SENSITIVITY ANALYSIS OF TRANSMISSION PARAMETERS IN A DIPHTHERIA-VACCINE-TREATMENT MODEL

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Abstract.
Diphtheria continues to pose a major public health concern, particularly across various regions of sub-Saharan Africa. Recent diphtheria outbreaks highlight the critical need for sustained high vaccination coverage within communities. Without vaccination and appropriate treatment, the disease remains highly dangerous, with a fatality rate of approximately 30% among unprotected individuals, posing an even greater threat to young children. This study introduces a diphtheria-vaccine-treatment compartmental model designed to capture the disease dynamics through eight distinct epidemiological states: Susceptible (unvaccinated) population ($\boldsymbol{S_U}$), fully vaccinated ($\boldsymbol{V_F}$), Partially vaccinated ($\boldsymbol{V_P}$), Exposed (E), Asymptomatic infected ($\boldsymbol{I_A}$), Symptomatic infected ($\boldsymbol{I_S}$), Treated (T), and Recovered (R). The basic reproduction number ($\boldsymbol{R_0}$) was calculated to be 0.1323. With $\boldsymbol{R_0} < 1$, the model predicts asymptotic stability, indicating that diphtheria transmission will gradually decline, ultimately leading to disease eradication over time. Sensitivity analysis revealed that the most positively sensitive parameter influencing $\boldsymbol{R_0}$ is the asymptomatic infection transmission rate, $\boldsymbol{\beta_1}$, where $\boldsymbol{S_{\beta_1}^{R_0}}$ = 0.7716799884. Conversely, the only negatively sensitive parameter is the proportion of the infectious population, $\boldsymbol{\rho}$, where $\boldsymbol{S_{\rho}^{R_0}}$ = -0.08281740530, suggesting that an increase in this parameter would lead to a reduction in $\boldsymbol{R_0}$. Based on these findings, targeted interventions should focus on reducing asymptomatic transmission, as asymptomatic carriers play a critical role in sustaining disease spread. Strengthening surveillance systems to improve early detection, enhancing vaccination coverage to increase immunity, and ensuring timely treatment of both symptomatic and asymptomatic cases are essential measures for controlling diphtheria transmission.
Keywords: Basic reproduction Number, Diphtheria, Epidemiology, Mathematical modeling, sensitivity Analysis.

Introduction

Diphtheria is an acute bacterial infection that is highly contagious and vaccine-preventable. Diphtheria is primarily caused by *Corynebacterium diphtheriae* but can also be caused by *Corynebacterium ulcerans (WHO,2023; NCDC, 2023;* Elsinga, van Meijeren, and Reubsaet, 2023; *Kanchanarat, Chinviriyasit, and Chinviriyasit, 2022;* Acosta and Tiwari, 2020; Wharton, 2006*).* It primarily spreads from person to person through direct contact or airborne transmission

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via respiratory droplets (WHO, 2023; Medugu, *et al.,* 2023; Marshall, *et al.,* 2022; Sornbundit, Triampo, and Modchang, 2017). The disease can impact individuals of all age groups, but unimmunized children face the highest risk. Symptoms typically develop gradually, starting with a sore throat and fever. In severe cases, the bacteria release a toxin that forms a thick gray or white membrane at the back of the throat. This can obstruct the airways, leading to difficulty in breathing or swallowing and resulting in a characteristic barking cough. Swelling of the neck may also occur due to enlarged lymph nodes. Diphtheria continues to pose a global public health challenge, especially in areas with insufficient vaccination coverage. Although immunization programs have greatly decreased cases in many nations, outbreaks still emerge, particularly in regions affected by conflict, displacement, or weakened healthcare systems. Recent diphtheria outbreaks highlight the critical need for sustained high vaccination coverage within communities. Without vaccination and appropriate treatment, the disease remains highly dangerous, with a fatality rate of approximately 30% among unprotected individuals, posing an even greater threat to young children (WHO, 2023). Diphtheria occurrence and resurgence in Nigeria are highly attributed to vaccination gaps, wanning immunity, and treatment inaccessibility. To understand the transmission dynamics of diphtheria and evaluate treatment and vaccination strategies, many studies have proposed and developed different mathematical models to satisfy their objectives (Rahmi and Pratama, 2023; *Kanchanarat, Chinviriyasit and Chinviriyasit, 2022;* Chang *et al.,* 2022; Islam *et al.,* 2022; Amalia and Toaha, 2022; Izzati and Andriani, 2021; Ahmed and Rahman, 2021; Finger *et al.,* 2019; Husain, 2019). Mathematical modeling is a useful tool to guide outbreak control decision-making (Gamboa and Lopez-Herrero, 2022; Hethcote,2020; Kretzschmar and Wallinga, 2009). Mathematical modeling offers a precise and concise approach to synthesizing existing knowledge about a biological process. (Villaverde *et al*., 2022). Mathematical models are extensively employed to analyze, interpret, and forecast the transmission dynamics of infectious diseases. Models specific to globally significant diseases have been instrumental in shaping public health strategies for disease control and prevention (Wu et al, 2013). These models replicate the spread of pathogens within populations, offering valuable insights that guide public health interventions and policy formulation. An essential component of improving these models is sensitivity analysis, which evaluates the impact of changes in model parameters on predicted outcomes.

