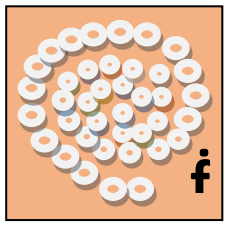

International Journal of Mathematical Analysis and Modelling

(Formerly Journal of the Nigerian Society for Mathematical Biology)

Volume 8 Issue 2, 2025

ISSN (Print): 2682 - 5694
ISSN (Online): 2682 – 5708
www.tnsmb.org

Human infertility due to undetected asymptomatic chlamydia infections: A mathematical modelling approach

T.T. Ashezua[*†], **R.I. Gweryina**[†] , and **F.D. Son-nen**[†]

Abstract

Chlamydia remains one of the commonest sexually transmitted infections (STIs) around the world, which has caused infertility and public health concern to many families and communities in both underdeveloped and developed countries. Chlamydia trachomatis has been observed to have negative health consequences in humans hence much research work is needed to avert the ugly trend of the disease in the population. In this work, a mathematical model for chlamydia, which splits the asymptomatic population into detected and undetected asymptomatic population is developed and analyzed. The reproduction number (R_c) was obtained using the next generation method. The model upon qualitative analysis exhibits the phenomenon of forward bifurcation near $R_c = 1$. The existence of forward bifurcation in the model shows that having the reproduction number less than one is enough pointer to guarantee the elimination of chlamydia in a community no matter the initial sizes of the infected subpopulation. Intuitively, this implies that the disease-free equilibrium of the model whenever $R_c < 1$ is globally asymptotically stable. Analytical and numerical results shows that the reproduction number (R_c) is a decreasing function of the treatment rate (τ_1). Results from sensitivity analysis reveal that the chlamydia transmission rates and treatment rate are the prominent parameters that significantly drive the dynamics of chlamydia in the population. A close attention should be paid on these parameters in order to check the spread of the disease in the population. Numerical simulation results suggest that a low detection rate (10%) of the asymptomatic individuals (i.e., from undetected to detected state) is a potential threat to human fertility, no matter the level of treatment given to the identified persons and thus not sufficient for Chlamydia elimination in about 40 years time. Further, it is also observed that a high detection rate (70%) of individuals infected with asymptomatic infection (from undetected to detected state) leads to the elimination of undetected asymptomatic individuals with the disease in the population in about 12 years time with the administration of sufficient treatment rate. Hence, identifying more cases of undetected asymptomatic individuals immediately for treatment will help in reducing human infertility due to chlamydia infections in families and communities. In that light, preventive measures and optimized treatment was introduced into the basic model to formulate the optimal control model. The Pontrayagin's maximum principle is utilized and the study shows that condom use and optimized treatment could be the best options for curbing the menace of chlamydia in the family and community cycles.

Keywords and phrases: Chlamydia; reproduction number; human infertility; stability; bifurcation

1 Introduction

Chlamydia trachomatis, a preventable and curable sexually transmitted infections (STIs), is one of the commonest STIs that can be contracted from anal, oral and vagina sex. Bacterium Chlamydia trachomatis is the major cause of the disease [9, 39, 10]. It is estimated in the year 2020 that, about 128.5 million new infections associated with Chlamydia trachomatis was reported worldwide amongst adults between 15 to 49 years of age and about 4.0 percent of the global prevalence were recorded for women and 2.5 percent for men [39]. Furthermore, reports from Statista indicate that in Africa about

*Corresponding Author; E-mail: timothy.ashezua@uam.edu.ng
†Department of Mathematics, Joseph Sarwuan Tarka University, P.M.B. 2373, Makurdi, Nigeria

25.5 million people had Chlamydia, with 14.7 million females and 10.8 million males infected with the disease [36].

The symptoms linked to chlamydia are often mild or absent and these include: In females, bleeding between menstrual period, abnormal discharge from the vagina, discomfort/pain in the lower abdomen while males experience burning sensation when urinating, discomfort/pain in the testicle and discharge from the penis [9, 39, 10, 33]. It is instructive to note that 70 percent of infected females and about 50 percent of males infected with the disease do not show symptoms [23, 34].

The World Health Organization (WHO) defined infertility as a disease of the male or female reproductive system characterized by the inability to achieve pregnancy after several attempts of unprotected sexual intercourse. This condition affects millions of people and has recorded negative consequences to many families and communities. Other details about infertility can be found in [39, 22].

Reports from Cleveland Clinic, indicate that most of the chlamydia cases are asymptomatic in nature, which means there are no signs or symptoms of infection and most of these cases go unreported (undetected) [33]. Individuals who do not know their asymptomatic status continue to infect others and subsequently become infertile, hence causing pain to their families/communities. Antibiotics are used to successfully treat Chlamydia infections in about a week or two. Apart from taking antibiotics, patients should avoid unprotected sexual activities while on medication to prevent re-infection. Susceptible individuals can avoid getting chlamydia by abstaining from anal, oral or vaginal sex with an individual who has a chlamydia infection. Individuals who can not abstain from sexual activities are advised to use condoms correctly to prevent them from contracting the disease [10].

Mathematical models on infectious diseases have been utilized over the years in providing useful insights into the transmission dynamics, prevention and control of infectious diseases [32]. Theoretical studies on numerous epidemic models are extensively discussed in [34, 32, 19, 35, 14, 4, 1, 17, 13, 27]. Research works on the use of mathematical models in studying the transmission dynamics, prevention and control of Chlamydia are very few [33]. For example, [21, 25] developed a discrete-time population-level models while [5, 30] designed a continuous-time models. A delayed differential equation model was formulated by [6]. In the works of Wilson [40, 41, 42], several differential equation models were developed for studying different aspects of Chlamydia dynamics in vivo. Further, [24, 37] designed Chlamydia models in various forms involving the use of an individually-based stochastic model and semi-parametric threshold regression analysis [43]. Also, [33, 34, 35] developed and rigorously analyzed a two group deterministic mathematical model for the spread of Chlamydia trachomatis in a population. Mushayabasa [26] designed and analyzed a co-infection deterministic mathematical model for assessing the epidemiological consequences of chlamydia-gonorrhea in a population. In another research work by Samanta and Sharma [31], a delayed chlamydia epidemic model with pulse vaccination was analyzed while Sharma and Samanta [32], formulated and analyzed a Chlamydia epidemic model using mass action incidence function.

Recently, [3] formulated and analyzed a mathematical model for chlamydia trachomatis transmission dynamics. In their work, the entire (sexually active) population at time t, denoted by $N(t)$, is compartmentalized into the susceptible individuals $(S(t))$, exposed individuals $(E(t))$, asymptomatic infected individuals $(I_a(t))$, symptomatic infected individuals $(I_s(t))$, treated individuals who failed treatment $Q(t)$ and individuals who recover from chlamydia infection due to successful treatment $(R(t))$. The model in [3] did not consider splitting the asymptomatic infected individuals into detected and undetected asymptomatic individual subgroups. It is also important to state that all other works on chlamydia transmission dynamics mentioned in this work did not also consider the splitting of the asymptomatic class as mentioned above to the best of our knowledge. The present study complements all the outlined research works (particularly the one by [3]) by developing and analyzing, a Chlamydia transmission model that considers the splitting of the asymptomatic class (individuals) into detected and undetected asymptomatic infected individuals, respectively. However, the compartment of treated individuals who failed treatment Q incorporated in [3] has been dropped in the current study. The reason is that the goal of the present study is to examine human infertility arising from undetected

asymptomatic infections (I_{au}) and not from individuals who failed treatment. This is because human infertility is largely attributed to: prolonged untreated chlamydia infection and undetected asymptomatic carriers. The failed treatment class (Q) does not directly contribute to the human infertility under investigation. It is worthy to mention that mathematically, including the (Q) compartment does not change the force of infection and the reproduction number structure in the present study.

The aim of this study therefore, is to explore from a mathematical modelling point of view the effect of undetected asymptomatic cases of chlamydia infections and to determine whether or not splitting the asymptomatic class (individuals) into detected and undetected asymptomatic individuals, respectively will change the qualitative (equilibrium) and quantitative dynamics of the chlamydia model presented in [3].

The paper is arranged as follows. The Chlamydia model is developed in section 2, and analyzed in section 3. Sensitivity and optimal control analysis of the model are presented in sections 4 and 5, respectively. Numerical simulations are conducted in section 6 and conclusion of the paper in section 7.

2 Model formulation

The total sexually active population at time t, denoted by $N(t)$, is compartmentalized into the susceptible $(S(t))$, exposed $(E(t))$, asymptomatic infected $(I_a(t))$, detected infected asymptomatic $I_{ad}(t)$, undetected infected asymptomatic $I_{au}(t)$, symptomatic infected $(I_s(t))$ and recovered $(R(t))$ individuals at time t, respectively.

