2h + 2q + 2\alpha + 2\gamma + 2\sigma)\mu + (a + h + q + \alpha + \gamma)\sigma + q(a + h + \alpha + \gamma))}{(\mu + q)(\sigma + \mu)(\gamma + a + h + \alpha + \mu)} < 0 \\ \xi_q^{R_0} &= -\frac{q}{q + \mu} < 0 & \xi_{\gamma}^{R_0} &= -\frac{\gamma}{\gamma + a + h + \alpha + \mu} < 0 & \xi_a^{R_0} &= -\frac{a}{\gamma + a + h + \alpha + \mu} < 0 \\ \xi_{\alpha}^{R_0} &= -\frac{\alpha}{\gamma + a + h + \alpha + \mu} < 0 & \xi_h^{R_0} &= -\frac{h}{\gamma + a + h + \alpha + \mu} < 0 \end{aligned}$$

The sensitivity analysis reveals the impact of each parameter on the basic reproduction number R_0 . The transmission rate β has a sensitivity index of 1, indicating that any increase in β will lead to a proportional increase in R_0 , emphasizing its significant role in disease spread. Similarly, the recruitment rate Λ also has a sensitivity index of 1, meaning that higher recruitment into the susceptible population directly increases R_0 , highlighting the importance of managing the influx of susceptible individuals. The rate of progression from exposed to infectious σ shows a positive sensitivity index, indicating that an increase in σ raises R_0 , though the effect is moderated by the balance between progression to the infectious stage and the mortality rate μ . On the other hand, the mortality rate μ has a negative sensitivity index, implying that an increase in μ decreases R_0 , suggesting that higher mortality can reduce the potential for disease spread.

The rate of entry into quarantine q also shows a negative sensitivity index, meaning that enhancing quarantine measures can reduce R_0 , emphasizing the role of quarantine in disease control. Similarly, the recovery rate γ has a negative sensitivity index, indicating that improving recovery decreases R_0 , which underscores the importance of effective treatment strategies. Additionally, the rate of entry into antibiotic treatment a and the rate of access to healthcare resources h both have negative sensitivity indices, suggesting that increasing these rates can reduce R_0 and thereby contribute to controlling the disease. The disease-induced death rate α also negatively influences R_0 , meaning that an increase in α can help limit the spread of the disease. Overall, this sensitivity analysis provides valuable insights into the parameters that most strongly influence R_0 and highlights potential strategies for reducing the spread of the disease by targeting these key parameters.

4. Discussion of Results

The impact of quarantine on the susceptible and quarantined populations is evident as shown in Figure 2 and 3 respectively. As the rate of entry into quarantine (q) increases, the susceptible population ($S(t)$) experiences a more rapid decline over time. When there is no quarantine ($q = 0$), the susceptible population decreases very slowly, leaving a significant portion of the population vulnerable to infection. However, with the implementation of quarantine ($q > 0$), the decline in the susceptible population becomes steeper, indicating that more individuals are being removed from the susceptible pool either through exposure, quarantine, or recovery. The quarantined population ($Q(t)$) exhibits a substantial increase as q rises. Without quarantine ($q = 0$), the quarantined population remains at zero, while higher values of q result in a larger and quicker rise in the quarantined population, which eventually peaks before gradually declining. These results highlight the effectiveness of quarantine as a strategy for controlling the spread of diphtheria by isolating susceptible individuals and preventing further transmission.

The rate of entry into antibiotic treatment (a) plays a crucial role in the dynamics of the infectious ($I(t)$) and antibiotic treatment ($A(t)$) populations as seen in Figure 4 and 5. As a increases, more individuals from the infectious class are moved into the antibiotic treatment class. This transfer reduces the number of people who remain infectious, thereby lowering the peak and overall magnitude of the $I(t)$ curve. A higher value of a leads to a faster decline in the infectious population, as more individuals receive treatment that helps them recover sooner, reducing their infectious period and the likelihood of spreading the disease. Concurrently, as a increases, the population in the antibiotic treatment class ($A(t)$)

risers. More individuals being treated with antibiotics causes the $A(t)$ curve to peak higher and potentially earlier, depending on how quickly the infectious individuals are identified and treated.