Sensitivity analysis serves as a fundamental tool in understanding disease transmission dynamics by quantifying the influence of individual parameters on model outcomes. This analytical approach is essential for guiding experimental design, improving data assimilation, and optimizing model simplification, particularly in complex nonlinear systems. By incorporating sensitivity analysis, researchers can evaluate the stability and reliability of model predictions, addressing uncertainties that may arise from data collection errors or assumed parameter values (Riaz et al., 2024; Rui et al., 2024; Bai et al., 2023; Ni et al., 2022; Rodrigues et at., 2013).

1 A key advantage of sensitivity analysis is its ability to identify parameters with the most significant impact on the basic reproduction number ($\boldsymbol{R_0}$), thereby informing the implementation of targeted intervention strategies. Sensitivity indices offer a quantitative assessment of how parameter variations influence model variables. However, without considering sensitivity analysis in the mathematical modeling of infectious diseases, interventions may be misdirected, leading to inefficient allocation of resources and suboptimal disease control outcomes.

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2 Model Development

A mathematical model is a structured framework for conveying insights into disease transmission within human populations over time (t). In this study, we introduce a Diphtheria-Vaccine-Treatment model to study the transmission dynamics of Diphtheria disease with vaccine and treatment interventions (see Fig.1). The model integrates compartments for susceptible (unvaccinated) (S_U), Exposed (E), Asymptomatic Infected (I_A), Symptomatic Infected (I_S), Fully Vaccinated (V_F), Partially Vaccinated (V_P), Treated (T) and Recovered (R).

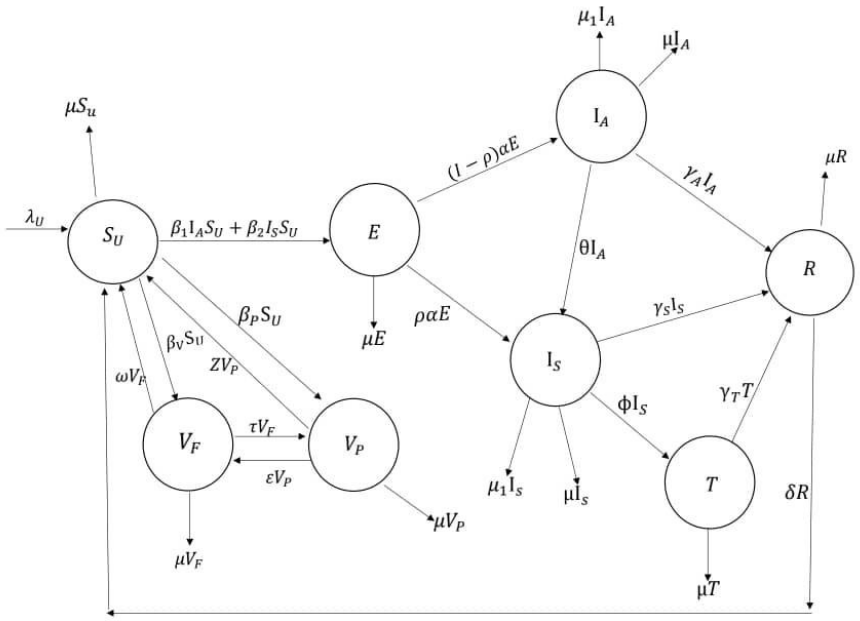

Fig. 1. Schematic Diagram of the Model

$$\frac{dS_u}{dt} = \lambda_u - (\beta_1 I_A + \beta_2 I_S)S_u + \delta R + \omega V_F + zV_P - (\beta_V + \beta_P + \mu)S_u, \quad (1)$$

$$\frac{dV_F}{dt} = \beta_V S_u + \varepsilon V_p - (\omega + \tau + \mu)V_F, \quad (2)$$

$$\frac{dV_P}{dt} = \beta_P S_u + \tau V_F - (z + \varepsilon + \mu)V_P, \quad (3)$$

$$\frac{dE}{dt} = (\beta_1 I_A + \beta_2 I_S)S_u - [(1-\rho)\alpha + \rho\alpha + \mu_1 + \mu]E, \quad (4)$$

$$\frac{dI_A}{dt} = (1-\rho)\alpha E - (\theta + \mu_1 + \mu + \gamma_A)I_A, \quad (5)$$

$$\frac{dI_S}{dt} = \rho\alpha E + \sigma I_A - (\gamma_S + \mu_1 + \mu + \phi)I_S, \quad (6)$$

$$\frac{dT}{dt} = \phi I_S - (\gamma_T + \mu)T, \quad (7)$$

$$\frac{dR}{dt} = \gamma_A I_A + \gamma_S I_S + \gamma_T T - (\delta + \mu)R. \quad (8)$$

2.1 Equilibrium States of the Model

A disease-free equilibrium state remains stable when there are no infectious individuals in the population, meaning it consists solely of susceptible, fully vaccinated, and partially vaccinated individuals.

