Mathematical Modeling of the Transmission Dynamics of Secondary Syphilis Co-Infected with Measles

Innocent Cleopas Eli*

Department of Mathematics and Statistics, Federal University Otuoke, Bayelsa State, Nigeria

***Corresponding Author**

DOI: https://doi.org/10.51584/IJRIAS.2025.10020050

Received: 10 February 2025; Accepted: 14 February 2025; Published: 20 March 2025

ABSTRACT

Disease generally are disorder in plants or animals. The study examined the transmission dynamics of secondary syphilis that is co-infected with measles. The work basically is divided into four important compartments which are immigration factor in the susceptible, syphilis infected, syphilis latent and measles infected compartment. It was observed that no infection free equilibrium exists analytically due to immigration factor, thus, the endemic equilibrium points as the only equilibrium point was obtained. The analytical investigation of the behaviour of the sub-models for secondary syphilis and measles was done with the help of deterministic techniques. It is observed that the asymptotically stable system since all coefficients of equation are positive. Finally, the numerical investigation with the help of MATLAB established the sensitivity of the parameters such that while an increase in all parameters considered increased, the co-infected class did not show any effect on co-infected class. Due to the introduction of immigration factor, the disease-free equilibrium did not exist. Through analytical studies, it is determined that the endemic equilibrium point through which the establishment of the stability of the secondary syphilis and measles sub-models and the coinfection model were achieved. The study went further to numerically simulate the results of the proposed model and obtained the time series plots for each sub-model and the coinfection model. It is observed that the numerical results agreed with analytical findings. It also established the sensitivity of the parameters $\alpha_{MS}, \sigma, \varphi_M, \varphi_S$ and φ_V and observed while an increase in all parameters considered increased in the co-infected class though φ_V did not show any effect on co-infected class.

Keywords: Disease, Mathematical Model, Transmission Dynamics, Syphilis, Co-infected and Measles.

INTRODUCTION

A disease is any harmful deviation from the normal structural and functional state of an organism, generally associated with certain signs and symptoms indicative of an organism abnormal state.

Dynamics in this context, refers to the way people interact and work together. The dynamics of any infections disease are heavily dependent on the rate of transmission from infections to susceptible hosts.

Mathematical modeling is the earliest method used to formulate epidemic spread [1]. The first mathematical model of infectious disease transmission was constructed in 1760 [2], in other to determine the effectiveness of relation, a crude form of small pox vaccination.

In 1906, [2] proposed a discrete time model to understand the recurrence of measles epidemics [1]. In 1911, [1] equally developed differential equations to investigate the effectiveness of various strategies for malaria. [3] then extent [1] models to form a dynamic system model of infectious disease transmission, which is also called compartment model. They found that only if the basic reproduction number was larger than a threshold value, could an infectious disease spread in a susceptible population. The population is assumed to be homogenous, well-mixed, and aggregated into a small set of compartments according to individual health states [4] divided infectious individuals into two sub-groups: super spreaders and regular spreaders, when they studied super spreading events by using compartment models. Also, [5] integrated human behaviour into the variable of average infection rate in order to study the impact that human behaviour change have on epidemic spread. The

ISSN No. 2454-6194 | DOI: 10.51584/IJRIAS |Volume X Issue II February 2025

pattern of human mobility is a determine factor of epidemic diffusion [6]. The random walk-model [7] is used to represent human mobility patterns. This model formulation of a path consists of a succession of random steps and explains that an individual move within a finite space where the individual can move to each position the same probability.

Syphilis is a major severally transmitted disease and has been affecting millions of individuals both in low-and-high-income countries of the world [8]. It is a systemic disease caused by Treponema pallidum bacterium which is mainly transmitted through sex, blood contact, mother to child during birth [9]. Diagnosis, treatment, and using condom are the basic control mechanisms [8]. If left untreated, syphilis progresses through four stages: Primary, Secondary, Latent, and Tertiary [10]. The first three infection stages can transmit the disease to other susceptible groups of individuals, the transmission can occur via sexual contact and in most cases, the tertiary stage is not transmissible through sexual contact [11]. Approximately, 90% of new syphilis substantial morbidity and mortality data are recorded in low-in-come countries around the world [12]. Co-infection is an infection of an individual with two or more micro-organisms species [13].

Measles is an infectious disease which was first acknowledged in Boston in 1675 by [14]. It is acute and highly infectious vital disease caused by morbillivirus (measles virus) for which humans are the only reservoirs [15]. In the last two decades, the global cases of measles have been decking before the emergence of covid-19 pandemic. The number of measles infections increased in 2019, reaching 869, 770 cases 207,500 deaths which is the highest incidence of the disease since 1996 [16]. Recently there has been an increase in measles infections in sub-saharan Africa with 17,500 cases altogether as of January 2022, a 400% spike from cases reported in 2021 [17]. The primary source of transmission is through direct contact with the nose and throat secretions of an infected person or by aerosolized droplets [15]. When measles virus infects a non-immune population, almost everyone will become infected [18]. According to [17], the virus survives in the atmosphere for up to two hours when an infected individual's coughs or sneezes.

