International Journal of Artificial Intelligence and Mathematical Sciences
June 2025 Vo4. Issue No. 01
e-ISSN: 2663-7073
DOI: https://doi.org/10.58921/ijaims.v4i1

Global dynamics of a staged progression model for whooping cough

[1*]Samuel Tosin Akinyemi, [2]Bigben Ogbuagu, [2]Mohammed Dago Maigemu, [2]Sani Fakai Abubakar

sammysalt047@gmail.com, bigbenogbuagu@gmail.com, mmdago70@gmail.com, saniabu2k9@yahoo.com

[1]Wigwe University, Isiokpo, Rivers State, Nigeria, [2]Department of Mathematics, Kebbi State University of Science & Technology, Aliero, Nigeria

Received: 13-02-2025; Accepted: 19-04-2025; Published: 1-7-2025

Abstract
This paper introduces a comprehensive stability analysis of a pertussis (whooping cough) model that incorporates staged disease progression. To examine the asymptotic and symptomatic behavior of the disease with respect the model's equilibria, a qualitative analysis of the model is conducted. The local stability of the disease-free equilibrium is demonstrated using the Jacobian stability method, demonstrating its local asymptotic stability. Additionally, the comparison method is utilized to demonstrate the global stability of the model, establishing that the disease-free equilibrium achieves global asymptotic stability when the basic reproduction number falls below one. Numerical simulations based on baseline data further validate the analytical results. Furthermore, the research explores the influence of varying some of the model parameters.

Keywords: Whooping cough disease; Mathematical model; Equilibria; Global Stability.

1. INTRODUCTION

According to Jamal et al., (2022), whooping cough, sometime referred to as pertussis, is an acute bacterial illness that affects the respiratory system and is contagious. It is a respiratory condition that ranks among the world's main causes of illness in both adults and children, even after decades of existence, it continues to be a major worry in the medical field in both industrialized and developing nations

*Email: sammysalt047@gmail.com

License Type: CC-BY
This article is open access and licensed under a Creative Commons Attribution 4.0 International License.
Published bi-annually by © Sindh Madressatul Islam University (SMIU) Karachi.

Less than a year-old infant, especially those under six months old, face the highest complications of disease and are a major victim of the illness and its mortality (De Cellès *et al*., 2018; Fabricius *et al.,* 2018; Tilahun *et al*., 2018; Stepanikova *et al*., 2024). The disease complications include apnea, pneumonia, convulsions, and even death.

Bordetella pertussis, a Gram-negative bacterium, is the causative agent of whooping cough. It is an airborne disease, as indicated in (Mattoo and Cherry, 2005; Koenig et al., 2019), the disease can travel through droplets in the air when an infected person coughs or sneezes. A healthy individual can contract the infection by breathing in the contaminated air. This result to infection of normal individual. Incubation period of the disease ranges from 7 to 10 days. While brain disease and convulsions are uncommon, pneumonia is a quite common side effect. It is characterized by coughing fits that last four to eight weeks which is very contagious in the three weeks of infection.

The history of whooping cough trace back to the late 15^{th} century (Bokhari et al., 2012), with the earliest documented outbreak occurring in France in 1578. A significant epidemic struck Cape Town in 1947, resulting in 107 fatalities (Joshi et al., 2019). In the early 2010s, outbreaks were reported in the USA, Ireland, and Israel. In 2014, California experienced over 10,000 cases of whooping cough, marking it as the most severe outbreak since 1947. According to a report published in 2014, there were about 24.1 million cases of whooping symmetry 2023, cough with 160,700 deaths in younger children around the world (Alqarni et al., 2022). In line with WHO, there were more than 151,000 whooping cough cases in 2018 (Alqarni et al., 2022).

Effective vaccination is essential for lowering the risk of whooping cough. Currently available vaccines include acellular vaccines made of highly purified whooping cough antigens and whole-cell vaccines made of inactivated Bortedella pertussis. In certain areas, adults are also given booster doses of whooping cough vaccine to strengthen their immune systems, and doses are given to expectant mothers to protect preterm infants. The scientific community has been very interested in mathematical modelling because of its ability to explain real-world occurrences and offer a deeper understanding of the system being studied. It has been used to represent problems in a variety of fields, including economics, chemistry, biology and physics (Ibragimov *et al.,* 2017; Serovajsky*,* 2021; Azizi, 2024). Primarily, mathematical models have been employed to furnish policymakers in the field of public health with enhanced comprehension regarding the unpredictable nature and dynamic transmission of many illnesses (Brauer *et al.,* 2019; Ullah *et al.,* 2020; Chahine *et al.,* 2024).

Ordinary differential equation-based Mathematical model can pinpoint factors that either inhibit or accelerate the spread of infectious diseases. These include; Pertussis (Ogbuagu *et al*., 2024), Monkeypox (Akinyemi et al., 2023; Manivel *et al*., 2024), Tuberculosis (Dago et al., 2015), Cholera (Abubakar and Ibrahim, 2022), Ebola (Wang et al., 2023; Akinyemi *et*

al., 2023), and HIV (Ibrahim *et al*., 2015; Ayoade *et al*., 2024; Odebiyi *et al*., 2024). Many of these mathematical models do not exhibit global stability, so suitable methods are frequently employed. Some mathematical models with stability analysis can be found in Akinyemi et al., 2016; Xu, 2011; Vargas-De-León, 2013; Sun et al., 2015; Gharahasanlou et al., 2022; Ji, 2014; Huang et al., 2012; Yakubu et al., 2021; Tan et al., 2015; Jenkins et al., 2020; Xuan et al., 2020; Carbonetti, 2015; Carrasquilla et al., 2020; Muloiwa et al., 2018 proposed that a mathematical model exhibiting local stability may not be stable for some initial condition and may seem to diverge after a small disturbance, thus global stability analysis are performed.

Consequently, since this study proposed a mathematical model with stability analysis, it is also crucial to apply the proper initial conditions to ensure stability of the analysis and prevent divergence as a result of disruption. Also, the investigation of the model's feasibility region and stability analysis is essential for generating an accurate predictive outcome (Keeling & Rohani, 2011; Brauer *et al.,* 2019; Muniyappan *et al*., 2022). This work aims to conduct a stability analysis of an updated mathematical model that builds upon the framework introduced by Aisha et al. (2020). Unlike the earlier model, this version incorporates both asymptomatic infected individuals and vaccination classes.

The aim of this paper is to examine and explore the dynamical behavior of the whooping cough model, specifically examining how different population groups interact under stability analysis. By integrating vaccination and asymptomatic infected classes, the model provides a deeper insight into the disease dynamic. The layout of this paper is as follows: Section 2 outlines the model formulation; Section 3 focuses on equilibrium states and stability analysis; Section 4 includes numerical simulations with result discussions; and Section 5 wraps up the study.