At equilibrium, we define

$$\frac{dS_u}{dt} = \frac{dV_F}{dt} = \frac{dV_P}{dt} = \frac{dE}{dt} = \frac{dI_A}{dt} = \frac{dI_S}{dt} = \frac{dT}{dt} = \frac{dR}{dt} = 0.$$

Solving we obtain the following as the Disease-free equilibrium points

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$$\begin{pmatrix} S_u \\ V_F \\ V_p \\ E \\ \mathrm{I}_A \\ \mathrm{I}_S \\ T \\ R \end{pmatrix} = \begin{pmatrix} \dfrac{k_2k_3k_4}{\beta_1\alpha(1-\rho)k_4+\beta_2\alpha\left(\rho k_3+(1-\rho)\theta\right)} \\ \dfrac{(\varepsilon\beta_P-\beta_V k_8)k_2k_3k_4}{(k_4k_8-\varepsilon\tau)\left[\left(\beta_1\alpha(1-\rho)k_4+\beta_2\alpha\left(\rho k_3+(1-\rho)\theta\right)\right)\right]} \\ \dfrac{(\tau\beta_v+\beta_P k_7)A}{(k_7k_8-\varepsilon\tau)} \\ 0 \\ 0 \\ 0 \\ 0 \\ 0 \end{pmatrix}, \tag{9}$$

where $k_2=(1-\rho)\alpha+\rho\alpha+\mu_1+\mu$,

$k_3=\theta+\mu_1+\mu+\gamma_A$,

$k_4=\gamma_S+\mu_1+\mu+\phi$,

$k_8=z+\varepsilon+\mu$.

2.2 Determination of Basic Reproduction Number, R_0

The basic reproduction number represents the average number of secondary infections generated by a single infected individual throughout the infectious period (Diekmann *et al.,*1990). When the reproduction ratio exceeds one, the disease will continue to spread throughout the population. Conversely, if it falls below one, the infection will gradually decline and eventually disappear. The basic reproduction number serves as a key indicator of the disease's progression (Oguntolu *et al*.,2022).

In the model equation, the infectious compartments include E, I_A, I_s and the expected secondary infections depend on these classes. The rate of appearance of new infections in compartments *i* is given by the matrix.

$F=\left(\dfrac{\partial f_i\left(E^0\right)}{\partial x_i}\right)$, $x_j=E,I_A,I_s$ for $j=1,2,3$ and E^0 is the disease-free equilibrium.

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$$F = \frac{\partial F_i}{\partial x_j}\left(E_0\right).$$

$$V = \frac{\partial V_i}{\partial x_j}\left(E_0\right).$$

$$F_i = \begin{pmatrix} \left(\beta_1 I_A^* + \beta_2 I_S^*\right) S_u^\circ \\ 0 \\ 0 \end{pmatrix},$$

$$F = \begin{pmatrix} 0 & \beta_1 S_u^\circ & \beta_2 S_u^\circ \\ 0 & 0 & 0 \\ 0 & 0 & 0 \end{pmatrix}.$$

$$V = V^- - V^+ = \begin{pmatrix} -k_2 E^* \\ (1-\rho)\alpha E^* - k_3 I_A^* \\ \rho\alpha E^* + \theta I_A^* \end{pmatrix},$$

where

$$V^- = \begin{pmatrix} -k_2 E^* \\ -k_3 I_A^* \\ -k_4 I_S^* \end{pmatrix}; V^+ = \begin{pmatrix} 0 \\ (1-\rho)\alpha E^* \\ \rho\alpha E^\circ + \theta I_A^* \end{pmatrix},$$

$$V = \begin{pmatrix} k_2 & 0 & 0 \\ -(1-\rho)\alpha & k_3 & 0 \\ -\rho\alpha & -\theta & k_4 \end{pmatrix},$$

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$$V^{-1}=\begin{pmatrix} \frac{1}{k_2} & 0 & 0 \\ \frac{-(1-\rho)\alpha}{k_2k_3} & \frac{1}{k_3} & 0 \\ \frac{-\alpha(\theta+\rho k_3+\rho\theta)}{k_2k_3k_4} & \frac{\theta}{k_3k_4} & \frac{1}{k_4} \end{pmatrix},$$

$$FV^{-1}=\begin{pmatrix} 0 & \beta_1 S_u^{\circ} & \beta_2 S_u^{\circ} \\ 0 & 0 & 0 \\ 0 & 0 & 0 \end{pmatrix}\begin{pmatrix} \frac{1}{k_2} & 0 & 0 \\ \frac{-(1-\rho)\alpha}{k_2k_3} & \frac{1}{k_3} & 0 \\ \frac{-\alpha(\theta+\rho k_3+\rho\theta)}{k_2k_3k_4} & \frac{\theta}{k_3k_4} & \frac{1}{k_4} \end{pmatrix}.$$

To determine the basic reproduction number, we compute the eigenvalues. By extracting the dominant eigenvalue from the matrix FV^{-1} and performing the necessary calculations $|A-\lambda I|=0$, we obtain

$$FV^{-1}=\begin{pmatrix} -\frac{\beta_1k_4(-1+\rho)\alpha}{\beta_1\alpha(1-\rho)k_4+\beta_2\alpha(\rho k_3+(1-\rho)\theta)}-\frac{\beta_2\alpha(\rho\theta-\rho k_3-\theta)}{\beta_1\alpha(1-\rho)k_4+\beta_2\alpha(\rho k_3+(1-\rho)\theta)}-\lambda & \frac{\beta_1k_2k_4}{\beta_1\alpha(1-\rho)k_4+\beta_2\alpha(\rho k_3+(1-\rho)\theta)}+\frac{\beta_2k_2\theta}{\beta_1\alpha(1-\rho)k_4+\beta_2\alpha(\rho k_3+(1-\rho)\theta)} & \frac{\beta_2k_2k_3}{\beta_1\alpha(1-\rho)k_4+\beta_2\alpha(\rho k_3+(1-\rho)\theta)} \\ 0 & 0-\lambda & 0 \\ 0 & 0 & 0-\lambda \end{pmatrix}=0,$$