To study the dynamics of measles illness spread, numerous researchers have designed various mathematical models [19] developed a mathematical model of measles, transmission dynamics for measles epidemiology considering the impact of exposed individuals to the latest period and discussed through stability analysis and numerical simulation [20] formulated the SEIRV model for measles and the model has shown importance of measles vaccination in preventing transmission within a population. They conclude from their findings that the spread of a disease largely depends on the contact rates and also the proportion of the population that is immune exceed the herds immunity level of measles. [21] investigated an infection in which population is divided into susceptible, latent, infected, post infection and recovered using ordinary differential equation. Another simulation of measles transmission dynamics under the intervention of vaccination was performed by [22] to investigate the transmission of measles virus using the five categories of susceptible, vaccinated, exposed infectious and recovered individuals with demographic factors using the deterministic compartment model. [23] developed a model of measles transmission dynamics with double dose vaccination. The model was used to determine the significant role of stochastic approach and the analysis of positivity of solution, invariant region of the solution, the existence of equilibrium points and their stability and sensitivity analysis of parameters of the basic reproductive number of both the model analyzed and done in deterministic and stochastic approaches. A model formulated by [24] on measles dynamics of network tries to emphasize a transmission rate and theoretically examine the threshold dynamics to investigate the influence of heterogeneity and warning immunity of measles transmission dynamics. [25] recently developed open a novel transmission dynamics model to evaluate the effects of monitored vaccination program to control and eliminate measles. In this paper, we studied the transmission dynamics of secondary syphilis co-infected with measles.

Mathematical Formulation

Model Variables Definition

The total sexually active population at time t, denoted by $N(t)$ is subdivided into the mutually exclusive compartments of susceptible individuals $(N(t))$, vaccinated individuals for measles infection $(V(t))$, population of secondary syphilis infected and infectious individuals $(I_S(t))$, latently infected syphilis population $(L_S(t))$, measles infected individuals $(I_M(t))$, who are capable of transmitting the disease,

ISSN No. 2454-6194 | DOI: 10.51584/IJRIAS |Volume X Issue II February 2025

population of infectious individuals with secondary stage syphilis and measles co-infection $(I_{MS}(t))$, individuals who recover from the infection $(R(t))$ and individuals undergoing treatment for secondary syphilis $(T(t))$.

The constant recruitment of secondary syphilis infected and infectious individuals, latently infected syphilis individuals and measles infected individuals into the population will cause the disease never to die out hence no disease-free equilibrium.

Basic Assumptions of the Model

The proposed model has the following basic assumptions:

- The local density of the total population is a constant though the total population size may vary with time.
- Individuals infected with secondary syphilis can be infected with measles and vice versa.
- Individuals co-infected with secondary syphilis and measles can transmit either syphilis or measles.
- Co-infected individuals can recover from either secondary syphilis or measles at the same time.
- There are two different infection rates, namely, the infection rate of secondary syphilis (β_S) and the infection rate of measles(β_M). Infection rate for singly infected and co-infected individuals are assumed to be the same.
- Vaccinated individuals automatically recovers from measles infection but could be infected with secondary syphilis by coming in contact with syphilis infectious individuals.
- Recovered individuals acquire permanent immunity and are not susceptible.
- The recovery rates for all compartments are different.
- Co-infected individuals have a higher death rate than singly infected individuals do.
- Natural death rate is the same for all compartments.

Model Parameters Definition

The parameters used in the proposed model are defined as follows

$\Lambda =$ Rate of recruitment

$\beta_S =$ Force of infection between susceptible, syphilis infected and co-infected individuals

$\beta_M =$ Force of infection between susceptible, measles infected and co-infected individuals

$\beta_V =$ Force of infection between vaccinated and syphilis infected individuals

$\delta =$ Fraction of syphilis infected individuals to become latent for syphilis

$\rho =$ Treatment rate of syphilis latent individuals

$\alpha_M =$ Rate at which co-infected individuals recover from measles

$\alpha_S =$ Rate at which co-infected individuals recover from secondary syphilis

ISSN No. 2454-6194 | DOI: 10.51584/IJRIAS |Volume X Issue II February 2025

α_{MS} = Rate at which co-infected individuals recover from the co-infection

σ = Rate at which susceptible individuals receive measles vaccine

d_S = Death rate due to secondary syphilis infection

d_M = Death rate due to measles infection

d_{MS} = Death rate due to co-infection

ε = Recovery rate of measles infected individuals

τ = Recovery rate individuals undergoing syphilis treatment

γ = Recovery rate of measles vaccinated individuals

μ = Natural death rate

φ_M = Contact rate between susceptible individuals and measles infected individuals