It is assumed that Λ is the recruitment rate of newborns and individuals who are sexually active (assumed susceptible) into the susceptible class (S). The chlamydia transmission rates for infected individuals in I_a and I_s classes are represented by β_1 and β_2, respectively. Further, $\rho\eta$ and $(1-\rho)\eta$ represents the proportion of exposed individuals who are asymptomatic and symptomatic, respectively. Individuals in class I_a progress to class I_s at rate σ_1 and equally progress to classes I_{ad} and I_{au} at rates σ_2 and σ_3, respectively. The terms $\sigma_1 m$, $\sigma_2 m$ and $\sigma_3 m$ represent the proportion of individuals in class I_a who progress to classes I_s, I_{ad} and I_{au}, respectively. Also, the parameters τ_1 and τ_2 represents the treatment rates for individuals in classes I_s and I_{ad}, respectively while ψ is the recovery rate of individuals in class R. The parameter ϕ accounts for the rate of detection of undetected asymptomatically infected individuals. Furthermore, natural death rate μ occurs in all the classes.

Collectively, the above assumptions and definitions, the description of the state variables and parameters on Table 1 and schematic diagram shown in Figure 1, led to the following chlamydia model in (1):

$$\begin{aligned}
\frac{dS(t)}{dt} &= \Lambda - \lambda S - \mu S + \psi R,\\
\frac{dE(t)}{dt} &= \lambda S - [\rho\eta + (1-\rho)\eta + \mu]E,\\
\frac{dI_a(t)}{dt} &= \rho\eta E - [\sigma_1 m + \sigma_2 m + \sigma_3 m + \mu]I_a,\\
\frac{dI_{ad}(t)}{dt} &= \sigma_2 m I_a + \phi I_{au} - (\mu + \tau_2)I_{ad},\\
\frac{dI_{au}(t)}{dt} &= \sigma_3 m I_a - (\mu + \phi)I_{au},\\
\frac{dI_s(t)}{dt} &= (1-\rho)\eta E + \sigma_1 m I_a - (\mu + \tau_1)I_s,\\
\frac{dR(t)}{dt} &= \tau_1 I_s + \tau_2 I_{ad} - (\mu + \psi)R,
\end{aligned} \tag{2.1}$$

where,

$$\lambda = \Big(\frac{\beta_1 I_a + \beta_2 I_s}{N}\Big), \tag{2.2}$$

and

$$N(t) = S(t) + E(t) + I_a(t) + I_{ad}(t) + I_{au}(t) + I_s(t) + R(t). \tag{2.3}$$

In summary, Chlamydia model (1) is developed based on the assumptions below:

i. Allowing for the recovery of infected individuals who are successfully treated for chlamydia infection as reported in [39, 10].

ii. The asymptomatic individuals in class I_a are split into detected asymptomatic (I_{ad}) and undetected asymptomatic (I_{au}) individuals (classes), respectively. This assumption is in line with the information obtained from [39].

iii. The present study adopts the use of standard incidence function since it is more appropriate for large population as stated in [28].

iv. The chlamydia infection is a non lethal disease.

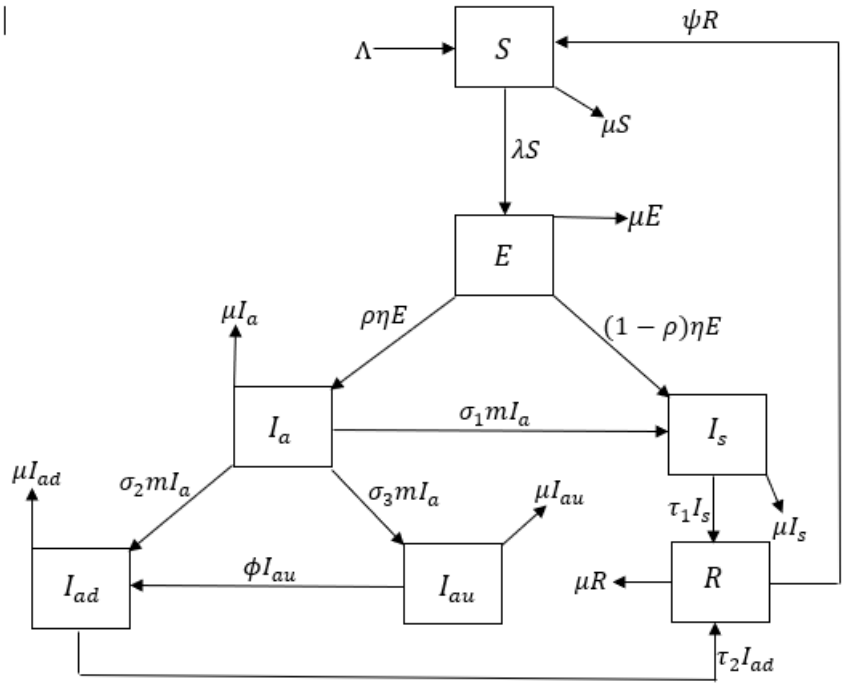

Figure 1: Schematic diagram for model (1)

2.1 Basic properties

For the model equations in (1) to be epidemiologically meaningful, it is vital to show that all its state variables are non-negative for all time t. That is, the solutions of the model equations in (1) with positive initial data will remain positive for all $t \geq 0$.

2.1.1 Positivity and boundedness of solution.

The model (1) deals with human population, so all its state variables and parameters are non-negative. The biologically feasible region in (4) is considered.

$$\Omega = \{(S, E, I_a, I_{ad}, I_{au}, I_s, R) \in \mathbb{R}^7_+ : N \leq \frac{\Lambda}{\mu}\}. \tag{2.4}$$

Table 1: Description of state variables/parameters of model (1).

Variables/parameters	Description
S	Susceptible population
E	Exposed population
I_a	Population of asymptomatic individuals
I_{ad}	Detected asymptomatic individuals
I_{au}	Undetected asymptomatic individuals
I_s	Symptomatic individuals
R	Recovered individuals
Λ	Recruitment rate
β_1	Transmission rate from I_a to S
β_2	Transmission rate from I_s to S
$\rho\eta$	Proportion of exposed individuals who are asymptomatic
$(1-\rho)\eta$	Proportion of exposed individuals who are symptomatic
μ	Natural death rate
ϕ	Rate of detection of undetected asymptomatic infection
τ_1	Treatment rate for individuals in I_s
τ_2	Treatment rate for individuals in I_{ad}
ψ	Wanning immunity rate
λ	Force of infection
$\sigma_1, \sigma_2, \sigma_3, \eta, m$	Progression rates
$\sigma_1 m, \sigma_2 m, \sigma_3 m$	Proportion of asymptomatic individuals who progresses to I_s, I_{ad} and I_{au} classes, respectively

It is proved in Lemma 2.1 that the set Ω is a positively invariant set and a global attractor of the system in (1). This implies that, any phase trajectory initiated anywhere in the non-negative region $\mathbb{R}^7_+$ of the phase space will eventually enter the region Ω and remains in Ω thereafter.

Lemma 2.1. *The region Ω is positively invariant for model (1).*

Proof. The rate of change of the total population is given by

$$\frac{dN}{dt} = \Lambda - \mu N. \tag{2.5}$$

Since the right hand side of (5) is bounded by $\Lambda - \mu N$, we can show using a standard comparison theorem [20] that

$$N(t) \leq N(0)exp^{-\mu t} + \frac{\Lambda}{\mu}\big(1 - exp^{-\mu t}\big). \tag{2.6}$$

Precisely, if $N(0) \leq \dfrac{\Lambda}{\mu}$, then $N(t) \leq \dfrac{\Lambda}{\mu}$. Therefore, Ω is positively invariant. Thus, no solution path escapes through any boundary of Ω and it is worth while to consider the dynamics of model (1) in Ω. In this region, the model can be considered as being mathematically and epidemiologically well posed [18].

3 Mathematical analysis

3.1 The disease-free equilibrium (DFE)

The model equations in (1) has a DFE given by $E_1 = (S^*, E^*, I_a^*, I_{ad}^*, I_{au}^* I_s^*, R^*) = \Big(\dfrac{\Lambda}{\mu}, 0, 0, 0, 0, 0, 0\Big)$. The next generation operator method is used to prove the linear stability of E_1 on the system (1) [11, 38]. By adopting the notations in [38], it follows that the matrices F and V, for the new infection terms and the remaining terms, respectively, are given by

$$F = \begin{pmatrix} 0 & \frac{\beta_1\Lambda}{\mu} & 0 & 0 & \frac{\beta_2\Lambda}{\mu} \\ 0 & 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 & 0 \end{pmatrix} \text{ and } \quad V = \begin{pmatrix} k_1 & 0 & 0 & 0 & 0 \\ -\rho\eta & k_2 & 0 & 0 & 0 \\ 0 & -\sigma_2 m & k_3 & -\phi & 0 \\ 0 & -\sigma_3 m & 0 & k_4 & 0 \\ -k_5 & -\sigma_1 m & 0 & 0 & k_6 \end{pmatrix},$$

where,

$$\begin{aligned} &k_1 = [\rho\eta + (1-\rho)\eta + \mu], k_2 = (\sigma_1 m + \sigma_2 m + \sigma_3 m + \mu), k_3 = (\mu + \tau_2), \\ &k_4 = (\mu + \phi), k_5 = (1-\rho)\eta, k_6 = (\mu + \tau_1). \end{aligned} \tag{3.1}$$

Hence, the reproduction number of the model (1), is given by

$$R_c = \rho(FV^{-1}) = \frac{\beta_1\Lambda\rho\eta}{\mu k_1 k_2} + \frac{\beta_2\Lambda(\eta m\rho\sigma_1 + k_2 k_5)}{\mu k_1 k_2 k_6}, \tag{3.2}$$

where $\rho(FV^{-1})$ is the spectral radius of the matrix (FV^{-1}).
Consequently, the result in Lemma 3.1 follows from Theorem 2 in [38].