$$FV^{-1}=\begin{pmatrix} 0 \\ 0 \\ \frac{\alpha(\rho\beta_1k_3-\rho\theta\beta_2-\rho\beta_1k_4+\theta\beta_2+\beta_1k_4)}{\beta_1\alpha(1-\rho)k_4+\beta_2\alpha(\rho k_3-\rho\theta+\theta)} \end{pmatrix}, \quad (10)$$

$$\lambda_1=\frac{\alpha(\rho\beta_1k_3-\rho\theta\beta_2-\rho\beta_1k_4+\theta\beta_2+\beta_1k_4)}{\beta_1\alpha(1-\rho)k_4+\beta_2\alpha(\rho k_3-\rho\theta+\theta)},$$

$$\lambda_2=0,\ \lambda_3=0.$$

Clearly, the dominant eigenvalue, λ_1, is taken to be the basic reproduction number. Therefore

$$R_0=\frac{\alpha(\rho\beta_1k_3-\rho\theta\beta_2-\rho\beta_1k_4+\theta\beta_2+\beta_1k_4)}{\beta_1\alpha(1-\rho)k_4+\beta_2\alpha(\rho k_3-\rho\theta+\theta)}, \quad (11)$$

where R_0 is the basic reproduction number.

Sensitivity Analysis for the Parameter Using Basic Reproductive Number

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Sensitivity Analysis (SA) highlights the significance of model parameters be revealing their relative influence on the dynamics of diphtheria. It is a crucial tool for identifying key factors that drive disease transmission, offering valuable insights for implementing timely and effective intervention strategies. According to Powell *et al* (2005), Sensitivity analysis is widely employed to assess the reliability of model predictions by evaluating their dependence on parameter values. Omitting this crucial step in modeling is often considered misleading, as it undermines the credibility and accuracy of the results. Sensitivity indices measure the relative changes in a variable when a parameter changes (Arriola and Hyman (2007); Chitnis *et al*. (2008); Mikuchi *et al* (2012) and Abdulrahman *et al*. (2013). In particular, the normalized forward sensitivity index expresses the proportional change in a given variable relative to changes in a specific parameter. When the variable is a differentiable parameter function, the sensitivity index can also be defined through partial derivatives, providing a rigorous mathematical framework for assessing parameter sensitivity.

$$S_{\psi}^{R_0} = \frac{\partial R_0}{\partial \psi} x \frac{\psi}{R_0}, \tag{12}$$

where $\psi \in Q = \{\beta_1, \beta_2, \gamma_A, \gamma_s, \varphi, \mu, \rho, \theta, \delta, \mu_1\}$and R_0 is the basic reproduction number.

3 Variables and Parameter Values Estimation

The values for the population-dependent parameters of the model are presented in Table 1.

Table 1. Values for the Population-Dependent Parameter of the Model

Variables	Values	Source
S_u	1787416	NCDC
V_F	2306303	NCDC
V_p	1410329	NCDC
E	20725	NCDC
I_A	1251	NCDC
I_s	3466	NCDC/Oduoye et al (2024)
T	214	NCDC
R	1000	Assumed

The values in Table 2 were obtained from either self-estimation or authors who have conducted similar research on diphtheria infection.

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Table 2. Estimation of Parameters

Parameters	Value	Unit	Reference	Description
λ_U	100	1 / day	Madubueze, Tijani & Fatmawati (2023)	Recruitment rate
μ	0.0000491431	1 / day	Madubueze, Tijani & Fatmawati (2023)	Natural death rate
μ_1	0.011	1 / day	Calculated	Diphtheria-induced death rate
β_1	**0.201***	1 / day	Estimated	Asymptomatic infection transmission rate
β_2	**0.0709***	1 / day	Estimated	Symptomatic infection transmission rate
β_V	0.95	-	NCDC	The rate at which susceptible individuals become fully vaccinated
β_P	**0.503***	-	Estimated	The rate at which susceptible individuals become partially vaccinated

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ω	**0.0114***	-	Estimated	The rate at which fully vaccinated individuals become susceptible
Z	**0.00777***	-	Estimated	The rate at which partially vaccinated individuals become susceptible
τ	**0.0289***	-	Estimated	The rate at which individuals go from being fully vaccinated to partially vaccinated
ε	**0.0707***	-	Estimated	The rate at which partially vaccinated individuals become fully vaccinated
ρ	0.2	-	Madubueze, Tijani & Fatmawati (2023)	Proportion of infectious population
α	**0.146***	-	Estimated	Rate of progression from the exposed class to either the asymptomatic compartment or the infected compartment

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θ	**0.000104***	-	Estimated	The rate at which asymptomatic infected individuals become symptomatic infected
ϕ	**0.00567***	-	Estimated	The rate at which symptomatic infected become treated
γ_A	0.0714	1 / day	Madubueze, Tijani & Fatmawati (2023)	The recovery rate for asymptomatic infected individuals
γ_S	0.042	1 / day	Madubueze, Tijani & Fatmawati (2023)	The recovery rate for symptomatic infected individuals
γ_T	0.0714	1 / day	Assumed	The recovery rate for treated individuals
δ	0.0011	1 / day	Calculated	The rate at which recovered individuals become susceptible (loss rate of immunity)

***Optimized values**

4 Results

The basic reproduction number,R_0, represents the average number of secondary infections generated by a single infected individual in a fully susceptible population. Utilizing the parameter values presented in Table 2, we calculated R_0 to be 0.1323. Since $R_0 < 1$, this result

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indicates that the model is asymptotically stable, suggesting that the disease will gradually decline over time. Furthermore, Table 3 illustrates the variations in R_0 under different parameter values, offering additional insights into its dynamic behaviour. A graphical representation of these variations is provided in Fig.

