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Dynamical Analysis of a Diphtheria Transmission Model with Epidemiological Data Fitting

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Abstract

Diphtheria is a serious infectious disease caused by *Corynebacterium diphtheriae*, which affects the respiratory system and can lead to severe complications if not properly controlled. In this study, a compartmental deterministic epidemiological model governed by a system of nonlinear differential equations was formulated to investigate the transmission dynamics of diphtheria. Rigorous analysis of the model showed that the disease-free equilibrium was both locally and globally asymptotically stable when the basic reproduction number was less than unity, indicating that the spread of the disease could be effectively controlled under this condition. Real-life data on diphtheria were collected and fitted into the model in order to estimate key parameters. These estimated parameter values were then used to perform numerical simulations using MATLAB, which helped validate the analytical results obtained from the model. The simulations further explored the interaction dynamics of diphtheria in humans, including transmission patterns, disease progression, and its effects on the host population. Based on the findings, recommendations were made to healthcare policymakers on effective strategies for controlling and reducing the spread of the disease and minimizing its public health burden.

Keywords:

Diphtheria; Data fitting; Sensitivity analysis; Basic reproduction number; Numerical simulation.

Introduction

Diphtheria is an acute and potentially fatal infectious disease caused primarily by toxigenic strains of *Corynebacterium diphtheriae*, a Gram-positive bacterium that produces a potent exotoxin responsible for severe tissue damage and systemic complications. Although largely controlled in many countries through vaccination, diphtheria remains a public health concern in regions with low immunization coverage and weakened health systems. The disease typically affects the respiratory tract but may also present as cutaneous infection, especially in vulnerable

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populations [1]. The toxin produced inhibits protein synthesis in host cells, leading to local necrosis and systemic toxicity such as myocarditis and neuropathy [2]. Transmission of diphtheria occurs mainly through respiratory droplets from infected individuals or carriers, as well as direct contact with contaminated skin lesions or fomites. Once inhaled, the bacterium colonizes the upper respiratory tract, where it produces a thick gray pseudomembrane that may obstruct the airway and cause respiratory distress. This form of obstruction is a hallmark clinical feature and is associated with significant mortality in untreated cases [3]. In addition, asymptomatic carriers play an important role in sustaining transmission within communities, particularly in overcrowded settings [4, 15,16].

The clinical presentation of diphtheria ranges from mild pharyngitis to severe systemic illness. Early symptoms include sore throat, fever, malaise, and swollen cervical lymph nodes, which can rapidly progress to respiratory obstruction and systemic toxin-mediated complications. Severe cases may result in myocarditis, arrhythmias, renal failure, or peripheral neuropathy, all of which significantly increase mortality risk [5]. The variability in disease severity is influenced by host immunity and vaccination status. Despite the availability of effective vaccines, diphtheria outbreaks continue to occur globally, particularly in regions affected by conflict, migration, or disrupted healthcare systems. Recent epidemiological evidence indicates a resurgence of cases in several countries, linked to declining immunization coverage and population displacement [6]. Studies have also shown that changes in circulating strains and toxin gene acquisition among non-toxigenic strains may contribute to re-emergence risks [7,18,19]. Global health organizations emphasize sustained immunization, surveillance, and rapid outbreak response as essential strategies for diphtheria control [8,9]. The World Health Organization recommends maintaining high routine vaccination coverage and ensuring booster doses across the lifespan to prevent susceptibility gaps. Without consistent vaccination efforts, diphtheria can rapidly re-emerge, even in regions where it was previously eliminated [2,4].

Tafrikan et al [10], developed a mathematical model to study diphtheria transmission dynamics incorporating vaccination and treatment. The model classified the population into susceptible, infected, treated, and recovered compartments. Their results showed that increased vaccination coverage reduced disease transmission significantly, while treatment shortened infection duration. They concluded that combining vaccination and treatment was effective in achieving disease control and stability of the disease-free equilibrium. Amalia et al [11] formulated a diphtheria transmission model using optimal control theory to evaluate the impact of vaccination, booster doses, and treatment. The study introduced time-dependent control variables to minimize infection spread. Their findings showed that booster vaccination greatly reduced transmission, and the best outcomes were achieved when all control strategies were applied together. They concluded that optimal control significantly improved disease management.

Gatto et al [12] developed a SEIR-based model to analyse COVID-19 transmission and the effect of containment measures. The model incorporated mobility reduction and contact tracing effects. Their results showed that lockdown measures significantly reduced transmission rates and flattened the epidemic curve. They concluded that SEIR models were useful for evaluating real-time intervention strategies during pandemics. Zhang et al [13] developed a SEIR model to study measles transmission dynamics under vaccination influence. The study analysed how different vaccination levels affected outbreak size. Their findings showed that increasing vaccination coverage reduced outbreak probability and could eliminate endemic transmission

when herd immunity thresholds were reached. They concluded that vaccination remained the most effective control strategy. Zhao et al [14] developed a SEIR-type model to study Ebola virus disease transmission with isolation and hospitalization compartments. The model captured key outbreak control mechanisms. Their results showed that rapid isolation of infected individuals significantly reduced transmission and outbreak size. They concluded that timely intervention and strong healthcare response were critical in controlling Ebola outbreaks.

The aim of this study is to formulate a mathematical model that captures the transmission dynamics of diphtheria and to use it to analyze the spread and control of the disease in a population. The study also seeks to provide meaningful insights that can support effective public health interventions and policy decisions to; (i) analyze the proposed mathematical model and determine its qualitative properties, including the stability of the disease-free and endemic equilibria, with emphasis on global asymptotic stability. (ii) compute and analyze the basic reproduction number in order to understand the transmission potential of diphtheria within the population (iii) collect and analyze real-life diphtheria data from relevant health authorities for use in model validation and assessment. (iv) fit the collected real-life data into the proposed model in order to estimate unknown parameters and improve model accuracy. (v) simulate the mathematical model using the estimated parameters and interpret the results, and finally provide recommendations to health policymakers on effective strategies for controlling and reducing the spread of diphtheria.

The novelty of this study lies in the development of a compartmental deterministic epidemiological model governed by nonlinear differential equations to describe the transmission dynamics of diphtheria in a human population. The model was rigorously analyzed to establish the stability of the disease-free equilibrium, showing that it was both locally and globally asymptotically stable when the basic reproduction number was less than unity, thereby confirming conditions under which effective disease control could be achieved. Unlike many theoretical studies, real-life diphtheria data were incorporated into the model through data fitting and parameter estimation, making the model more realistic and applicable to actual epidemic situations.

Furthermore, the estimated parameters obtained from real-world data were used to conduct numerical simulations in MATLAB, which validated the analytical results and provided deeper insights into the transmission dynamics of diphtheria. The simulations also illustrated the interaction patterns of the disease within the host population and highlighted its impact over time. In addition, the study contributed a predictive framework for forecasting diphtheria infection trends, thereby enhancing its practical relevance. The findings ultimately provided evidence-based recommendations for policymakers on effective control and mitigation strategies to reduce the disease burden in the population.