φ_S = Contact rate between susceptible individuals and secondary syphilis infected individuals

φ_V = Contact rate between measles vaccinated individuals and secondary syphilis infected individuals

κ = Recovery rate for syphilis infected population

Model Formulation

The mathematical model for the spread of secondary syphilis co-infected with measles based on the model description and basic assumptions is given by the following system of nonlinear ordinary differential equations.

$$\frac{dS}{dt} = (1-a-b-c)\Lambda N - (\sigma + \mu + \beta_M + \beta_S)S \quad (3.1)$$

$$\frac{dI_S}{dt} = a\Lambda N + (\beta_S - \beta_M)S - (\mu + d_S + \kappa + \delta)I_S + \alpha_M I_{MS} + \beta_V V \quad (3.2)$$

$$\frac{dI_M}{dt} = c\Lambda N + (\beta_M - \beta_S)S - (\mu + d_M + \varepsilon)I_M + \alpha_S I_{MS} \quad (3.3)$$

$$\frac{dI_{MS}}{dt} = (\beta_M + \beta_S)S - (\mu + d_{MS} + \alpha_M + \alpha_S + \alpha_{MS})I_{MS} \quad (3.4)$$

$$\frac{dL_S}{dt} = b\Lambda N + \delta I_S - (\mu + \rho + d_s)L_S \quad (3.5)$$

$$\frac{dT}{dt} = \rho L_S - (\mu + \tau + d_s)T \quad (3.6)$$

$$\frac{dV}{dt} = \sigma S - \beta_V V - (\mu + \gamma)V \quad (3.7)$$

$$\frac{dR}{dt} = \kappa I_S + \varepsilon I_M + \alpha_{MS} I_{MS} + \tau T + \gamma V - \mu R \quad (3.8)$$

With initial conditions

$$S(0) > 0, I_S(0) \geq 0, I_M(0) \geq 0, I_{MS}(0) \geq 0, L_S(0) \geq 0, T(0) \geq 0, V(0) \geq 0 \text{ and } R(0) \geq 0. \quad (3.9)$$

ISSN No. 2454-6194 | DOI: 10.51584/IJRIAS |Volume X Issue II February 2025

Where

$$\beta_S = \frac{\varphi_S(I_S+I_{MS})}{N} \quad (3.10)$$

$$\beta_M = \frac{\varphi_M(I_M+I_{MS})}{N} \quad (3.11)$$

$$\beta_V = \frac{\varphi_V I_S}{N} \quad (3.12)$$

Model Analysis

To understand the dynamics of the proposed model, we find the equilibrium points of the system and investigate the dynamics of the equilibrium points. Since no infection free equilibrium exist due to immigration factor, the endemic equilibrium point is the only equilibrium point under consideration. The analysis will be done by investigating the behavior of the sub-models for secondary syphilis and measles.

Determination of Endemic Equilibrium Point of the Syphilis Submodel

Without considering the infections of people with measles, the syphilis sub-model is given as

$$\frac{dS}{dt} = (1-a-b-c)\Lambda N - (\mu+\beta_S)S \quad (3.13)$$

$$\frac{dI_S}{dt} = a\Lambda N + \beta_S S - (\mu + d_S + \kappa + \delta)I_S \quad (3.14)$$

$$\frac{dL_S}{dt} = b\Lambda N + \delta I_S - (\mu + \rho + d_s)L_S \quad (3.15)$$

$$\frac{dT}{dt} = \rho L_S - (\mu + \tau + d_s)T \quad (3.16)$$

$$\frac{dR}{dt} = \kappa I_S + \tau T - \mu R \quad (3.17)$$

and

$$\beta_S = \frac{\varphi_S I_S}{N} \quad (3.18)$$

We obtain the steady state solution by letting

$$\frac{dS}{dt} = \frac{dI_S}{dt} = \frac{dL_S}{dt} = \frac{dT}{dt} = \frac{dR}{dt} = 0$$

We obtain the steady state solution by letting

$$\frac{dS}{dt} = \frac{dI_S}{dt} = \frac{dI_M}{dt} = \frac{dI_{MS}}{dt} = \frac{dL_S}{dt} = \frac{dT}{dt} = \frac{dV}{dt} = \frac{dR}{dt} = 0$$

in equations $(3.13 - 3.17)$ and solving the resulting equations for S, I_S, L_S, T and R.