Lemma 3.1. *The DFE (E_1) of the model (1) is locally asymptotically stable if $R_c < 1$ and unstable if $R_c > 1$.*

The threshold value, R_c is the reproduction number of chlamydia infection. By definition, it is the average number of secondary chlamydia infections produced by an infected individual in a completely susceptible population [38]. The Lemma 3.1 implies that when $R_c < 1$, the eradication of chlamydia in the population can be achievable so long as the initial sizes of the subpopulation of model (1) are in the basin of attraction of the DFE (E_1). Thus, a little influx of chlamydia-infected persons into

the population will not result into large chlamydia outbreaks, and the disease will diminish with time. Further, in order to guarantee that the disease eradication is independent of the initial sizes of the subpopulations, it is important to show that the disease-free equilibrium is globally asymptotically stable if $R_c < 1$.

Theorem 3.1. *The DFE (E_1) of the model (1) is globally asmptotically stable in Ω whenever $R_c \leq 1$.*

Proof. The infected classes in the model (1) can be written in the matrix-vector form as in (9):

$$\frac{dZ(t)}{dt} = \Big[(F-V) - \Big(1 - \frac{S}{N}\Big)W\Big]Z(t), \tag{3.3}$$

where $Z(t) = \big(E(t), I_a(t), I_{ad}(t), I_{au}(t), I_s(t), R(t)\big)^T$ and the matrices F and V are given in Section 3. Furthermore,

$$W = \begin{pmatrix} 0 & \frac{\beta_1\Lambda}{\mu} & 0 & 0 & \frac{\beta_2\Lambda}{\mu} \\ 0 & 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 & 0 \end{pmatrix}.$$

Since W is a nonnegative matrix and $S \leq N$ in Ω, it follows that

$$\frac{dZ(t)}{dt} \leq \big[(F-V)\big]Z(t). \tag{3.4}$$

By utilizing the fact that the eigenvalues of the matrix $F - V$ all have negative real parts (that is, $\rho(FV^{-1}) < 1$ if $R_c < 1$.), it follows that the linearized differential inequality (10) is stable so long as $R_c < 1$. Thus, by comparison theorem [20],

$$\lim_{t\to\infty} \big(E(t), I_a(t), I_{ad}(t), I_{au}(t), I_s(t), R(t)\big) = \Big(0,0,0,0,0,0\Big). \tag{3.5}$$

It can be shown by substituting (11) into (1) that, $S(t) \to \dfrac{\Lambda}{\mu}$, as $t \to \infty$. Hence,

$$\lim_{t\to\infty} \big(S(t), E(t), I_a(t), I_{ad}(t), I_{au}(t), I_s(t), R(t)\big) = \Big(\frac{\Lambda}{\mu}, 0,0,0,0,0,0\Big) = E_1. \tag{3.6}$$

Thus, every solution to the equation of the model (1) and initial conditions in Ω, approaches the DFE (E_1) as $t \to \infty$ whenever $R_c < 1$. It is important to state that the global stability result for the DFE in Theorem 3.1 is valid under the assumption of standard incidence and an asymptotically constant population (i.e., $N(t) \to \dfrac{\Lambda}{\mu}$), which is consistent with equation (5) and Lemma 2.1 [18].

3.2 Forward bifurcation analysis

3.2.1 Existence of unique endemic equilibrium

Here, the existence of a unique endemic equilibrium of model (1) is explored. To prove the existence of endemic equilibria of model (1), let $E_2 = \{S^{**}, E^{**}, I_a^{**}, I_{au}^{**}, I_{ad}^{**}, I_s^{**} R^{**}\}$ be any arbitrary equilibrium of the model equations in (1) and are solved in terms of the force of infection (FOI) at steady state to get

$$\begin{aligned} S^{**} &= \frac{\Lambda}{(\lambda^{**}M_2+\mu)}, E^{**} = \frac{\lambda^{**}\Lambda}{k_1(\lambda^{**}M_2+\mu)}, I_a^{**} = \frac{\lambda^{**}\Lambda M_3}{(\lambda^{**}M_2+\mu)}, I_{au}^{**} = \frac{\lambda^{**}\Lambda M_4}{(\lambda^{**}M_2+\mu)} \\ I_{ad}^{**} &= \frac{\lambda^{**}\Lambda M_5}{(\lambda^{**}M_2+\mu)}, I_s^{**} = \frac{\lambda^{**}\Lambda M_6}{(\lambda^{**}M_2+\mu)}, R^{**} = \frac{\lambda^{**}\Lambda M_0}{(\lambda^{**}M_2+\mu)}, \end{aligned} \tag{3.7}$$

where,

$$
\begin{aligned}
&k_1 = [\rho\eta + (1-\rho)\eta + \mu], k_2 = (\sigma_1 m + \sigma_2 m + \sigma_3 m + \mu), k_3 = (\mu + \tau_2),\\
&k_4 = (\mu + \phi), k_5 = (1-\rho)\eta, k_6 = (\mu + \tau_1), k_7 = \mu + \psi, M_1 = \psi M_0, M_2 = 1 - M_1\\
&M_3 = \frac{\rho\eta}{k_1 k_2}, M_4 = \frac{\sigma_3 m \rho\eta}{k_1 k_2 k_4}, M_5 = \frac{\eta m \rho(\phi\sigma_3 + k_4\sigma_2)}{k_1 k_2 k_3 k_4}, M_6 = \frac{(\eta m \rho\sigma_1 + k_2 k_5)}{k_1 k_2 k_6},\\
&M_0 = \frac{\left[\eta m \rho(\phi k_6\sigma_3\tau_2 + k_3 k_4\sigma_1\tau_1 + k_4 k_6\sigma_2\tau_2) + k_2 k_3 k_4 k_5\tau_1\right]}{k_1 k_2 k_3 k_4 k_6 k_7}.
\end{aligned}
\tag{3.8}
$$

The FOI at steady state, λ^{**} is expressed as

$$
\lambda^{**} = \frac{(\beta_1 I_a^{**} + \beta_2 I_s^{**})}{N^{**}}. \tag{3.9}
$$

The expressions in (13) and (14) are substituted into (15) to get

$$
(1 + \lambda^{**} M_7) = \frac{\beta_1\rho\eta k_6 + \beta_2(\eta m\rho\sigma_1 + k_2 k_5)}{k_1 k_2 k_6}
$$

which yields
$(1 + \lambda^{**} M_7) = \frac{\mu}{\Lambda} R_c$.
Further simplification shows that
$\lambda^{**} = \frac{1}{M_7}(\frac{\mu}{\Lambda} R_c - 1) > 0$, where $M_7 = \left(\frac{1}{k_1} + M_3 + M_4 + M_5 + M_6 + M_0\right)$.

Thus, a unique endemic equilibrium exists for model (1) whenever $R_c > 1$.

3.2.2 Existence of forward bifurcation analysis.

It is very important to categorize the type of bifurcation model (1) can exhibit. The following result is claimed.

Theorem 3.2. *Model (1) exhibits forward bifurcation at $R_c = 1$ whenever a bifurcation coefficient, denoted by a is negative.*

Proof. Suppose $E_2 = (S^{**}, E^{**}, I_a^{**}, I_{ad}^{**}, I_{au}^{**}, I_s^{**}, R^{**})$ is an arbitrary endemic equilibrium of model (1) (that is, an equilibrium where at least one of the infected components is non-zero). The existence of forward bifurcation will be explored using the centre manifold theory [7, 8]. In order to apply this theory, the following change of variables is performed. Let $S = x_1, E = x_2, I_a = x_3, I_{ad} = x_4, I_{au} = x_5, I_s = x_6$ and $R = x_7$. Also, the vector notation $X = (x_1, x_2, ..., x_7)^T$ is adopted, and model (1) is thus written in the form $\frac{dX}{dt} = F(X)$ with $F = (f_1, f_2, ..., f_7)^T$, as follows

$$
\begin{aligned}
\frac{dx_1}{dt} &\equiv f_1 = \Lambda - (\lambda + \mu)x_1 + \psi x_7,\\
\frac{dx_2}{dt} &\equiv f_2 = \lambda x_1 - k_1 x_2,\\
\frac{dx_3}{dt} &\equiv f_3 = \rho\eta x_2 - k_2 x_3,\\
\frac{dx_4}{dt} &\equiv f_4 = \sigma_2 m x_3 + \phi x_5 - k_3 x_4,\\
\frac{dx_5}{dt} &\equiv f_5 = \sigma_3 m x_3 - k_4 x_4,\\
\frac{dx_6}{dt} &\equiv f_6 = k_5 x_2 + \sigma_1 m x_3 - k_6 x_6,\\
\frac{dx_7}{dt} &\equiv f_7 = \tau_1 x_6 + \tau_2 x_4 - k_7 x_7.
\end{aligned}
\tag{3.10}
$$

where, $k_i, i = 1, 2, ..., 7$ are as earlier defined by equation (14) and, the FOI takes the form in (17)

$$\lambda = \frac{(\beta_1 x_3 + \beta_2 x_6)}{N}, \tag{3.11}$$

with $N = x_1 + x_2 + x_3 + x_4 + x_5 + x_6 + x_7$.
The case where $\beta_1 = \beta_2 = \beta^*$ is considered as the bifurcation parameter. Solving for $\beta_1 = \beta_2 = \beta^*$ from $R_c = 1$, yields

$$\beta_1 = \beta_2 = \beta^* = \frac{\mu k_1 k_2 k_6}{\Lambda[\eta\rho(m\sigma_1 + k_6) + k_2 k_5]}. \tag{3.12}$$