Model Formulation

The total population of the people at time *t*, denoted $N(t)$, is split into (5) mutually exclusive compartments of susceptible individual $S(t)$, $E(t)$ Exposed individuals to diphtheria, Vaccinated individual with diphtheria $V(t)$, infected individual with diphtheria $I(t)$, treatment class for individuals with diphtheria, and Set of individual that recovered from the

disease $R(t)$. The bacteria, Coryne-bacterium is denoted $B(t)$. The recruitment rate of individuals into the susceptible population is at the rate Λ, β_H is the effective contact rate of humans with the probability of been infected per contact with an infected individual. We also denote β_1 as the bacteria shedding rate into surroundings, θ as the rate at which the exposed humans become infected with Diphtheria, σ is the rate at which the infected humans are treated, p_1 and p_2 are the shedding rate the bacteria into the surrounding, ε is the rate as which treated individuals recovered, μ, is the natural death rate of humans and the disease induced death of humans is δ and ϕ as the modification parameter that accounts for reduced death in the treatment class. The model assumed a uniform natural death rate across all compartments of the population. It also assumed that infected individuals receive treatment and that vaccination is applied to the susceptible population to reduce infection risk. Diphtheria transmission was considered to occur through bacterial infection in humans. In addition, the model incorporated disease-induced death rates for both infected individuals and those under treatment. Finally, it was assumed that recovered individuals do not acquire permanent immunity and may return to the susceptible class.

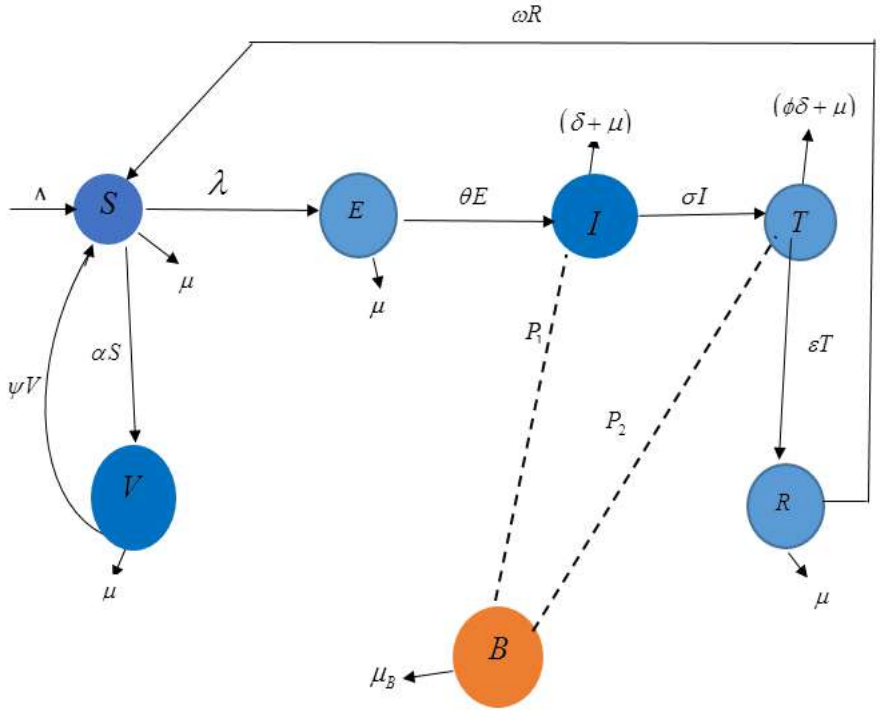

Fig 1: Schematic Flow Diagram of the diphtheria Model

Table 1. Parameters and variables description

Variables	Description
$S(t)$	Individuals susceptible to diphtheria
$E(t)$	Individuals exposed to diphtheria
$I(t)$	Individuals that are infected with diphtheria
$T(t)$	Treatment for diphtheria

$V(t)$	Vaccination class
Parameters	**Description**
Λ	Recruitment rate into susceptible class
β	The rate at which susceptible individuals gets in contact with diphtheria
θ	Progression rate from exposed to infected
β_1	Bacteria contact rate
σ	Treatment rate for diphtheria
ε	The rate at which those treated of diphtheria recovered
α	Rate at which susceptible individuals are vaccinated
ψ	Waning rate of vaccine
p_1, p_2	Shedding rate of the bacteria in the environment
μ_B	Bacteria natural death rate
μ	Human natural death rate
ω	Rate at which those that recovered become susceptible
K	Density of the bacteria in the environment
δ	Disease induced death rate
ϕ	Modification parameter that accounts for diphtheria induced death in treatment class

Model Equations

$$\begin{aligned}
\frac{dS}{dt} &= \Lambda - \lambda S + \omega R + \psi V - \alpha S - \mu S \\
\frac{dE}{dt} &= \lambda S - (\theta + \mu) E \\
\frac{dI}{dt} &= \theta E - (\sigma + \delta + \mu) I \\
\frac{dT}{dt} &= \sigma I - (\varepsilon + \phi\delta + \mu) T \\
\frac{dV}{dt} &= \alpha S - (\psi + \mu) V \\
\frac{dB}{dt} &= P_1 I + P_2 T - \mu_B \\
\frac{dR}{dt} &= \varepsilon T - (\omega + \mu) R
\end{aligned} \qquad (1)$$

Where λ the force of infection of the Diphtheria model (1) isis given as:

$$\lambda = \frac{\beta IS}{N} + \frac{\beta_1 B}{K+B}$$

Let $M_1 = (\theta + \mu)$, $M_2 = (\sigma + \delta + \mu)$, $M_3 = (\varepsilon + \phi\delta + \mu)$ $M_4 = (\psi + \mu)$ and $M_5 = (\omega + \mu)$

Model Analysis

Invariant region of the diphtheria model

Lemma 1.

The solution of Diphtheria is feasible for all $t > 0$

Proof

The total population of the humans in the Diphtheria model is given as:

$$N(t) = S(t) + E(t) + I(t) + T(t) + V(t) + R(t)$$

The sum of the differential equations is

$$N(t) = S(t) + E(t) + I(t) + T(t) + V(t) + R(t)$$

$$\frac{dN}{dt} = \Lambda - (S + E + I + T + V + R)\mu - \delta I - \phi\delta T$$

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

Solving the differential equation using the integrating factor method

$$\frac{d}{dt}\left(Ne^{ut}\right) \le \Lambda e^{ut}$$

$$d\left(Ne^{ut}\right) \le \Lambda e^{ut} dt$$

Integrating both sides

$$N(t) \le \frac{\Lambda}{\mu} + ce^{-\mu t}$$

Putting the initial l condition at t =0

$$N(0) \le \frac{\Lambda}{\mu} + c$$

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

$N0 \le N \le \frac{\Lambda}{\mu}$ as $t \to \infty$ so therefore model (1) is feasible thus, Thus, in this region, the Diphtheria model can be considered as being epidemiologically and mathematically well posed.

Positivity of solution of the Diphtheria model

It is necessary to show that all state variable of the Diphtheria model are nonnegative for all time (t). This is done by considering $\left\{ (S, E, I, T, V, B, R) \ge 0 \in R_+^7 \right\}$

Lemma 2:

Let the initial data for the model (1) be $(S, E, I, T, V, B, R) > 0$. Then the solutions (S, E, I, T, V, B, R) of the model (1) are positive for all time $t > 0$

From the first equation that

$$\frac{ds}{dt} = \Lambda - \lambda s + \omega R + \psi V - \alpha S - \mu S$$

$$\frac{ds}{dt} \ge -(\lambda + \alpha + \mu) S$$

By separating the variable and integrating

$$\int \frac{ds}{ds} \ge \int -(\lambda + \alpha + \mu) dt$$

$$InS \ge -(\lambda + \alpha + \mu) t + C$$

$$S(t) \ge Ce^{-(\lambda+\alpha+\mu)t}$$

Applying the initial condition at $t = 0$

Therefore, $S(t) \ge S(0) e^{-(\lambda+\alpha+\mu)t} \ge 0$ Since $(\lambda + \alpha + \mu) \ge 0$

Similarly it can be shown that $E, I, T, V, R > 0$

Asymptotic stability of the disease-free equilibrium of the Diphtheria model

The steady state where there is no infection (or absence of the disease), a point where $E = I = T = B = R = 0$ is called the disease-free equilibrium point (DFE) [23].