2. MODEL FORMULATION

In order to comprehend disease flow patterns and develop effective disease control measures, mathematical models of infectious disease are essential. Thus, it is crucial to concentrate on the steps involved in determining the disease's epidemiology and to figure out the most crucial and manageable characteristics for disease control when building a mathematical model for infectious diseases. This part presents an enhanced version of the model from Aisha et al. (2020), which strategies the total human population over time $Z(t)$ categorized into six separate and mutually exclusive subgroups: individuals with maternally derived immunity $Y_1(t)$, susceptible individuals $Y_2(t)$, vaccinated individuals $Y_3(t)$, asymptomatic individuals $Y_4(t)$, infectious individuals $Y_5(t)$, and recovered individuals $Y_6(t)$, so that

$$Z(t) = Y_1(t) + Y_2(t) + Y_3(t) + Y_4(t) + Y_5(t) + Y_6(t) \quad (1)$$

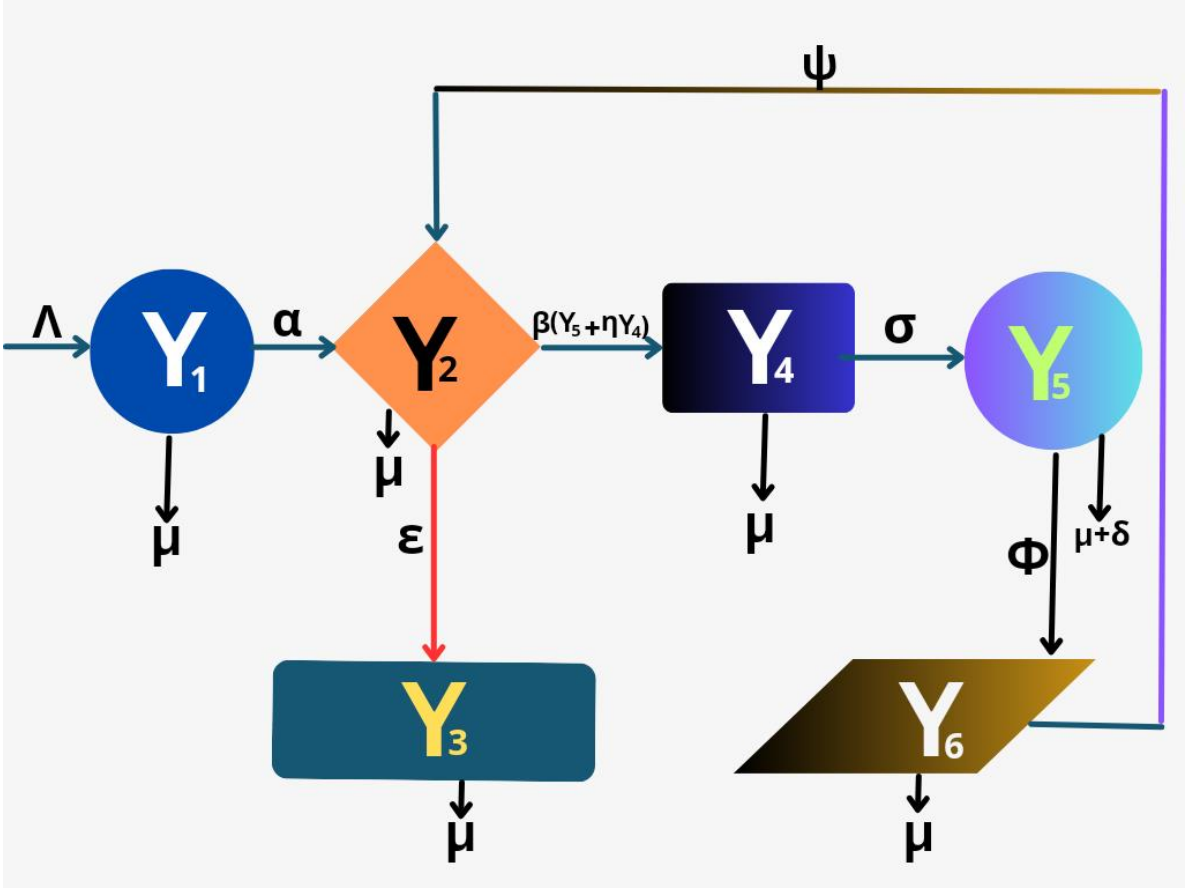

Fig. 1: Schematic diagram of the whooping cough model

Fundamental Assumption of the Model

The formulation of the model is based on the following assumptions:

1) The model considers a mass incidence function $\lambda = \beta(Y_5 + \eta Y_4)$
2) Only symptomatic humans are assumed to receive treatment.
3) There is no assumption of permanent immunity, transition from the R compartment to the S compartment is possible for individuals.
4) The birth rate and the death rate are not equal.
5) It is assumed that those who have had vaccinations are completely immune to whooping cough.

Therefore, the model is constructed as a nonlinear deterministic system with six equations:

$$\left.\begin{aligned}
\frac{dY_1}{dt} &= \Lambda - \alpha Y_1 - \mu Y_1 \\
\frac{dY_2}{dt} &= \alpha Y_1 - \varepsilon Y_2 - \beta(Y_5 + \eta Y_4)Y_2 - \mu Y_2 + \psi Y_6 \\
\frac{dY_3}{dt} &= \varepsilon Y_2 - \mu Y_3 \\
\frac{dY_4}{dt} &= \beta(Y_5 + \eta Y_4)Y_2 - \sigma Y_4 - \mu Y_4 \\
\frac{dY_5}{dt} &= \sigma Y_4 - \phi Y_5 - (\mu + \delta)Y_5 \\
\frac{dY_6}{dt} &= \phi Y_5 - \psi Y_6 - \mu Y_6
\end{aligned}\right\} \quad (2)$$

The simplified form of system (2) is expressed as:

$$\left.\begin{aligned}
\frac{dY_1}{dt} &= \Lambda - K_1 Y_1 \\
\frac{dY_2}{dt} &= \alpha Y_1 - (\lambda + K_2)Y_2 + \psi Y_6 \\
\frac{dY_3}{dt} &= \varepsilon Y_2 - \mu Y_3 \\
\frac{dY_4}{dt} &= \lambda Y_2 - K_3 Y_4 \\
\frac{dY_5}{dt} &= \sigma Y_4 - K_4 Y_5 \\
\frac{dY_6}{dt} &= \phi Y_5 - K_5 Y_6
\end{aligned}\right\} \quad (3)$$