The rate of access to healthcare resources (h) significantly impacts both the infectious ($I(t)$) and healthcare resources ($H(t)$) compartments as displayed in Figure 6 and 7. As the rate of access to healthcare resources (h) increases, more individuals from the infectious class are moved to the healthcare resources class. This transition reduces the number of individuals who remain in the infectious state, leading to a decrease in the peak and overall number of infectious individuals over time. Essentially, a higher h means that infectious individuals are receiving necessary healthcare interventions sooner, which not only helps them recover faster but also minimizes the period during which they can transmit the disease to others. Consequently, increasing h contributes to controlling the spread of the disease by reducing the infectious population. Simultaneously, as h increases, the population in the healthcare resources class (H) grows. This increase reflects the higher number of infectious individuals accessing healthcare.

The rate of progression from the quarantined state to the infectious state (σ_q) plays a critical role in influencing both the infectious (I) and quarantined (Q) populations within the model as depicted in Figure 8 and 9. As the rate σ_q increases, more individuals who were quarantined progress to the infectious class. This transition results in an increase in the number of individuals in the infectious state. A higher σ_q suggests that the quarantine is less effective in preventing the transition to the infectious state, potentially due to the premature release from quarantine or ineffective quarantine measures. Consequently, the infectious population may experience a rise as σ_q increases, leading to a higher risk of transmission within the community and a prolonged epidemic. Conversely, an increase in σ_q reduces the size of the quarantined population, as more individuals are moving from the quarantine to the infectious class. This reduction means that fewer individuals remain in quarantine, potentially shortening the time they are isolated from the rest of the population.

Increasing and decreasing the recovery rate from quarantine (γ_q) impacts both the quarantined (Q) and recovered (R) compartments as shown in Figure 10 and 11. As γ_q rises, individuals in quarantine transition to the recovered state more quickly. This results in a faster decrease in the number of quarantined individuals, as they move out of the quarantine compartment at an accelerated rate. Consequently, the quarantined population diminishes more rapidly over time. Conversely, a lower γ_q means

that individuals remain in quarantine longer, leading to a higher number of individuals in quarantine for an extended period. With a higher γ_q , the number of individuals transitioning to recovery from quarantine increases, which leads to a more rapid accumulation of recovered individuals. This accelerated transition results in a higher peak and quicker rise in the recovered population. On the other hand, a lower γ_q slows down the recovery process, leading to a slower increase in $R(t)$ and a delayed peak, as individuals remain in quarantine longer before recovering.

The recovery rate with antibiotic treatment (γ_a) has impact on both the antibiotic treatment compartment (A) and the recovered compartment (R) as illustrated in Figure 12 and 13. When γ_a is increased, individuals receiving antibiotic treatment recover more quickly, which leads to a faster decrease in its population. This is because a higher γ_a means that more individuals transition from (A) to (R) at a quicker rate, reducing the number of individuals receiving treatment over time. The increase in γ_a accelerates the growth of the recovered population. With more individuals moving from the antibiotic treatment compartment to the recovered state more rapidly, the number of recovered individuals (R) rises faster and reaches a higher peak more quickly. This reflects the efficient recovery process facilitated by faster antibiotic treatment. When γ_a is decreased, the recovery from antibiotic treatment slows down. As a result, individuals remain in the antibiotic treatment compartment for a longer period, leading to a slower reduction in (A).

The recovery rate with healthcare resources (γ_h) has effects on both the healthcare resources compartment (H) and the recovered compartment (R) as shown in Figure 14 and 15. When γ_h is increased, individuals with access to healthcare resources recover more quickly, leading to a more rapid decrease in the healthcare resources compartment (H). This is because a higher γ_h accelerates the transition of individuals from H to R , thereby reducing the number of individuals receiving healthcare resources at any given time. As the recovery rate with healthcare resources increases, the number of individuals in the recovered compartment (R) also rises more swiftly. With individuals moving from H to R more quickly, the recovery process is expedited, resulting in a faster and potentially higher peak in the recovered population. This indicates that the healthcare system is effectively facilitating quicker recovery, which contributes to reducing the overall burden of the disease. On the other hand, if γ_h is decreased, the recovery from healthcare resources slows down. This results in a slower reduction in the population of individuals in H since individuals take longer to recover and transition to the recovered state.