From the susceptible and vaccination classes we have;

$$\frac{ds}{dt} \ge -\lambda + \omega R + \psi V - \alpha S - \mu S$$

$$0 \geq -\lambda - (\alpha + \mu) S + \psi V$$

$$(\alpha + \mu) S = \Lambda + \psi V$$

$$S = \frac{\Lambda + \psi V}{\alpha + \mu}$$

But $\frac{dV}{dt} \geq \alpha S - (\psi + \mu) V$

$$0 = \alpha S - (\psi + \mu) V$$

$$V = \frac{\alpha S}{\psi + \mu}$$

Putting S into V gives:

$$V = \frac{\Lambda \alpha}{(\alpha + \mu)(\psi + \mu) - \psi \alpha} \Rightarrow V = \frac{\Lambda \alpha}{\alpha \mu + \psi \mu + \mu^2}$$

Putting V back to S gives:

$$S = \frac{\Lambda (\alpha + \mu)}{\alpha \mu + \psi \mu + \mu^2}$$

Hence, the disease-free equilibrium is given by:

$$DDFEP = \{S^*, E^*, I^*, T^*, B^*, R^*\} = \left\{ \frac{\Lambda (\alpha + \mu)}{\alpha \mu + \psi \mu + \mu^2} 0, 0, 0, 0, \frac{\Lambda \alpha}{\alpha \mu + \psi \mu + \mu^2}, 0 \right\}$$

Basic Reproduction Number of the Diphtheria Model

The basic reproduction number of Diphtheria infected individuals denoted by R_0 is defined as the average number of secondary infections produced by a single Diphtheria infectious individual introduced in a wholly susceptible population during his or her entire infectious period [23, 24]. We calculate the basic reproduction number by using the next generation operator method on the dynamical system (1).

Hence, it follows that,

$R_0 = \rho\left(FV^{-1}\right)$ Where ρ is the dominant Eigen value of FV^{-1}

$$F=\begin{bmatrix} 0 & \frac{\beta(\psi+\mu)}{\alpha+\psi+\mu} & 0 & \frac{\Lambda\beta_1}{\mu K} \\ 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 \end{bmatrix}, \qquad V=\begin{bmatrix} M_1 & 0 & 0 & 0 \\ -\theta & M_2 & 0 & 0 \\ 0 & -\sigma & M_3 & 0 \\ 0 & -P_1 & -P_2 & \mu_B \end{bmatrix}$$

$$V^{-1}=\begin{bmatrix} \frac{1}{M_1} & 0 & 0 & 0 \\ \frac{\theta}{M_1M_2} & \frac{1}{M_2} & 0 & 0 \\ \frac{\sigma\theta}{M_2M_1M_3} & \frac{\sigma}{M_2M_3} & \frac{1}{M_3} & 0 \\ \frac{\theta(M_3P_1+P_2\sigma)}{M_3M_2M_1\mu_B} & \frac{M_3P_1+P_2\sigma}{M_3M_2\mu_B} & \frac{P_2}{M_3\mu_B} & \frac{1}{\mu_B} \end{bmatrix}$$

$$F.V^{-1}=\begin{bmatrix} \frac{\beta E_1\theta}{E_2M_1M_2}+\frac{\Lambda\beta_1\theta(M_3P_1+P_2\sigma)}{\mu KM_3M_2M_1\mu_B} & \frac{\beta E_1}{E_2M_2}+\frac{\Lambda\beta_1(M_3P_1+P_2\sigma)}{\mu KM_3M_2\mu_B} & \frac{\Lambda\beta_1P_2}{\mu KM_3\mu_B} & \frac{\Lambda\beta_1}{\mu K\mu_B} \\ 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 \end{bmatrix}$$

Where $E_1=(\psi+\mu),\ E_2=\alpha+\psi+\mu$

The Eigen values are:

$$\lambda_1=0,\lambda_2=0,\lambda_3=0 \text{ and}$$

$$\lambda_4=\frac{\theta(\mu KM_3\mu_B\beta E_1+E_2M_3P_1\Lambda\beta_1+E_2P_2\sigma\Lambda\beta_1)}{E_2M_1M_2\mu KM_3\mu_B}$$

The basic reproduction number which is the greatest Eigen value is given as

$$R_0=\frac{\theta(\mu KM_3\mu_B\beta(\psi+\mu)+E_2M_3P_1\Lambda\beta_1+E_2P_2\sigma\Lambda\beta_1)}{(\alpha+\psi+\mu)M_1M_2\mu KM_3\mu_B}$$

Local Asymptotic Stability of the DFE of the Diphtheria Model

Theorem 1

The disease-free equilibrium point of the Diphtheria only is locally asymptotically stable (LAS) if $R_0<1$, and unstable if $R_0>1$.

Proof

Using Jacobian matrix to prove the local stability of the disease-free equilibrium point

$$J(\varsigma_0)=\begin{bmatrix} -M & 0 & -\frac{\beta E_1}{E_2} & 0 & \psi & \frac{-\Lambda\beta_1}{\mu K} & \omega \\ 0 & -M_1 & \frac{\beta E_1}{E_2} & 0 & 0 & \frac{\Lambda\beta_1}{\mu K} & 0 \\ 0 & \theta & -M_2 & 0 & 0 & 0 & 0 \\ 0 & 0 & \sigma & -M_3 & 0 & 0 & 0 \\ \alpha & 0 & 0 & 0 & -M_4 & 0 & 0 \\ 0 & 0 & P_1 & P_2 & 0 & -\mu_B & 0 \\ 0 & 0 & 0 & \varepsilon & 0 & 0 & -M_5 \end{bmatrix}$$

Where $M=(\alpha+\mu)$, $M_1=(\theta+\mu)$, $M_2=(\sigma+\delta+\mu)$, $M_3=(\varepsilon+\phi\delta+\mu)$, $M_4=(\psi+\mu)$, $M_5=(\omega+\mu)$, $E_1=(\psi+\mu)$ and $E_2=\alpha+\psi+\mu$

The characteristics polynomial of the $J(\varsigma_0)$ above is given as

$$p(\lambda)=\lambda^7+l_1\lambda^6+l_2\lambda^5+l_3\lambda^4+l_4\lambda^3+l_5\lambda^2+l_6\lambda+l_7$$

Where:

$$l_1=-M_5-\mu_B-M_4-M_3-M_2-M_1-M$$

$$l_2=\frac{\begin{pmatrix}(M+M_1+M_2+M_3+M_4+M_5)\mu_B+(M+M_2+M_3+M_4+M_5)M_1+(M+M_3+M_4+M_5)M_2+(M+M_4+M_5)M_3\\+(M+M_5)M_4+MM_5-\psi\alpha\end{pmatrix}E_2-\theta\beta E_1}{E_2}$$

$$l_3=\frac{\begin{pmatrix}\begin{pmatrix}((M+M_1+M_2+M_4+M_5)M_3+(M+M_1+M_2+M_4)M_5+(M+M_2+M_4)M_1+(M+M_4)M_2+MM_4-\psi\alpha)\mu_B\\+((M+M_1+M_2+M_4)M_5+(M+M_2+M_4)M_1+(M+M_4)M_2+MM_4-\psi\alpha)M_3+((M+M_2+M_4)M_1+(M+M_4)M_2+MM_4-\psi\alpha)M_5\\+((M+M_4)M_2+MM_4-\psi\alpha)M_1+M_2(MM_4-\psi\alpha)\end{pmatrix}E_2-\theta\beta E_1(M+\mu_B+M_3+M_4+M_5)\end{pmatrix}\mu K-E_2P_1\theta\Lambda\beta_1)}{E_2\mu K}$$

