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Modeling Diphtheria Dynamics and Intervention Strategies in Nigeria: An SEIRP-H Compartmental Model Approach

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ABSTRACT:
Diphtheria remains a significant public health threat in regions with low vaccination coverage and limited healthcare infrastructure, such as Nigeria. This study introduces an SEIRP-H model (Susceptible, Exposed, Infectious, Recovered, Protected, and Hospitalized) to capture the complex dynamics of diphtheria transmission and control strategies. The model is designed to reflect the critical stages of disease progression, incorporating key compartments that account for hospital isolation, vaccination, and immunity post-recovery. Parameters for infection rate, hospitalization, vaccination efficacy, and immunity waning are estimated using available epidemiological data, providing a realistic foundation for simulation. Our analysis focuses on understanding the impact of hospitalization and vaccination efforts on transmission rates, while also exploring the role of immunity (both short- and long-term) in controlling outbreaks. Through sensitivity analysis, we identify the most influential parameters affecting the disease dynamics, which helps highlight priority areas for intervention. The model simulations suggest that increasing vaccination rates and enhancing hospital capacity can significantly reduce the basic reproduction number (R_0) and slow the spread of diphtheria. Our findings underscore the importance of targeted vaccination campaigns, strict isolation of infectious individuals, and robust healthcare response systems to effectively manage diphtheria outbreaks in Nigeria.

Keywords: Diphtheria Transmission, SEIRP-H Model, Vaccination Efficacy, Hospitalization Impact
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1 Introduction

Diphtheria is a serious bacterial infection caused by Corynebacterium diphtheriae, primarily affecting the respiratory system and leading to severe complications such as myocarditis and neuropathy if untreated [1]. Although effective vaccines have existed since the early 20th century, which drastically reduced diphtheria incidence in regions with robust vaccination programs, the disease remains a significant public health concern in regions with inconsistent vaccination coverage. Periodic outbreaks continue to be reported in Nigeria, highlighting the challenge of sustaining high immunization rates in settings with limited healthcare infrastructure [2, 3]. This persistence underscores the importance of achieving and maintaining strong vaccination programs to curb transmission, especially in high-risk areas [4].

Mathematical modeling provides powerful tools to explore and understand disease transmission dynamics, offering valuable insights for designing effective health interventions [5]. Through the construction of mathematical representations of epidemiological processes, researchers can simulate disease behavior under different conditions, which helps inform strategies for disease management [6]. Simple compartmental frameworks, like the Susceptible-Infected-Recovered (SIR) model, are frequently used to explore the transmission patterns of infectious diseases [7]. However, the complexity of diseases such as diphtheria—especially in regions with diverse immunity levels and healthcare access—often requires models to be expanded or adapted to better reflect real-world scenarios.

Several recent studies have introduced innovative modeling approaches to account for the nuances of infectious disease

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transmission and control. Game-theoretic models, for example, have been applied to examine how individual vaccination choices impact community immunity [8]. Other studies have analyzed the effects of community size on disease persistence, revealing how larger populations sustain infections over longer periods [9]. Additionally, models that incorporate behavioral patterns and realistic contact networks [10, 11] as well as spatial-transmission models using partial differential equations [12] underscore the role of contact structure and geographic spread in disease dynamics. These diverse approaches illustrate the flexibility and adaptability of mathematical models to address complex disease behaviors.

In the context of diphtheria, researchers have employed a variety of compartmental models to study transmission dynamics and control strategies. For instance, Cheuvart et al. [13] used mathematical modeling of antibody decay to estimate seroprotection rates 10 years post-vaccination. Udofia et al. [14] developed an age-structured model of diphtheria transmission, employing non-linear differential equations to assess the global stability of the system. Similarly, Islam et al. [15] utilized a next-generation matrix approach for global stability analysis and parameter estimation. Studies by Ahmed et al. [16] explored quarantine's impact on diphtheria dynamics, highlighting the role of early detection in controlling the spread. Further, Islam et al. [17] developed an optimal control model to determine cost-effective strategies for reducing transmission, incorporating both cost and vaccination effectiveness. Other works, such as Olayiwola and Alaje [18], emphasize vaccination's impact on outbreak dynamics through simulation-based modeling and sensitivity analysis. George [19] conducted a sensitivity analysis of diphtheria transmission parameters, identifying key areas for intervention. Sanusi et al. [20] analyzed data from Nigeria's Isin Local Government Area to assess gender effects on transmission, while Ilahi and Widiana [21] examined vaccine efficacy using stability analysis within the SEIR model framework. Finally, Izzati and Andriani [22] provided a dynamical analysis of diphtheria with natural immunity rates, exploring stability under different equilibrium conditions.