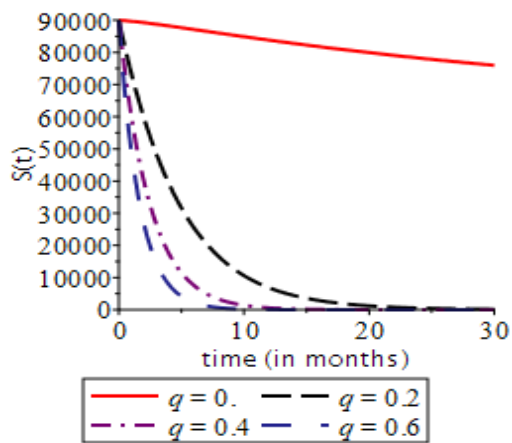


Figure 2: Effect of rate of entry into quarantine on the susceptible class

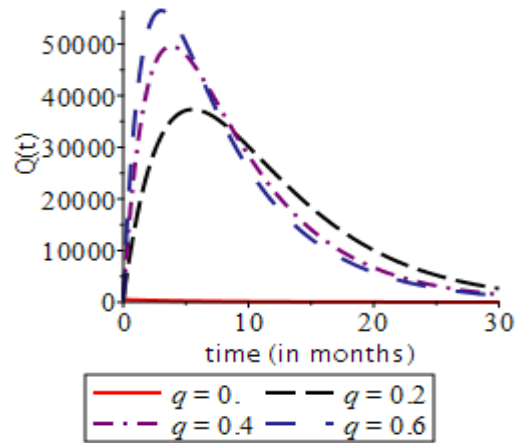


Figure 3: Effect of rate of entry into quarantine on the quarantine class

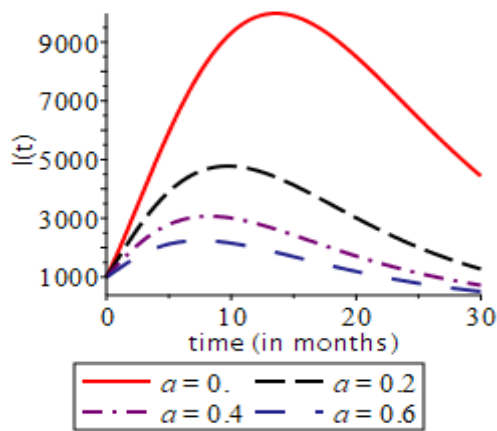


Figure 4: Effect of rate of entry into antibiotic treatment on infectious class

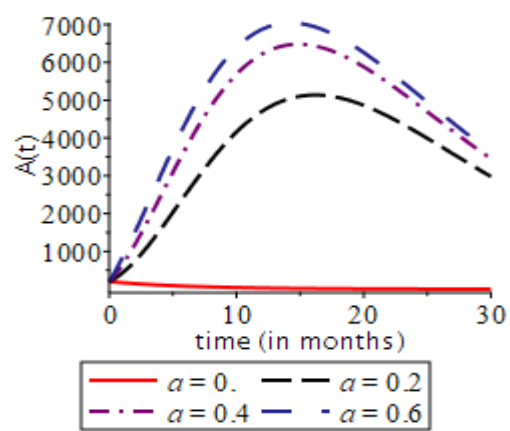


Figure 5: Effect of rate of entry into antibiotic treatment on individuals receiving antibiotic treatment

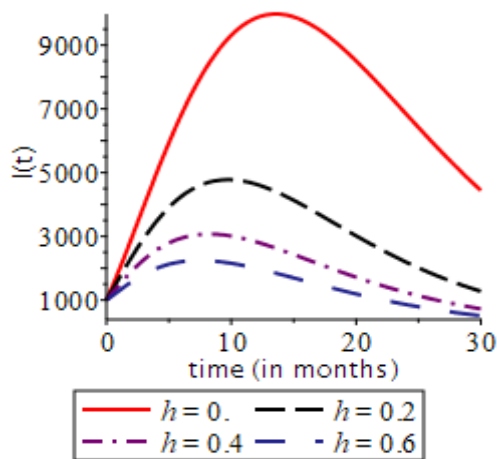


Figure 6: Effect of rate of access to healthcare resources on infectious.

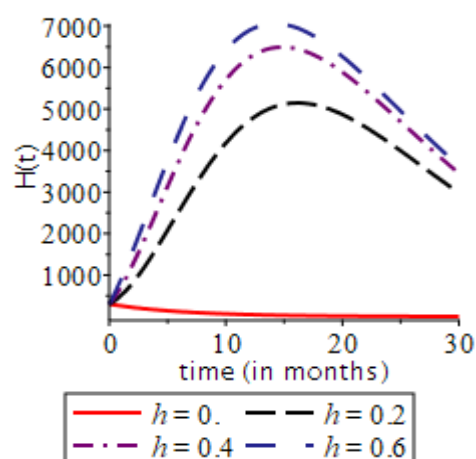


Figure 7: Effect of rate of access to healthcare resources on H class.