$$l_4=\frac{1}{E_2\mu K}\begin{pmatrix}\begin{pmatrix}\begin{pmatrix}((M+M_1+M_2+M_4)\mu_B+(M+M_1+M_2)M_4+(M_1+M_2)M-\psi\alpha+M_1M_2)M_5\\+((M+M_1+M_2)M_4+(M_1+M_2)M-\psi\alpha+M_1M_2)\mu_B+((M_1+M_2)M+M_1M_2)M_4)M_3\\+MM_1M_2-\alpha\psi(M_1+M_2)\end{pmatrix}\\+(((M+M_1+M_2)M_4+(M_1+M_2)M-\psi\alpha+M_1M_2)\mu_B+((M_1+M_2)M+M_1M_2)M_4+MM_1M_2-\alpha\psi(M_1+M_2))M_5\\+(((M_1+M_2)M+M_1M_2)M_4+MM_1M_2-\alpha\psi(M_1+M_2))\mu_B+M_1M_2(MM_4-\psi\alpha)\end{pmatrix}E_2\\-\beta E_1\theta\begin{pmatrix}(M+\mu_B+M_4+M_5)M_3\\+(M+\mu_B+M_4)M_5+(M+M_4)\mu_B+MM_4-\psi\alpha\end{pmatrix}\end{pmatrix}\mu K-\theta\Lambda\beta_1E_2(MP_1+M_3P_1+M_4P_1+M_5P_1+P_2\sigma)$$

$$l_5=\frac{1}{E_2\mu K}\begin{pmatrix}\begin{pmatrix}\begin{pmatrix}(((M+M_1+M_2)M_4+(M_1+M_2)M-\psi\alpha+M_1M_2)\mu_B+((M_1+M_2)M+M_1M_2)M_4+MM_1M_2-\alpha\psi(M_1+M_2))M_3\\+((((M_1+M_2)M+M_1M_2)M_4+MM_1M_2-\alpha\psi(M_1+M_2))\mu_B+M_1M_2(MM_4-\psi\alpha)\end{pmatrix}M_5\\+(((M_1+M_2)M+M_1M_2)M_4+MM_1M_2-\alpha\psi(M_1+M_2))M_3+\mu_BM_1M_2(MM_4-\psi\alpha)\end{pmatrix}E_2\\-\beta E_1(((M+\mu_B+M_4)M_3+(M+M_4)\mu_B+MM_4-\psi\alpha)M_5+((M+M_4)\mu_B+MM_4-\psi\alpha)M_3+\mu_B(MM_4-\psi\alpha))\theta\end{pmatrix}\mu K$$

$$-E_2\theta((MP_1+M_3P_1+M_4P_1+P_2\sigma)M_5+P_1(M+M_4)M_3+(MP_1+P_2\sigma)M_4+MP_2\sigma-\alpha\psi P_1)\Lambda\beta_1$$

$$l_6=\frac{1}{E_2\mu K}\begin{pmatrix}\begin{pmatrix}(((((M_1+M_2)M+M_1M_2)M_4+MM_1M_2-\alpha\psi(M_1+M_2))\mu_B+M_1M_2(MM_4-\psi\alpha))M_3+\mu_BM_1M_2(MM_4-\psi\alpha))\mu K\\-(P_1(M+M_4)M_3+(MP_1+P_2\sigma)M_4+MP_2\sigma-\alpha\psi P_1)\theta\Lambda\beta_1\\-(MM_4-\psi\alpha)(-\mu K\mu_BM_1M_2M_3+\theta\Lambda\beta_1(M_3P_1+P_2\sigma))\end{pmatrix}M_5\\+(((M+M_4)\mu_B+MM_4-\psi\alpha)M_3+\mu_B(MM_4-\psi\alpha))M_5+\mu_BM_3(MM_4-\psi\alpha))\end{pmatrix}E_2$$

$$-\beta E_1\theta\mu K(((M+M_4)\mu_B+MM_4-\psi\alpha)M_3+\mu_B(MM_4-\psi\alpha))M_5+\mu_BM_3(MM_4-\psi\alpha))$$

$$\lambda^7 = MM_4\mu K\mu_B E_2 M_1 M_2 M_3 M_4\left(1-R_0\right)$$

Applying Routh-Hurwitz criterion (Hassan et al 2022) to the Characteristics polynomial, we have that

$$\left(1-R_0\right)>0$$
$$\Rightarrow R_0<1$$

Thus the DFE point of the Diphtheria only model is locally asymptotically stable.

Global Asymptotic Stability of the Disease-free equilibrium point of the Diphtheria Model.
To investigate the global stability of the disease-free equilibrium, we use the technique implemented by [25]

To do this, we write the equation in the uninfected class as

$$\frac{dX}{dt} = F\left(X,Z\right)$$

And we re-write the equation in the infected class as

$$\frac{dz}{dt} = G(X,Z)$$

Where $X=\left(S,V,R\right)\in\Re_+^3$ denotes the uninfected population and

$Z=\left(E,I,T,B\right)\in\Re_+^4$ Denotes the infected population

$\varepsilon_0=(X^*,0)$ Represent the disease-free equilibrium of the system, and it globally asymptotically stable if it satisfies the following conditions:

$H_1:\dfrac{dX}{dt}=F\left(X^*,0\right),X^*$ is globally asymptotically stable

$H_2:\dfrac{dZ}{dt}=D_Z G\left(X^*,0\right)Z-\hat{G}\left(X,Z\right)$

$\hat{G}\left(X,Z\right)\geq 0$ for all $\left(X,Z\right)\in D$ and where $D_Z G\left(X^*,0\right)$ is an M- matrix (i.e the diagonal elements are no-negative and it is also the Jacobian of $\hat{G}\left(X,Z\right)\geq 0$ evaluated at $(X^*,0)$. If the system satisfies the above condition, then the theorem below holds.

Theorem 2

The equilibrium point $\varsigma_0=(X^*,0)$ *is globally asymptotically stable if* $R_0\leq 1$

$$F\left(X,Z\right)=\begin{bmatrix}\Lambda-\lambda S+\omega R+\psi V-\alpha S-\mu S\\ \alpha S-\left(\psi+\mu\right)V\\ \varepsilon T-\left(\omega+\mu\right)R\end{bmatrix},\quad G\left(X,Z\right)=\begin{bmatrix}\lambda S-\left(\theta+\mu\right)E\\ \theta E-\left(\sigma+\delta+\mu\right)I\\ \sigma I-\left(\varepsilon+\phi\delta+\mu\right)T\\ P_1 I+P_2 T-\mu_B\end{bmatrix}$$

At disease free equilibrium,

$$H_1 : \frac{dS}{dt} = \Lambda + \psi V - \alpha S - \mu S$$

$$\frac{dV}{dt} = \alpha S - (\psi + \mu) S \text{ And } \frac{dR}{dt} = 0$$

$$H_2 : D_z G(X^*, 0) \mathrm{Z} = \begin{bmatrix} -(\theta + \mu) E + \dfrac{\beta(\psi + \mu)}{\alpha + \psi + \mu} I + \dfrac{\Lambda \beta_1}{\mu K} B \\ \theta E - (\sigma + \delta + \mu) I \\ \sigma I - (\varepsilon + \phi\delta + \mu) T \\ P_1 I + P_2 T - \mu_B \end{bmatrix}$$

$$\hat{G}(X, Z) = D_Z G(X^*, 0) Z - G(X, Z)$$

$$G(X, Z) = \begin{bmatrix} \dfrac{\beta(\psi + \mu)}{\alpha + \psi + \mu} + \dfrac{\Lambda \beta_1}{\mu K} \left(1 - \dfrac{SN + S(K + B) + S^2}{N(K + B)} \right) \\ 0 \\ 0 \\ 0 \end{bmatrix} \geq 0$$

Clearly, $1 \geq \dfrac{SN + S(K + B) + S^2}{N(K + B)}$ this implies that $\hat{G}(X, Z) \geq 0$.