The Jacobian of the transformed system (16), evaluated at the DFE (E_1) with $\beta_1 = \beta_2 = \beta^*$, is given by

$$J^* = \begin{pmatrix} -\mu & 0 & -\beta^* & 0 & 0 & -\beta^* & \psi \\ 0 & -k_1 & \beta^* & 0 & 0 & \beta^* & 0 \\ 0 & \rho\eta & -k_2 & 0 & 0 & 0 & 0 \\ 0 & 0 & \sigma_2 m & -k_3 & \phi & 0 & 0 \\ 0 & 0 & \sigma_3 m & 0 & -k_4 & 0 & 0 \\ 0 & k_5 & \sigma_1 m & 0 & 0 & -k_6 & 0 \\ 0 & 0 & 0 & \tau_2 & 0 & \tau_1 & -k_7 \end{pmatrix}.$$

Matrix $J(E_1)$ has a right eigenvector given by $w = [w_1, w_2, w_3, w_4, w_5, w_6, w_7]^T$, where

$$\begin{aligned} w_1 &= -\frac{[\beta^*(w_3 + w_6) - \psi w_7]}{\mu}, \\ w_2 &= w_2 > 0, \\ w_3 &= \frac{\rho\eta}{k_2} w_2 > 0, \\ w_4 &= \frac{(\sigma_2 m w_3 + \phi w_5)}{k_3} > 0, \\ w_5 &= \frac{\sigma_3 m}{k_4} w_3 > 0, \\ w_6 &= \frac{(k_5 w_2 + \sigma_1 m w_3)}{k_6} > 0, \\ w_7 &= \frac{(\tau_2 w_4 + \tau_1 w_6)}{k_7} > 0. \end{aligned} \tag{3.13}$$

Furthermore, J^* has a left eigenvector, $v = (v_1, v_2, v_3, v_4, v_5, v_6, v_7)$, satisfying $v.w = 1$, with

$$\begin{aligned} &v_1 = 0, v_2 = v_2 > 0, v_3 = \frac{(\beta^* v_2 + \sigma_1 m v_6)}{k_2}, v_4 = v_5 = 0, \\ &v_6 = \frac{\beta^*}{k_6} v_2, v_7 = 0. \end{aligned} \tag{3.14}$$

It follows from Theorem 4.1 in [8], if we compute the associated non-zero partial derivatives of $F(X)$ at the DFE (E_1), and the associated bifurcation coefficients, a and b, defined by

$a = \sum_{k,i,j=1}^{7} v_k w_i w_j \frac{\partial^2 f_k}{\partial x_i \partial x_j}(E_1)$,

and

$b = \sum_{k,i=1}^{6} v_k w_i \frac{\partial^2 f_k}{\partial x_i \partial \beta^*}(E_1)$

are computed to be

$a = -\frac{2\beta^* \mu v_2}{\Lambda}[(w_3 + w_6)(w_2 + w_4 + w_5 + w_7) + w_3(w_3 + 2w_6) + w_6^2] < 0$

and
$b = v_2(w_3 + w_6) > 0.$
It is instructive to note that the eigenvectors $v_2, w_2, w_3, ..., w_7$ are all positive. Hence, it follows from Theorem 4.1 in [8] that model (1), or the transformed model (16) exhibits a forward bifurcation at $R_c = 1$. As stated in [12], the epidemiological implication of forward bifurcation is that the DFE loses its stability and a stable endemic equilibrium surfaces whenever the associated reproduction number is slightly greater than one.

4 Sensitivity Analysis

Sensitivity analysis (SA) is performed on the parameters of model (1) using the parameter values in Table 2. The aim of this analysis is to determine the relative importance of each parameter in the model that depicts Chlamydia transmission dynamics. A method similar to the ones outlined in the works of [3, 29, 2] were utilized to obtain the sensitivity index of all the parameters connected to the reproduction number using the formula in (21).

$$\Upsilon_{\gamma}^{R_c} = \frac{\partial R_c}{\partial \gamma} \times \frac{\gamma}{R_c}, \tag{4.1}$$

where γ denotes model parameters contained in R_c. The sensitivity indices of the parameters of the model are as presented in Table 3. The parameters with the largest positive indices are β_1 and β_2 thus making them the key drivers of chlamydia transmission in the population as their values keep increasing. Also, the parameter whose sensitivity index is negative and has a great potential in reducing chlamydia burden in the population is τ_1 especially as its value keeps growing.

From the results of the SA presented in Table 3, some of the parameters with high positive indices are the transmission rates of chlamydia infection from infectives in the asymptomatic and symptomatic infection stages, denoted by β_1 and β_2, respectively while the treatment rate (τ_1) shows a negative indices. These parameters significantly determine whether the dynamics of Chlamydia in the population will persist or not. Consequently, to curb the spread of the disease in the population, these parameters must be adequately targeted by policy makers in the health sector for the effective control of chlamydia. In Figure 2, a global sensitivity analysis is performed and the results show that β_1, β_2 and τ_1 significantly drive the dynamics of chlamydia burden (that is, the persistence or otherwise) in the population. It is worthy to state that absolute care should be in the estimation of these parameters as absence of precision in the estimation of these model parameters can lead to uncertainties and even affect the value of the reproduction number.

Therefore, graphical illustration of the sensitivity indices in Table 3 is presented in Figure 2.

Table 2: The parameter values of model (1)

Parameter	Nominal value ($year^{-1}$)	Reference
Λ	1000	[34]
β_1	0.1	[32]
β_2	0.15	[32]
μ	0.014	[33]
ρ	0.70	[33]
η	0.50	[32]
ϕ	0.70	Assumed
τ_1	0.85	Assumed
τ_2	0.70	Assumed
$\sigma_1, \sigma_2, \sigma_3, m$	0.50	Implied from [32]
ψ	0.60	[32]

Table 3: Sensitivity indices of some parameters values

Parameter	Sensitivity indices
β_1	$+0.4994$
β_2	$+0.5006$
ρ	$+0.0537$
η	$+0.0272$
σ_1	-0.0176
σ_2, σ_3	-0.2343
τ_1	-0.4925
m	-0.4863

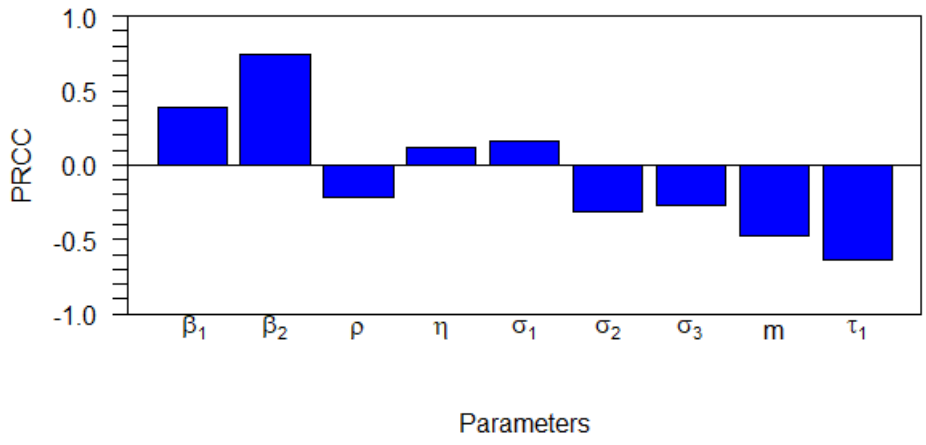

Figure 2: Plot of sensitivity indices of parameters on R_c

5 Optimal control analysis

Here, we are most concerned in finding the optimal control measures of curbing Chlamydia transmission based on the global sensitivity assessment. It is clear that with the base treatment value in Table 2, the disease seems to persistent since $R_c = 1.2111 > 1$. Therefore, to minimize the infected population size, optimal preventive and curative controls listed below are needed to be included into the basic chlamydia model in Equation (1).

u_1 : Preventive measures such as use of condoms to protect susceptible from contracting Chlamydia infections from asymptomatic and symptomatic individuals.

u_2 : Optimal treatment control for treating the detected asymptomatic and symptomatic individuals

