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Mathematical model for transmission of *Chlamydia* due to sexual activity and unhygienic environment

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Abstract

Aim: Sexually transmitted diseases (STDs) need to be studied systematically to better understand their global spread. Transmission of *Chlamydia trachomatis* is a severe public health issue, with roughly 90 million new cases per year. Globally, *Chlamydia trachomatis* is the most frequent bacterial cause of STDs.

Methods: To better understand the dynamics and transmission of *Chlamydia*, the susceptible-exposed-infected-recovered-susceptible (SEIRS) model was constructed. Using a system of nonlinear ordinary differential equations, a basic reproduction number has been calculated at an equilibrium point, and the system is locally and globally asymptotically stable at both disease-free and endemic equilibrium points. Numerical simulations illustrate the behavior and flow of *Chlamydia* infections in different compartments.

Results: Conclude from the proposed study that 25% of individuals have been exposed to *Chlamydia*, of which 20% of individuals get infections due to sexual activity and 55% of individuals get recovered. Twenty percent of individuals have been exposed to *Chlamydia*, of which 37% of individuals have been infected due to an unhygienic environment. Of those, 43% of individuals recovered. Also, it has been found that people are more likely to get infections because of an unhygienic environment than sexually active people. The recovery rate is also much better for people who have been infected because of an unhygienic environment.

Conclusions: Sexually transmitted infections can be reduced by up to 10%. While infection due to an unhygienic environment can be controlled up to a certain intensity. According to this research, public awareness campaigns and the improvement of personal hygiene will play a major role in reducing the spread of the epidemic in the future.

Keywords

Chlamydia, mathematical model, transmission dynamics, stability, numerical simulation

Introduction

Among sexually transmitted diseases (STDs), *Chlamydia trachomatis* infection is the most common [1]. According to the World Health Organization (WHO), there will be 129 million cases of *Chlamydia trachomatis* infection in 2020 [2]. The bacteria *Chlamydia trichromatic* causes *Chlamydial* infection. It can be transmitted in two main ways: one is through sexual activity with an infected individual, while the other is due to an unhygienic environment. Once infected, a person may transmit the disease to their partners via intercourse, anal sex, or oral sex. Whereas, a non-sexual method of transmission includes direct hand-to-hand contact, sharing of bedding, clothing, or towels, and transmission by flies that have come into contact with an infected person's discharge from the eyes or nose. In rare situations, infected vaginal fluid or semen might come into contact with a person's eye, producing conjunctivitis. *Chlamydia trachomatis* is also the leading cause of blindness worldwide [3]. It is a very common STD that can happen to both men and women, affecting about 4.2% of women and 2.7% of men worldwide [4, 5], but it is more common in women. However, *Chlamydia* is more prevalent among young individuals who engage in sexual activity, whereas infection rates are greater in younger women aged fifteen to twenty-four [6]. In women, *Chlamydial* infection affects the throat, rectum, and cervix, causing serious damage to the reproductive system. Moreover, it causes pelvic inflammatory disease (PID) with a subsequent risk of infertility. As a result, pregnancy may become difficult or impossible for a woman. Aside from ectopic pregnancy, it may also cause miscarriage [7, 8]. The transmission of *Chlamydia* from an infected mother to her baby may occur during vaginal delivery [6]. Also, the symptoms of *Chlamydia* infection in women include vaginal discharge with a bad smell, vaginal bleeding, vaginal itching and burning, abdominal pain, cramping during menstruation, and fever. In men, the symptoms include pain and swelling in the testicles, pain, and burning when urinating, and turbid discharge from the penis. *Chlamydia* has an incubation period of seven to twenty days. It refers to the time between infection and the development of the disease in a person. Infections with *Chlamydia* are treatable and curable. Azithromycin is an antibiotic that is often provided in a single, high-dose prescription or doxycycline is an antibiotic that must be taken twice a day for about one week before it will be effective. It is essential to avoid any sexual activity throughout the therapy period. Even if an infected individual has successfully cured a previous infection, it is still possible to transmit and get *Chlamydia* if exposed to the same person again.

Literature survey

Mathematical models have proven to be one of the most useful tools for studying the spread of any infection. The mathematical epidemic model of STDs is used to study the behavior of STDs and their impacts on society. These models were originally used to demonstrate the relevance of the contact structure and dynamic characteristics of infections [9]. A compartmental mathematical model to study the *Chlamydia* resurgence [10]. In the absence of tools to change sexual networks, a vaccine will be necessary to stop infection transmission. *Chlamydia trachomatis* and gonorrhea co-dynamics models with optimum control analysis have been studied and examined to assess the impact of targeted treatment for each of the diseases on their co-infections in a population [11]. Mathematical modeling and study of the transmission dynamics of blinding trachoma with the impact of awareness programs and found a lack of competent health care systems and public awareness programs to blame for the outbreak of the blinding trachoma disease [12]. A sophisticated investigation of *Chlamydia trachomatis* infection sensitivity was performed using a susceptible-exposed-infected-recovered-susceptible (SEIRS) model, and they also analyzed the population turnover and the impact of screening [13]. When the asymptomatic interval is longer than the symptomatic phase, the impact of a screening program is more apparent. To understand how various forms of policy analysis are employed and how the studies have evolved with changes in the field, it is examined by published *Chlamydia* models [14].