Therefore the disease free equilibrium of the Diphtheria only model is globally asymptotically stable.

Endemic Equilibrium Point of the Diphtheria Model

The endemic equilibrium point is the steady state where there is persistence or prevalence of a disease in the population.

Theorem 3

The endemic equilibrium points of the Cholera model in (1) is stable if $R_0 > 1$ and unstable if $R_0 < 1$.

Proof

To obtain the endemic equilibrium we set the RHS of the differential equations in (1) to zero and solve for the state variables.

Thus, at the endemic equilibrium point,

$$\frac{dS}{dt} = \frac{dE}{dt} = \frac{dI}{dt} = \frac{dT}{dt} = \frac{dV}{dt} = \frac{dR}{dt} = 0$$

Let $\eta^{**} = (S^{**}, E^{**}, I^{**}, T^{**}, R^{**}, B^{**})$ be the endemic equilibrium point.

We have that,

$$S^{**}=\frac{\Lambda M_4}{M_4(\alpha+\lambda+\mu-\omega)-\alpha\psi},\ E^{**}=\frac{\Lambda M_4\lambda}{M_1\left(M_4(\alpha+\lambda+\mu-\omega)-\alpha\psi\right)},$$

$$I^{**}=\frac{\theta\Lambda M_4\lambda}{M_1\left(M_4(\alpha+\lambda+\mu-\omega)-\alpha\psi\right)M_2},$$

$$T^{**}=\frac{\theta\Lambda M_4\lambda\sigma}{M_1\left(M_4(\alpha+\lambda+\mu-\omega)-\alpha\psi\right)M_2M_3},\ V^{**}=\frac{\Lambda\alpha}{M_4(\alpha+\lambda+\mu-\omega)-\alpha\psi},$$

$$B^{**}=\frac{(M_3P_1+P_2\sigma)\theta\Lambda M_4\lambda}{M_1M_2\left(M_4(\alpha+\lambda+\mu-\omega)-\alpha\psi\right)M_3\mu_B},$$

$$R^{**}=\frac{\theta\Lambda M_4\lambda\sigma\grave{o}}{M_1M_2\left(M_4(\alpha+\lambda+\mu-\omega)-\alpha\psi\right)M_3M_5}$$

By Substituting the above into the force of infection, $\lambda^{**}=\frac{\beta I}{N}+\frac{\beta_t B}{K+B}$, we obtained t

$$\lambda^{**}=\frac{M_5M_1M_2M_3(R_0-1)}{M_1M_3\mu_BM_2\left(\left((M_3+\sigma)M_5+\sigma\grave{o}\right)\theta+M_5M_3M_2\right)K\mu^2+\begin{pmatrix}-2M_1M_3\mu_BM_2\left(\left((M_3+\sigma)M_5+\sigma\grave{o}\right)\theta+M_5M_3M_2\right)K\omega\\+2M_1M_3\mu_BM_2\left(\left((M_3+\sigma)M_5+\sigma\grave{o}\right)\theta+M_5M_3M_2\right)K\alpha\\+\theta(M_3P_1+P_2\sigma)\begin{pmatrix}\left(\left((-M_3-\sigma)M_5-\sigma\grave{o}\right)\theta-M_5M_3M_2\right)\beta_1\\+M_5M_3M_1M_2\end{pmatrix}\Lambda\\+2KM_1^{\,2}M_2^{\,2}M_3^{\,2}M_5\mu_B\end{pmatrix}\mu+M_1M_3\mu_BM_2\left(\left((M_3+\sigma)M_5+\sigma\grave{o}\right)\theta+M_5M_3M_2\right)K\omega^2}$$

From above we observed that for $\lambda^{**}>1$, then $R_0>1$.

Sensitivity Analysis of the Diphtheria Model

Sensitivity analysis is carried out to determine the parameters that enhance the spread as well as control of an infection in a population [27]. The sensitivity index of the reproduction number of the Cholera model with respect to any parameter say p is given by:

$$\Im_p^{R_0}=\frac{\partial R_0}{\partial p}\times\frac{p}{R_0}$$

$$R_0=\frac{\theta\left(\mu KM_3\mu_B\beta(\psi+\mu)+E_2M_3P_1\Lambda\beta_1+E_2P_2\sigma\Lambda\beta_1\right)}{(\alpha+\psi+\mu)M_1M_2\mu KM_3\mu_B}$$

$$\Im_\beta^{R_0}=\frac{\mu K\mu_B(\psi+\mu)(\delta\phi+\grave{o}+\mu)\beta}{(\alpha+\psi+\mu)\left(P_1\mu+(\delta\phi+\grave{o})P_1+\sigma P_2\right)\Lambda\beta_1+\mu K\mu_B(\psi+\mu)(\delta\phi+\grave{o}+\mu)\beta}=0.1002$$

$$,\ \Im_\theta^{R_0}=\frac{\mu}{\theta+\mu}=0.0763,$$

$$\Im_{\phi}^{R_0} = -\frac{\delta(\alpha+\psi+\mu)P_2\sigma\Lambda\beta_1\phi}{(\delta\phi+\grave{o}+\mu)\left((\alpha+\psi+\mu)\left(P_1\mu+(\delta\phi+\grave{o})P_1+\sigma P_2\right)\Lambda\beta_1+\mu K\mu_B(\psi+\mu)(\delta\phi+\grave{o}+\mu)\beta\right)} = -0.0007$$

$$\Im_{\psi}^{R_0} = \frac{\mu K\mu_B\alpha\beta(\delta\phi+\grave{o}+\mu)\psi}{(\alpha+\psi+\mu)\left((\alpha+\psi+\mu)\left(P_1\mu+(\delta\phi+\grave{o})P_1+\sigma P_2\right)\Lambda\beta_1+\mu K\mu_B(\psi+\mu)(\delta\phi+\grave{o}+\mu)\beta\right)} = 0.0557$$

$$\Im_{\alpha}^{R_0} = -\frac{\mu K\mu_B(\psi+\mu)(\delta\phi+\grave{o}+\mu)\beta\alpha}{(\alpha+\psi+\mu)\left((\alpha+\psi+\mu)\left(P_1\mu+(\delta\phi+\grave{o})P_1+\sigma P_2\right)\Lambda\beta_1+\mu K\mu_B(\psi+\mu)(\delta\phi+\grave{o}+\mu)\beta\right)} = -0.0532$$

$$\Im_{\delta}^{R_0} = -0.0159,$$

$$\Im_{\varepsilon}^{R_0} = -\frac{(\alpha+\psi+\mu)P_2\sigma\Lambda\beta_1\grave{o}}{(\delta\phi+\grave{o}+\mu)\left((\alpha+\psi+\mu)\left(P_1\mu+(\delta\phi+\grave{o})P_1+\sigma P_2\right)\Lambda\beta_1+\mu K\mu_B(\psi+\mu)(\delta\phi+\grave{o}+\mu)\beta\right)} = -0.4162$$

$$\Im_{P_1}^{R_0} = \frac{(\delta\phi+\grave{o}+\mu)(\alpha+\psi+\mu)P_1\Lambda\beta_1}{(\alpha+\psi+\mu)\left(P_1\mu+(\delta\phi+\grave{o})P_1+\sigma P_2\right)\Lambda\beta_1+\mu K\mu_B(\psi+\mu)(\delta\phi+\grave{o}+\mu)\beta} = 0.4615$$

$$\Im_{\mu}^{R_0} = -0.1441,$$

$$\Im_{P_2}^{R_0} = \frac{\sigma\Lambda\beta_1P_2(\alpha+\psi+\mu)}{\mu K\mu_B(\psi+\mu)(\delta\phi+\grave{o}+\mu)\beta+(\delta\phi+\grave{o}+\mu)(\alpha+\psi+\mu)P_1\Lambda\beta_1+\sigma\Lambda\beta_1P_2(\alpha+\psi+\mu)} = 0.4383$$

$$\Im_{\mu_B}^{R_0} = -\frac{(\alpha+\psi+\mu)\Lambda\beta_1\left((\delta\phi+\grave{o}+\mu)P_1+\sigma P_2\right)}{(\alpha+\psi+\mu)\Lambda\beta_1\left((\delta\phi+\grave{o}+\mu)P_1+\sigma P_2\right)+\mu K\mu_B(\psi+\mu)(\delta\phi+\grave{o}+\mu)\beta} = -0.8997$$

