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Epidemiological Pattern and the Dynamics of Diphtheria Outbreak in Nigeria (A SIR and SEIR Modeling Approach)

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ABSTRACT

Diphtheria is highly prevalent in the African countries especially among the Sub-Saharan Africa. Factors such as declining herd immunity due to low vaccination are key determinants of the outbreak in Nigeria, while the high mortality rate recorded has been attributed to the non-availability of diphtheria antitoxin (DAT). Hence, this study examined the dynamics of the spread of diphtheria in Nigeria during the epidemic period using the SIR and SEIR Modeling approach with a set of data collated monthly from the monthly publications of the NCDC. The results of the SIR model revealed value of 0.14 estimated for the transmission rate suggesting moderate transmission rate, and removal rate of 0.50 which indicated a 50% chance of recovery, death, or complete removal from the entire population. Also, results of SEIR Model revealed estimated value of 0.42 for the transmission rate suggesting moderate rate of spread with an average latent period of 5 days. The computed average reproduction rate for SIR model was approximately 0.28 while that of SEIR model was approximately 0.84 since R0 <1, this indicates that one infected individual cause less than 1 new infection which can further be explained as a maximum control in the rate of spread. However, the computed value of herd immunity obtained for the SIR model was 0.72 while 0.16 was estimated for SEIR Model. Since both estimated values of herd immunity are lower than 80%, it indicates that an insignificant portion of the susceptible population is yet to develop strong immunity against diphtheria infection.

INTRODUCTION

Diphtheria is a disease caused by a bacterium that affects the upper respiratory tract and, less often, the skin (World Health Organization [WHO], 2024). Although highly contagious, it is a vaccine-preventable disease (WHO, 2024).

Gaston Ramon at the Pasteur Institute in Paris and Alexander Thomas Glenny at the Wellcome Research Laboratories in London independently developed an inactivated version of diphtheria toxoid in 1923 (American History Museum, Gavi, 2021; National Vaccine Information Center [NVIC], 2024). The vaccine now administered through immunization to curb the spread of the disease is the combined diphtheria, tetanus, and pertussis (DTaP) vaccine.

In October 2023, UNICEF reported a cumulative 14,482 suspected cases of diphtheria, of which 9,486 were confirmed. Cases were reported from 19 states and 128 Local Government Areas (LGAs), with 95% of cases originating from five states in northwestern and northeastern Nigeria (Kano, Katsina, Yobe, Bauchi, and Borno) (UNICEF Nigeria, 2023a, 2023b).

In June 2022, Australia and several European countries reported a diphtheria outbreak that lasted until September 2022, affecting Austria, Germany, Norway, Belgium, France, Switzerland, and the United Kingdom. During this outbreak, 144 cases were suspected, of which 97 were classified as clinically compatible and 44 were laboratory-confirmed (World Health Organization Regional Office for Europe, 2022).

Diphtheria remains highly prevalent in many African countries, particularly in sub-Saharan Africa. In 2023, four African Union member states which comprise Algeria, Guinea, Niger, and Nigeria, experienced recurrent diphtheria outbreaks (Fouda *et al.*, 2025; WHO, 2024). Nigeria accounted for a substantial proportion of these cases, with 13,145 reported infections and 493 deaths as of October 5, 2023 (Africa CDC, 2023).

The primary causes of recurrent diphtheria outbreaks and high mortality rates in Nigeria have been attributed to waning herd immunity resulting from low DTP vaccination coverage and inadequate availability of diphtheria antitoxin (Abdulrasheed *et al.*, 2023). Nigeria has experienced previous diphtheria outbreaks, including a notable outbreak in 2011 that affected rural communities in Borno State (Agrawal *et al.*, 2023; Oduoye *et al.*, 2024). Other factors, including overcrowding, poor health status, substandard living conditions, incomplete immunization, and immunocompromised conditions, increase susceptibility to diphtheria and facilitate disease transmission (Lo, 2025). The persistent occurrence of diphtheria outbreaks in Nigeria highlights the need for further studies to better understand the dynamics of disease transmission. Such knowledge will support healthcare providers and policymakers in developing effective preventive strategies and educating the public to

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reduce disease incidence. Consequently, compartmental epidemiological models such as the SIR and SEIR models provide valuable tools for understanding disease dynamics and informing interventions aimed at achieving a diphtheria-free society.