Where $K_1 = \alpha + \mu$, $K_2 = \mu + \varepsilon$, $K_3 = \mu + \sigma$, $K_4 = \phi + \mu + \delta$, $K_5 = \psi + \mu$

Given the initial condition:

$$Y_1(0) \geq 0,\ Y_2(0) > 0,\ Y_3(0) \geq 0,\ Y_4(0) \geq 0,\ Y_5(0) \geq 0,\ Y_6(0) \geq 0$$

Table 1: Compartments and parameters Description

Y_1	Maternally Derived Immune individuals
Y_2	Susceptible individuals

Y_3	Vaccinated individuals
Y_4	Asymptotic infected individuals
Y_5	Infectious individuals
Y_6	Recovered individuals
Z	Total population
Λ	Recruitment of individuals
α	The movement from the passively immune group
ψ	The progression rate due to immunity loss
ε	Effectiveness of the vaccine
ϕ	Rate of treatment of the infected individuals
δ	whooping cough induce death rate
η	Adjustment parameter caused by infection
β	Rate of contact
μ	Natural death rate
σ	Rate at which asymptomatic becomes symptomatic infectious

Lemma 1: the close set $D=\left\{\left(Y_1,Y_2,Y_3,Y_4,Y_5,Y_6\right)\in \square_+^6 : Z\le \frac{\Lambda}{\mu}\right\}$ remains positively invariant and attracts with respect to system (3).

Proof

From (3) we note that $\frac{dZ}{dt}+\mu Z\le \Lambda$ and establish that $Z(t)\le \frac{\Lambda}{\mu}+e^{-\mu t}\left(Z(0)-\frac{\Lambda}{\mu}\right)$ using a standard comparison theorem (Lakshmikantham et al., 1989). It is shown that $Z(t)$ approaches $\frac{\Lambda}{\mu}$ as $t\to\infty$, ensuring that system (3) remains positively invariant and attracting within D. Therefore, the model holds significance from both mathematical and epidemiological perspectives in D (Hethcote, 2000), considering solutions in D is sufficient for the analysis.

3. EXISTENCE OF EQUILIBRIUM STATES

The disease-free equilibrium for system (3) is obtained as

$$\Theta = \begin{pmatrix} Y_{1,0} \\ Y_{2,0} \\ Y_{3,0} \\ Y_{4,0} \\ Y_{5,0} \\ Y_{6,0} \end{pmatrix} = \begin{pmatrix} \dfrac{\Lambda}{K_1} \\ \dfrac{\alpha\Lambda}{K_1K_2} \\ \dfrac{\varepsilon\alpha\Lambda}{\mu K_1K_2} \\ 0 \\ 0 \\ 0 \end{pmatrix}$$

To examine the stability of the model at Θ, the effective reproduction number R_e, will be applied. This is obtained through the application of the next-generation method described in (Hefferman et al., 2005), with F and G representing the matrices for new infection terms and transition terms at Θ, respectively. hence

$$F = \begin{pmatrix} \beta\eta\dfrac{\alpha\Lambda}{K_1K_2} & \beta\dfrac{\alpha\Lambda}{K_1K_2} \\ 0 & 0 \end{pmatrix} \qquad G = \begin{pmatrix} K_3 & 0 \\ -\sigma & K_4 \end{pmatrix} \tag{4}$$

$$R_e = \frac{\beta(\eta K_4 + \sigma)\alpha\Lambda}{K_1K_2K_3K_4} \tag{5}$$

$$R_e = R_{e1} + R_{e2} \tag{6}$$

Thus,

$$R_{e1} = R_e - R_{e2} \tag{7}$$

Where

$$R_{e1} = \frac{\beta\eta\alpha\Lambda}{K_1K_2K_3} \quad \text{and} \quad R_{e2} = \frac{\beta\alpha\Lambda\sigma}{K_1K_2K_3K_4} \tag{8}$$

3.1. LOCAL STABILITY ANALYSIS OF EQUILIBRIUM STATES

Theorem 1: The disease-free equilibrium of the system described in equation (3) is locally asymptotically stable if $R_e < 1$, whereas it becomes unstable if $R_e > 1$.

Proof

The Jacobian matrix of the system (3), evaluated at Θ is given as

$$J(\Theta)=\begin{bmatrix} -K_1 & 0 & 0 & 0 & 0 & 0 \\ \alpha & -K_2 & 0 & \frac{-\beta\eta\Lambda\alpha}{K_1K_2} & \frac{-\beta\Lambda\alpha}{K_1K_2} & \psi \\ 0 & \varepsilon & -\mu & 0 & 0 & 0 \\ 0 & 0 & 0 & \frac{\beta\eta\Lambda\alpha}{K_1K_2}-K_3 & \frac{\beta\Lambda\alpha}{K_1K_2} & 0 \\ 0 & 0 & 0 & \sigma & -K_4 & 0 \\ 0 & 0 & 0 & 0 & \phi & -K_5 \end{bmatrix} \quad (9)$$

The characteristic equation of (9) takes the form

$$=(K_1+\chi)(K_2+\chi)(\mu+\chi)(K_5+\chi)\left[\chi^2+a_1\chi+a_2\right]=0, \quad (10)$$

where χ represents the eigenvalue,

We have

$$a_1=K_3+K_4-\frac{\beta\eta\Lambda\alpha}{K_1K_2}$$

$$a_2=K_3K_4\left(1-\frac{\beta\Lambda\alpha(\eta K_4+\sigma)}{K_1K_2K_3K_4}\right)$$

Expressing a_1 and a_2 in terms of R_e, with aid of (4) and (6) to have

$$a_1=K_3+K_4(1-R_e+R_{e_2})$$

$$a_2=K_3K_4(1-R_e)$$

It is evident that all the roots of equation (10) are negative whenever $R_e<1$. Therefore, based on the Routh Hurwitz criterion, system (3) can be considered locally asymptotically stable as both and satisfy the stability criteria since $a_1>0$ and $a_2>0$. Epidemiologically, according to Theorem 1, controlling the spread of whooping cough in the society is achievable (when $R_e<1$) if the initial-population sizes of the model fall within the attraction region of the disease-free equilibrium Θ, otherwise, the disease will persist and spread within the population.

3.2. Global Stability Analysis of Equilibrium States

To demonstrate qualitatively that the system's dynamic behavior remains unchanged regardless of the initial subpopulation sizes, global stability analysis is done by comparison method as outlined by Okuonghae, (2012). Thus, the next result is ascertained.

Theorem 3: The disease-free equilibrium of system (3) is globally asymptotically stable whenever $R_e < 1$ and unstable if $R_e > 1$.