In this study, we introduce an SEIRP-H model (Susceptible-Exposed-Infectious-Recovered-Protected-Hospitalized) tailored to capture the specific transmission dynamics of diphtheria in Nigeria. This model extends the traditional SEIR framework by adding compartments for individuals with long-term immunity ("Protected") and those receiving treatment in hospitals ("Hospitalized"). By emphasizing both the role of immunity and the impact of medical isolation on disease control, the SEIRP-H model offers a nuanced representation of diphtheria dynamics, particularly suited to settings where hospitalization and fluctuating immunity play key roles in outbreak management.

To ensure that model predictions are accurate and reflective of actual conditions, the SEIRP-H model employs parameter values obtained from the Nigeria Centre for Disease Control (NCDC) and refined through the Quasi-Newton method. This approach enhances the alignment between model projections and real-world data, making the SEIRP-H model a useful tool for public health planning. Additionally, a sensitivity analysis of the model highlights the most influential factors in disease transmission, providing valuable guidance on where vaccination and hospital-based interventions may have the greatest impact. Through its unique structure and rigorous parameterization, the SEIRP-H model presents a comprehensive framework for understanding and managing diphtheria outbreaks in Nigeria's public health landscape.

By adapting mathematical modeling techniques to the specific challenges posed by diphtheria in Nigeria, this study offers an improved tool for public health officials to design and implement effective interventions. The SEIRP-H model integrates critical factors—such as vaccination, hospitalization, and long-term immunity—providing actionable insights into disease management. By refining the model's components to accurately represent real-world conditions, this study enhances our understanding of diphtheria dynamics and offers targeted strategies to mitigate outbreaks in regions with varied epidemiological contexts.

2 Model Formulation

The SEIRP-H model is developed to capture the transmission dynamics of diphtheria, with specific adaptations for the epidemiological context in Nigeria, where vaccination coverage and healthcare resources vary. This model builds on the SEIR framework by incorporating additional compartments to account for long-term immunity and hospitalization, both crucial for managing diphtheria outbreaks. The compartments in the SEIRP-H model are defined as follows:

- Susceptible (S): Individuals at risk of infection.
- Exposed (E): Individuals exposed to Corynebacterium diphtheriae but not yet infectious.
- Infectious (I): Symptomatic individuals capable of transmitting the disease.
- Recovered (R): Individuals with temporary immunity following recovery.
- Protected (P): Individuals with long-term immunity due to vaccination or recovery.
- Hospitalized (H): Infectious individuals isolated for treatment, with limited transmission potential.

2.1 Model Equations

The dynamics of the SEIRP-H model are governed by the following system of differential equations:

$$\frac{dS}{dt} = -\beta S\frac{I}{N} - \omega S + \theta P, \tag{1}$$
$$\frac{dE}{dt} = \beta S\frac{I}{N} - \gamma E, \tag{2}$$
$$\frac{dI}{dt} = \gamma E - \alpha I - \delta I, \tag{3}$$
$$\frac{dR}{dt} = \alpha I - \rho R, \tag{4}$$
$$\frac{dP}{dt} = \omega S + \rho R - \theta P, \tag{5}$$
$$\frac{dH}{dt} = \delta I - \sigma H, \tag{6}$$

where the parameters represent the following:

- β: transmission rate,
- γ: rate of progression from exposed to infectious,
- α: recovery rate,
- δ: hospitalization rate,
- σ: discharge rate from hospitalization,
- ω: vaccination rate,
- ρ: rate at which recovered individuals gain long-term immunity,
- θ: rate of immunity waning.

The system (1) describes the transitions between compartments based on diphtheria progression, immunity acquisition, hospitalization, and vaccination.