Thus, with the above measures, the Chlamydia model (1) now take the form as in equation (22)

$$\begin{aligned}
\frac{dS(t)}{dt} &= \Lambda - (1-u_1(t))(\frac{\beta_1 I_a + \beta_2 I_S}{N})S - \mu S + \psi R,\\
\frac{dE(t)}{dt} &= (1-u_1(t))(\frac{\beta_1 I_a + \beta_2 I_s}{N})S - [\rho\eta + (1-\rho)\eta + \mu]E,\\
\frac{dI_a(t)}{dt} &= \rho\eta E - (m\sum_{i=1}^{3}\sigma_i + \mu)I_a,\\
\frac{dI_{ad}(t)}{dt} &= \sigma_2 m I_a + \phi I_{au} - (\mu + \tau_2 + u_2(t))I_{ad},\\
\frac{dI_{au}(t)}{dt} &= \sigma_3 m I_a - (\mu + \phi)I_{au},\\
\frac{dI_s(t)}{dt} &= (1-\rho)\eta E + \sigma_1 m I_a - (\mu + \tau_1 + u_2(t))I_s,\\
\frac{dR(t)}{dt} &= (\tau_1 + u_2(t))I_s + (\tau_2 + u_2(t))I_{ad} - (\mu + \psi)R,
\end{aligned} \tag{5.1}$$

where N is defined by equation (3) subject to the initial conditions $S(0) = S_0, I_a(0) = I_a^0, I_{ad}(0) = I_{ad}^0, I_{au}(0) = I_{au}^0, I_s(0) = I_s^0$ and $R(0) = R_0$.
The aim of the optimal control is to minimize the number of Chlamydia infected individuals using the combined linear and quadratic form of the objective functional given by equation (5.2)

$$J(u_1, u_2) = \int_0^T \Big[h_1 E + h_2 I_{ad} + h_3 I_{au} + m_1 I_a + m_2 I_s + \sum_{i=1}^{2}\frac{c_i}{2}u_i^2\Big]dt, \tag{5.2}$$

where T is the maximum time for implementing the controls. $h_i, i = 1, 2, 3$ are the positive balancing constants, m_1 and m_2 refers to the weight constants associated with individuals in class I_a and I_s, respectively. c_1 and c_2 are the cost constants corresponding to the controls u_1 and u_2, respectively. The choice of the objective functional follows from [16]. When $c_i = 0$ indicates no implementation of the control u_i while $c_i = 1$ implies complete usage of the control u_i. Note that when $c_i = 0$ in equation (5.2), the dynamics of the chlamydia model is dominated by infected individuals and the disease remain endemic even after period T. Further, the quadratic form $\frac{c_i}{2}u_i^2$ is standard in optimal control to reflect increasing marginal costs and prevent unrealistic solutions. Applying the Pontryagin's maximum principle as used by the authors [14, 16, 15], we obtain the optimal controls $(u_1^*, u_2^*) \in U$ such that equation (5.3) is met.

$$J(u_1^*, u_2^*) = min\{J(u_1, u_2) \mid (u_1, u_2) \in U\} \tag{5.3}$$

alongside the Hamiltonian function

$$H = h_1 E + h_2 I_{ad} + h_3 I_{au} + m_1 I_a + m_2 I_s + \sum_{i=1}^{2}\frac{c_i}{2}u_i^2 + \sum_{i=1}^{6} g_i y_i, \tag{5.4}$$

where y_i is the ith right hand side of equation (5.1) and g_i is the ith adjoint that satisfy the co-state functions given below

$$g_i' = -\frac{\partial H}{\partial x_i}, i = 1, 2, ..., 6 \tag{5.5}$$

where $x_1 = S, x_2 = E, x_3 = I_a, x_4 = I_{ad}, x_5 = I_{au}, x_6 = I_s$ and $x_7 = R$, and the expanded form of (5.5) is as follows

$$\begin{aligned}
g_1' &= (g_1 - g_2)(1 - u_1(t))(\frac{\beta_1 I_a + \beta_2 I_s}{N})(1 - \frac{S}{N}) + g_1\mu, \\
g_2' &= -h_1 + (g_2 - g_1)(1 - u_1(t))(\frac{\beta_1 I_a + \beta_2 I_s}{N})\frac{S}{N} + \rho\eta(g_2 - g_3) + (1 - \rho)\eta(g_2 - g_6) + g_2\mu, \\
g_3' &= -m_1 + (g_2 - g_1)(1 - u_1(t))(\beta_1 - \frac{\beta_1 I_a + \beta_2 I_s}{N})\frac{S}{N} + m(\sigma_1(g_3 - g_6) + \sigma_2(g_3 - g_4) + \sigma_3(g_3 - g_5)) + g_3\mu, \\
g_4' &= -h_2 + (g_2 - g_1)(1 - u_1(t))(\frac{\beta_1 I_a + \beta_2 I_s}{N})\frac{S}{N} + (\tau_2 + u_2(t))(g_4 - g_7) + g_4\mu, \\
g_5' &= -h_3 + (g_2 - g_1)(1 - u_1(t))(\frac{\beta_1 I_a + \beta_2 I_s}{N})\frac{S}{N} + \phi(g_5 - g_4) + g_5\mu, \\
g_6' &= -m_2 + (g_2 - g_1)(1 - u_1(t))(\beta_2 - \frac{\beta_1 I_a + \beta_2 I_s}{N})\frac{S}{N} + (g_6 - g_7)(\tau_1 + u_2(t)) + g_6\mu, \\
g_7' &= (g_2 - g_1)(1 - u_1(t))(\frac{\beta_1 I_a + \beta_2 I_s}{N})\frac{S}{N} + \varphi(g_7 - g_1) + g_7\mu,
\end{aligned} \tag{5.6}$$

and the final conditions $g_i(T) = 0, i = 1, 2, ..., 7$.
At this point, the optimal conditions are given by equation (5.7)

$$\frac{\partial H}{\partial u_1^*} = 0, \frac{\partial H}{\partial u_2^*} = 0, \tag{5.7}$$

from which the following optimal controls in equation (5.8) are obtained

$$\begin{aligned}
u_1^* &= max\{0, min(1, (g_2 - g_1)\frac{(\beta_1 I_a + \beta_2 I_s)S}{N c_1}))\}, \\
u_2^* &= max\{0, min(1, \frac{(g_4 - g_7)I_{ad} + (g_6 - g_7)I_s}{c_2})\}.
\end{aligned} \tag{5.8}$$

The numerical results of the optimal controls in equation (5.1) is discussed in the next section.

6 Numerical Simulations

Numerical simulations are performed on model (1) by utilizing the parameter values in Table 2. The model (1) is solved numerically using MATLAB ODE45 solver. Figure 3 shows the effect of low detection rate of individuals from the undetected to the detected classes of asymptomatic stages of chlamydia infection. A low rate of 10% detection of individuals infected with asymptomatic infection (from undetected to detected state) when treatment is applied leads to the continued existence of undetected individuals with the disease in the population as shown in Figure 3 (d). This implies that chlamydia may possible remain in the population for life thus causing infertility as a result of prolonged stay of the disease in the human body without treatment. Figure 4 on the other hand shows the effect of high detection rate of individuals who are infected with the disease in the undetected to the detected classes of asymptomatic stages of chlamydia infection. A high rate of detection of individuals infected with asymptomatic infection (from undetected to detected state) leads to the timely elimination of undetected individuals with the disease in the population as shown in Figure 4 (d). In fact, the elimination of chlamydia in the population is achievable in about 12 years time, provided the detection rate of those infected with the disease is high. Hence, concerted effort should be put in place by health workers to see that every individual who comes to the health facility for medical check up are tested for chlamydia

infection. This will help reduce the number of asymptomatic cases in the population hence reducing the number of infertility cases in families and communities as noted in [10]. Consequently, infected persons undergoing treatment or those who have successfully completed treatment are encouraged not to engage in any form of unprotected sexual activity until at least 7 days after treatment or correctly use condoms to avoid reinfection.

We demonstrate numerically in Figures 5, the relationship between the treatment rate (τ_1) and the reproduction number (R_c). The reproduction number (R_c) is plotted as a function of the treatment rate (τ_1). From Figure 5, it is observed that an increase in the treatment rate of individuals in the symptomatic stage of infection leads to a decrease in the reproduction number.