Proof

The comparison method requires making use of the F and G matrices expressed in (4) by writing the infected classes as

$$\frac{dX}{dt} = (F - G)X - JX,\ X = (Y_4, Y_5).$$

Where

$$F = \begin{pmatrix} \beta\eta \frac{\alpha\Lambda}{K_1 K_2} & \beta \frac{\alpha\Lambda}{K_1 K_2} \\ 0 & 0 \end{pmatrix} \text{ and } G = \begin{pmatrix} K_2 & 0 \\ -\sigma & K_3 \end{pmatrix}.$$

Then

$$J = \left(1 - \frac{Y_2}{Z}\right) \begin{pmatrix} \beta\eta \frac{\alpha\Lambda}{K_1 K_2} & \beta \frac{\alpha\Lambda}{K_1 K_2} \\ 0 & 0 \end{pmatrix}$$

J is a non-negative matrix since $Y_2(t) \le Z(t) \le \frac{\Lambda}{\mu}$, in the invariant set. Hence it follows that

$$\frac{dX}{dt} \le (F - G)X$$

Given that all eigenvalues of the matrix $F - G$ possess negative real parts, R_e<1. Hence, it can be inferred that the linearized differential inequality system retains stability whenever R_e<1, $(Y_4, Y_5, Y_6) \to (0,0,0)$ as $t \to \infty$. Substituting $Y_4 = Y_5 = Y_6 = 0$ in (3) gives $Y_2(t) \to Y_{2,0}$ as $t \to \infty$. Thus, $(Y_1(t), Y_2(t), Y_3(t), Y_4(t), Y_5(t), Y_6(t)) \to (Y_{1,0}, Y_{2,0}, Y_{3,0}, 0, 0, 0)$ $as \to \infty$ for R_e <1. Thus, Θ is globally asymptotically stable if $R_e < 1$.

4. NUMERICAL SIMULATION AND DISCUSSION OF RESULTS

This section addresses that the qualitative results for the new pertussis model presented in Section 4 are validated quantitatively (numerically). Thus, for the purpose of simulation, we choose $Y_1(0) = 76489400$, $Y_2(0) = 120197600$, $Y_3(0) = 13112470$, $Y_4(0) = 4150$, $Y_5(0) = 2190$, and $Y_6(0) = 7430401$ to be the initial condition for the model such that

the total population $Z \leq \frac{\Lambda}{\mu}$ and the value of the parameters presented in Table 1 are used to numerically simulate the model in MATLAB

Table 2: The values of population independent model parameters

S/N	Parameter	Description	Values	Source(s)
1.	Λ	Proportion of immunized individuals against infection	10140	Estimated
2.	α	Migration form M to S	0.02	Estimated
3.	ψ	Progression rate due to loss of immunity	0.02	Estimated
4.	ϕ	Treatment rate from I to R	(0,1)	Control parameter
5.	δ	Pertussis induced death rate	0.01	(WHO 2015)
6.	μ	Natural death rate	0.00005	Calculated
7.	β	Contact rate	(0,1)	(Yeung et al., 2017)
8.	ε	Vaccine efficacy	(0,1)	Control parameter
9.	η	Modification parameter due to infection	0.04	Skoff et al., (2015)
10.	σ	Rate at which close contacts becomes asymptotic infectious	0.048	Calculated

Fig. 2 Depicts the population profile of the asymptomatic infected human $Y_4(t)$ with respect to time in days. It reveals that when $R_e = 0.0150 < 1$, $Y_4(t) \to 0$ as $t \to \infty$ despite having different initial conditions. Furthermore, this validates the theoretical result presented by Theorem 3.2.

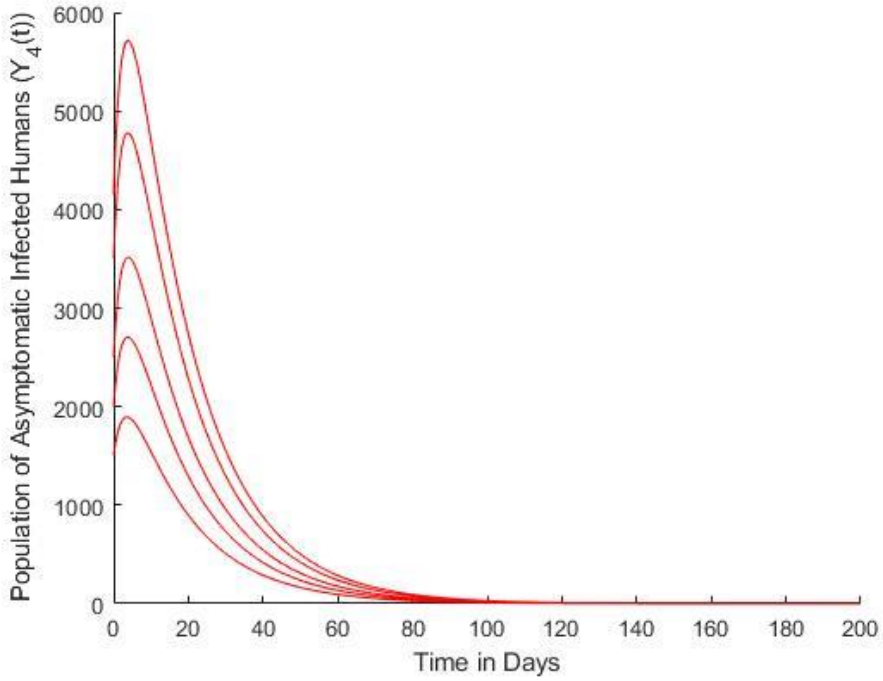

Fig. 2. Global Stability Result for $Y_4(t)$ when $R_e < 1$

The population profile for symptomatic humans $Y_5(t)$ against time in days is presented in Fig 3 and is generated by setting $\beta = 0.75 \times 10^{-7}$, $\varepsilon = 0.25$, $\phi = 0.25$ while Table 1 shows that the parameter values are fixed. The figure demonstrates that whenever $R_e = 0.0150 < 1$, then $Y_5(t) \to 0$ as $t \to \infty$. Hence validating Theorem 3.2.