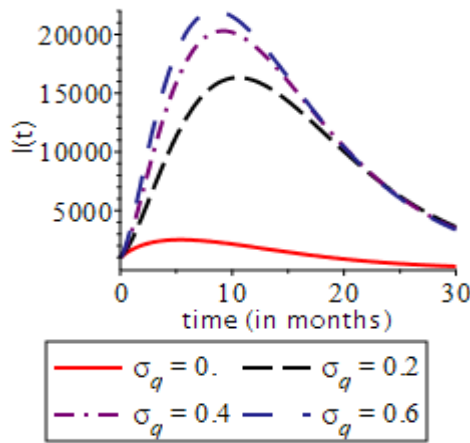


Figure 8: Effect of rate of progression from quarantined to infectious on the infectious

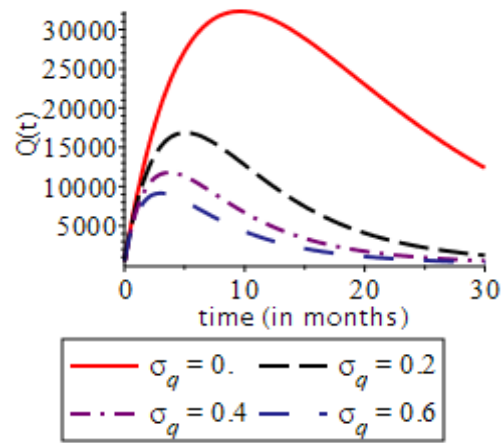


Figure 9: Effect of rate of progression from quarantined to infectious on the quarantine.

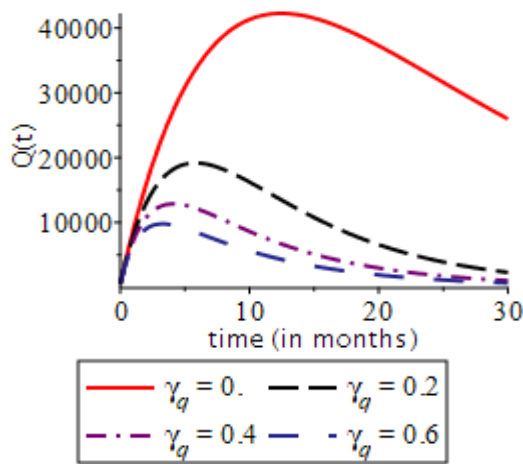


Figure 10: Effect of rate of recovery from quarantine on quarantine

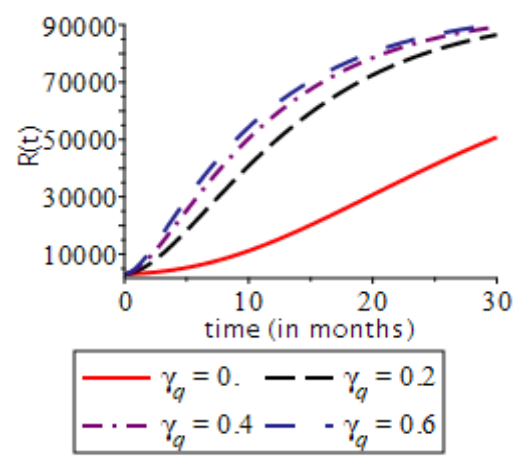


Figure 11: Effect of rate of recovery from quarantine on quarantine

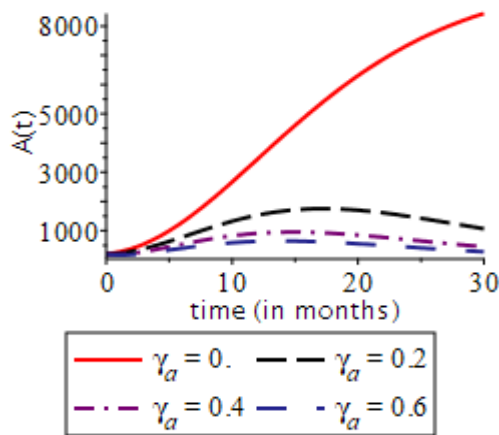


Figure 12: Effect of rate of recovery with antibiotic treatment on antibiotic treatment