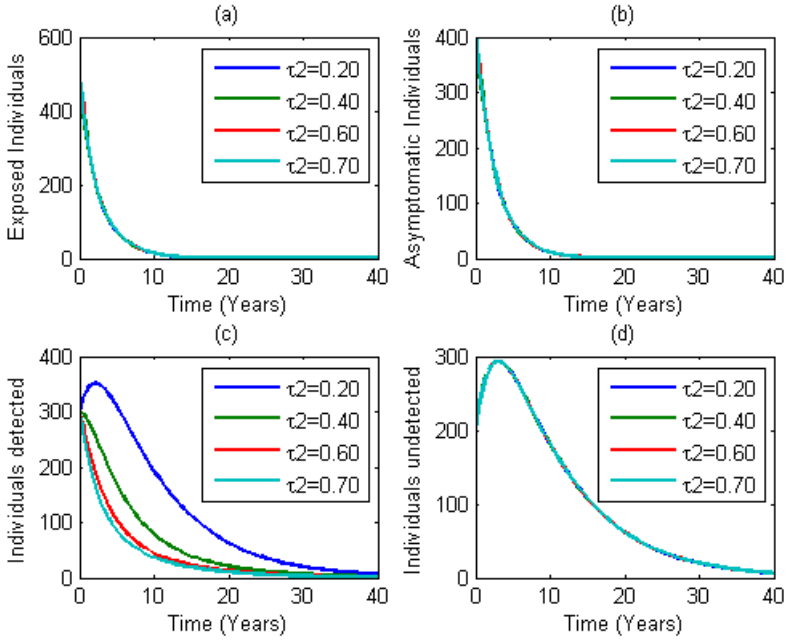

Figure 3: Simulation of model (1) showing the effect of low detection rate (ϕ) from the undetected to detected infected individuals. Here, τ_2 is varied from 0.20 to 0.70 with $\phi = 0.10$.

6.1 Impact of optimal control on the model

Here we numerically investigate the impact of the following control,strategies on the spread and transmission of chlamydia disease.

Strategy 1: use of condoms only

Strategy 2: use of treatment control only

Strategy 3: combination of the use of condoms and treatment controls

The above strategies are implemented using the forward backward scheme [15]. We assume that $c_1 < c_2$ since the cost of buying condoms is cheaper than treating infected people with chlamydia. To this end, we have $c_1 = 20$ and $c_2 = 95$. The balancing constants are taken to be $h_1 = 10, h_2 = h_3 = 20, m_1 = 50$ and $m_2 = 23$. The parameter values are as given in Table 2. The initial subpopulations are chosen as $S(0) = 1200, E(0) = 500, I_a(0) = 10, I_{au}(0) = 23, I_{ad}(0) = 25, I_s(0) = 10$ and $R(0) = 25$.

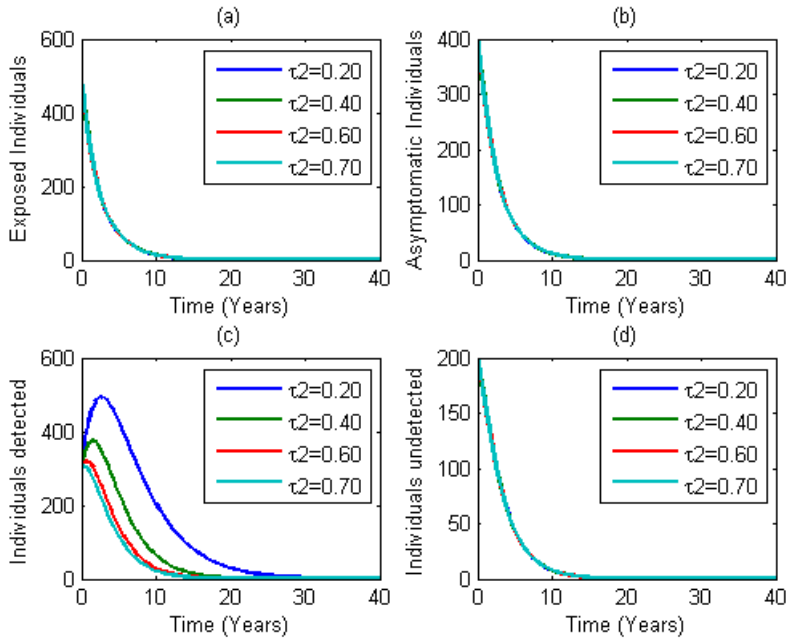

Figure 4: Simulation of model (1) showing the effect of high detection rate (ϕ) from the undetected to detected infected individuals. Here, τ_2 is varied from 0.20 to 0.70 with $\phi = 0.70$.

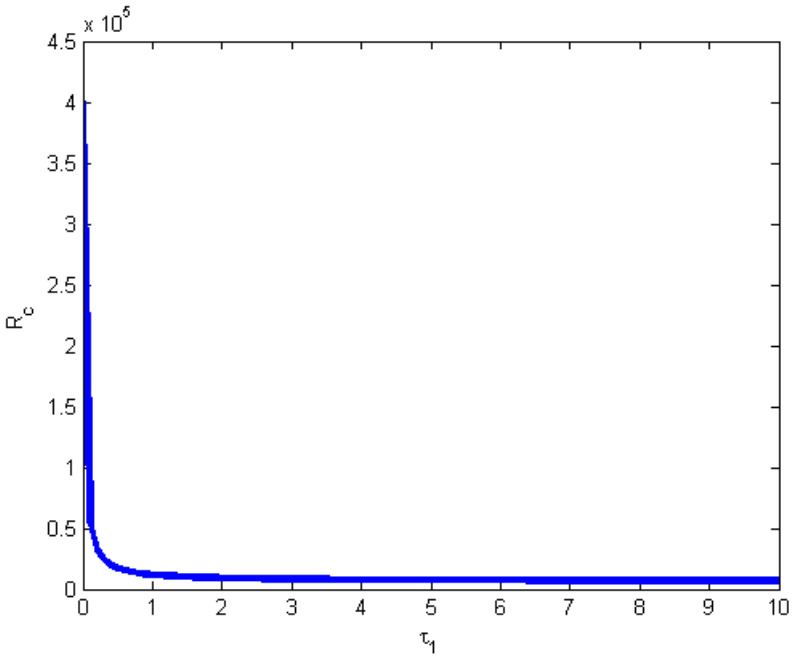

Figure 5: Plot of reproduction number, R_c as a function of treatment rate, τ_1. Parameter values used are as in Table 2.

6.1.1 Strategy 1:

The preventive control measures such as condoms u_1 is used to optimize the objective functional J while treatment control strategy u_2 is set to zero. Figure 6 shows that the number of asymptomatic infectives (detected and undetected), and those with the disease symptoms decreased with time in the presence of an effective preventive strategy u_1. Conversely, without control u_1, the infected population increased slightly above. This is actually as expected because condom use help to reduce the risk in transmission of chlamydia and other sexually transmitted diseases [22]. The control profile for this strategy in Figure 7 (a) reflects that maximum use of u_1 is necessary for at least six years to achieve the slow space in chlamydia transmission, before decreasing to the end of the simulation period. The decrease in the profile implies that maintaining preventive strategy throughout an epidemic period is almost impossible for the public, therefore other means of control can be jointly used.

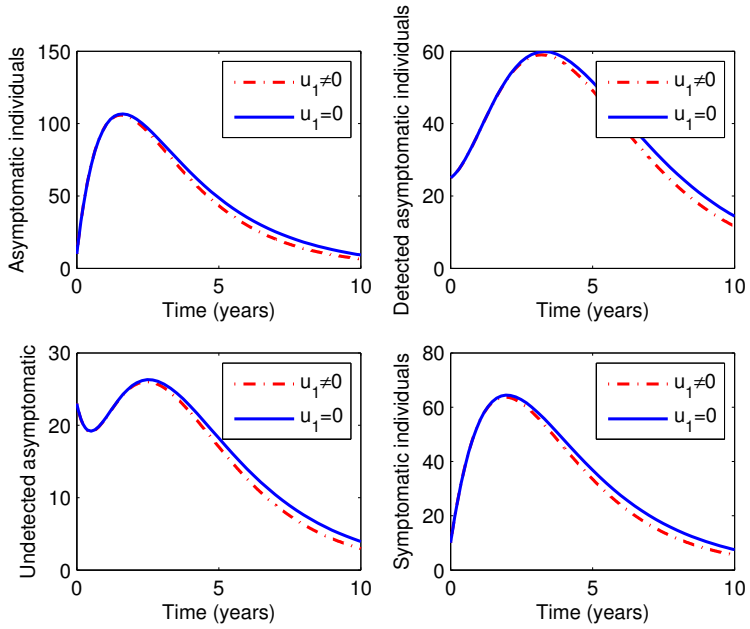

Figure 6: Impact of strategy u_1 on chlamydia dynamics.

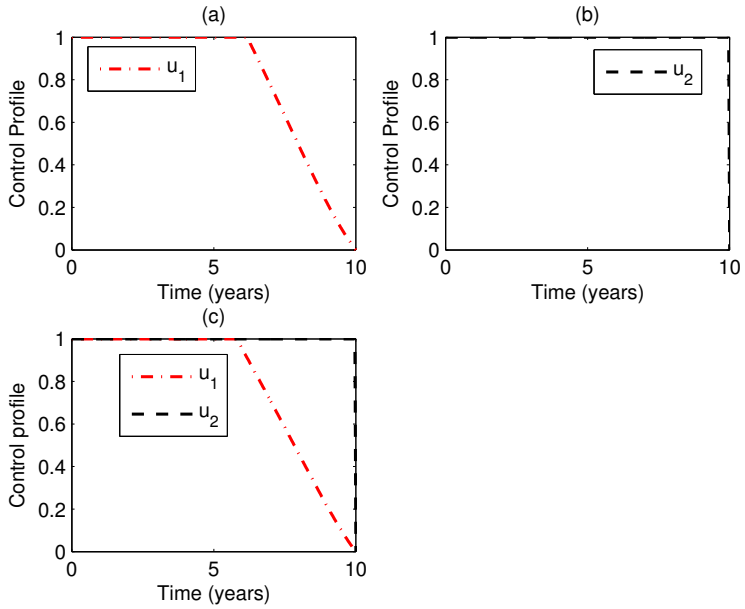

Figure 7: Control profiles for (a) strategy 1, (b) strategy 2, and (b) strategy 3, respectively.