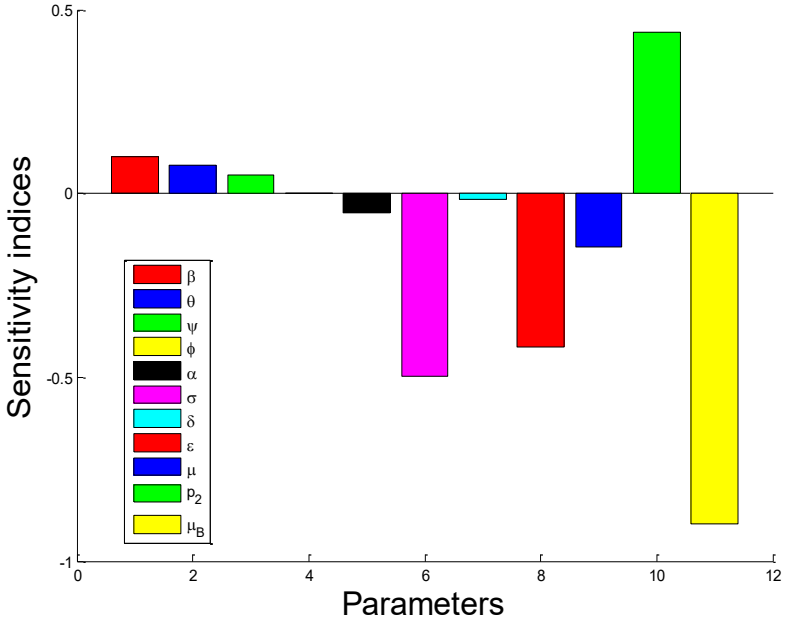

Figure 2 Bar chat of Diphtheria sensitivity Indices

Interpretation of the diphtheria Sensitivity Analysis

From the sensitivity analysis above, it is observed that the parameters like β, which are the contact rate of susceptible and infected humans, progression rate from exposed class to infected class θ, waning rate of vaccine ψ, shedding rate of bacteria p_1 *and* p_2, are all with positive sensitivity indices which enhances the spread of Diphtheria within the human population [26,27]. Also the parameters like ϕ modification parameter that accounts for diphtheria induced death, rate at which susceptible individuals are vaccinated α, the rate at which treated individuals recovered ε, disease induced death rate δ, Natural death rate μ and bacteria Natural death rate μ_B are with negative sensitivity indices and will reduces the prevalence of diphtheria within the human population.

Data fitting for Diphtheria

We estimated some parameters in the Diphtheria-only model by fitting the model with the weekly number of active cases in Nigeria; the data goes over a period of 51 weeks, from 1st December to 24th December, 2023 as obtained from Nigeria Centre for Disease Control (NCDC). The initial conditions for the state variables used to calibrate the model on 24th December, 2023 were determined based on our estimation of Nigeria's total population. Using the fmincon algorithm in MATLAB, we fitted the system (1) to the cumulative number of active Diphtheria cases. We used the fitting to estimate the Diphtheria effective contact rate β, progression rate from exposed Diphtheria to human infected class θ, the bacteria contact rate β_1, Progression rate from infected individuals to treatment class σ

Table 4: Real life data for diphtheria from NCDC for 2023

Date	Week 1-3	Week 4-5	Week 6-9	Week 17-20	Week 21-24	Week 25-28	Week 48	Week 51
Cases	89	56	102	54	160	579	190	93

Link:
https//:ncdc.gov.ng/sitreps/?name=An%20Update%20of%20diphtheria%20Outbreak20in%

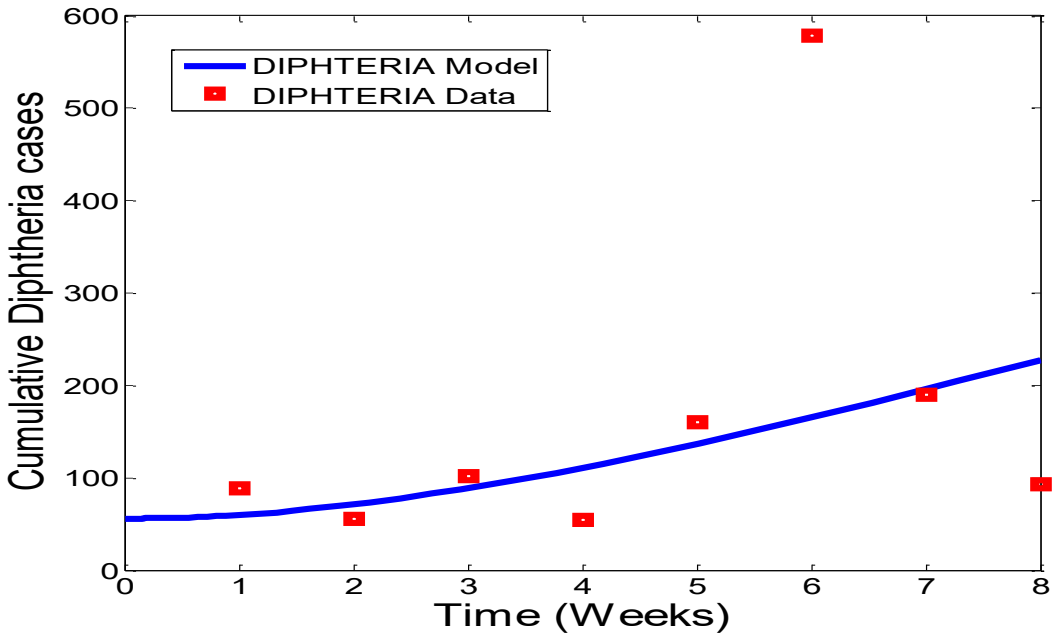

Fig 3: Number of active diphtheria cases in Nigeria

Parameter Values and Sources

Parameter	Value	Source
β	0.5700	Fitted
θ	0.230	Fitted,
μ	0.019	[20]
K	0.005	[20]
μ_B	0.047	[17]
δ	0.006	Fitted
ϕ	0.1	[22]
ε	0.37	[21]
α	0.7	[17]
ψ	0.6	[20
P_1	0.007	[22]
Λ	0.0014	[17
β_1	0.561	Fitted
P_2	0.007	[20]
σ	0.37	Fitted

Numerical Simulations and Discussion

The graphs of our numerical simulations are presented below as well as their respective interpretations. The initial conditions of the state variables used for the numerical simulations are given as follows: $S(0)$= 3600000, $E(0)$ = 200000 $I(0)$ = 200000, $T(0)$ = 1000000, $V(0)$ = 57000, $B(0)$=5000 $R(0)$=3000.