Organization of proposed study

A model has been constructed in this paper to better understand how *Chlamydia* spreads. Section 2 contains the model's formulation and description and also contains the calculation of the basic

reproduction number at equilibrium points, while section 3 contains the computation of stability on a local and global scale, and section 4 contains the computation of numerical simulation in such a way that it helps in the analysis of *Chlamydia* infection and the effect of recovery rate on disease transmission. Section 5 concludes the model.

Formulation and description of the *Chlamydia* model

To analyze the transmission dynamics of *Chlamydia*, a compartmental model is constructed. This compartment model consists of two groups of populations with two strains of infectious stages: the transmission of *Chlamydia* due to sexual activity and an unhygienic environment. The total population of humans at the time *t*, *N(t)* is divided into five compartments, each with a class of susceptible individuals *S(t)*, who are healthy but can get infected through direct and indirect contact with infectious individuals. Class of exposed individuals *E(t)*, who have been infected due to sexual activity and an unhygienic environment but are not yet infectious. $I_s(t)$ and $I_u(t)$ a class of infected individuals who are infected and can transmit the disease due to sexual activity and an unhygienic environment, respectively. *R(t)* class of recovered individuals who have been infected and then recovered from the disease. The transmission dynamics of *Chlamydia* are described graphically in Figure 1, and the parameters used in the model are described in Table 1.

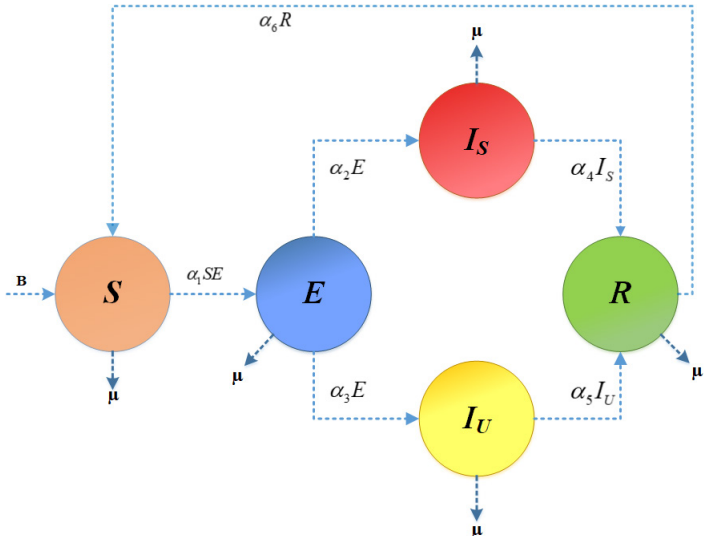


Figure 1. Transmission dynamics of *Chlamydia*

Table 1. Description of model parameters

Parameters	Description	Value	Source
B	Birth rate	0.018	Calculated
α_1	Rate of transmission from *S* to *E*	0.8	Assumed
α_2	Transmission rate from *E* to I_S	0.67	Calculated
α_3	Transmission rate from *E* to I_U	0.32	Calculated
α_4	Recovery rate from I_S	0.92	Calculated
α_5	Recovery rate from I_U	0.95	Calculated
α_6	Rate of transmission from *R* to *S*	0.05	Assumed
μ	Escape rate	0.01	Assumed

A dynamical system of non-linear ordinary differential equations for the model is formulated as follows:

$$\frac{dS}{dt} = B - \alpha_1 SE + \alpha_6 R - \mu S,$$
$$\frac{dE}{dt} = \alpha_1 SE - \alpha_2 E - \alpha_3 E - \mu E,$$

$$\frac{dI_S}{dt} = \alpha_2 E - \alpha_4 I_S - \mu I_S,$$
$$\frac{dI_U}{dt} = \alpha_3 E - \alpha_5 I_U - \mu I_U,$$
$$\frac{dR}{dt} = \alpha_4 I_S + \alpha_5 I_U - \alpha_6 R - \mu R. \quad (1)$$

The total human population of this model is presented as:

$N(t) = S(t) + E(t) + I_S(t) + I_U(t) + R(t)$

Adding the non-linear ordinary differential equation of system (1), we have

$\frac{d}{dt} = (S + E + I_S + I_U + R) \leq B - \mu N.$

This implies that $\lim_{t\to\infty} sup\ (S + E + I_S + I_U + R) \leq \frac{B}{\mu}$.

Thus, the feasible region for the model is Λ, which is a positively invariant. *i.e.,* every solution of the model, with initial conditions Λ remains there for all $t > 0$.

$$\Lambda = \{(S, E, I_S, I_U, R) \in R_+^5 : S + E + I_S + I_U + R \leq \frac{B}{\mu}, S > 0, E \geq 0, I_S \geq 0, I_U \geq 0, R \geq 0\} \quad (2)$$

Existence of the equilibrium points

To obtain the disease-free equilibrium point E_0 for the system of non-linear differential equations, put the right-hand side of Eq. (1) equal to zero thus, $E_0 = (\frac{B}{\mu}, 0, 0, 0, 0)$. (3)

This means when there is no infection $E = I_S = I_U = R = 0$. This model has a unique disease-free equilibrium point.

Due to sexual activity or the use of unhygienic environments, there will always be an optimum number of individuals who will be sitting in each compartment. This point is referred to as an endemic point in epidemiology.