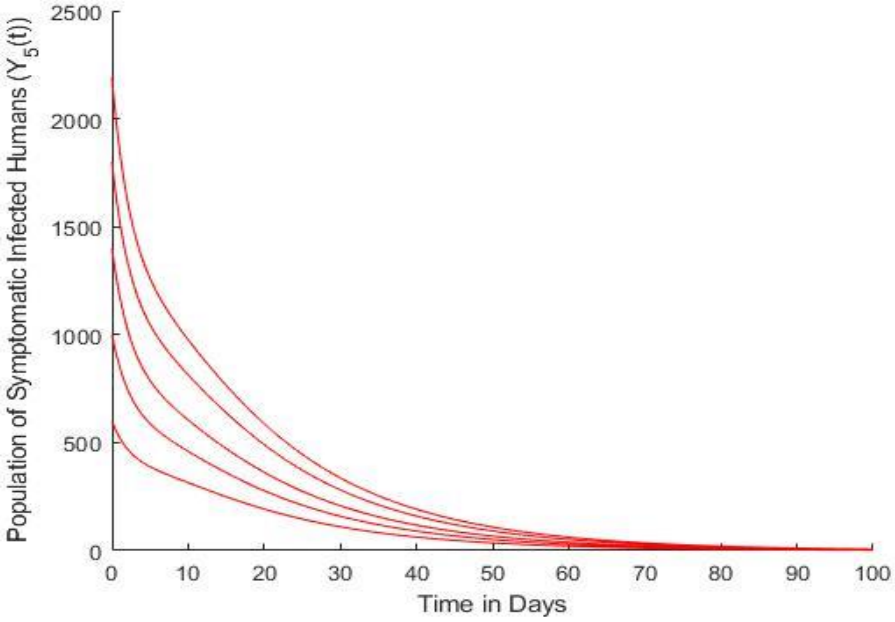

Fig. 3. Global Stability Result for $Y_5(t)$ when $R_e < 1$

The effect of varying the parameter value for β on the population dynamics of $Y_4(t)$ and $Y_5(t)$ against time in days are shown in Fig 4 and Fig 5 respectively. Both figures illustrate that as β increases, the population of $Y_4(t)$ and $Y_5(t)$ increases. This suggest that the number of those infected with whooping cough will increase as β increases. Hence, the implementation of control measures targeted to reduce the value of β should be encouraged and maintained.

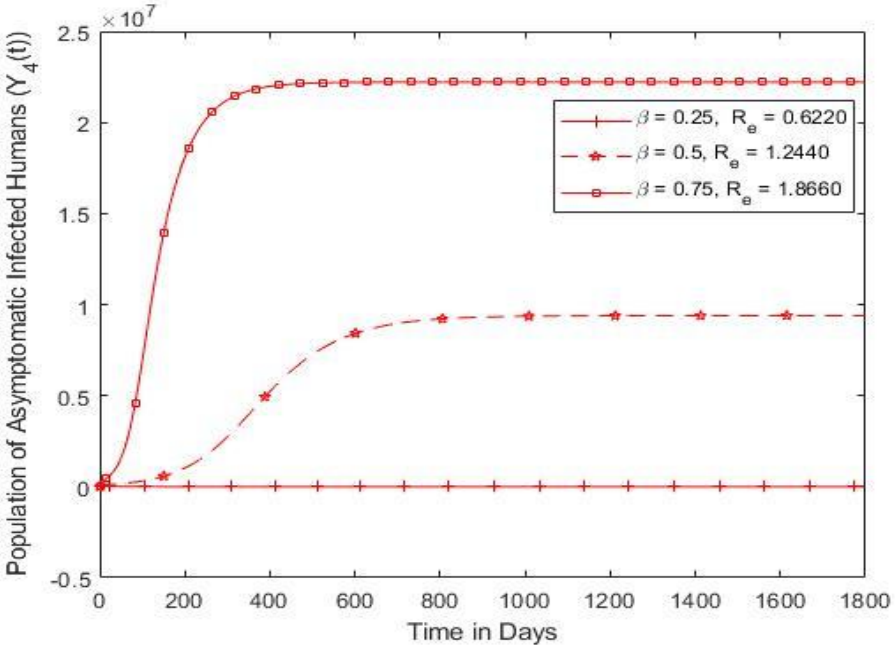

Fig. 4. Effect of varying β on $Y_4(t)$

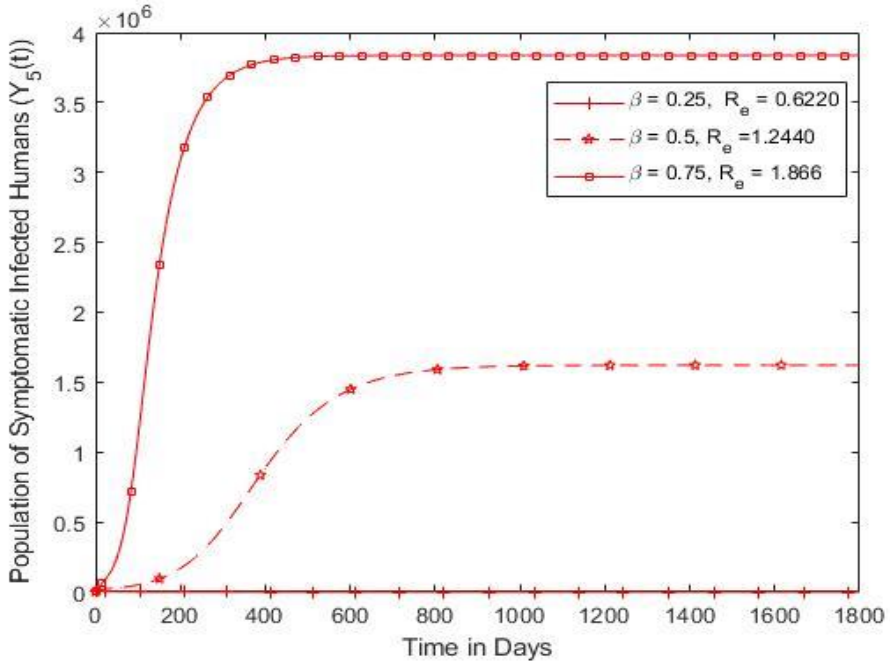

Fig. 5. Effect of varying β on $Y_5(t)$

To investigate the effect of the parameter $\mathcal{E}$ on the distribution of whooping cough, the population profile of $Y_4(t)$ and $Y_5(t)$ against time in days while varying the parameter value of $\mathcal{E}$ is displayed in Fig. 6 and Fig 7 correspondingly.

The figures demonstrate that as the value of $\mathcal{E}$ increases the population of both $Y_4(t)$ and $Y_5(t)$ reduces. This implies that parameter ε is a control measure needed to curb or reduce the menace of whooping cough in the society.