Table 3. Basic Reproduction Number

	Varying Values		
Parameter	1	**2**	3
β_1	0.0201	0.201	0.901
γ_A	0.00714	0.0714	0.714
β_2	0.00709	0.0709	0.709
γ_s	0.0042	0.042	0.42
θ μ_1	0.0000104 0.0011	0.000104 0.011	0.00104 0.11
μ	0.00000491431	0.0000491431	0.00491431
ϕ	0.000567	0.00567	0.0567
ρ	0.02	0.2	0.9
$\boldsymbol{R_0}$	0.01622443361	0.1321666826	0.7647496103

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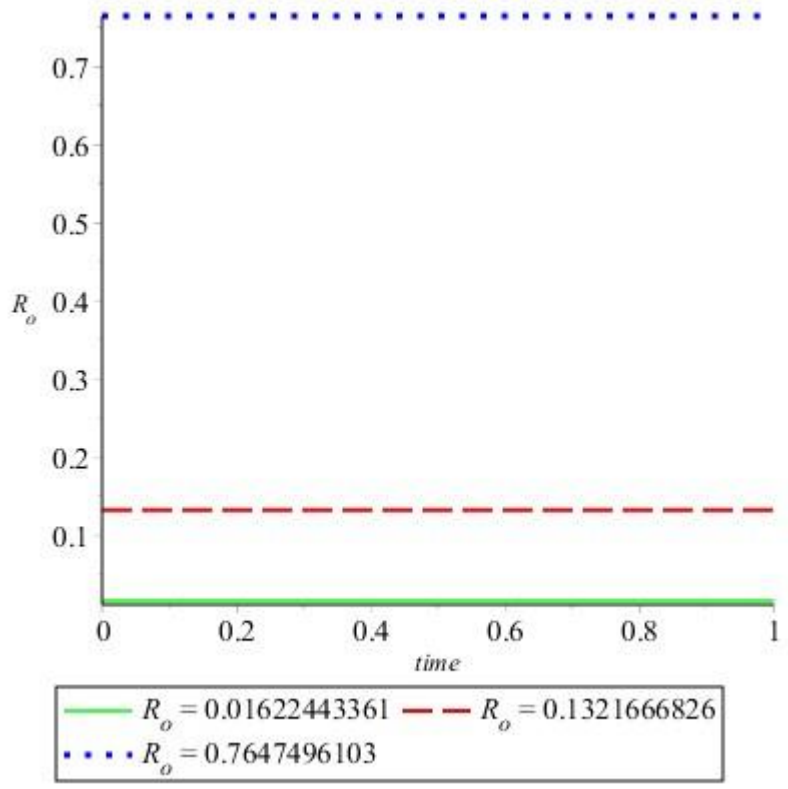

Fig. 2. Plot of Varying Basic Reproduction Numbers

5 Sensitivity of Basic Reproduction Number

Table 4 presents the sensitivity indices of the parameters of the basic reproduction number. The sensitivity analysis of the basic reproduction number by interpretation is as follows: The parameters with negative sensitivity indices tend to have an effect of reducing the disease burden in the community, and if the reduction in the basic reproduction number of the disease is a result of the decrease in the parameter values. In contrast, the positive sensitivity indices can expand the spread of the disease if the parameter values increase.

The most positive sensitive parameter is the asymptomatic infection transmission rate, β_1, where $S_{\beta_1}^{R_0} = 0.7716799884$.

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Other parameters with positive sensitivity indices include:

The recovery rate for symptomatic infected individuals, γ_S, $S_{\gamma_S}^{R_0}$ = 0.5519590004.

Diphtheria-induced death rate, μ_1, $S_{\mu_1}^{R_0}$ = 0.1592500914.

Symptomatic infection transmission rate, β_2, $S_{\beta_2}^{R_0}$ = 0.1107969999.

The recovery rate for asymptomatic infected individuals,

γ_A, $S_{\gamma_A}^{R_0}$ = 0.09534756537.

The rate at which symptomatic infected become treated,

ϕ, $S_{\phi}^{R_0} = 0.07451446506$.

Natural death rate, μ, $S_{\mu}^{R_0}$ =0.0007114584699.

The rate at which asymptomatic infected individuals become symptomatic

infected, θ, $S_{\theta}^{R_0}$ =0.0006944080394.

The only negatively sensitive parameter is the proportion of the infectious population, ρ, where $S_{\rho}^{R_0}$ = -0.08281740530, indicating that an increase in this parameter would reduce the basic reproduction number. Figs. 3-11 are the plots of the sensitivity of varying parameters on the basic reproduction number.