Endemic equilibrium point $E_{end}^* = (S^*, E^*, I_S^*, I_U^*, R^*)$ (4)

where $S^* = \frac{\alpha_2 + \alpha_3 + \mu}{\alpha_1}$,

$E^* = (\alpha_5 + \mu)(\alpha_6 + \mu)(\alpha_4 + \mu)(-\mu^2 + (-\alpha_2 - \alpha_3)\mu + B\alpha_1)/(\alpha_1\mu(\mu^3 + (\alpha_2 + \alpha_3 + \alpha_4 + \alpha_5 + \alpha_6)\mu^2 + ((\alpha_2 + \alpha_3 + \alpha_5 + \alpha_6)\alpha_4 + (\alpha_2 + \alpha_3 + \alpha_6)\alpha_5 + \alpha_6(\alpha_2 + \alpha_3))\mu + ((\alpha_2 + \alpha_3 + \alpha_6)\alpha_5 + \alpha_3\alpha_6)\alpha_4 + \alpha_2\alpha_5\alpha_6))$,

$I_S^* = (\alpha_5 + \mu)\alpha_2(\alpha_6 + \mu)(-\mu^2 + (-\alpha_2 - \alpha_3)\mu + B\alpha_1)/(\alpha_1\mu(\mu^3 + (\alpha_2 + \alpha_3 + \alpha_4 + \alpha_5 + \alpha_6)\mu^2 + ((\alpha_2 + \alpha_3 + \alpha_4 + \alpha_6)\alpha_5 + (\alpha_2 + \alpha_3 + \alpha_6)\alpha_4 + \alpha_6(\alpha_2 + \alpha_3))\mu + ((\alpha_2 + \alpha_3 + \alpha_6)\alpha_4 + \alpha_6\alpha_2)\alpha_5 + \alpha_3\alpha_4\alpha_6))$,

$I_U^* = (\alpha_6 + \mu)(\alpha_4 + \mu)\alpha_3(-\mu^2 + (-\alpha_2 - \alpha_3)\mu + B\alpha_1)/(\alpha_1\mu(\mu^3 + (\alpha_2 + \alpha_3 + \alpha_4 + \alpha_5 + \alpha_6)\mu^2 + ((\alpha_2 + \alpha_3 + \alpha_5 + \alpha_6)\alpha_4 + (\alpha_2 + \alpha_3 + \alpha_6)\alpha_5 + \alpha_6(\alpha_2 + \alpha_3))\mu + ((\alpha_2 + \alpha_3 + \alpha_6)\alpha_5 + \alpha_3\alpha_6)\alpha_4 + \alpha_2\alpha_5\alpha_6))$,

$R^* = ((\alpha_2\alpha_4 + \alpha_3\alpha_5)\mu + \alpha_4\alpha_5(\alpha_2 + \alpha_3))(-\mu^2 + (-\alpha_2 - \alpha_3)\mu + B\alpha_1)/(\alpha_1\mu(\mu^3 + (\alpha_2 + \alpha_3 + \alpha_4 + \alpha_5 + \alpha_6)\mu^2 + ((\alpha_2 + \alpha_3 + \alpha_5 + \alpha_6)\alpha_4 + (\alpha_2 + \alpha_3 + \alpha_6)\alpha_5 + \alpha_6(\alpha_2 + \alpha_3))\mu + ((\alpha_2 + \alpha_3 + \alpha_6)\alpha_5 + \alpha_3\alpha_6)\alpha_4 + \alpha_2\alpha_5\alpha_6))$.

Basic reproduction number

To get the threshold value for the transmission of *Chlamydia*, a basic reproduction number is formulated using the next-generation matrix (NGM) algorithm [15]. The basic reproduction number for the system is obtained as the spectral radius of the matrix (fv^{-1}) around the disease-free equilibrium point.

Let $X = (S, E, I_S, I_U, R)$ then model rewrite as $X' = F(X) - V(X)$ where $F(X)$ represents the rate of appearance of new infections in the compartment and $V(X)$ represents the rate of transfer individuals which are given by,

$$F(X) = \begin{bmatrix} \alpha_1 SE \\ 0 \\ 0 \\ 0 \\ 0 \end{bmatrix} \quad \text{and} \quad V(X) = \begin{bmatrix} E(\alpha_2 + \alpha_3 + \mu) \\ -\alpha_2 E + I_S(\alpha_4 + \mu) \\ -\alpha_3 E + I_U(\alpha_5 + \mu) \\ -\alpha_4 I_S - \alpha_5 I_U + R(\alpha_6 + \mu) \\ -B + \alpha_1 SE - \alpha_6 R + \mu S \end{bmatrix} \quad (5)$$