MATERIALS AND METHODS

Data Source

Data of 217,841 were gathered form the official website of the NCDC based on the monthly publications of the situation reports. Data collected include the number of suspected cases of infection, number of confirmed cases, number of deaths and the number of persons with no history of vaccination. Other relevant data extracted includes the number of confirmed cases distributed by states in the north.

Variable(s) Description

The variables of the SIR and SEIR epidemic models are stated as

Susceptible (S): this represents the number of susceptible people per interval of time (t) during the outbreak.

Exposed (E): this represents the number of latent individuals or the number of persons in the incubation phase, per interval of time.

Infectious (I): This represents the number of persons who have been infected and are capable of recreating new infections in susceptible persons per given interval of time.

Removed (R): this represents the population of those who have either died or have recovered from the aliment.

Data presentation

Table 1 presents the summary statistics for SIR model where the total number found in the susceptible compartment represents the number of persons with no history of vaccination while the infected compartment represents incidences of clinically confirmed cases and manifestations of diphtheria, while the removed compartment represents the total number of deaths or those who had recovered from the ailment. The variance indicated a wide variation or gap in the data points and as such the mean is less representative of the data set this could have happened as a result of an outlier or some irregularity experienced during the process of data collection.

Models Formulation

The SIR and SEIR epidemic models are useful tools for modeling an infectious disease under a certain conditions such that, during the spread of an infectious disease, the decreasing rate of the number of susceptible individual (S) is proportional to the number of infectious individual (I), Only a fraction of α of infected individuals who are in the infectious period (In) are confirmed and reported as daily new cases (yn), at every given time, N = S + E + I + R.

This study leveraged on the concepts of deterministic epidemiology due to the fact that the available set of data adopted for this study fits better than stochastic approach. The choice of exploring two models is in a quest to examine the model that best describes the spread pattern.

The spatial autocorrelation techniques were also explored in a quest to find out if there exist some spatial relationship among the recorded cases in the various states.

Mathematical representation of SIR Model

The equations for the SIR model are mathematically presented as:

$$\frac{ds}{dt} = -\frac{\beta SI}{N} \quad (1)$$

$$\frac{dI}{dt} = \frac{\beta SI}{N} - \gamma I \quad (2)$$

$$\frac{dR}{dt} = \gamma I \quad (3)$$

Mathematical representation of SEIR Model

The equations for the SEIR model are mathematically presented as:

$$\frac{dS}{dt} = -\frac{\beta SI}{N} \quad (4)$$

$$\frac{dE}{dt} = \frac{\beta SI}{N} - \sigma E \quad (5)$$

$$\frac{dI}{dt} = \sigma E - \gamma I \quad (6)$$

$$\frac{dR}{dt} = \gamma I \quad (7)$$

Model Evaluation using Root Mean Squared Error, Robustness Coefficient

Root Mean Square Error (RMSE): The RMSE measures the average difference between predicted values and actual values predicted by a model. It is computed as

$$\frac{\sqrt{\sum(y_i - \hat{y})2}}{N} \quad (8)$$

A value of root mean square error close to 1 indicates a good fit.

Robustness Coefficient (RC): This is defined as the ratio between the smallest and the largest final epidemic size. A value of RC close to 1 indicates a good model prediction. (Yang *et al.*, 2021).