6.1.2 Strategy 2:

Use of treatment control u_2. Applying treatment control in Figure 8 indeed reduces to almost half of the maximum number of asymptomatic individuals detected without control. A similar trend is observed in symptomatic individuals. However, treatment has no reasonablet effect on infected individuals whose Chlamydia status has not been detected. As indicated on the control profile in Figure 7 (b), treatment ought to be carried out optimally throughout the simulation period (10 years) in order to achieve the overall control of the disease.

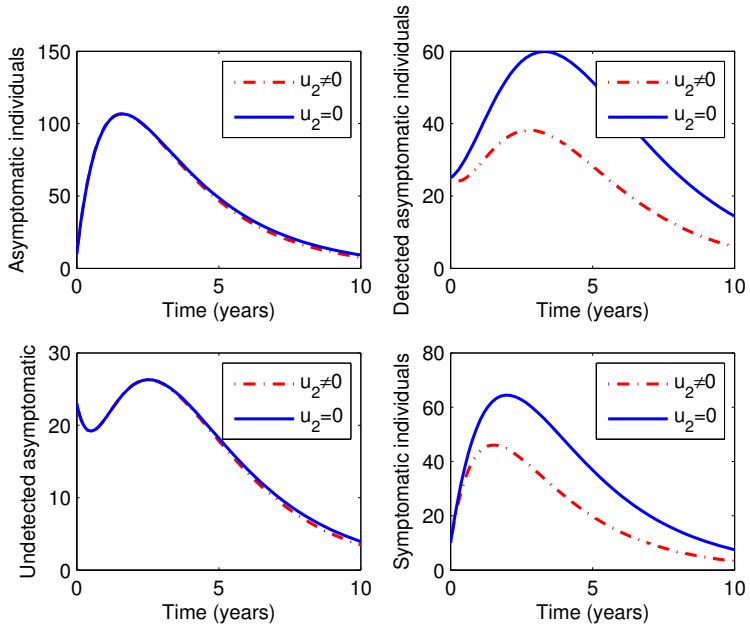

Figure 8: Impact of strategy u_2 on chlamydia dynamics.

6.1.3 Strategy 3:

Combined use of condoms and treatment for the control of the disease. Figure 9 demonstrates clearly that simultaneous use of condoms alongside treatment have depopulated significantly both the mild cases and infectious cases of chlamydia. On the other hand, when controls are not implemented, asymptomatic and symptomatic cases grow in number. It is obvious from Figure 10 that, combined strategy is the best for reducing chlamydia cases. This is consistent with the outcome of the work of [14] which says, that preventive and treatment should be combined for an effective eradication of sexually transmitted diseases.

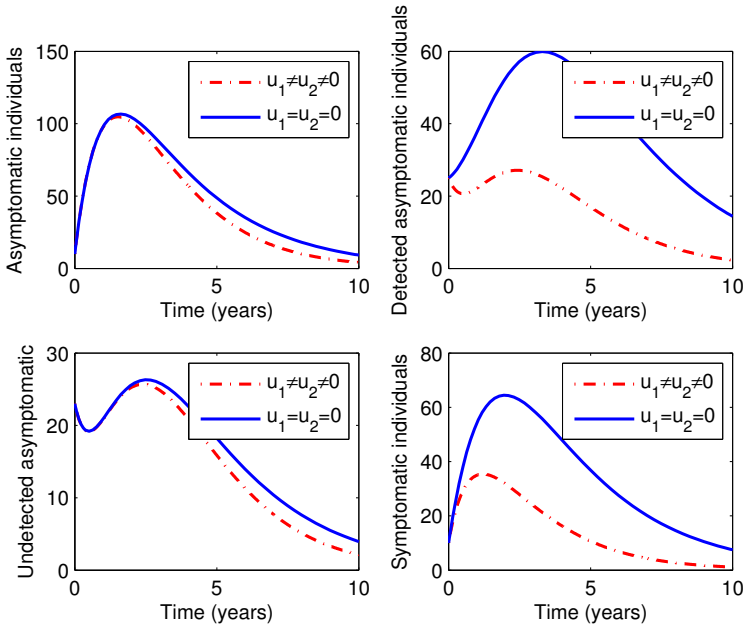

Figure 9: Impact of strategy u_{12} on chlamydia dynamics.

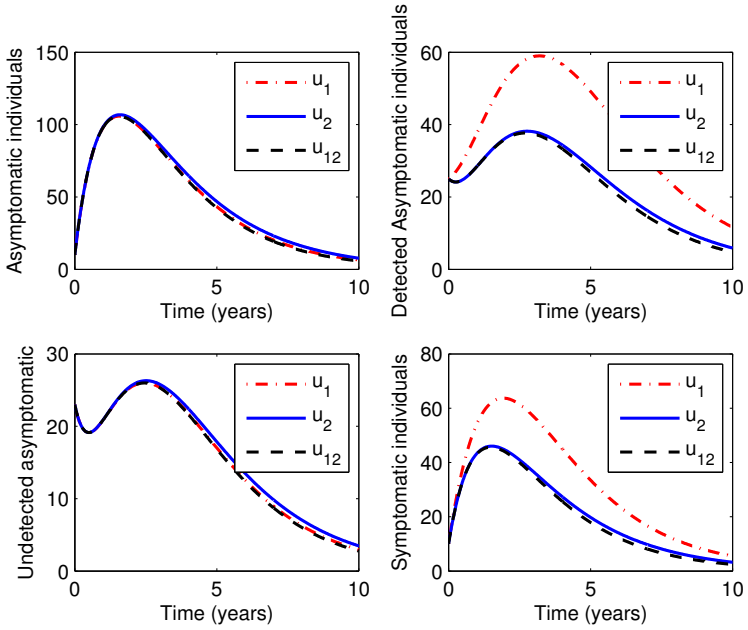

Figure 10: Impact of comparing strategies $1, 2$ and 3 on chlamydia dynamics.

7 Conclusion

In this work, a mathematical model that splits the asymptomatic population into detected and undetected sub-population is developed and analyzed. The aim of this study is basically to examine the effect of undetected asymptomatic cases of chlamydia infection. The model (1) upon qualitative analysis exhibits the phenomenon of forward bifurcation near the point $R_c = 1$. The meaning of this phenomenon as explained in [12] is that, the disease-free equilibrium loses its stability and a stable endemic equilibrium surfaces when the associated reproduction number is slightly greater than one. Hence, The existence of forward bifurcation in the model (1) shows that having $R_c < 1$ is enough pointer to guarantee the elimination of chlamydia in the population irrespective of the initial sizes of the infected subpopulations. Intuitively, this implies the global asymptotic stability of the disease-free equilibrium of the model whenever $R_c < 1$. Analytical and numerical results show a relationship between the treatment rate τ_1 and the reproduction number R_c. This implies that (as demonstrated in Figure 5) treatment of infected individuals has a positive impact in minimizing the burden of chlamydia transmission dynamics in the population. Sensitivity analysis results reveal that the most vital parameters that significantly affect the reproduction number of model (1) are the Chlamydia transmission rates (i.e., β_1 and β_2) and treatment rate (τ_1) in the population. This implies that reducing the transmission rates and increasing the treatment has a huge impact in curtailing Chlamydia burden in the population, hence an eye should be kept on these parameters in order to effectively control the spread of the disease. Results from the numerical simulations suggest that a low detection rate (10%) of the asymptomatic individuals (from undetected to detected state) alongside high treatment rate is a potential threat to human fertility, and thus not sufficient for Chlamydia elimination in about 40 years time. Further, it is also observed that a high detection rate (70%) of individuals infected with asymptomatic infection (from undetected to detected state) leads to the elimination of undetected asymptomatic individuals with the disease in the population in about 12 years time. Thus, identifying more cases of undetected asymptomatic individuals immediately for treatment will help in reducing human infertility due to chlamydia infection in families and communities. In that light, preventive measures and optimized treatment was introduced into the basic model to formulate the optimal control model. Using the Pontrayagin′s maximum principle, the study shows that the use of condoms and optimized treatment could be the best option for curbing the menace of chlamydia in families and community cycles.

In summary, this study unfolds the existence of forward bifurcation in the Chlamydia transmission dynamic model (1). Additionally, the study shows the effect of undetected chlamydia asymptomatic infections in individuals hence one of the possible causes of infertility in some families and communities. Finally, it is established that, splitting the asymptomatic population into detected and undetected asymptomatic subpopulation alters the qualitative nature of the chlamydia model in [3].

This study can be extended as follows:

i. Incorporating the effect of media awareness campaign and screening

ii. Conduct cost-effectiveness analysis of condom and treatment control strategies in curbing chlamydia in the population.

iii. Conduct sensitivity analysis on the weight constants linked to individuals in I_a and I_s.