By calculating the Jacobian matrices at E_0, we find that $D(F(E_0)) = \begin{bmatrix} f & 0 \\ 0 & 0 \end{bmatrix}$ and $D(V(E_0)) = \begin{bmatrix} v & 0 \\ J_1 & J_2 \end{bmatrix}$ where, f and v are 5 × 5 matrices defined as $f = \frac{\partial F_i}{\partial X_j}(E_0)$ and $v = \frac{\partial v_i}{\partial X_j}(E_0)$. Finding f and v we get,

$$f = \begin{bmatrix} \alpha_1 S & 0 & 0 & 0 & \alpha_1 E \\ 0 & 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 & 0 \end{bmatrix} \text{ and } v = \begin{bmatrix} \alpha_2 + \alpha_3 + \mu & 0 & 0 & 0 & 0 \\ -\alpha_2 & \alpha_4 + \mu & 0 & 0 & 0 \\ -\alpha_3 & 0 & \alpha_5 + \mu & 0 & 0 \\ 0 & -\alpha_4 & -\alpha_5 & \alpha_6 + \mu & 0 \\ \alpha_1 S & 0 & 0 & -\alpha_6 & \alpha_1 E + \mu \end{bmatrix}. \quad (6)$$

Here, v is a non-singular matrix that we can find v^{-1}. Now we calculate the NGM fv^{-1} and the largest modulus of eigenvalues of fv^{-1} is the basic reproduction number of the model. The formulated basic reproduction number $R_0 = \frac{\alpha_1 B}{\mu(\alpha_2 + \alpha_3 + \mu)}$. (7)

Stability

In this section, we will discuss the local stability and global stability for equilibrium points.

Local stability

Theorem-1

Disease-free equilibrium point E_0 of the model is locally asymptotically stable if $\frac{B}{\mu} < \frac{\alpha_2 + \alpha_3 + \mu}{\alpha_1}$.

Proof: Evaluating the Jacobian matrix for the model at point E_0 (disease-free equilibrium point) gives,

$$J(E_0) = \begin{bmatrix} -\mu & \frac{-\alpha_1 B}{\mu} & 0 & 0 & \alpha_6 \\ 0 & \frac{\alpha_1 B}{\mu} - \alpha_2 - \alpha_3 - \mu & 0 & 0 & 0 \\ 0 & \alpha_2 & -\alpha_4 - \mu & 0 & 0 \\ 0 & \alpha_3 & 0 & -\alpha_5 - \mu & 0 \\ 0 & 0 & \alpha_4 & \alpha_5 & -\alpha_6 - \mu \end{bmatrix}.$$

Thus, the eigenvalues of $J(E_0)$ are given by $\lambda_1 = -\mu$, $\lambda_2 = -(\alpha_6 + \mu)$, $\lambda_3 = -(\alpha_5 + \mu)$, $\lambda_4 = -(\alpha_4 + \mu)$, and $\lambda_5 = \frac{B\alpha_1 - \mu(\alpha_2 + \alpha_3 + \mu)}{\mu}$. Clearly, λ_1, λ_2, λ_3 and λ_4 are negative. Also, if $\frac{B}{\mu} < \frac{\alpha_2 + \alpha_3 + \mu}{\alpha_1}$ then $\lambda_5 < 0$.

As all eigenvalues of the matrix are negative therefore disease-free equilibrium point E_0 of the model is locally asymptotically stable.

Theorem-2

The endemic equilibrium point E^*_{end} is locally asymptotically stable if it satisfies the following condition, $S \leq \max\{\frac{\alpha_5}{\alpha_1}, \frac{\mu^2}{\alpha_1 \alpha_5}\}$.

Proof: Linearizing the system around the endemic equilibrium point E^*_{end} gives the Jacobian matrix

$$J(E^*) = \begin{bmatrix} -\alpha_1 E^* - \mu & -\alpha_1 S^* & 0 & 0 & \alpha_6 \\ \alpha_1 E^* & \alpha_1 S^* - \alpha_2 - \alpha_3 - \mu & 0 & 0 & 0 \\ 0 & \alpha_2 & -\alpha_4 - \mu & 0 & 0 \\ 0 & \alpha_3 & 0 & -\alpha_5 - \mu & 0 \\ 0 & 0 & \alpha_4 & \alpha_5 & -\alpha_6 - \mu \end{bmatrix}.$$

The characteristic equation of the Jacobian matrix is $\lambda^5 + \alpha_4\lambda^4 + \alpha_3\lambda^3 + \alpha_2\lambda^2 + \alpha_1\lambda + \alpha_0$ where $\alpha_4 = E\alpha_1 + \alpha_2 + \alpha_3 + \alpha_4 + \alpha_6 + 5\mu + (\alpha_5 - S\alpha_1)$,

$a_3 = E\alpha_1(\alpha_2 + \alpha_3 + \alpha_4 + \alpha_5 + \alpha_6 + 4\mu) + \alpha_2(\alpha_4 + \alpha_5 + \alpha_6 + 4\mu) + \alpha_3(\alpha_4 + \alpha_5 + \alpha_6 + 4\mu) + \alpha_4(\alpha_6 + 4\mu) + 4\mu\alpha_6 + 9\mu^2 (\alpha_4\alpha_5 - S\alpha_1\alpha_4) + (\alpha_5\alpha_6 - S\alpha_1\alpha_6) + (4\alpha_5\mu - 4S\alpha_1\mu) + (\mu^2 - S\alpha_1\alpha_5)$,