Computations for Moran Index

$$I = \frac{N}{\sum W_{ij}} \times \frac{\sum i \sum j W_{ij}(X_i - \hat{X})(X_j - \widehat{X})}{\sum(X - \hat{X})2} \quad (9)$$

Where,

W = sum of all weights Wij or the spatial weights between i and j

N = number of spatial unit indexed i and j

X_i, X_j = the values for units i and j

$\underline{X}$ = mean of

Wij= Wij the elements of a matrix of spatial weight

$(X_i - X\hat{})(X(X_j - (X)\hat{}$ = The product of deviations from the mean of neighboring units

Test Statistic

$$Z_i = \frac{I - E(I)}{\sqrt{V(I)}} \quad (10)$$

$$\text{Where } E(I) = \frac{-1}{(n-1)}$$

$$Var(I) = E(I^2) - E(I)^2 \quad (11)$$

RESULTS AND DISCUSSION

Table 1 presents the summary statistics for SIR model where the total number found in the susceptible compartment represents the number of persons with no history of vaccination while the infected compartment represents incidences of clinically confirmed cases and manifestations of diphtheria, while the removed compartment represents the total number of deaths or those who had recovered from the ailment. The variance indicated a wide variation or gap in the data points and as such the mean is less representative of the data set this could have happened as a result of an outlier or some irregularity experienced during the process of data collection.

Table 1: Summary Statistics of the Data for SEIR Model

Compartment	Total	Number of observations	Minimum	Maximum	Mean	Variance	Standard deviation
Susceptible	50983	357	253	22293	142.81	2613966.31	1616
Infected	28395	357	111	13387	79.54	907073.98	952.4
Removed	1486	357	22	598	4.16	1911.21	43.72

Table 2 gives a description of the data for SEIR epidemic model with a cognizant attention been paid to the exposed population. These exposed population here is being defined as the category of persons who even though are infected, they are not yet infectious. The variance here also indicated a wide variation or gap between the data points and as such the mean is less representative of the data set which also suggests the presence of an outlier in the dataset.

Table 2: Summary Statistics of the Data for SEIR Model

Compartment	Total	Number of Observations	Minimum	Maximum	Mean	Variance	Standard Deviation
Susceptible	56,113	357	500	23,879	157.18	2,902,479.34	1,703.67
Exposed	50,983	357	253	22,293	142.81	2,613,966.31	1,616.00
Infected	28,395	357	111	13,387	79.54	907,073.98	952.4
Removed	1,486	357	22	598	4.16	1,911.21	43.72

Description of the Parameters of SIR/SEIR Model

Table 3: Parameters of SIR and SEIR Models

Parameters	Description	Computation	Source
Infectious rate (β)	This is defined as the rate of spread of an infection between a susceptible and an infectious individual.	$\beta = \Theta I/N$ where Θ is the contact rate and I/N is the proportion of infected individuals	Subhash Kumar Yadav and Yusuf Akhter.,2021
Incubation rate(σ)	This represents the incubation rate or the rate of latent individuals becoming infectious.	Where $1/\sigma$ is defined as average duration of days in incubation	Subhash Kumar Yadav and Yusuf Akhter.,2021
Recovery rate (ɣ)	This represents the rate of recovery or mortality due to the infection.	$\gamma = 1/D$ where D represents the rate of death.	Subhash Kumar Yadav and Yusuf Akhter.,2021

Parameter Estimates for SIR and SEIR Models

Table 4 provides the estimated parameter values for SIR model where a value of 0.14 was estimated for the rate of transmission which suggests that in every 0.5% proportion of an infected population of 1000 susceptible population with a contact of 28 persons, there will always be a minimum transmission rate of 0.14%. And a removal rate of 0.50 was estimated which indicated a 50% chance of recovery, death, or complete removal from the entire population.

Table 4: Estimates for SIR Model

Parameter	Parameter value	P value
Beta(β)	0.14	0.001
Gamma(ɣ)	0.50	0.001

Table 5 gives the estimated parameter value for SEIR Model, an estimated value of 0.42 was obtained for the rate of transmission which suggests that in every 0.5% proportion of infective population where there are 1000 susceptible with a contact of 84 persons, there will always be about 42 infections indicating a moderate rate of spread. An average latent period of 5 days was estimated in the model as an incubation rate which indicated the duration of time between being infected and becoming infectious.