References

[1] N. I. Akinwande, S. A. Somma, R. O. Olayiwola, T. T. Ashezua, R. I. Gweryina, and et al. Modelling the impacts of media campaign and double dose vaccination in controlling COVID-19 in Nigeria. *Alexandria Engineering Journal*, 80:167–190, 2023.

[2] S. Annas, M. I. Pratama, M. Rifandi, W. Sanusi, and S. Side. Stability Analysis and Numerical Simulation of SEIR Model for pandemic COVID-19 Spread in Indonesia. *Chaos, Solitons and Fractals*, 139(110072), 2020.

[3] T. T. Ashezua, J. J. Ibekwe, and S. A. Somma. Modelling and analysis of a model for chlamydia trachomatis transmission dynamics. *International Journal of Mathematical Analysis and Modelling*, 6(2):13–30, 2023.

[4] T.T. Ashezua, R.I. Gweryina, and F.S. Kaduna. Population dynamics of a mathematical model for monkeypox. *International Journal of Mathematical Analysis and Modelling*, 6(1):40–63, 2023.

[5] R. C. Brunham, B. Pourbohloul, S. Mak, R. White, and M. I. Rekart. The unexpected impact of a Chlamydia trachomatis infection control program on susceptibility to reinfection. *J. Infec. Dis.*, 192:1836–1844, 2005.

[6] J. A. Burns, I. M. Cliff, and S. E. Doughty. Sensitivity analysis and parameter estimation for a model of Chlamydia trachomatis infection. *J. Inverse III-posed Probl.*, 15(3):243–256, 2007.

[7] I. Carr. Applications of centre manifold theory. 1981.

[8] C. Castillo-Chavez and B. Song. Dynamical models of tuberculosis and their applications. *Mathematical Biosciences and Engineering*, 2(2004).

[9] CDC. Chlamydia statistics. retrieved on August 16, 2023 from https://www.cdc.gov/std/chlamydia/stat.htm. 2023.

[10] Cleveland Clinic. Clamydia. retrieved on September 18, 2024 from https://my.clevelandclinic.org/health/diseases/4023-chlamydia. 2024.

[11] O. Diekmann, J.A.P. Heesterbeek, and J.A.J. Metz. On the definition and computation of the basic reproduction ratio r_0 in models for infectious disease in heterogeneous population. *Journal of Mathematical Biology*, 28:365–382, 1990.

[12] A. B. Gumel. Causes of backward bifurcations in some epidemiological models. *Journal of Mathematical Analysis and Applications*, 395(2012):355–365, 2012.

[13] A. B. Gumel, J. M. S. Lubuma, O. Sharomi, and Y. A. Terefe. Mathematics of a sex-structured model for syphilis transmission dynamics. *Mathematical Methods in Applied Sciences*, 41(18):8488–8513, 2017.

[14] A. B. Gumel, J. M. S. Lubuma, O. Sharomi, and Y. A. Terefe. Mathematics of a sex-structured model for syphilis transmission dynamics. *Mathematical Methods in Applied Sciences*, 41(18):8488–8513, 2018.

[15] R. I. Gweryina, C. Alfiniyah, C. E. Madubueze, and K. O. Achema. Nonlinear dynamics model of HIV/AIDS: Assessing the impacts of condoms, vaginal microbicides, and optimized treatment. *Partial Differential Equations in Applied Mathematics*, 12:100933, 2024.

[16] R. I. Gweryina, M. Y. Kura, and T. T. Ashezua. Optimal control model for the infectiology of staphylococcus aureus with dual transmission pathways. *Results in Control and Optimization*, 14:100364, 2024.

[17] R. I. Gweryina, C. E. Madubueze, and F. S. Kaduna. Mathematical assessment of the role of denial on COVID-19 transmission with non-linear incidence and treatment functions. *Scientific African*, 12:e00811, 2021.

[18] H. W. Hethcote. The mathematics of infectious diseases. *SIAM Rev.*, 42(4):599–653, 2000.

[19] E. Iboi and D. Okuonghae. Population dynamics of a mathematical model for syphilis. *Applied Mathematical Modelling*, 40:3573–3590, 2016.

[20] S. Lakshmikantham, S. Leela, and A. A. Martynyuk. Stability Analysis of Nonlinear Systems, Marcel Dekker, New York. 1989.

[21] C. F. Martin, I. J. S. Allen, and M. S. Stamp. An analysis of the transmission of Chlamydia in a closed population. *J. Difference Equ. Appl.*, 2(1):1–29, 1996.

[22] Mayo Clinic. Clamydia trachomatis. retrieved on September 18, 2024 from https://www.mayoclinic.org/diseases-conditions/chlamydia/symptoms-causes/syc-20355349. 2024.

[23] Medical News Today. Everything you need to know about chlamydia. retrieved on September 18, 2024 from https://www.medicalnewstoday.com/articles/8181. 2024.

[24] K. Mirjam, W. Robert, A. van den Hock, and P. J. Maarten. Comparative model-based analysis of screening programs for Chlamydia trachomatis infections. *Amer. J. Epidemiology*, 153(1):90–101, 2001.

[25] K. Mirjam, T. H. Yvonne, P. van Duynhoven, and S. J. Anton. Modelling prevention strategies for gonnorrhea and Chlamydia using stochastic network simulations. *Amer. J. Epidemiology*, 144(3):306–317, 1996.

[26] S. Mushayabasa. The epidemiological consequences of Chlamydia and gonorrhea co-infection: Insights from a mathematical. *Int. J. Appl. Math. Comput.*, 4(3):295–306, 2012.

[27] B. I. Omede, U. B. Odionyenma, A. A. Ibrahim, and B. Bolaji. Third wave of COVID-19: mathematical model with optimal control strategy for reducing the disease burden in Nigeria. *International Journal of Dynamics and Control*, 11(2023):411–427, 2023.

[28] S. Pal, K. Kundu, and J. Chattopadhyay. Role of standard incidence in an eco-epidemiological system a mathematical study. *Ecological Modelling*, 199(3):229–329, 2006.

[29] Y. M. Rangkuti, Firmansyah, and A. Landong. Sensitivity analysis of seir epidemic model of covid-19 spread in Indonesia. *Journal of Physics: Conference Ssries*, 2193(2022), 2022.

[30] D. G. Regan, D. P. Wilson, and J. S. Hocking. Coverage is the key for effective screening of Chlamydia trachomatis in Australia. *J. Infec. Dis.*, 198:349–358, 2008.

[31] G. P. Samanta and S. Sharma. Analysis of a delayed Chlamydia epidemic model with pulse vaccination. *Appl. Math. Comput.*, 230:555–569, 2014.

[32] S. Sharma and G. P. Samanta. Analysis of a Chlamydia epidemic model. *Journal of Biological Systems*, 22(4):714–744, 2014.

[33] O. Sharomi and A. B. Gumel. Re-infection induced backward bifurcation in the transmission dynamics of Chlamydia trachomatis. *Math. Anal. Appl.*, 356:96–118, 2009.

[34] O. Sharomi and A. B. Gumel. Mathematical study of a risk-structured two group model for Chlamydia transmission dynamics. *Appl. Math. Modell.*, 35(8):3653–3673, 2011a.

[35] O. Sharomi and A. B. Gumel. Dynamical analysis of a sex-structured Chlamydia trachomatis transmission model with time delay. *Nonlinear Analysis :Real World Applications.*, 12:837–866, 2011b.

[36] Statista. Number of people infected with chlamydia in Africa as of 2020, by gender. retrieved on August 18, 2023 from https://www.statista.com/statistics/1128548/prevalence-of-chlamydia-in-africa-by-gender/: :text=as2023.

[37] K. M. Turner, E. J. Adams, N. Gay, A. C. Gham, C. Merler, and W. J. Edmunds. Developing a realistic sexual network model of Chlamydia transmission in Britain. *Theoret. Biol. Med. Model*, 3(3), 2006.

[38] P. van den Driessche and J. Watmough. Reproduction numbers and sub-threshold endemic equilibria for compartmental models of disease transmission. *Mathematical Biosciences*, 180:29–48, 2002.

[39] WHO. Clamydia. retrieved on August 16, 2023 from https://www.who.int/news-room/fact-sheets/detail/chlamydia: :text=in2023.

[40] D. P. Wilson. Mathematical modelling of Chlamydia. *ANZIAM J.*, 45(E):C201–C214, 2004a.

[41] D. P. Wilson, S. Mathew, C. Wan, A. N. Pettitt, and D. I. S. McElwain. Use of a quantitative gene expression assay based on micro-array techniques and a mathematical model for the investigation of Chlamydial generation time. *Bull. Math. Biol.*, 66(3):523–537, 2004b.

[42] D. P. Wilson, P. Timms, D. I. S. McElwain, and P. M. Bavoil. Type III secretion, contact-dependent model for the intracellular development of Chlamydia. *Bull. Math. Biol.*, 68:161–178, 2006.

[43] Z. Yu, W. Tu, and M. T. Lee. A semi-parametric threshold regression analysis of sexually transmitted infections in adolescent women. *Stat. Med.*, 28:3029–3042, 2009.