we get the following,

$$(1-a-b-c)\Lambda N - (\mu+\beta_S)S = 0 \quad (3.19)$$

$$a\Lambda N + \beta_S S - (\mu + d_S + \kappa + \delta)I_S = 0 \quad (3.20)$$

$$b\Lambda N + \delta I_S - (\mu + \rho + d_s)L_S = 0 \quad (3.21)$$

$$\rho L_S - (\mu + \tau + d_s)T = 0 \quad (3.22)$$

ISSN No. 2454-6194 | DOI: 10.51584/IJRIAS |Volume X Issue II February 2025

$$\kappa I_S + \tau T - \mu R = 0 \quad (3.23)$$

From equation 3.19,

$$S = \frac{(1-a-b-c)\Lambda N}{(\mu+\beta_S)} \quad (3.24)$$

Substitute equation 3.24 into equation 3.20, we get,

$$a\Lambda N + \beta_S \frac{(1-a-b-c)\Lambda N}{(\mu+\beta_S)} - (\mu + d_S + \kappa + \delta)I_S = 0$$

We solve for I_S and get

$$I_S = \frac{\beta_S(1-a-b-c)\Lambda N + a\Lambda N(\mu+\beta_S)}{(\mu+d_S+\kappa+\delta)(\mu+\beta_S)} \quad (3.25)$$

Substitute equation 3.25 into equation 3.18, we get a quadratic equation to be solved for β_S as shown below

$$(\mu + d_S + \kappa + \delta){\beta_S}^2 + [(\mu + d_S + \kappa + \delta)\mu - (1 - a - b - c)\Lambda\varphi_S - a\Lambda\varphi_S]\beta_S - a\Lambda\varphi_S\mu = 0$$

$$\beta_S = -\frac{[(\mu+d_S+\kappa+\delta)\mu-(1-a-b-c)\Lambda\varphi_S-a\Lambda\varphi_S]\pm\Delta}{2(\mu+d_S+\kappa+\delta)} \quad (3.26)$$

Where Δ is given as

$$\Delta = \sqrt{[(\mu + d_S + \kappa + \delta)\mu - (1 - a - b - c)\Lambda\varphi_S - a\Lambda\varphi_S]^2 + 4a\Lambda\varphi_S\mu(\mu + d_S + \kappa + \delta)}$$

Substitute equation 3.25 into equation 3.21,

$$b\Lambda N + \delta\frac{\beta_S(1-a-b-c)\Lambda N + a\Lambda N(\mu+\beta_S)}{(\mu+d_S+\kappa+\delta)(\mu+\beta_S)} - (\mu + \rho + d_s)L_S = 0$$

Then solving for L_S we get,

$$L_S = \frac{b\Lambda N}{(\mu+\rho+d_s)} + \frac{\delta[\beta_S(1-a-b-c)\Lambda N + a\Lambda N(\mu+\beta_S)]}{(\mu+\rho+d_s)(\mu+d_S+\kappa+\delta)(\mu+\beta_S)} \quad (3.27)$$

Substitute equation 3.27 into equation 3.22,

$$T = \frac{\rho}{(\mu+\tau+d_s)}\left[\frac{b\Lambda N}{(\mu+\rho+d_s)} + \frac{\delta[\beta_S(1-a-b-c)\Lambda N + a\Lambda N(\mu+\beta_S)]}{(\mu+\rho+d_s)(\mu+d_S+\kappa+\delta)(\mu+\beta_S)}\right] \quad (3.28)$$

Substitute equation 3.25 and equation 3.28 in equation 3.23 to get

$$\kappa\left[\frac{b\Lambda N}{(\mu+\rho+d_s)} + \frac{\delta[\beta_S(1-a-b-c)\Lambda N + a\Lambda N(\mu+\beta_S)]}{(\mu+\rho+d_s)(\mu+d_S+\kappa+\delta)(\mu+\beta_S)}\right]$$

$$+\tau\frac{\rho}{(\mu+\tau+d_s)}\left[\frac{b\Lambda N}{(\mu+\rho+d_s)} + \frac{\delta[\beta_S(1-a-b-c)\Lambda N + a\Lambda N(\mu+\beta_S)]}{(\mu+\rho+d_s)(\mu+d_S+\kappa+\delta)(\mu+\beta_S)}\right] - \mu R = 0$$

On solving for R, we get,

$$R = \frac{\kappa}{\mu}\left[\frac{b\Lambda N}{(\mu+\rho+d_s)} + \frac{\delta[\beta_S(1-a-b-c)\Lambda N + a\Lambda N(\mu+\beta_S)]}{(\mu+\rho+d_s)(\mu+d_S+\kappa+\delta)(\mu+\beta_S)}\right]$$
$$+\frac{\tau\rho}{\mu(\mu+\tau+d_s)}\left[\frac{b\Lambda N}{(\mu+\rho+d_s)} + \frac{\delta[\beta_S(1-a-b-c)\Lambda N + a\Lambda N(\mu+\beta_S)]}{(\mu+\rho+d_s)(\mu+d_S+\kappa+\delta)(\mu+\beta_S)}\right] \quad (3.29)$$

Due to the nature of β_S obtained in equation 3.26, two equilibria points exist.