Table 5: Estimates for SEIR Model

Parameter	Parameter value	P value
Beta(β)	0.14	0.001
Sigmma(σ)	0.20	0.002
Gamma(Ɣ)	0.50	0.001

Table 6 displays the RMSE which is the measured sum of the squared root difference between the actual values of a random variable and its corresponding predicted value by a model it helps to characterize the accuracy of a model's prediction. A RMSE close to 1 indicates a perfect prediction. Based on the above RMSE derived from the models, the SEIR model seems to have a better accuracy than the SIR model. On the other hand, the robustness coefficient (RC) which has been defined as the ratio between the smallest and the largest final epidemic size helps to quantify the consistency or reliability of an epidemic model's prediction. Both values of RC derived above gives an indication that both models are consistent and reliable, but however the SEIR model gives a more précised prediction.

Table 6: Model Evaluation Metrics

Model	RSME	RC
SIR	52	0.024
SEIR	37	0.030

Table 7: Summary of the Moran Index Results.

N	Total cases	µ	Weight	Moran index(I)	E(I)	VAR(I)	Zscore	P value
18	13379	743	60	-0.023	-0.058	2.39	0.0226	0.5199

From figure 1, the spatial autocorrelation represented among the distribution of confirmed cases giving a Zscore of 0.0226 indicates a random autocorrelation a situation where the values of confirmed cases are not related to each other based on spatial proximity.