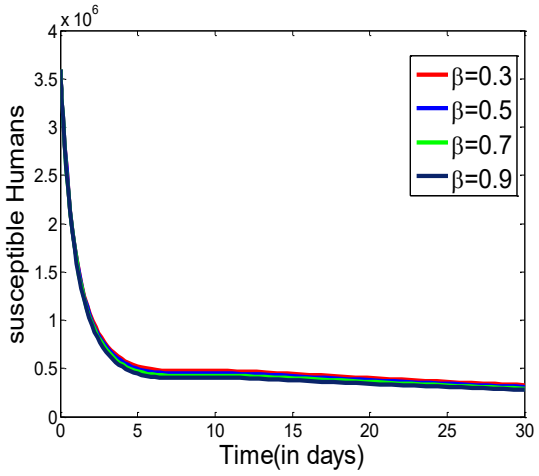

Fig 3(ii) Effect of varying β on $E(t)$

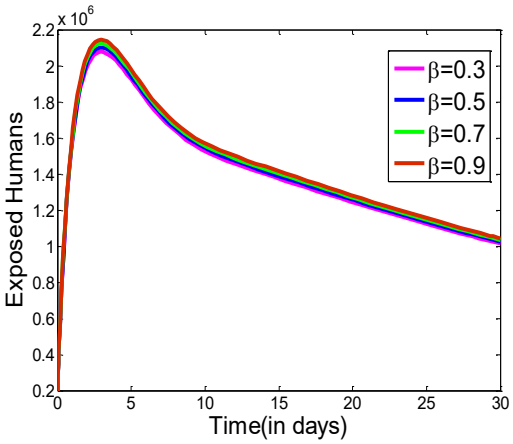

Fig 3(i) Effect of varying β on $S(t)$

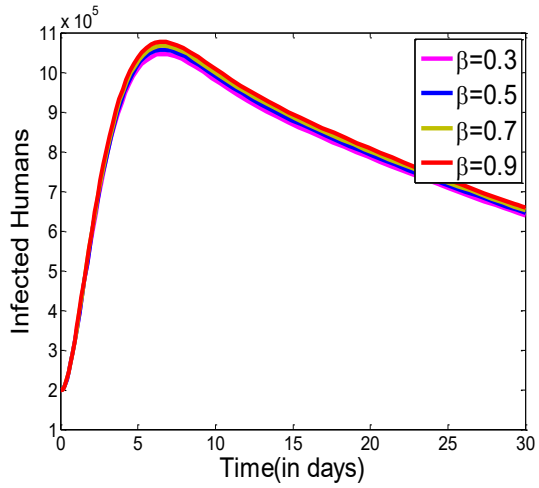

Fig 4(i) Effect of varying β on $I(t)$

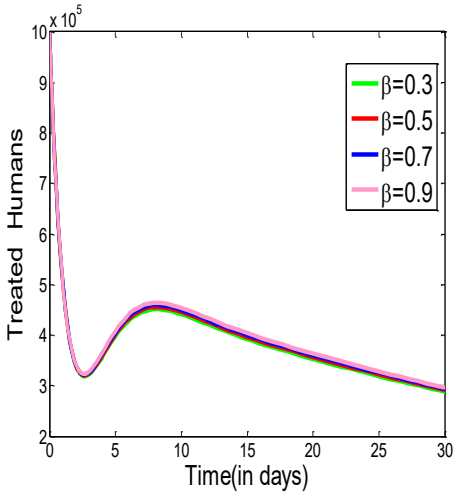

Fig 4(ii) Effect of varying β on $T(t)$

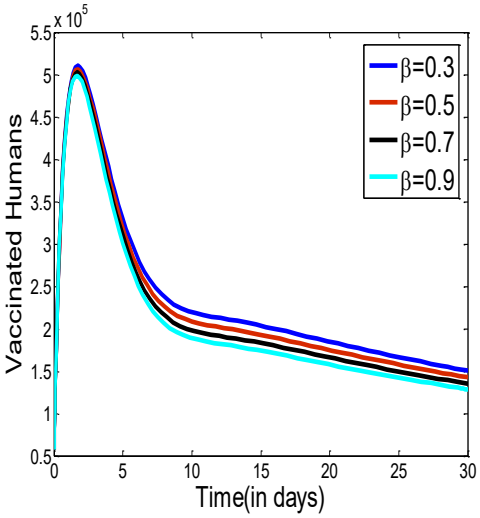

Fig 5(i) Effect of varying β on $V(t)$

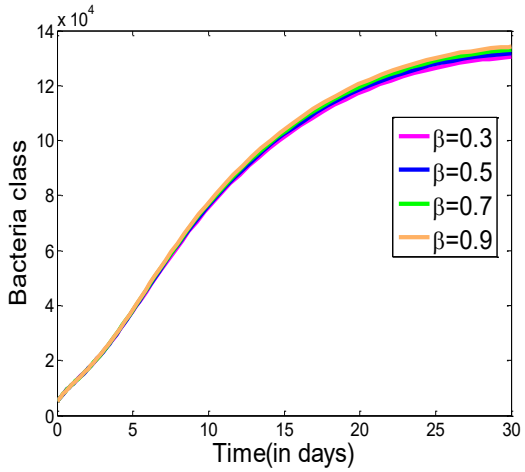

Fig 5(ii) Effect of varying β on $B(t)$

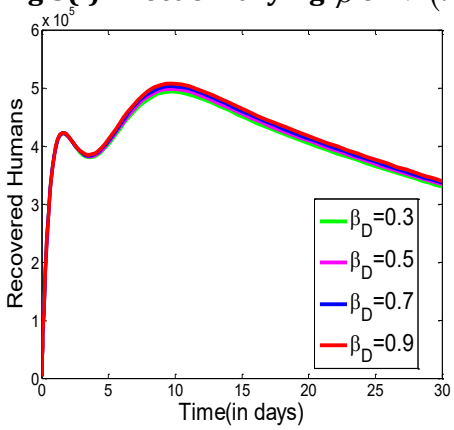

Fig 6(i) Effect of varying β on $R(t)$

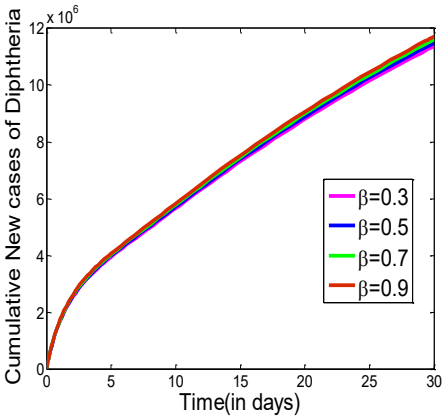

Fig 6(ii) Cumulative New Cases of Diphtheria

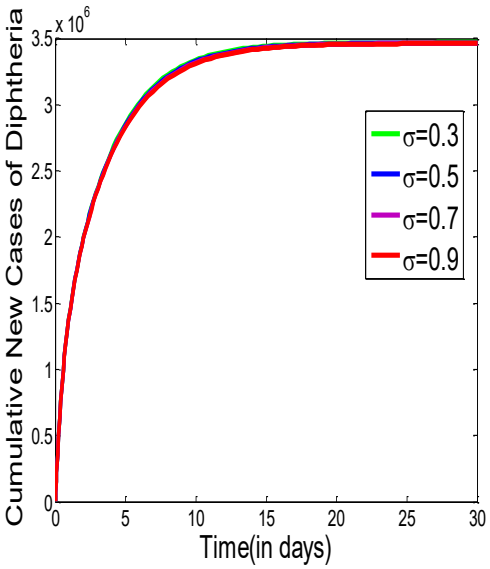

Fig 6(iii) Cumulative New Cases of Diphtheria

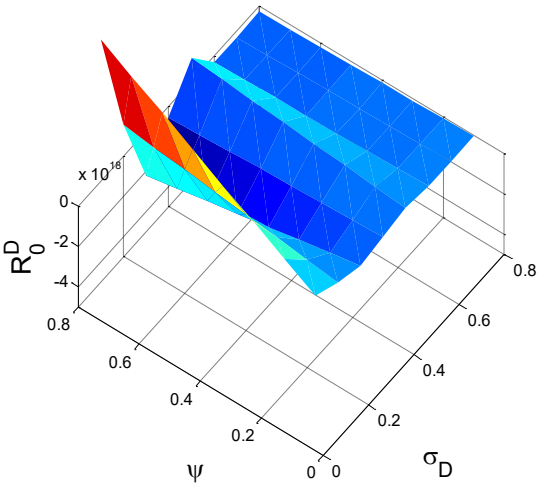

Fig 7(i) Surface plot of R_0^D against ψ and σ_D

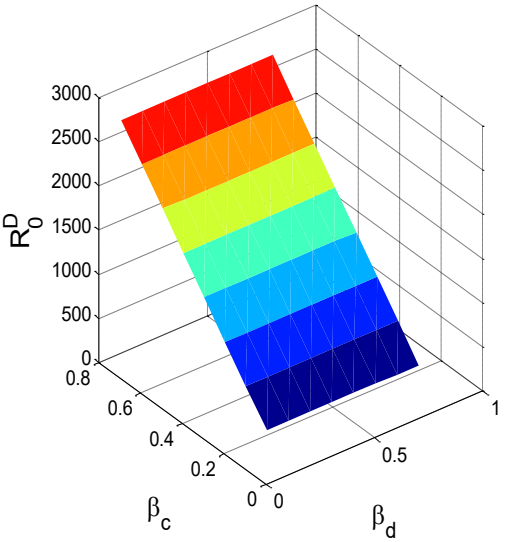

Fig 7(ii) Surface plot of R_0^D against β_1 and β

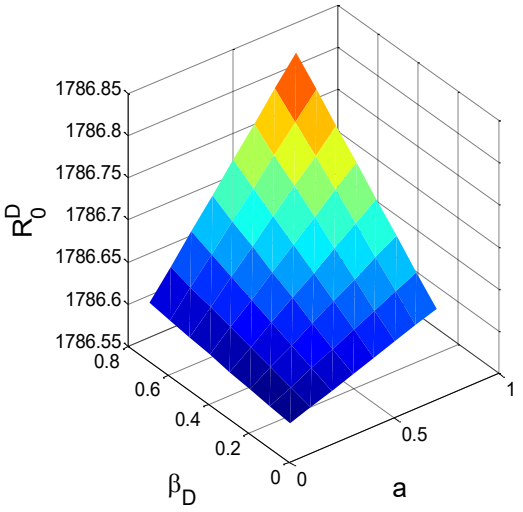

Fig 7(iii) Surface plot of R_0^D against β_D

From figure 3(i), an increase in the contact rate between susceptible individuals and infected individuals with diphtheria led to a decline in the susceptible population. From figure 3(ii), the exposed population initially increased and then declined rapidly as the infection rate increased. This suggests that, despite a reduction in the total susceptible population due to increasing infectiousness, there was a continuous movement of individuals from the susceptible class into the exposed class. In figure 4(i), the number of infected individuals increased initially and then declined afterward. Figure 4(ii) showed that the treated population initially decreased because the disease was not yet widely established; however, as the infection became more prevalent in the population, the number of individuals in the treatment class increased. Over time, the treated population later declined due to recovery resulting from effective treatment interventions. Figure 5(i) shows an increase in the vaccination rate led to a reduction in the number of infected individuals. From figure 11(ii), the infected population increased due to the presence of bacteria in the environment, which contributed to continued transmission. In figure 6(i), the recovered population increased as the contact rate decreased due to treatment interventions. In figure 6(ii), an increase in the contact rate between susceptible and infected individuals led to a rise in cumulative new diphtheria cases, indicating that reducing contact through measures such as social distancing would help lower disease burden.

It was observed from figure 6(iii) that increasing the number of treated individuals did not completely eliminate the disease but only reduced the number of new cases. This suggests that while treatment is important, additional efforts such as prevention and improved healthcare resources are necessary to effectively reduce diphtheria prevalence in the population.

Figure 7(i) represents the surface plot of R_0^D against ψ and σ_D, we observed that the basic reproduction number of Diphtheria is reduced as a result of these two parameters. It is evident that the $R_0^D < 1$, implying that these parameters reduces the endemicity of Diphtheria. Figure 7(ii) illustrates the surface plot of R_o^D against β_C and β_D ,we observed that the basic reproduction number of Diphtheria increases as a result of increase in the values of these