ISSN No. 2454-6194 | DOI: 10.51584/IJRIAS |Volume X Issue II February 2025

Local Stability of Endemic Equilibrium Points

Theorem 3.3.1: The endemic equilibrium point is locally asymptotically stable if all eigenvalues of its characteristic polynomial are negative.

Proof:

We linearize equations $(3.13 - 3.17)$ by making the following substitutions and obtaining the Jacobian matrix as shown below;

$$f_1 = (1 - a - b - c)\Lambda N - (\mu + \beta_S)S$$
$$f_2 = a\Lambda N + \beta_S S - (\mu + d_S + \kappa + \delta)I_S$$
$$f_3 = b\Lambda N + \delta I_S - (\mu + \rho + d_s)L_S$$
$$f_4 = \rho L_S - (\mu + \tau + d_s)T$$
$$f_5 = \kappa I_S + \tau T - \mu R$$

$$J = \begin{bmatrix} \frac{\partial f_1}{\partial S} & \frac{\partial f_1}{\partial I_S} & \frac{\partial f_1}{\partial L_S} & \frac{\partial f_1}{\partial T} & \frac{\partial f_1}{\partial R} \\ \frac{\partial f_2}{\partial S} & \frac{\partial f_2}{\partial I_S} & \frac{\partial f_2}{\partial L_S} & \frac{\partial f_2}{\partial T} & \frac{\partial f_2}{\partial R} \\ \frac{\partial f_3}{\partial S} & \frac{\partial f_3}{\partial I_S} & \frac{\partial f_3}{\partial L_S} & \frac{\partial f_3}{\partial T} & \frac{\partial f_3}{\partial R} \\ \frac{\partial f_4}{\partial S} & \frac{\partial f_4}{\partial I_S} & \frac{\partial f_4}{\partial L_S} & \frac{\partial f_4}{\partial T} & \frac{\partial f_4}{\partial R} \\ \frac{\partial f_5}{\partial S} & \frac{\partial f_5}{\partial I_S} & \frac{\partial f_5}{\partial L_S} & \frac{\partial f_5}{\partial T} & \frac{\partial f_5}{\partial R} \end{bmatrix} \quad (3.30)$$

At endemic equilibria

$$J = \begin{bmatrix} -(\mu + \beta_S) & -\frac{\varphi_S S}{N} & 0 & 0 & 0 \\ \beta_S & \frac{\varphi_S S}{N} - (\mu + d_S + \kappa + \delta) & 0 & 0 & 0 \\ 0 & 0 & \delta - (\mu + \rho + d_s) & 0 & 0 \\ 0 & 0 & \rho & -(\mu + \tau + d_s) & 0 \\ 0 & \kappa & 0 & \tau & -\mu \end{bmatrix}$$

$|J - \lambda I| = 0 \Rightarrow$

$$\begin{vmatrix} -(\mu + \beta_S) - \lambda & -\frac{\varphi_S S}{N} & 0 & 0 & 0 \\ \beta_S & \frac{\varphi_S S}{N} - (\mu + d_S + \kappa + \delta) - \lambda & 0 & 0 & 0 \\ 0 & 0 & \delta - (\mu + \rho + d_s) - \lambda & 0 & 0 \\ 0 & 0 & \rho & -(\mu + \tau + d_s) - \lambda & 0 \\ 0 & \kappa & 0 & \tau & -\mu - \lambda \end{vmatrix} = 0 \quad (3.31)$$

On solving equation 3.31, we get,

$$\lambda^5 + A\lambda^4 + B\lambda^3 + C\lambda^2 + D\lambda + E = 0 \quad (3.32)$$

Where

$$A = \left((\mu + d_S + \kappa + \delta) + \beta_S + (\mu + \tau + d_s) - \delta + 2\mu + (\mu + \rho + d_s) - \frac{\varphi_S S}{N} \right)$$