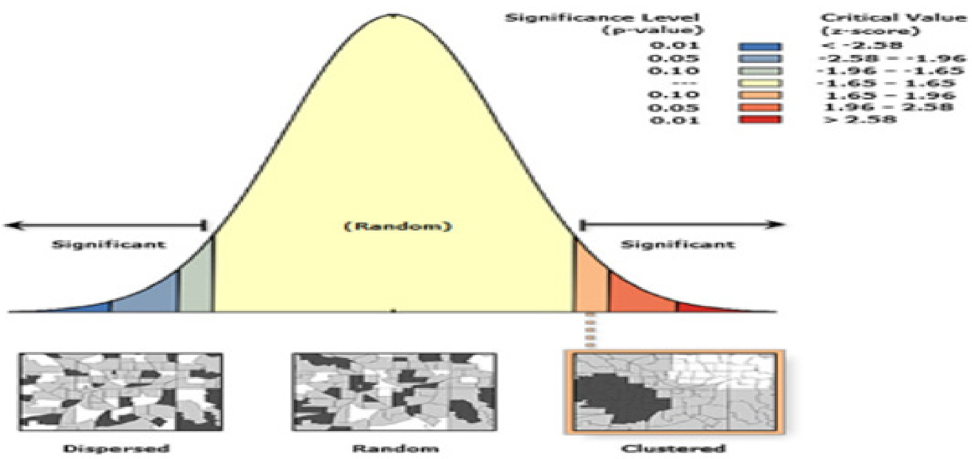

Figure 1: Interpretation of Moran Index

Graphical Representations of Models Results

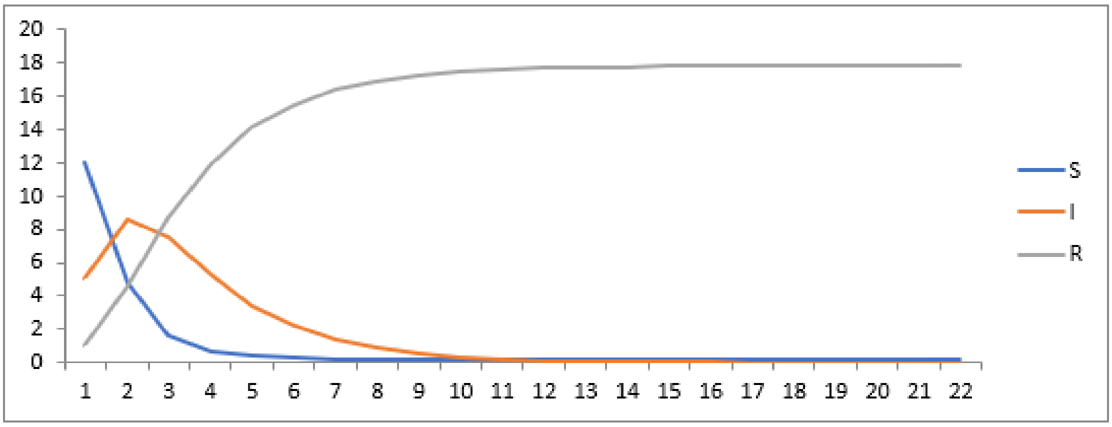

Figure 2 : Epidemic Wave Report by SIR Model

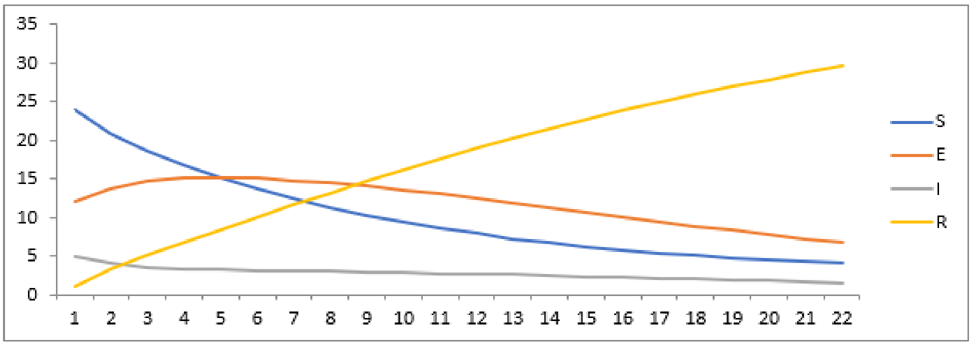

Figure 3 : Epidemic Wave Report by SEIR Model

Discussion of findings

The dynamics of the spread of Diphtheria described by the models revealed an epidemic pattern with a time varying rate of transmission (β).

at the early periods of the transmission, there was a continuous rise in the number of confirmed cases by week, which later became minimal due to factors such as increased awareness about its mode of transmission, other possible intervention measures employed by policy makers like the opening of isolation centers to reduce contacts with infected individual, deployment of diphtheria antitoxins in the rural settlements. At the last week of the epidemic wave, there was an indication that the rate of transmission has dropped drastically while the susceptible population continues to increase.

The statistic revealed by the Moran I indicate a weak spatial autocorrelation, which suggests that at 5% level of significance, there are no evidence to reject the null hypothesis, hence the study concludes that there is no spatial autocorrelation or association among the confirmed cases recorded in the cases presented above and as such, there could be other factors apart peculiar to geographical zones apart from poor vaccination history which may have aided the fast rate of transmission in the affected places.

CONCLUSION

The SIR and SEIR models have shown the interwoven relationship that existed within the compartments; various peaks of the infection dissemination were established according to the reported waves by the models, among the various peaks established, it was discovered that there were more incidences of infections recorded in the sixth wave than in the other waves. Based on the value of the basic reproduction number, a conclusion can be drawn that the rate of transmission of the disease has been curbed. Although the value of herd immunity indicated that a significant proportion of the population have not developed a strong immunity which puts the country at further risk should an incidence of its re-emergence should occur in the future and it was discovered as well that there was no spatial relationship among the confirmed cases. The distribution of the confirmed cases between the various states were random or all incidences of the confirmed cases happened as they were without any interference the other cases reported in the neighboring states as revealed by the Moran I statistics.

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