The sensitivity analysis of the basic reproduction number (R_0) provides crucial insights into the factors that most influence diphtheria transmission dynamics. The findings indicate that the asymptomatic infection transmission rate (β_1) is the most positively sensitive parameter, meaning that even a slight increase in asymptomatic transmission can significantly elevate R_0, exacerbating the spread of diphtheria. This underscores the critical role of asymptomatic carriers in sustaining disease transmission within the population. The symptomatic infection transmission rate (β_2), recovery rates for both symptomatic (γ_S) and asymptomatic (γ_A) individuals, and the rate at which symptomatic individuals receive treatment (ϕ), suggest that changes in these parameters also influence the spread of disease. Notably, a higher recovery rate for symptomatic individuals (γ_S) correlates with an increase in R_0, possibly because a faster recovery allows individuals to return to the community while still capable of transmitting the disease if not adequately monitored. The diphtheria-induced death rate (μ_1) also has a positive sensitivity, implying that mortality among infected individuals does not significantly

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reduce transmission and may instead be indicative of widespread infection. The positive sensitivity value of the natural death rate (μ) indicates that an increase in the natural death rate leads to a slight increase in the basic reproduction number (R_0). However, the impact is minimal due to the small magnitude of the sensitivity index. The negative sensitivity index of the proportion of the infectious population (ρ) indicates that an increase in this parameter would reduce the R_0. This suggests that transmission could be reduced if a larger proportion of infections result in symptomatic cases, which are more likely to be detected and treated.

Table 4. Table 4: Sensitivity indices of $\boldsymbol{R_0}$ to the model parameters

Parameters	**Value**	**Sensitivity Index**
β_1	0.201	0.7716799884
γ_A	0.0714	0.09534756537
β_2	0.0709	0.1107969999
γ_s	0.042	0.5519590004
θ	0.000104	0.0006944080394
μ_1	0.011	0.1592500914
μ	0.0000491431	0.0007114584699
ϕ	0.00567	0.07451446506
ρ	0.2	-0.08281740530

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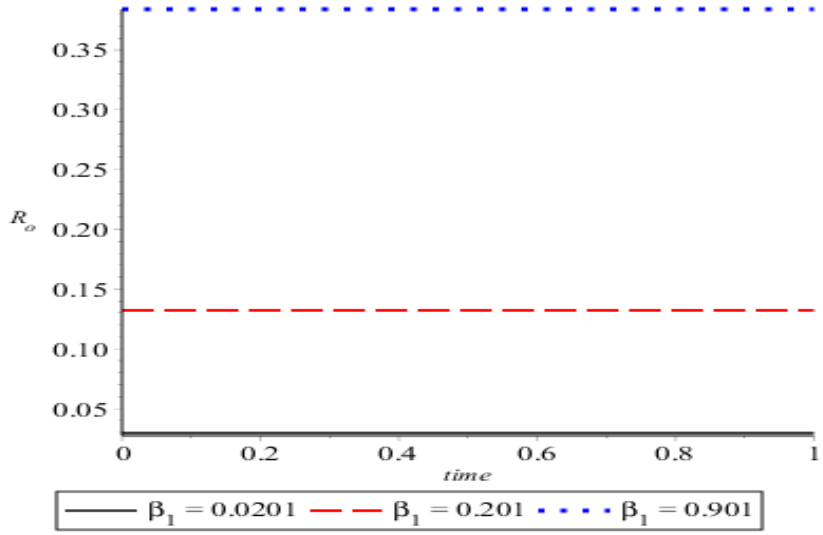

Fig. 3. Plot of Sensitivity for β_1

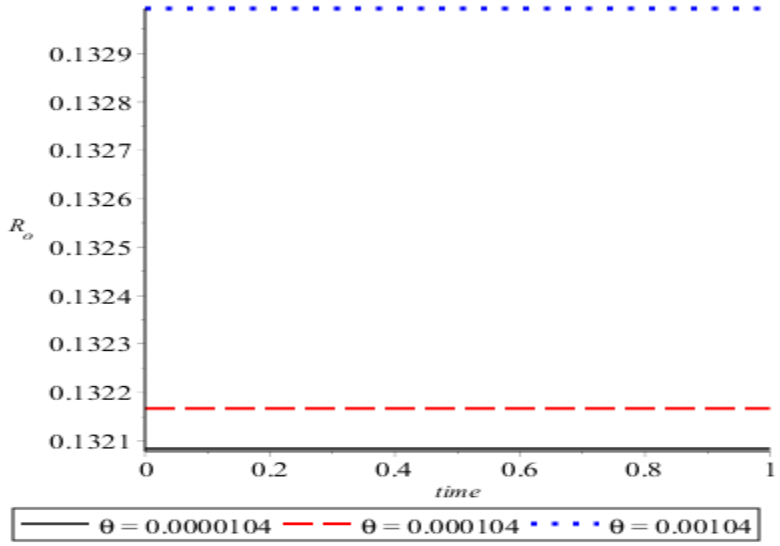

Fig. 4. Plot of Sensitivity for θ

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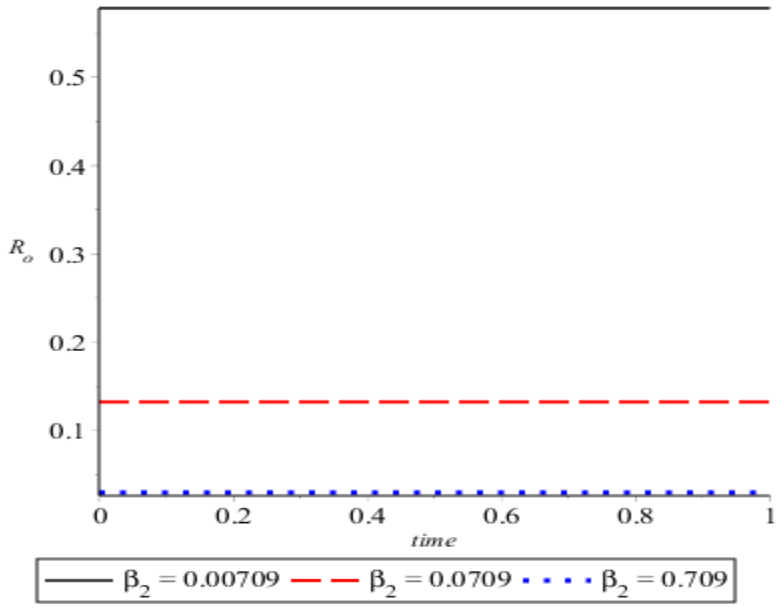