$a_2 = 7\mu^3 + (6E\alpha_1 + 6\alpha_2 + 6\alpha_3 + 5\alpha_4 + 5\alpha_6)\mu^2 + (3E(\alpha_2 + \alpha_3 + \alpha_4 + \alpha_5 + \alpha_6)\alpha_1 + (\alpha_2 + \alpha_3 + \alpha_6)3\alpha_4 + 3(\alpha_5 + \alpha_6)(\alpha_2 + \alpha_3))\mu + E((\alpha_2 + \alpha_3 + \alpha_5 + \alpha_6)\alpha_4 + (\alpha_2 + \alpha_3 + \alpha_5)\alpha_6 + \alpha_5(\alpha_2 + \alpha_3))\alpha_1 + ((\alpha_5 + \alpha_6)\alpha_4 + \alpha_5\alpha_6)(\alpha_2 + \alpha_3)(\alpha_4\alpha_5\alpha_6 - S\alpha_1\alpha_4\alpha_6)(3\alpha_4\alpha_5\mu - 3S\alpha_1\alpha_4\mu)(3\alpha_5\alpha_6\mu - 3S\alpha_1\alpha_6\mu)(6\alpha_5\mu^2 - 6S\alpha_1\mu^2)(\alpha_4\mu^2 - S\alpha_1\alpha_4\alpha_5)(\alpha_6\mu^2 - S\alpha_1\alpha_5\alpha_6)(3\mu^3 - 3S\alpha_1\alpha_5\mu)$,

$a_1 = 2\mu^4 + (4E\alpha_1 + 4\alpha_2 + 4\alpha_3 + 2\alpha_4 + 2\alpha_6)\mu^3 + (3E(\alpha_2 + \alpha_3 + \alpha_4 + \alpha_5 + \alpha_6)\alpha_1 + (3\alpha_2 + 3\alpha_3 + 2\alpha_6)\alpha_4 + 3(\alpha_5 + \alpha_6)(\alpha_2 + \alpha_3))\mu^2 + 2E((\alpha_2 + \alpha_3 + \alpha_5 + \alpha_6)\alpha_4 + (\alpha_2 + \alpha_3 + \alpha_5)\alpha_6 + \alpha_5(\alpha_2 + \alpha_3))\alpha_1 + 2((\alpha_5 + \alpha_6)\alpha_4 + \alpha_5\alpha_6)(\alpha_2 + \alpha_3)\mu + E(((\alpha_3 + \alpha_5)\alpha_6 + \alpha_5(\alpha_2 + \alpha_3))\alpha_4 + \alpha_2\alpha_5\alpha_6)\alpha_1 + \alpha_4\alpha_5\alpha_6(\alpha_2 + \alpha_3) + (4\alpha_5\mu^3 - 4S\alpha_1\mu^3) + (3\alpha_5\alpha_6\mu^2 - 3S\alpha_1\alpha_6\mu^2) + (3\alpha_5\alpha_4\mu^2 - 3S\alpha_1\alpha_4\mu^2) + (2\alpha_4\alpha_5\alpha_6\mu - 2S\alpha_1\alpha_4\alpha_6\mu) + (\alpha_4\alpha_6\mu^2 - S\alpha_1\alpha_4\alpha_5\alpha_6) + (2\alpha_4\mu^3 - 2S\alpha_1\alpha_4\alpha_5\mu) + (2\alpha_6\mu^3 - 2S\alpha_1\alpha_5\alpha_6\mu) + (3\mu^4 - 3S\alpha_1\alpha_5\mu^2)$,

$a_0 = (E\alpha_1 + \alpha_2 + \alpha_3)\mu^3 + (E(\alpha_2 + \alpha_3 + \alpha_4 + \alpha_5 + \alpha_6)\alpha_1 + (\alpha_4 + \alpha_5 + \alpha_6)(\alpha_2 + \alpha_3))\mu^2 + (E((\alpha_2 + \alpha_3 + \alpha_5 + \alpha_6)\alpha_4 + (\alpha_2 + \alpha_3 + \alpha_6)\alpha_5 + \alpha_6(\alpha_2 + \alpha_3))\alpha_1 + ((\alpha_5 + \alpha_6)\alpha_4 + \alpha_5\alpha_6)(\alpha_2 + \alpha_3)\mu + E(((\alpha_2 + \alpha_3 + \alpha_6)\alpha_5\alpha_3\alpha_6)\alpha_4 + \alpha_2\alpha_5\alpha_6)\alpha_1 + \alpha_4\alpha_5\alpha_6(\alpha_2 + \alpha_3))\mu + (\alpha_5\mu^4 - S\alpha_1\mu^4) + (\alpha_4\alpha_5\mu^3 - S\alpha_1\alpha_4\mu^3) + (\alpha_5\alpha_6\mu^3 - S\alpha_1\alpha_6\mu^3) + (\alpha_4\alpha_5\alpha_6\mu^2 - S\alpha_1\alpha_4\alpha_6\mu^2) + (\alpha_4\alpha_6\mu^3 - S\alpha_1\alpha_4\alpha_5\alpha_6\mu) + (\alpha_6\mu^4 - S\alpha_1\alpha_5\alpha_6\mu^2) + (\alpha_4\mu^2 - S\alpha_1\alpha_4\alpha_5\mu^2)(\mu^5 - S\alpha_1\alpha_5\mu^3)$.

The endemic equilibrium point E^*_{end} is locally asymptotically stable [16] if it satisfies, $S\alpha_1 < \alpha_5$ and $S\alpha_1\alpha_5 < \mu^2$ which implies that $S < \frac{\alpha_5}{\alpha_1}$ and $S < \frac{\mu^2}{\alpha_1\alpha_5}$. Hence, the endemic equilibrium point E^*_{end} is locally asymptotically stable if $S \leq \max\{\frac{\alpha_5}{\alpha_1}, \frac{\mu^2}{\alpha_1\alpha_5}\}$.