2.2 Model Assumptions

The SEIRP-H model is constructed under the following assumptions:

1. Homogeneous Mixing: All individuals have an equal probability of contact, simplifying the network structure of interactions.
2. Vaccination-Induced Immunity: Vaccination moves individuals from S to P, with a waning immunity rate θ representing a gradual return to susceptibility.
3. Temporary Immunity Post-Recovery: Recovered individuals initially have temporary immunity, with some gaining long-term immunity at rate ρ while others return to susceptibility.
4. Hospital Isolation: Hospitalized individuals in H are isolated, reducing transmission risk and enhancing recovery prospects.
5. Constant Population Size: The model assumes a closed population, ignoring births and natural deaths, which is reasonable for short-term epidemic modeling.
6. No Reinfection During Immunity: Individuals in R and P compartments are immune, with reinfection considered only after waning immunity, as defined by θ.

These assumptions provide a structured balance between model complexity and analytical tractability, capturing essential transmission and intervention mechanisms for understanding diphtheria dynamics and control in the context of Nigeria.

3 Disease-Free Equilibrium

The Disease-Free Equilibrium (DFE) represents the steady-state condition where no infections exist within the population, with individuals occupying only the susceptible, protected, or recovered compartments. This equilibrium state is essential for evaluating the stability of the system and understanding the conditions under which diphtheria transmission will cease in the population.

Let $(S^*, E^*, I^*, R^*, P^*, H^*)$ denote the equilibrium values of each compartment. At the DFE, where no infection exists, we assume:

$$E^* = 0, \quad I^* = 0, \quad H^* = 0.$$

Therefore, the DFE is expressed as:

$$(S^*, E^*, I^*, R^*, P^*, H^*) = \left(S^*, 0, 0, 0, \frac{\omega S^*}{\theta}, 0\right).$$

To achieve equilibrium, each differential equation governing the SEIRP-H model must equal zero.

1. Susceptible compartment: The rate of change for the susceptible population is defined as

$$\frac{dS}{dt} = -\beta S \frac{I}{N} - \omega S + \theta P = 0.$$

   At equilibrium, where $I = 0$, this simplifies to $\omega S^* = \theta P^*$, indicating that the vaccination and waning immunity rates balance the flow between susceptible and protected individuals.

2. Exposed, Infectious, Recovered, and Hospitalized compartments: Since $E = 0$, $I = 0$, $H = 0$, and $R = 0$ at the DFE, the corresponding differential equations are trivially satisfied.

3. Protected compartment: The protected population dynamics at equilibrium are given by

$$\frac{dP}{dt} = \omega S + \rho R - \theta P = 0.$$

   Given $R = 0$, this yields $P^* = \frac{\omega S^*}{\theta}$, establishing the balance between vaccination-induced protection and waning immunity.

Thus, the DFE is characterized by the state:

$$(S^*, E^*, I^*, R^*, P^*, H^*) = \left(S^*, 0, 0, 0, \frac{\omega S^*}{\theta}, 0\right).$$

3.1 Derivation of the Basic Reproduction Number R_0

The basic reproduction number, R_0, is a fundamental epidemiological threshold representing the expected number of secondary infections produced by a single infectious individual in a fully susceptible population. For the SEIRP-H model, R_0 reflects the balance of transmission, progression, and recovery rates within the population, determining the stability of the DFE.

To derive R_0, we analyze the dynamics at the onset of an outbreak, assuming that the population is predominantly susceptible (i.e., $S \approx N$), while the exposed (E), infectious (I), and hospitalized (H) compartments contain only a few individuals. The principal pathways of interest are as follows:

1. Infection Rate: Susceptible individuals become exposed at a rate proportional to $\beta S \frac{I}{N}$, where β is the transmission rate.

2. Progression to Infectious State: Exposed individuals progress to the infectious state at a rate γ.

3. Exit from the Infectious Compartment: Infectious individuals leave the compartment either by recovering at rate α or by being hospitalized at rate δ, resulting in an effective exit rate of $\alpha + \delta$.