ISSN No. 2454-6194 | DOI: 10.51584/IJRIAS |Volume X Issue II February 2025

$$B = (\mu + d_S + \kappa + \delta)\left(\beta_S + (\mu + \tau + d_s) - \delta + 2\mu + (\mu + \rho + d_s)\right) + (\mu + \tau + d_s)\left(\beta_S - \delta + 2\mu + (\mu + \rho + d_s) - \frac{\varphi_S S}{N}\right) + (\mu + \rho + d_s)\left(\beta_S + 2\mu - \frac{\varphi_S S}{N}\right) - \beta_S\delta + \beta_S\mu - 2\delta\mu + \frac{\delta\varphi_S S}{N} + \mu^2$$

$$C = (\mu + d_S + \kappa + \delta)(\mu + \tau + d_s)\left(\beta_S - \delta + 2\mu + (\mu + \rho + d_s)\right) + (\mu + d_S + \kappa + \delta)(\mu + \rho + d_s)(\beta_S + 2\mu) + (\mu + \rho + d_s)(\mu + \tau + d_s)\left(\beta_S + 2\mu - \frac{\varphi_S S}{N}\right) + (\mu + d_S + \kappa + \delta)\beta_S(\mu - \delta) + (\mu + \tau + d_s)\beta_S(\mu - \delta) + \frac{\varphi_S S}{N}(\mu + \tau + d_s)(\delta - 2\mu) + \mu^2(\mu + d_S + \kappa + \delta) - 2\delta\mu(\mu + d_S + \kappa + \delta) - \beta_S\mu\delta + \beta_S\mu(\mu + \rho + d_s) - 2\delta\mu(\mu + \tau + d_s) - \delta\mu^2 + \mu^2(\mu + \tau + d_s)$$

$$D = (\mu + d_S + \kappa + \delta)(\mu + \tau + d_s)\left(\beta_S\mu - \beta_S\delta + \beta_S(\mu + \rho + d_s) - 2\mu\delta + \mu^2 + 2\mu(\mu + \rho + d_s)\right) + (\mu + \rho + d_s)(\mu + d_S + \kappa + \delta)(\beta_S\mu + \mu^2) + (\mu + \rho + d_s)(\mu + \tau + d_s)\left(\beta_S\mu + \mu^2 - 2\mu\frac{\varphi_S S}{N}\right) - (\mu + d_S + \kappa + \delta)\delta\mu(\beta_S + \mu) + (\mu + \tau + d_s)\left(-\beta_S\delta\mu - \delta\mu^2 + 2\delta\frac{\varphi_S S}{N} - \mu^2\frac{\varphi_S S}{N}\right) + \delta\mu^2\frac{\varphi_S S}{N} - \mu^2\frac{\varphi_S S}{N}(\mu + \rho + d_s)$$

$$E = \mu(\mu + d_S + \kappa + \delta)(\mu + \tau + d_s)\left(\beta_S(\mu + \rho + d_s) - \beta_S\delta\mu - \delta\mu + \mu(\mu + \rho + d_s)\right) + \mu^2\frac{\varphi_S S}{N}(\mu + \tau + d_s)\left(\delta - (\mu + \rho + d_s)\right)$$

All eigenvalues of equation 3.32 will be negative if one or all values β_S and S produce non-negative coefficients. This fact will be verified numerically in subsequent sections of this project

Determination of Endemic Equilibrium Point of the Measles Submodel

Without considering the infections of people with syphilis, the measles sub-model is given as

$$\frac{dS}{dt} = (1 - a - b - c)\Lambda N - (\sigma + \mu + \beta_M)S \quad (3.33)$$

$$\frac{dI_M}{dt} = c\Lambda N + \beta_M S - (\mu + d_M + \varepsilon)I_M \quad (3.34)$$

$$\frac{dV}{dt} = \sigma S - (\mu + \gamma)V \quad (3.35)$$

$$\frac{dR}{dt} = \varepsilon I_M + \gamma V - \mu R \quad (3.36)$$

And

$$\beta_M = \frac{\varphi_M I_M}{N} \quad (3.37)$$

We obtain the steady state solution by equating equations (3.33 − 3.36) to zero and solve for the variables.

$$(1 - a - b - c)\Lambda N - (\sigma + \mu + \beta_M)S = 0 \quad (3.38)$$

$$c\Lambda N + \beta_M S - (\mu + d_M + \varepsilon)I_M = 0 \quad (3.39)$$

ISSN No. 2454-6194 | DOI: 10.51584/IJRIAS |Volume X Issue II February 2025

$$\sigma S - (\mu + \gamma)V = 0 \quad (3.40)$$

$$\varepsilon I_M + \gamma V - \mu R = 0 \quad (3.41)$$

From equation 3.38,

$$S = \frac{(1-a-b-c)\Lambda N}{(\mu+\sigma+\beta_M)} \quad (3.42)$$

Substitute equation 3.42 into equations 3.39 and 3.40, we get,

$$c\Lambda N + \beta_M \frac{(1-a-b-c)\Lambda N}{(\mu+\sigma+\beta_M)} - (\mu + d_M + \varepsilon)I_M = 0$$

$$I_M = \frac{\beta_M(1-a-b-c)\Lambda N + c\Lambda N(\mu+\sigma+\beta_M)}{(\mu+\sigma+\beta_M)(\mu+d_M+\varepsilon)} \quad (3.43)$$