Global stability

Here, we discuss the global stability behavior of the equilibrium point E_0 and E^*_{end} by Lyapunov's function [17].

Theorem-3

The disease-free equilibrium point E_0 is globally asymptotically stable.

Proof: The disease-free equilibrium point E_0 is global asymptotically stable in the feasible region Λ.

Consider the Lyapunov function $L_1(t) = S(t) + E(t) + I_S(t) + I_U(t) + R(t)$

$L_1'(t) = S'(t) + E'(t) + I_S'(t) + I_U'(t) + R'(t)$

$L_1'(t) = B - \mu(S + E + I_S + I_U + R)$

$L_1'(t) = 0$

Since E_0 belongs to the feasible region Λ, S is bounded above by $\frac{B}{\mu}$, this implies $\frac{dL_1}{dt} \leq 0$. Moreover, $\frac{dL_1}{dt} = 0$. Therefore, the only trajectory of the system on which $\frac{dL_1}{dt} = 0$ is E_0. Hence, by LaSalle's Invariant Principle [18], E_0 is globally asymptotically stable.

Theorem-4

The endemic equilibrium point E^*_{end} is globally asymptomatically stable in the feasible region Λ.

Proof: Consider the Lyapunov function,

$L_2(t) = \frac{1}{2}[(S(t) - S^*) + (E(t) - E^*) + (I_S(t) - I_S^*) + (I_U(t) - I_U^*) + (R(t) - R^*)]^2$

$\therefore \frac{dL_2}{dt} = [(S(t) - S^*) + (E(t) - E^*) + (I_S(t) - I_S^*) + (I_U(t) - I_U^*) + (R(t) - R^*)](S'(t) + E'(t) + I_S'(t) + I_U'(t) + R'(t))$

$= [(S(t) - S^*) + (E(t) - E^*) + (I_S(t) - I_S^*) + (I_U(t) - I_U^*) + (R(t) - R^*)](B - \mu(S + E + I_S + I_U + R))$

$= [(S(t) - S^*) + (E(t) - E^*) + (I_S(t) - I_S^*) + (I_U(t) - I_U^*) + (R(t) - R^*)](-\mu[(S(t) - S^*) + (E(t) - E^*) + (I_S(t) - I_S^*) + (I_U(t) - I_U^*) + (R(t) - R^*)])$

$= -\mu[(S(t) - S^*) + (E(t) - E^*) + (I_S(t) - I_S^*) + (I_U(t) - I_U^*) + (R(t) - R^*)]^2 \leq 0.$

By putting $B = \mu S^* + \mu E^* + \mu I_S^* + \mu I_U^* + \mu R^*$, we get $\frac{dL_2}{dt} = -\mu[(S(t) - S^*) + (E(t) - E^*) + (I_S(t) - I_S^*) + (I_U(t) - I_U^*) + (R(t) - R^*)]^2 \leq 0$. Hence, E^*_{end} is globally asymptomatically stable.

Numerical simulation

We simulated the transmission dynamics of *Chlamydia* infection, using the parametric values given in Table 1. We carry out a simulation and interpret the behavior of *Chlamydia*.

The variation in the population of the respective compartment concerning time in months shown in Figure 2. This represents that a large population of exposed individuals becomes infected within

one month and the intensity of infected individuals decreases after around 33 days. It can be observed from the graph that infected individuals due to an unhygienic environment can be cured within five months. While infected individuals due to sexual activity can be reduced by up to 10% through proper medication and awareness.

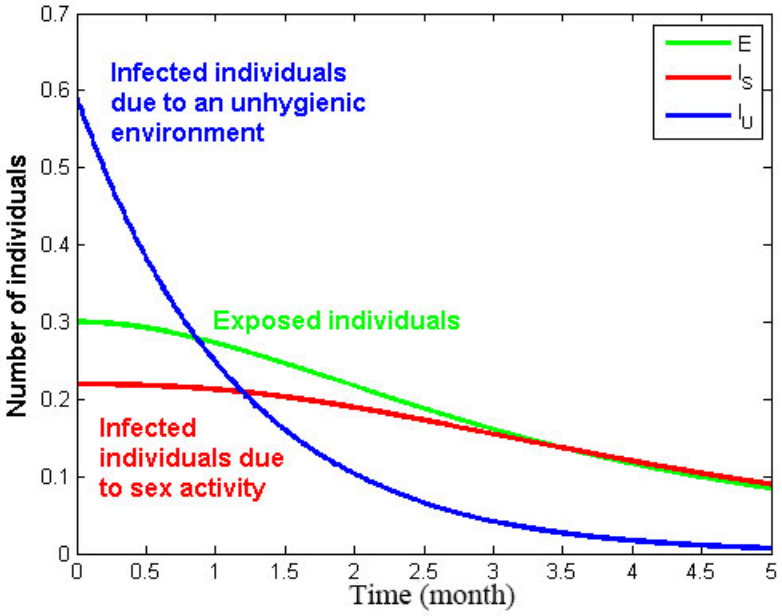


Figure 2. Density in the compartment with time

The change in infected individuals due to being sexually active for different values of α_2 (the rate at which exposed individuals are infected due to sexual activity) indicates Figure 3. It is observed that the number of infected individuals due to sexual activity initially increases by 5% as we increase the value of α_2 but this situation reverses after about 2.5 months, and infected individuals decrease by around 10%.