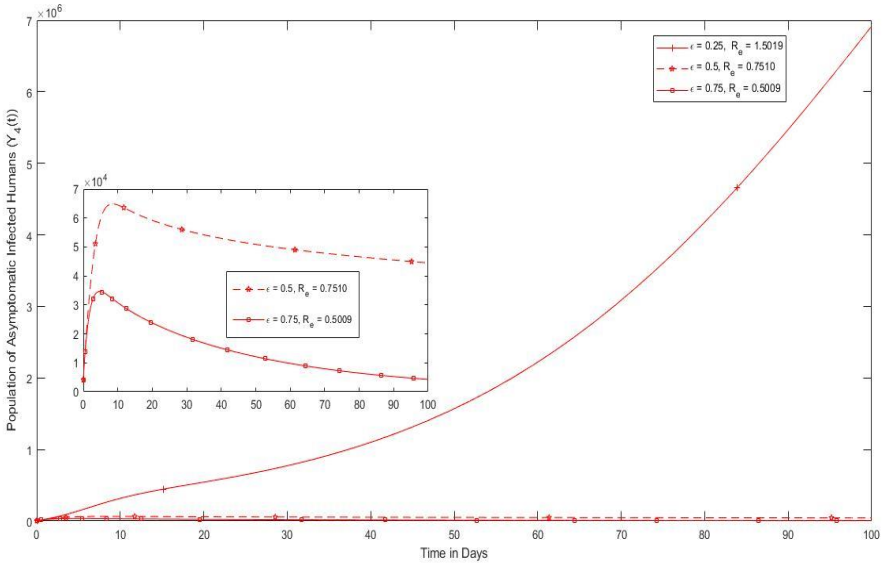

Fig. 6. Variation of $\mathcal{E}$ on the Asymptomatic Infected Humans

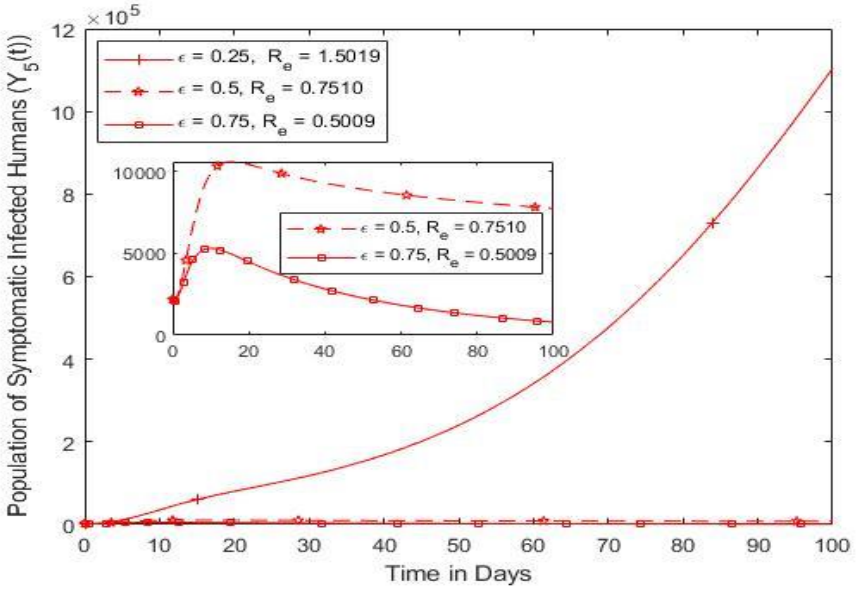

Fig. 7. Variation of $\mathcal{E}$ on the symptomatic infected Populations

The effect of changing the parameter value for ϕ on the population profile of $Y_4(t)$ and $Y_5(t)$ is explored through

numerical simulation and presented graphically by Fig 8 and 9. The figures depicts that increase in ϕ, reduces the number of those in $Y_4(t)$ and $Y_5(t)$ compartments. Consequently, ϕ is a control measure and should be implemented to reduce the prevalence of whooping cough