And

$$\sigma \frac{(1-a-b-c)\Lambda N}{(\mu+\sigma+\beta_M)} - (\mu + \gamma)V = 0$$

$$V = \frac{\sigma(1-a-b-c)\Lambda N}{(\mu+\sigma+\beta_M)(\mu+\gamma)} \quad (3.44)$$

Substitute equations 3.43 and 3.44 into equation 3.41,

$$\varepsilon \frac{\beta_M(1-a-b-c)\Lambda N + c\Lambda N(\mu+\sigma+\beta_M)}{(\mu+\sigma+\beta_M)(\mu+d_M+\varepsilon)} + \gamma \frac{\sigma(1-a-b-c)\Lambda N}{(\mu+\sigma+\beta_M)(\mu+\gamma)} - \mu R = 0$$

$$R = \frac{\gamma\sigma(\mu+\sigma+\beta_M)(1-a-b-c)\Lambda N + \varepsilon(\mu+\gamma)\left(\beta_M(1-a-b-c)\Lambda N + c\Lambda N(\mu+\sigma+\beta_M)\right)}{\mu(\mu+\sigma+\beta_M)(\mu+\gamma)(\mu+d_M+\varepsilon)} \quad (3.45)$$

To obtain β_M we substitute equation 3.43 into equation 3.37, a quadratic equation is obtained given as

$$(\mu + d_M + \varepsilon){\beta_M}^2 + [(\mu + d_M + \varepsilon)\mu - (1 - a - b - c)\Lambda\varphi_M - c\Lambda\varphi_M]\beta_M - c\Lambda\varphi_M\mu = 0$$

$$\beta_M = -\frac{[(\mu+d_M+\varepsilon)\mu-(1-a-b-c)\Lambda\varphi_M-c\Lambda\varphi_M]\pm\Delta}{2(\mu+d_M+\varepsilon)} \quad (3.45)$$

Where,

$$\Delta = \sqrt{[(\mu + d_M + \varepsilon)\mu - (1 - a - b - c)\Lambda\varphi_M - c\Lambda\varphi_M]^2 + 4c\Lambda\varphi_M\mu(\mu + d_M + \varepsilon)}$$

Due to the nature of β_S obtained in equation 3.26, two equilibria points exist.

Local Stability of Endemic Equilibrium Points

Theorem 3.5.1: The endemic equilibrium point is locally asymptotically stable if all eigenvalues of its characteristic polynomial are negative.

Proof:

We linearize equations $(3.33 - 3.36)$ by making the following substitutions and obtaining the Jacobian matrix as shown below

ISSN No. 2454-6194 | DOI: 10.51584/IJRIAS |Volume X Issue II February 2025

$$f_1 = (1-a-b-c)\Lambda N - (\sigma+\mu+\beta_M)S$$
$$f_2 = c\Lambda N + \beta_M S - (\mu + d_M + \varepsilon)I_M$$
$$f_3 = \sigma S - (\mu+\gamma)V$$
$$f_4 = \varepsilon I_M + \gamma V - \mu R$$

$$J = \begin{bmatrix} -(\sigma+\mu+\beta_M) & -\frac{\varphi_M S}{N} & 0 & 0 \\ \beta_M & \frac{\varphi_M S}{N} - (\mu + d_M + \varepsilon) & 0 & 0 \\ \sigma & 0 & -(\mu+\gamma) & 0 \\ 0 & \varepsilon & \gamma & -\mu \end{bmatrix}$$

$|J - \lambda I| = 0 \Rightarrow$

$$\begin{vmatrix} -(\sigma+\mu+\beta_M)-\lambda & -\frac{\varphi_M S}{N} & 0 & 0 \\ \beta_M & \frac{\varphi_M S}{N} - (\mu + d_M + \varepsilon) - \lambda & 0 & 0 \\ \sigma & 0 & -(\mu+\gamma)-\lambda & 0 \\ 0 & \varepsilon & \gamma & -\mu-\lambda \end{vmatrix} = 0 \quad (3.46)$$

We solve equation 3.46 and get

$$\lambda^4 + A\lambda^3 + B\lambda^2 + C\lambda + D = 0 \quad (3.47)$$

Where,

$$A = \beta_M + 4\mu + d_M + \varepsilon - \frac{\varphi_M S}{N} + \gamma + \sigma$$

$$B = (\mu + d_M + \varepsilon)(\beta_M + 3\mu + \gamma + \sigma) + 2\beta_M\mu + \beta_M\gamma - (3\mu + \gamma + \sigma)\frac{\varphi_M S}{N} + 3\mu^2 + 2\mu\gamma + 2\mu\sigma + \gamma\sigma$$