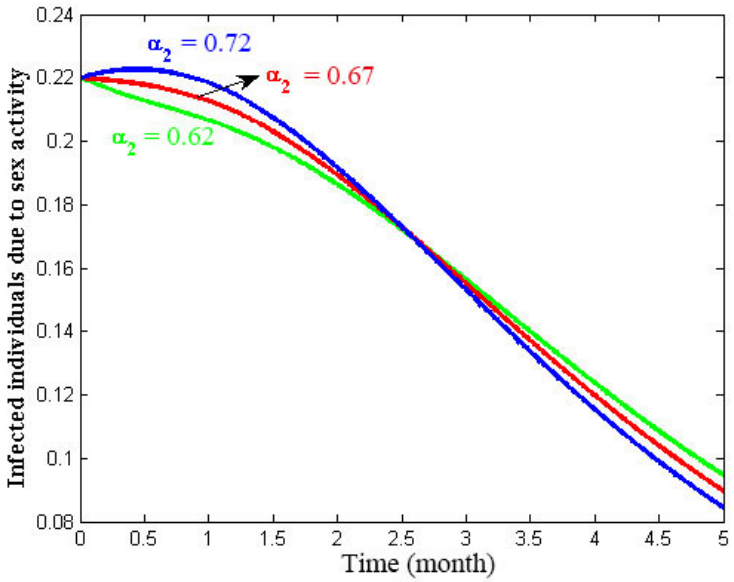
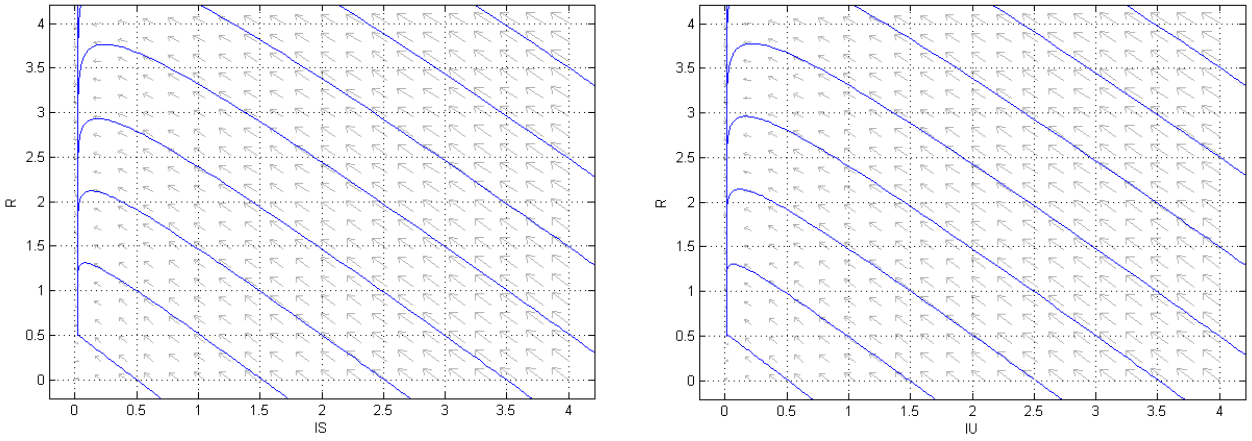


Figure 3. Impact on infected individuals due to sexual activity due to change in α_2

In Figure 4a and 4b, the trajectory field shows the intensity of infected individuals due to sexual activity and an unhygienic environment in the class of recovered individuals by *Chlamydia*, respectively. It can be observed from the Figure 4, that more infected individuals move toward the recovered individuals, but after some point of time it gets stable, and recovered cases decrease up to a certain level.



a b

Figure 4. Intensity of infected individuals in the class of recovered individuals

The movement of susceptible individuals toward the exposed individuals show in Figure 5a. Moreover, it shows the movement of exposed individuals towards the susceptible class at a lower intensity, which illustrates the awareness of exposed individuals to disease transmission and Figure 5b depicts the movement of recovered individuals towards the susceptible class with greater intensity and vice versa.