The basic reproduction number can thus be formulated as the ratio of the infection-generating potential to the rate of exiting the infectious state:

$$R_0 = \frac{\beta}{\alpha + \delta}.$$

3.2 Stability of the Disease-Free Equilibrium

The stability of the DFE depends directly on the value of R_0. If $R_0 < 1$, the DFE is stable, meaning that any introduction of the disease into the population will result in an eventual die-out, as each infectious individual will, on average, produce fewer than one secondary case. Conversely, if $R_0 > 1$, the DFE is unstable, leading to sustained transmission and potential outbreak growth.

To ensure disease control, public health interventions—such as increased vaccination rates or effective isolation of infectious individuals—are targeted to reduce R_0 below the critical threshold of 1, thereby stabilizing the DFE and preventing epidemic spread. This analysis of the DFE and R_0 offers critical insights into the conditions required to achieve a stable, disease-free population.

4 Endemic Equilibrium of the SEIRP-H Model

The Endemic Equilibrium (EE) of the SEIRP-H model describes a steady state where diphtheria persists at constant levels within the population, with each compartment maintaining a stable non-zero value. This equilibrium is crucial for understanding the long-term behavior of diphtheria within a community and assessing the conditions under which the disease will remain endemic.

4.1 Conditions for the Endemic Equilibrium

At the endemic equilibrium, the population in each compartment remains constant over time, so each differential equation is set to zero. Let the endemic equilibrium values for each compartment be denoted by $(S^e, E^e, I^e, R^e, P^e, H^e)$. Thus, we have the following system at equilibrium:

$$-\beta S^e \frac{I^e}{N} - \omega S^e + \theta P^e = 0, \tag{7}$$

$$\beta S^e \frac{I^e}{N} - \gamma E^e = 0, \tag{8}$$

$$\gamma E^e - \alpha I^e - \delta I^e = 0, \tag{9}$$

$$\alpha I^e - \rho R^e = 0, \tag{10}$$

$$\omega S^e + \rho R^e - \theta P^e = 0, \tag{11}$$

$$\delta I^e - \sigma H^e = 0. \tag{12}$$

The above system is solved in terms of the model parameters and the endemic equilibrium values are obtained as:

$$S^e = \frac{N(\alpha + \delta)}{\beta}, \tag{13}$$

$$E^e = \frac{(\alpha + \delta) I^e}{\gamma}, \tag{14}$$

$$I^e = \text{determined from initial conditions or specific } R_0, \tag{15}$$

$$R^e = \frac{\alpha I^e}{\rho}, \tag{16}$$

$$P^e = \frac{\omega N(\alpha + \delta) + \alpha I^e \beta}{\theta \beta}, \tag{17}$$

$$H^e = \frac{\delta I^e}{\sigma}. \tag{18}$$

4.2 Stability Analysis of the Endemic Equilibrium

The stability of the endemic equilibrium (EE) for the SEIRP-H model is determined by analyzing the eigenvalues of the Jacobian matrix J, evaluated at the EE. The Jacobian matrix J is given by:

$$J = \begin{pmatrix} -\beta\frac{I^e}{N} - \omega & 0 & -\beta\frac{S^e}{N} & 0 & \theta & 0 \\ \beta\frac{I^e}{N} & -\gamma & \beta\frac{S^e}{N} & 0 & 0 & 0 \\ 0 & \gamma & -(\alpha+\delta) & 0 & 0 & 0 \\ 0 & 0 & \alpha & -\rho & 0 & 0 \\ \omega & 0 & 0 & \rho & -\theta & 0 \\ 0 & 0 & \delta & 0 & 0 & -\sigma \end{pmatrix}.$$

The eigenvalues λ are obtained by solving the characteristic equation $\det(J - \lambda I) = 0$. Due to the complexity of (4.2), an analytical solution for the eigenvalues is not straightforward and requires numerical computation. However, some observations were made:

1. Isolated Eigenvalue: The term $-\sigma$ appears in the last row and column of J, indicating that $\lambda = -\sigma$ is an eigenvalue. This eigenvalue relates to the hospitalized compartment H and reflects the discharge rate.

2. Remaining Eigenvalues: The remaining eigenvalues correspond to the submatrix formed by excluding the row and column associated with H. These eigenvalues generally depend on parameters β, ω, α, δ, γ, θ, and ρ.