two parameters. It is evident that $R_0^D > 1$ suggests that increase in the value of these parameters raise the probability of Diphtheria endemicity. Figure 7(iii) illustrates the surface plot of R_o^D against β_D and a, we observed that the basic reproduction number of Diphtheria increases as a result of increase in the value of these two parameters. It is evident that $R_0^D > 1$, suggests that these parameters increase the probability of Diphtheria endemicity.

Conclusion

This study developed a deterministic mathematical framework to investigate the transmission dynamics of diphtheria, incorporating treatment as a key control strategy. The model was analyzed to determine the basic reproduction number (R_0), which played a central role in characterizing the disease dynamics. The analysis showed that the disease-free equilibrium was locally asymptotically stable when $R_0 < 1$, and globally asymptotically stable under the same condition, while the system admitted a stable endemic equilibrium when $R_0 > 1$.

A sensitivity analysis of the model parameters revealed that certain parameters positively influenced the basic reproduction number and therefore enhanced disease transmission. These included the contact rate between susceptible and infected individuals, the progression rate from exposed to infected class, the vaccine waning rate, and the bacterial shedding rate. On the other hand, parameters such as disease-induced death rate, vaccination rate, recovery rate of treated individuals, natural death rates, and other control-related parameters exhibited negative sensitivity indices, indicating their role in reducing diphtheria prevalence within the population.

Numerical simulations were carried out to validate the analytical results by varying key parameters, including the contact rate between susceptible and infected individuals, the contact rate between susceptible individuals and bacteria, and the treatment rate of infected individuals. The simulation results demonstrated that reducing contact between susceptible and infected individuals significantly lowered disease transmission, while increasing treatment rates among infected individuals effectively reduced the disease burden. The findings highlighted that a combination of reduced transmission contact, effective vaccination, and improved treatment strategies is essential for controlling and mitigating the spread of diphtheria in the population.

Based on the findings of this study, the following recommendations are made to reduce the burden of diphtheria in the society:

1. The government should increase its commitment to providing adequate treatment centers and improving access to healthcare services for individuals infected with diphtheria.
2. Public health awareness campaigns should be intensified to educate people on the importance of proper hygiene and safe disposal of human excreta, which will help reduce environmental contamination and bacterial transmission through food and water.
3. Sensitization programs should be organized to encourage individuals to maintain appropriate physical distance from people showing symptoms such as coughing or sneezing, thereby reducing the spread of diphtheria bacteria in the population.

4. The government and health authorities should strengthen routine immunization programs and ensure high vaccination coverage to reduce susceptibility and prevent outbreaks of diphtheria in the community.

Future research should focus on improving and extending the current model to better capture real-world complexities of diphtheria transmission. This can be achieved by incorporating time-dependent optimal control strategies to reduce disease burden more effectively. In addition, age-structured models should be developed to examine how diphtheria spreads across different age groups.

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