Fig. 5. Plot of Sensitivity for $\boldsymbol{\beta_2}$

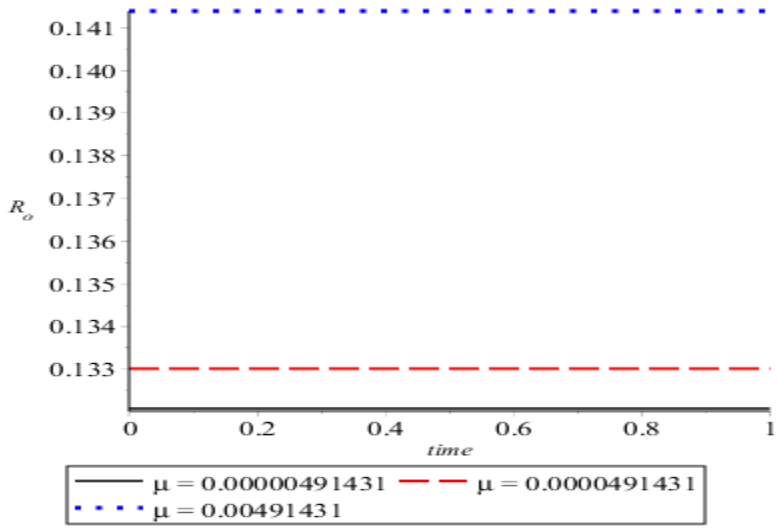

Fig. 6. Plot of Sensitivity for $\boldsymbol{\mu}$

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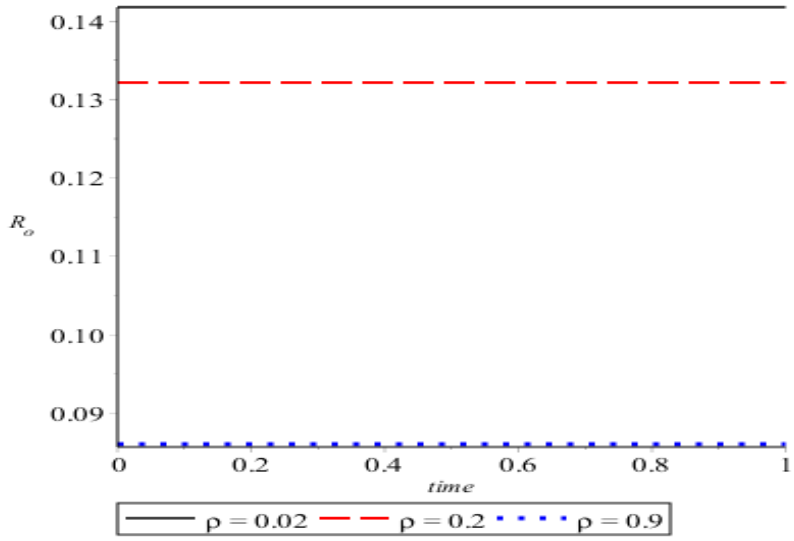