The stability of the EE can be assessed by examining the signs of the real parts of the eigenvalues of J. If all eigenvalues have negative real parts, the EE is stable; otherwise, instability occurs. This analysis can guide parameter adjustments in vaccination and isolation rates to promote disease control and move the system towards the disease-free equilibrium.

5 Bifurcation Analysis

Here, we examine how changes in parameters affect the qualitative dynamics of the SEIRP-H model, potentially shifting the system between disease-free and endemic states. This analysis focuses on the basic reproduction number R_0, which is a threshold parameter obtained as:

$$R_0 = \frac{\beta}{\alpha + \delta}.$$

A bifurcation occurs when $R_0 = 1$, marking a shift in the stability of the disease-free equilibrium (DFE). For $R_0 < 1$, the DFE is stable, causing infection levels to decay to zero over time and leading to disease elimination. When $R_0 > 1$, the DFE loses stability, and a stable endemic equilibrium (EE) emerges, resulting in persistent disease levels within the population.

To analyze this bifurcation behavior, we systematically vary the parameters to observe their influence on R_0 and the equilibrium states. A transcritical bifurcation is identified as R_0 crosses the threshold of 1. Figure 1 displays bifurcation diagrams, which illustrate how the system transitions between disease-free and endemic states at specific parameter values. This analysis underscores the critical importance of maintaining $R_0 < 1$ through targeted interventions, as this condition stabilizes the DFE and prevents the establishment of an endemic state.

6 Control and Intervention Strategy Analysis

To assess intervention strategies for controlling diphtheria, we simulate the effects of key parameter changes: vaccination rate (ω), transmission rate (β), recovery rate (α), and hospitalization rate (δ). Each intervention aims to reduce infection prevalence and guide the system toward a disease-free state.

The impact of these interventions is evaluated by examining peak infection levels, time to elimination, and cumulative cases. Four scenarios, corresponding to Figure 2, are analyzed:

1. Baseline: The baseline scenario, represented in Figure 2(a), shows disease progression with standard parameter values ($\beta = 0.25$, $\omega = 0.02$, $\alpha = 0.1$, $\delta = 0.05$) and no intervention.

2. Increased Vaccination Rate (ω): Raising ω shifts individuals from susceptible (S) to protected (P), reducing those at risk and effectively lowering R_0 as it is inversely related to ω:

$$R_0 \propto \frac{1}{\omega}.$$

   Figure 2(b) demonstrates this strategy's effect, resulting in a lower infection peak and faster approach to a disease-free state.