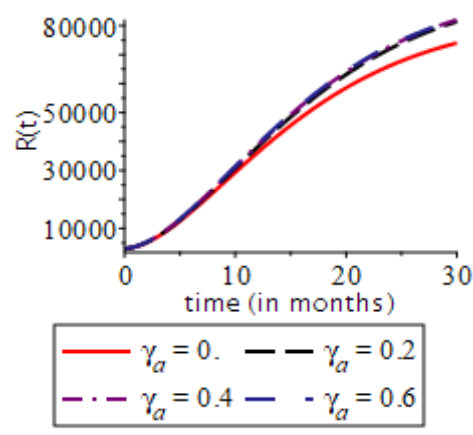


Figure 13: Effect of rate of recovery with antibiotic treatment on recovery class

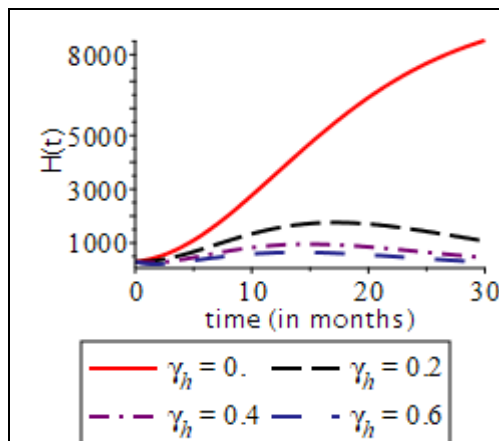


Figure 14: Effect of rate of recovery with healthcare resources on healthcare resources

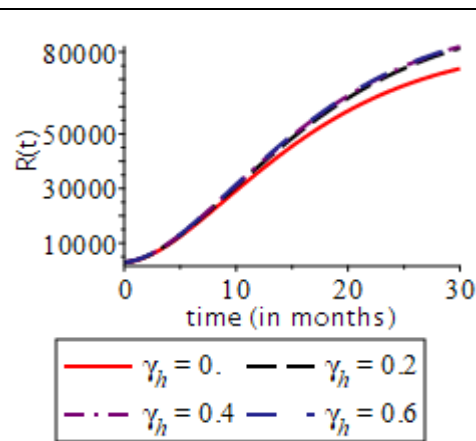


Figure 15: Effect of rate of recovery with healthcare resources on recovery class

5. Conclusion and Recommendation

The analysis of the mathematical model for diphtheria transmission provides valuable insights into effective disease management strategies. The findings demonstrate that implementing quarantine measures significantly impacts the dynamics of the disease by accelerating the decline in the susceptible population and increasing the number of individuals in quarantine. This highlights the effectiveness of quarantine in controlling the spread of diphtheria, although it also necessitates substantial resource allocation to ensure successful implementation. Additionally, the model reveals that higher recovery rates—whether through general recovery, antibiotic treatment, or access to healthcare resources—result in a lower peak of infectious individuals and a quicker rise in the recovered population. This underscores the critical role of effective recovery strategies in managing outbreaks. The rates of entry into antibiotic treatment and access to healthcare resources also play pivotal roles, with higher rates contributing to a reduction in the infectious population and an increase in recovery. However, balancing these rates with available resources is crucial to avoid overwhelming the healthcare system. Furthermore, a higher rate of progression from quarantine to the infectious state can elevate the infectious population and reduce the quarantined population, indicating the need for effective quarantine enforcement. Overall, the study emphasizes the importance of balancing disease control strategies with resource allocation to manage diphtheria outbreaks effectively.

To improve the management of diphtheria outbreaks, several key recommendations are proposed. Firstly, strengthening quarantine measures is essential to reduce disease spread, and this requires adequate resources to ensure the effectiveness and sustainability of quarantine practices. Enhancing recovery strategies by investing in healthcare infrastructure and resources can lead to higher recovery rates and a reduced disease burden. Additionally, optimizing antibiotic distribution is crucial to manage the infectious population efficiently while avoiding excessive strain on healthcare resources. Expanding access to healthcare resources will help reduce the infectious population and accelerate recovery, making it vital to ensure healthcare systems are prepared to handle increased patient numbers. Finally, regular monitoring

and adjustment of parameters such as quarantine rates, recovery rates, and healthcare access are necessary to respond effectively to changes in disease dynamics and resource availability. By implementing these recommendations, public health authorities can enhance their strategies for controlling diphtheria and improving overall disease management.

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