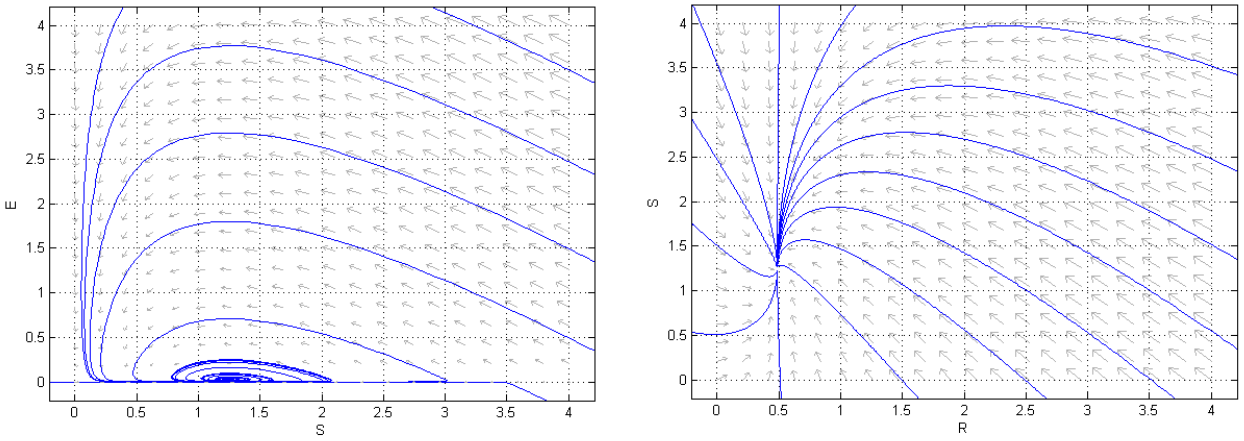


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Figure 5. Trajectory field and solution curve

In Figure 6 a pie chart shows the proportion of the *Chlamydia* model's compartments. *Chlamydia* is a disease that affects 10% of the population, 8% of whom are infected by sexual activity and another 18% by an unhygienic environment, from which 21% of these people can recover from the disease.

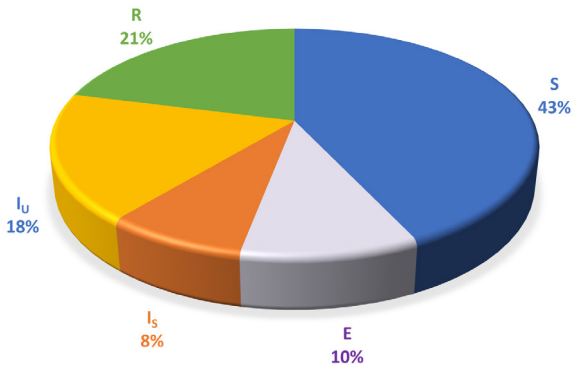

Figure 6. Percentage of all compartment

According to the pie chart in Figure 7a, 25% of people have been exposed to *Chlamydia*, and 20% of people get infections from sexual activity, with 55% of people recovering and Figure 7b shows that 20% of people have been exposed to *Chlamydia*, 37% have been infected as a result of an unhygienic environment, and 43% have recovered. It is also observed that individuals are more infected due to an unhygienic environment as compared to sexually active individuals and that the rate of recovery is much higher for those who get an infection because of an unhygienic environment.

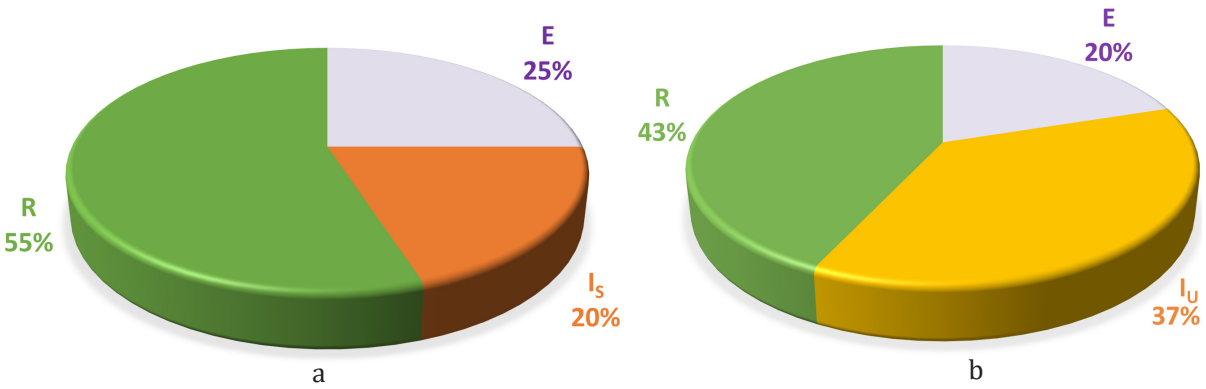

Figure 7. Percentage of exposed individuals and recovery rate due to infected individuals

Conclusions

A mathematical model is formulated to study the transmission of *Chlamydia* infection due to sexual activity and an unhygienic environment. Using a system of nonlinear ordinary differential equations, a basic reproduction number has been calculated at an equilibrium point, and the system is locally and globally asymptotically stable at both disease-free and endemic equilibrium points. Numerical simulations have illustrated the behavior and flow of *Chlamydia* infections in different compartments, which shows how exposed individuals are infected due to sexual activity and unhygienic environments, which demonstrates that sexually transmitted infections can be reduced by up to 10%. While the infection spreads due to an unhygienic environment, it can be controlled in five months. According to the conclusions of this research, public awareness campaigns and the improvement of personal hygiene will both play a major role in reducing the spread of the epidemic in the future.

Abbreviation

STDs: sexually transmitted diseases

Declarations

Author contributions

NHS gave the idea of the diseases and modeling. YNS detailed the conceptual facts. JNV and PMP constructed a model and did the simulation of the proposed system. JNV wrote the research paper and the remaining authors contributed to the write-up.

Conflicts of interest

The authors declare that they have no conflicts of interest.

Ethical approval

Not applicable.

Consent to participate

Not applicable.

Consent to publication

Not applicable.

Availability of data and materials

Not applicable.

Funding

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