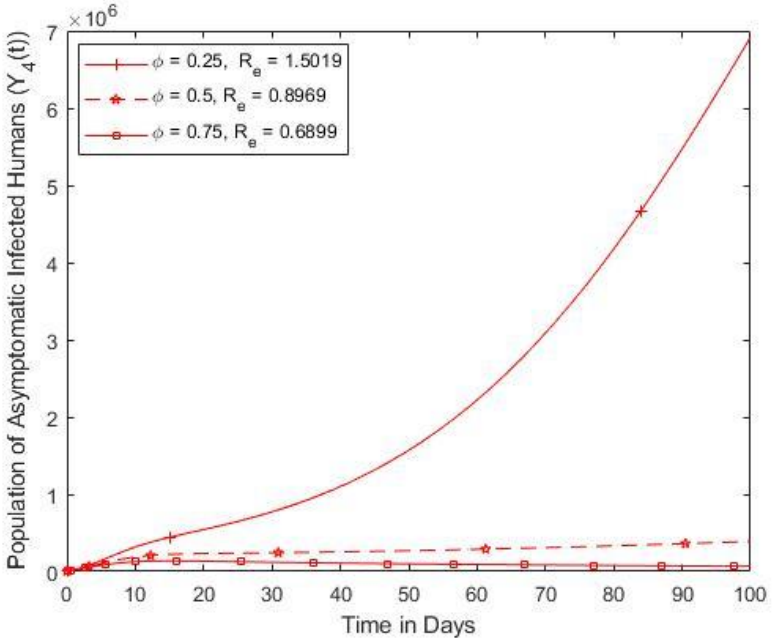

Fig. 8. Variation of ϕ on the Asymptomatic Infected Population

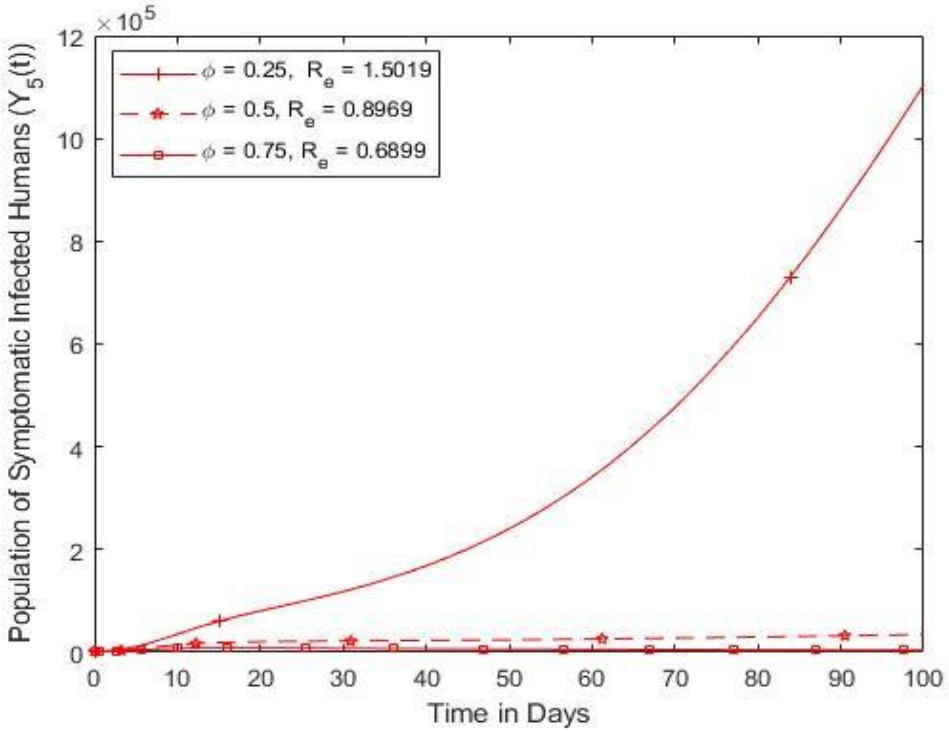

Fig. 9. Variation of ϕ on $Y_5(t)$

5. CONCLUSION

This paper examines the epidemiological aspects and global stability analysis of whooping cough, specifically incorporating asymptomatic infected and infectious classes. A non-linear model with six compartments was developed and analyzed to gain insights into the disease's behavior. The key findings are summarized below:

1. At the disease-free equilibrium, the model is globally asymptotically stable whenever the effective reproduction number R_e is less than unity.
2. Since a higher contact rate β would result in more people becoming infected, the implementation of control measure such as quarantine / isolation should be targeted towards reducing the value of β.
3. An improvement in vaccine effectiveness results to a decrease in the population of both the symptomatic and asymptomatic infected persons, this implies that vaccination is an essential control measure needed to curb or reduce the transmission of whooping cough in the society,
4. As explored through the numerical simulation presented graphically, the more treatment ϕ is administered, the more the individual in $Y_4(t)$ and $Y_5(t)$ compartments reduces. Consequently, treatment is a control measure and should be implemented to reduce the prevalence of whooping cough.

References

Abubakar, S. F., and Ibrahim, M. O. (2022). Optimal Control Analysis of Treatment Strategies of the Dynamics of Cholera. Journal of Optimization, 2022.

Aisha A.Y, Farah A. A, Ahmad I. I, and Yazariah M. Y. (2020). Dynamical Analysis on the Transmission of pertussis with Maternally Derived Immunity. Journal of mathematics and Statistics. Vol.16: 104. 112. DOI: 10.3844/jmssp.2020.104.112.

Akinyemi, S. T., Ibrahim, M. O., Usman, I. G., & Odetunde, O. (2016). Global stability analysis of sir epidemic model with relapse and immunity loss.

Akinyemi, S. T., Yemisi, O., Olarenwaju, I. M., and Bala, A. (2023). Approximate Solution of a Fractional-Order Ebola Virus Disease Model with Contact Tracing and Quarantine. Applied Mathematics and Computational Intelligence (AMCI), 12(1), 30-42.

Alqarni, M. M., Nasir, A., Alyami, M.A., Raza, A., Awrejcewicz, J., Rafiq, M., … and Mahmoud, E. E. (2022). A SEIR Epidemic Model of whooping cough-Like Infeciouss and its Dynamically Consistent Approximation. Complexity, 2022(1), 3642444.

Ayoade, A., Akinyemi, S., and Oyedepo, T. (2024). Minimization of HIV Infection among Nigerian Women through the Use of Microbicides: An Insight from Mathematical Modeling. **Journal of Advanced Mathematical Modeling**, 13(5), 1-22.

Azizi, T. (2024). 'Mathematical Modeling of Cancer Progression. AppliedMath, 4(3), 1065-1079.
Bokhari, H., bilal, I., and Zafar, S. (2012). BapC autotransporter protein of Bordetella pertussis is an adhesion factor. Journal of basic microbiology, 52(4), 390-396.

Brauer, F., Castillo-Chavez, C. and Feng, Z. (2019). Mathematical Models in Epidemiology; Springer: New York, NY, USA; Volume 32.

Carbonetti, N. H. (2015). Contribution of pertussis toxin to the pathogenesis of pertussis disease. Pathogens and disease, 73(8), ftv073.

Carrasquilla, G., Porras, A., Martinez, S., DeAntonio, R., Devadiga, R., Caceres, D. C., and Juliao, P. (2020). Incidence and mortality of pertussis disease in infants< 12 months of age following introduction of pertussis maternal universal mass vaccination in Bogotá, Colombia. Vaccine, 38(46), 7384-7392.

Chahine, M., Tzenios, N., & poh, O. B. J. (2024). How can mathematical models be used to predict the progression and impact of chronic diseases in the medical field?. Internalation journal of artificial intelligence, 4(07), 54-69.

Dago, M. M., Ibrahim, M. O., and Tosin, A. S. (2015). Stability Analysis of a Deterministic Mathematical Model for Transmission Dynamics of Tuberculosis. 5. International Journal of Advances in Science Engineering and Technology, ISSN, 2, 2321-9009.

De Cellès, M.D., Magpantay, F.M., King, A.A. and Rohani, P. (2018). The impact of past vaccination coverage and immunity on pertussis resurgence. Sci. Translat. Med., 10: 1748-1748. DOI: 10.1126/scitranslmed. aaj1748.

Fabricius, G., Aispuro P.M., Bergero P., Bottero D. and Gabrielli, M. (2018). Pertussis epidemiology in Argentina: TRENDS after the introduction of maternal immunisation. Epidemiol. Infect., 146: 858-866. DOI: 10.1017/S0950268818000808

Gharahasanlou, T. K., Roomi, V., and Hemmatzadeh, Z. (2022). Global stability analysis of viral infection model with logistic growth rate, general incidence function and cellular immunity. Mathematics and Computers in Simulation, 194, 64-79.

Hefferman, J., Smith, R., and Wahl, L. (2005). Perspectives on the basic reproduction ratio. Journal of the Royal Society interface 2, 281-293.

Hethcote, H.W. (2000). The mathematics of infectious diseases. SIAM Re-view. 42: 599-653

Huang, G., Beretta, E., and Takeuchi, Y. (2012). Global stability for epidemic model with constant latency and infectious periods. Mathematical Biosciences & Engineering, 9(2),297-312.

Ibragimov, R.N., Bakhtiyarov, S., and Zweigart, P. (2017). Correlation between three-dimensional sine sweep dynamics vibration testing and resonantly interacting internal gravity wave field. Mathematical Modelling of Natural Phenomena, 12(2), 62-93.