Fig. 7. Plot of Sensitivity for $\boldsymbol{\rho}$

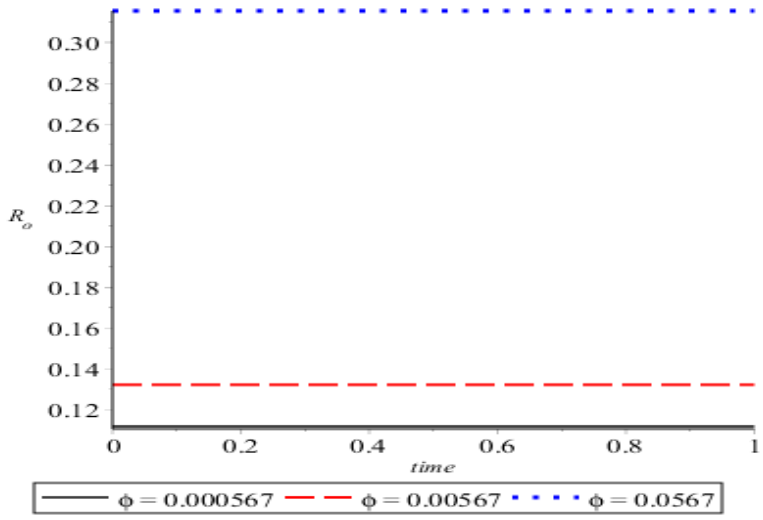

Fig. 8. Plot of Sensitivity for $\boldsymbol{\phi}$

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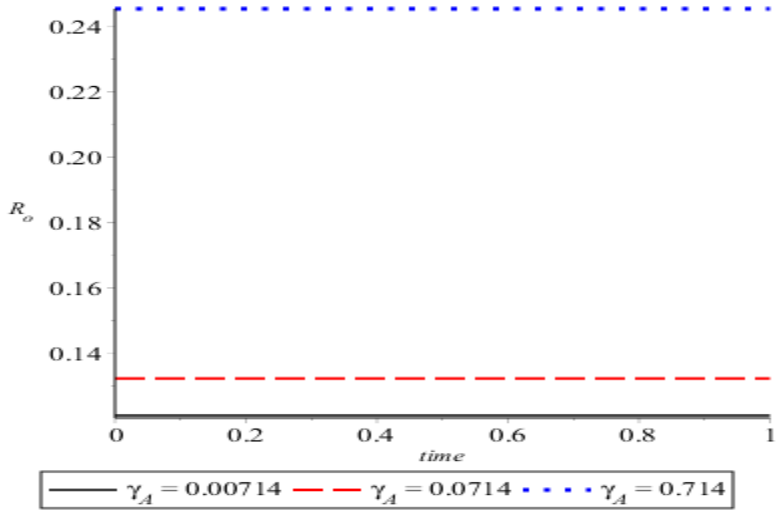

Fig. 9. Plot of Sensitivity for $\boldsymbol{\gamma_A}$

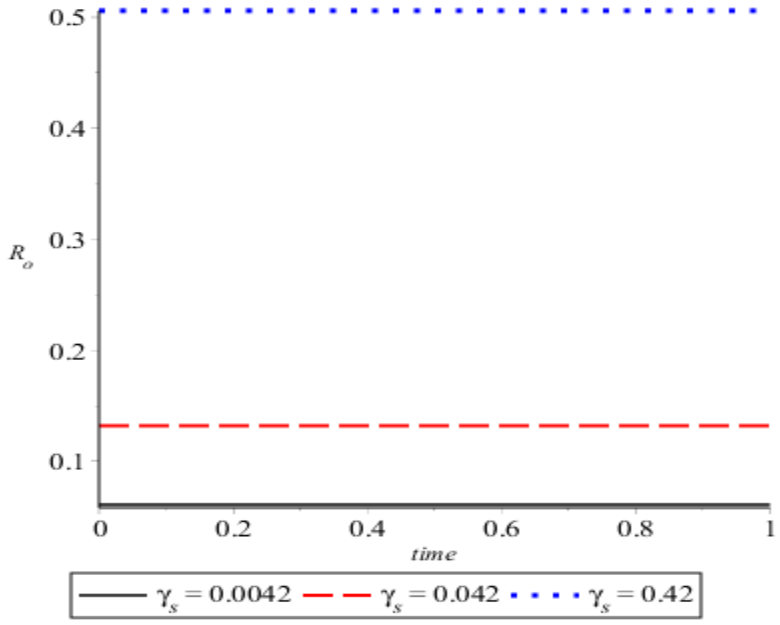

Fig. 10. Plot of Sensitivity for $\boldsymbol{\gamma_S}$

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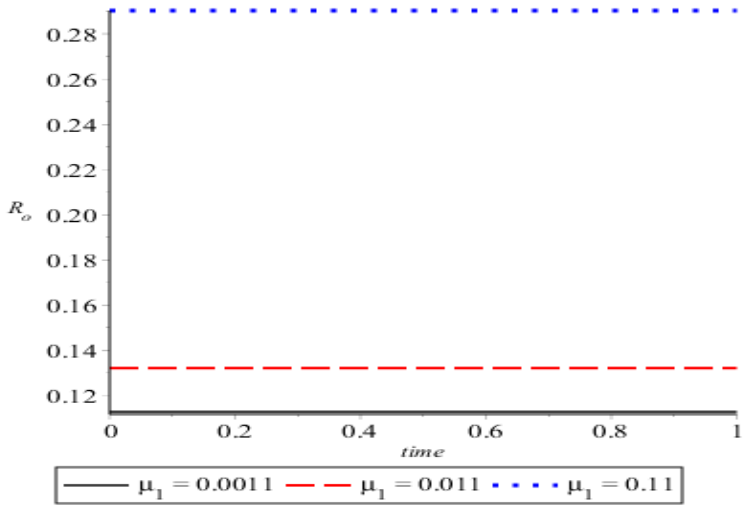

Fig. 11. Plot of Sensitivity for $\boldsymbol{\mu_1}$

6 Limitations

The study assessed the sensitivity of selected key parameters but did not fully evaluate or quantify their actual contribution to disease dynamics, limiting the ability to determine their true influence within the model.

7 Conclusion

In this study, we developed a diphtheria vaccine-treatment model consisting of eight distinct compartments: Susceptible (unvaccinated) population ($\boldsymbol{S_U}$), fully vaccinated ($\boldsymbol{V_F}$), Partially vaccinated ($\boldsymbol{V_P}$), Exposed (E), Asymptomatic infected ($\boldsymbol{I_A}$), Symptomatic infected ($\boldsymbol{I_S}$), Treated (T), and Recovered (R). A sensitivity analysis was conducted to evaluate the influence of each model parameter on the basic reproduction number ($\boldsymbol{R_0}$). The findings highlight the potential importance of asymptomatic carriers in the transmission dynamics of diphtheria, emphasizing the necessity of targeted interventions to mitigate their spread. Effective disease containment strategies should reduce transmission rates, strengthen surveillance systems, and ensure timely treatment. Based on the sensitivity analysis, this study provides targeted recommendations, including prioritizing the detection and control of asymptomatic carriers, minimizing both symptomatic and asymptomatic transmission, optimizing treatment and recovery strategies, addressing disease-related mortality while considering its impact on transmission, and enhancing surveillance and case detection efforts.

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