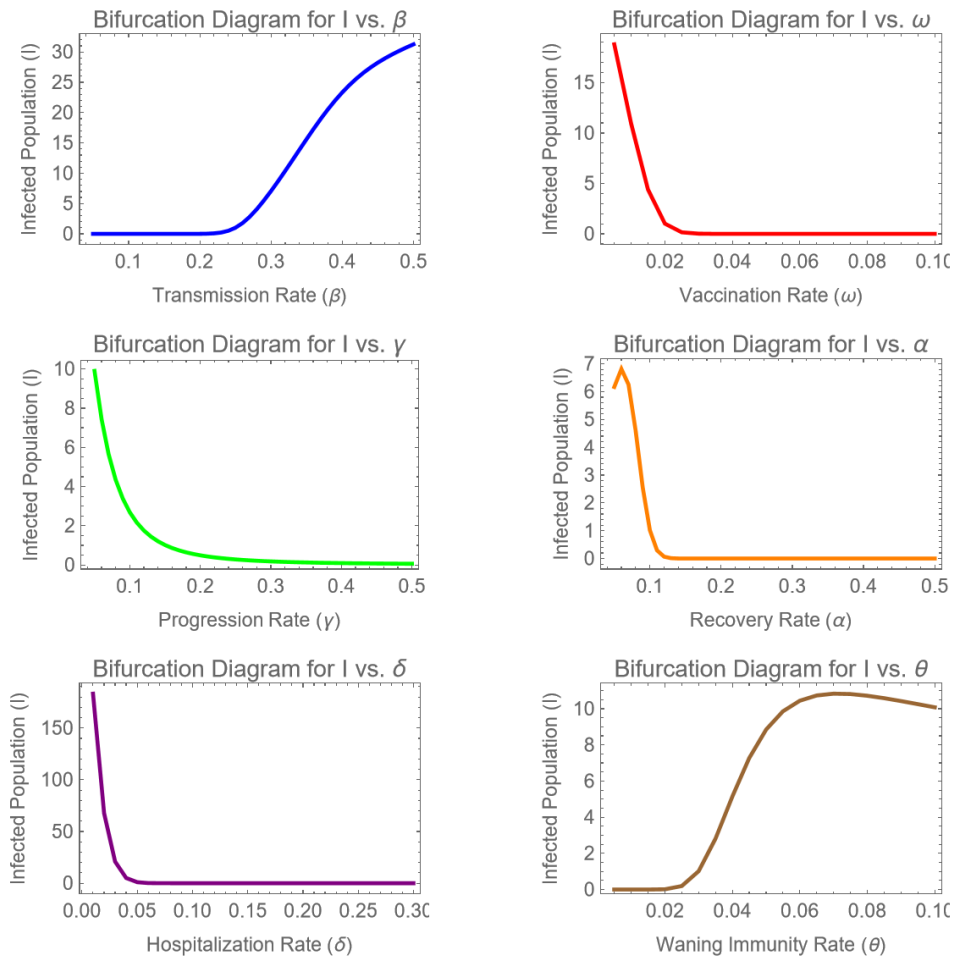

Figure 1: Bifurcation diagrams showing how varying parameters affect the stability of the disease-free equilibrium (DFE) and the transition to an endemic equilibrium (EE) in the SEIRP-H model.

3. Reduced Transmission Rate (β): Lowering β reduces R_0, defined as $\beta/(\alpha+\delta)$. Measures like social distancing and mask use achieve this reduction, as shown in Figure 2(c), producing a flatter infection curve:

$$R_0 = \frac{\beta}{\alpha+\delta}.$$

4. Increased Hospitalization Rate (δ): Increasing δ moves infectious individuals into isolation faster, shortening their infectious period and curtailing transmission. Figure 2(d) illustrates a more rapid decline in infections under this intervention.

These simulations reveal that combining increased ω with reduced β yields the most substantial reductions in prevalence, as both strategies effectively lower R_0 and accelerate the decline toward a disease-free state. Figure 2 thus highlights the strategic value of vaccination and transmission reduction in managing diphtheria outbreaks.

7 Discussion and Conclusion

This study develops and applies an SEIRP-H model tailored to analyze diphtheria transmission dynamics and control strategies within Nigeria, where vaccination rates and healthcare resources vary widely. By incorporating compartments for hospitalization and long-term immunity, the model captures the complex stages of diphtheria progression and allows for evaluation of interventions specific to Nigeria's public health context.