Ibrahim, M. O., Akinyemi, S. T., Dago, M. M., and Bakare, N. G. (2015). Mathematical Modelling of a Staged Progression HIV/AIDS Model with Control Measures. Journal of the Nigerian Association of Mathematical Physics, 29, 163-166.

Jamal, A., Jahan, S., Choudhry, H., Rather, I. A., and Khan, M.I. (2022). “A subtraction genomics-based approach to identify and characterize new drug targets in Bordetella pertussis: Whooping cough”. Vaccine, 10(11), 1915. 1-10.

Jenkins, V. A., Savic, M., and Kandeil, W. (2020). Pertussis in high risk groups: an overview of the past quarter century. Human vaccines & immune therapeutics, 16(11), 2609-2617.

Ji, Y. (2014). Global stability of a multiple delayed viral infection model with general incidence rate and an application to HIV infection. Mathematical Biosciences & Engineering, 12(3), 525-536.

Joshi, H. K., Sawant, S., and Rasaria, S. (2019). To assess the knowledge of Mothers in Relation to Selected Aspect of Immunization. Innovational: Journal of Nursing and Healthcare, 7-12.

Keeling, M. J., and Rohani, P. (2011). Modeling infectious diseases in humans and animals. Princeton University Press.

Koenig, K. L., Farah, J., McDonald, E. C., Thihalolipavan, S. and Burns, M. J. (2019). Pertussis: The identify, isolate,

inform tool applied to a re-emerging respiratory illness. Western Journal of Emergency Medicine, 20: 191-191. DOI: 10.5811/westjem.2018.11.40023

Lakshmikantham, V., Leela, S. and Martynyuk, A.A. (1989). Stability Analysis of nonlinear System. Marcel Dekker, Inc., New York and Basel.

Manivel, M., Venkatesh, A., Arunkumar, K., Prakash Raj, M., & Shyamsunder. (2024). A Mathematical Model of the Dynamicics of the Transmission of Monkeypox Disease Using Fractional Differential equations. Advanced theory and Simulations, 7(9), 2400330.

Mattoo, S. and Cherry, J.D. (2005). Molecular pathogenesis, epidemiology and clinical manifestations of respiratory infections due to Bordetella pertussis and other Bordetella subspecies. Clin. Microbiol. Rev., 18: 326-82. DOI: 10.1128/CMR.18.2.326-382.2005li

Muniyappan, A., Sundarappam, B., Manoharan, P., Hamdi, M., Raahemifar, K., Bourouis, S., & Varadarajan, V. (2022).

Stability and numerical solutions of second wave mathematical modeling on covid-19 and omicron and error analysis of approximate series solutions by using hpm. Mathematics, 10(3), 343.

Muloiwa, R., Wolter, N., Mupere, E., Tan, T., Chitkara, A. J., Forsyth, K. D., ... and Hussey, G. (2018). Pertussis in Africa: findings and recommendations of the Global Pertussis Initiative (GPI). Vaccine, 36(18), 2385-2393.

Odebiyi, O. A., Oladejo, J. K., Elijah, E. O., Olajide, O., Taiwo, A. A., & Taiwo, A. J. (2024). Mathematical Modeling on Assessing the impact of Screening of HIV/AIDS Transmission Dynamics. Journal of Applied Sciences and Environment Management, 28(8), 2347-2357.

Okuonghae, D. C. (2012). International Workshop on Mathematical Modeling and Simulations (IWMMAS). Mathematical analysis of epidemiological models for infectious diseases in the department of Mathematics, University of Benin city, Nigeria.

Ogbuagu, B., Maigemu, M. D., and Abubakar, S. F. (2024). Well-posedness of a novel mathematical model for pertussis with vaccination and asymptotic classes. Fudma journal of sciences, 8(3), 43-47.

Serovajsky, S. (2021). Mathematical Modelling; Chapman and Hall/CRC; Boca Raton, FL, USA.

Skoff, T. H., Kenyon, C. and Cocoros, N., Liko, J., Miller. L.,bKudish, K., …and Martin, S. W. (2015). Sources of infant pertussis infection in the United States. Pediatrics;136(4), 635-641.

Stepanikova, I., Baker, E., Oates, G., Acharya, S., Uddin, J., Thon, V., … & Kukla, L. (2024). Perinatal maternal stress and susceptibility to infectious diseases in later childhood: An early life programming perspective. In The psychology of Health and Illness (pp. 55-76). Routledge.

Sun, Q., Min, L., and Kuang, Y. (2015). Global stability of infection-free state and endemic infection state of a modified human immunodeficiency virus infection model. IET systems biology, 9(3), 95-103.

Tan, T., Dalby, T., Forsyth, K., Halperin, S. A., Heininger, U., Hozbor, D., ... and Von König, C. H. W. (2015). Pertussis across the globe: recent epidemiologic trends from 2000 to 2013. The Pediatric infectious disease journal, 34(9), e222-e232.

Tilahun, G.T., Makinde, O. D. and Malonza, D. (2018). Co-dynamics of pneumonia and typhoid fever diseases with cost effective optimal control analysis. Applied Math. Computer, 316: 438-459. DOI: 10.1016/j.amc.2017.07.063

Ullah, S., Ullah, O., Khan, M.A., and Gul, T. (2020). Optimal control analysis of tuberculosis (TB) with vaccination and treatment. Eur. Phys. J plus 2020, 135, 602.

Vargas-De-León, C. (2013). On the global stability of infectious diseases models with relapse. Abstraction and Application Magazine, 9, 50-61.

Wang, X., Li, J., Guo, S., and Liu, M. (2023). Dynamic analysis of an Ebola epidemic model incorporating limited

medical resources and immunity loss. Journal of Applied Mathematics and Computing, 69(6), 4229-4242.

WHO, (2015). Weekly epidemiological record Relevé épidémiologique hebdomadaire. World Health Organization
Xu, R. (2011). Global stability of an HIV-1 infection model with saturation infection and intracellular delay. Journal of Mathematical Analysis and Applications, 375(1), 75-81.a

Xuan, T. I. A. N., WANG, W. D., and Bo, L. I. (2020). Stability Analysis of a Pertussis Model with Family Factors. Journal of Southwest University, 42(3), 94-99.

Yakubu, A. A., Abdullah, F. A., Ismail, A. I. M., and Yatim, Y. M. (2021). Global stability analysis of pertussis transmission dynamics with maternally derived immunity compartment. In AIP Conference Proceedings 2423 (1). AIP Publishing.

Yeung, K.H.T., Duclos, P., Nelson, E.A.S., and Hutubessy, R.C.W. (2017). An update of the global burden of Pertusis in children younger than 5years: a modeling study. Lancet Infect Dis. 17(9):974-80. http://doi.org/10.1016/S1473-3 099(17)30390-0.