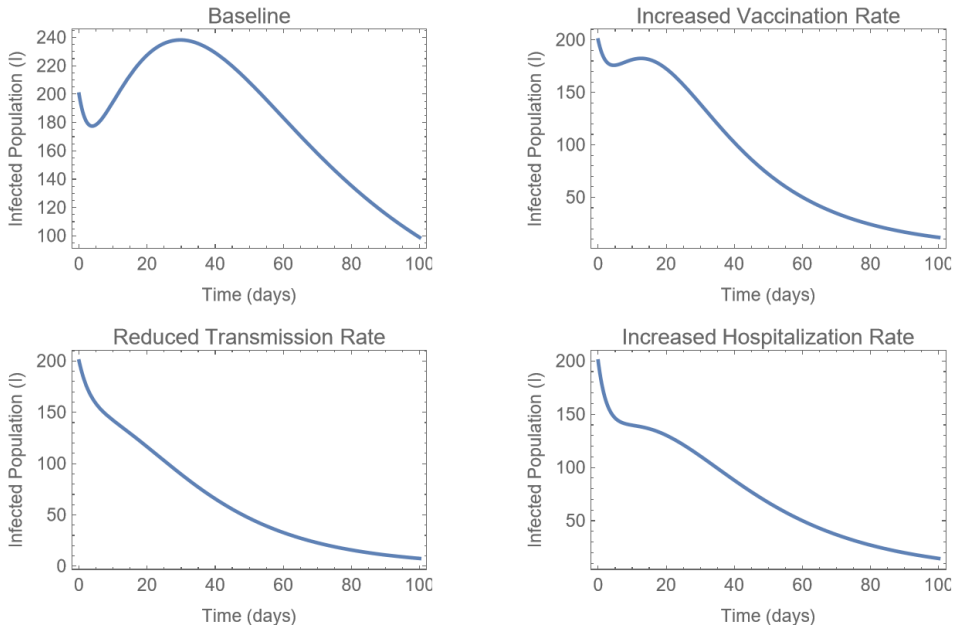

Figure 2: Effects of intervention strategies on diphtheria spread: (a) Baseline, (b) Increased vaccination rate (ω), (c) Reduced transmission rate (β), and (d) Increased hospitalization rate (δ). Each scenario shows infection dynamics over time under parameter adjustments.

Simulation results demonstrate that increasing vaccination rates (ω) is particularly effective in reducing disease prevalence. By moving individuals from the susceptible (S) to the protected (P) compartment, higher vaccination rates decrease the basic reproduction number R_0, thereby facilitating progress toward a disease-free state. Additionally, reducing the transmission rate (β) through public health measures, such as mask-wearing and social distancing, is shown to lower infection peaks and cumulative cases, which is essential in regions with limited vaccination coverage.

Enhancing healthcare access, through improved recovery (α) and hospitalization rates (δ), further supports disease management by reducing the infectious period and ensuring timely isolation of cases. The combined strategy of increased vaccination rates and reduced transmission yields the most substantial reduction in prevalence, as it effectively decreases R_0 and accelerates the system's shift toward a disease-free equilibrium. This approach is particularly relevant in Nigeria, where comprehensive vaccination and community-wide transmission control remain critical for managing diphtheria.

In conclusion, the SEIRP-H model provides a robust framework for assessing diphtheria control strategies, integrating both direct (vaccination) and indirect (isolation and transmission reduction) interventions. Future work could expand this model by examining population structure, the long-term impact of immunity waning, and adaptation to similar infectious diseases in Nigeria. These findings offer valuable guidance for Nigerian policymakers, underscoring the importance of targeted vaccination campaigns, effective isolation practices, and community health measures to control diphtheria outbreaks and protect public health in resource-limited settings.

Authors' Contributions

All authors participated actively in this research work and have read and approved the final manuscript.

Authors' Declaration

The authors declare no known conflict of interest.

Consent (where applicable)

Consent form has been approved by all authors.

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References

[1] Saket Kumar Jammar, Shraddha Sharma, Sunita Agarwal, Tanmaya Kataria, Prem Singh Jat, Shashank Nath Singh, Deepak Jain, Ritu Sehra, and Ajay Gupta. "Spectrum of Neurological Outcomes in Diphtheria: A Case Series". In: Indian Journal of Otolaryngology and Head & Neck Surgery (2021), pp. 1–6.

[2] AE Sadoh and RE Oladokun. "Re-emergence of diphtheria and pertussis: implications for Nigeria". In: Vaccine 30.50 (2012), pp. 7221–7228.

[3] AE Sadoh and WE Sadoh. "Diphtheria mortality in Nigeria: the need to stock diphtheria antitoxin". In: African Journal of Clinical and Experimental Microbiology 12.2 (2011).

[4] Nasir Abdulrasheed, Lukman Lawal, Abdulazeez B Mogaji, Ahmed O Abdulkareem, Abdulrahman K Shuaib, Sodiq G Adeoti, Opeyemi P Amosu, Abdulmujeeb O Muhammad-Olodo, Abdulwahab O Lawal, Tawakalitu A Jaji, et al. "Recurrent diphtheria outbreaks in Nigeria: A review of the underlying factors and remedies". In: Immunity, Inflammation and Disease 11.11 (2023), e1096.

[5] Guangping Huang and Ling Li. "A mathematical model of infectious diseases". In: Annals of Operations Research 168 (2009), pp. 41–80.

[6] GC Smith and CL Cheeseman. "A mathematical model for the control of diseases in wildlife populations: culling, vaccination and fertility control". In: Ecological Modelling 150.1-2 (2002), pp. 45–53.

[7] Ian Cooper, Argha Mondal, and Chris G Antonopoulos. "A SIR model assumption for the spread of COVID-19 in different communities". In: Chaos, Solitons & Fractals 139 (2020), p. 110057.

[8] Kabir KM Ariful, Islam M.D. Shahidul, and Mohammad Sharif Ullah. "Understanding the impact of vaccination and Self-Defense measures on epidemic dynamics using an embedded optimization and evolutionary game theory methodology". In: Vaccines 11.9 (2023), p. 1421.

[9] Matt J Keeling and Pejman Rohani. Modeling infectious diseases in humans and animals. Princeton university press, 2011.

[10] Zhen Wang, Michael A Andrews, Zhi-Xi Wu, Lin Wang, and Chris T Bauch. "Coupled disease–behavior dynamics on complex networks: A review". In: Physics of life reviews 15 (2015), pp. 1–29.

[11] Ken TD Eames and Matt J Keeling. "Modeling dynamic and network heterogeneities in the spread of sexually transmitted diseases". In: Proceedings of the national academy of sciences 99.20 (2002), pp. 13330–13335.

[12] Steven Riley. "Large-scale spatial-transmission models of infectious disease". In: Science 316.5829 (2007), pp. 1298–1301.

[13] Brigitte Cheuvart, Margaret Burgess, Fred Zepp, Jussi Mertsola, Joanne Wolter, and Lode Schuerman. "Anti-diphtheria antibody seroprotection rates are similar 10 years after vaccination with dTpa or DTPa using a mathematical model". In: Vaccine 23.3 (2004), pp. 336–342.

[14] Ekere Sunday Udofia, Ubong Dominic Akpan, Joy Ijeoma Uwakwe, and Henry Sylvester Thomas. "Age Structured Deterministic Model of Diphtheria Infection". In: Earthline Journal of Mathematical Sciences 14.3 (2024), pp. 391–404.

[15] Zahurul Islam, Shohel Ahmed, Rahman M.M., Karim M.F., and Amin M.R. "Global stability analysis and parameter estimation for a diphtheria model: A case study of an epidemic in Rohingya refugee camp in Bangladesh". In: Computational and Mathematical Methods in Medicine 2022.1 (2022), p. 6545179.

[16] Idris Ahmed, Chanakarn Kiataramkul, Mubarak Muhammad, and Jessada Tariboon. "Existence and Sensitivity Analysis of a Caputo Fractional-Order Diphtheria Epidemic Model". In: Mathematics 12.13 (2024), p. 2033.

[17] Zahurul Islam, Kabir K.M. Ariful, Rahman M.M., and Rahman M.D. Atikur. "A Cost-Effective Epidemiological Exposition of Diphtheria Outbreak by the Optimal Control Model: A Case Study of Rohingya Refugee Camp in Bangladesh". In: Complexity 2024.1 (2024), p. 6654346.

[18] Morufu Oyedunsi Olayiwola and Adedapo Ismaila Alaje. "Mathematical modelling of diphtheria transmission and vaccine efficacy using Nigeria". In: Modeling Earth Systems and Environment (2024), pp. 1–27.

[19] Isobeye George. "Diphtheria transmission dynamics: a sensitivity analysis." In: Faculty of Natural and Applied Sciences Journal of Scientific Innovations 5.1 (2023), pp. 130–140.

[20] Sanusi O.A., Ojo Olufemi David, and Onikola I.O. "Modeling the Transmission and Control Strategies of Diphtheria (A Case Study of Isin Local Government Area of Kwara State)". In: International Journal of Advances in Engineering and Management (IJAEM) 5 (2023), pp. 904–910.

[21] Ilahi F. and Widiana A. "The effectiveness of vaccine in the outbreak of diphtheria: mathematical model and simulation". In: IOP Conference Series: Materials Science and Engineering. Vol. 434. 1. IOP Publishing. 2018, p. 012006.

[22] Izzati N., Andriani A., and Robi'Aqolbi R. "Optimal control of diphtheria epidemic model with prevention and treatment". In: Journal of Physics: Conference Series. Vol. 1663. 1. IOP Publishing. 2020, p. 012042.