$$C = (\mu + d_M + \varepsilon)(2\beta_M\mu + \beta_M\gamma + 3\mu^2 + 2\mu\gamma + 2\mu\sigma + \gamma\sigma) - (3\mu^2 + 2\mu\gamma + 2\mu\sigma + \gamma\sigma)\frac{\varphi_M S}{N} + \beta_M\mu^2 + \beta_M\mu\gamma + \mu^3 + \mu^2\gamma + \mu^2\sigma + \mu\gamma\sigma$$

$$D = (\mu + d_M + \varepsilon)(\beta_M\mu^2 + \beta_M\mu\gamma + \mu^3 + \mu^2\gamma + \mu^2\sigma + \mu\gamma\sigma) - (\mu^3 + \mu^2\gamma + \mu^2\sigma + \mu\gamma\sigma)\frac{\varphi_M S}{N}$$

All eigenvalues of equation 3.47 will be negative if one or all values β_M and S produce non-negative coefficients. This fact will also be verified numerically in subsequent sections of this project.

Full Model Endemic Equilibrium Point and Stability

The co-infection model endemic equilibrium point is denoted by

$$E_{MS} = (S^*, I_S^*, I_M^*, I_{MS}^*, L_S^*, T^*, V^*, R^*)$$

The explicit calculations of the co-infection model endemic equilibrium point in terms of the model parameters are tedious analytically. We have shown its stability in the time series plot in the next chapter.

RESULTS

The results were obtained with the help of matlab as seen below.

ISSN No. 2454-6194 | DOI: 10.51584/IJRIAS |Volume X Issue II February 2025

Numerical Verification of Endemic Equilibrium Points

In the previous section , we obtained two equilibrium points for the secondary syphilis and measles sub models due to the nature of their respective forces of infections $\beta_S$and β_M. Using the parameter values in table 4.1 when substituted into equations 3.26 and 3.45 we obtain two results for β_M which are β_{M_1} = -0.35778 and $\beta_{M2} = 0.014153$. Since $0 < \beta_M < 1$, we choose $\beta_M = \beta_{M2} = 0.014153$. For the chosen β_M we obtain the following results;

$A = 1.3631, B = 0.61272, C = 0.10038$ and $D = 0.0049992 S = 248.28, I_M = 77.557, V = 653.37$and $R = 1156.8$.

We observe that the endemic equilibrium point given as $E_M = (248.28,77.557,653.37,1156.8)$ is asymptotically stable since all coefficients of equation 3.47 are positive.

Similarly, two results were obtained for β_S given as $\beta_{S_1} = 0.0022791$ and $\beta_{S2} = 0.16859$. Since both results occur in the feasible region of β_S i.e positive, we obtain two equilibrium points.

For β_{S_1}: $E_{S1} = (1625.5,77.833,463.3,2984.3,2521.7)$

For β_{S_2}: $E_{S2} = (580.07,214.19,532.64,3430.9,2899.1)$

We check the stability of each equilibrium point by computing A,B,C,D and E according to the equation 3.32. we obtain the following results;

For β_{S_1}: $A = 0.38933, B =$ -0.50801, $C =$ -0.25098, $D =$ -0.031861 and $E =$ -0.0011978.

For β_{S_2}: $A = 1.4965, B = 0.87613, C = 0.28162, D = 0.045576$ and $E = 0.0043393$.

From the results obtained, E_{S2} is asymptotically stable while E_{S1} is unstable.

Model Solution

In order to solve the model, we have used the following parameter values

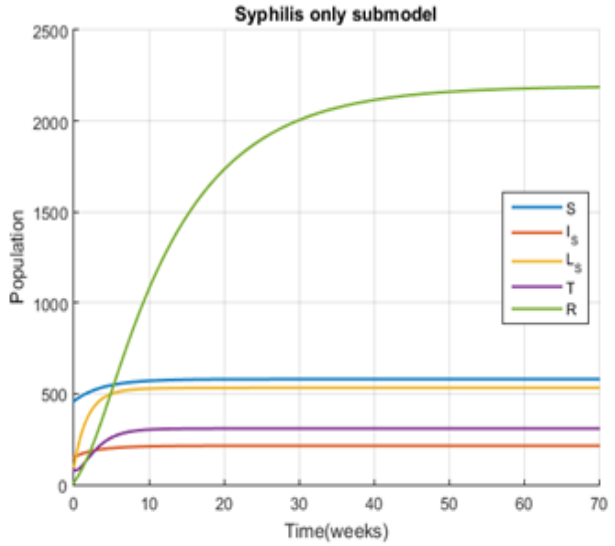
Table 4.1: Parameter values of proposed model

S/N	Parameter	Numeric value	S/N	Parameter	Numeric value
1	Λ	0.5	12	τ	0.5
2	δ	0.3	13	γ	0.1
3	ρ	0.4	14	μ	0.09
4	α_M	0.3	15	φ_M	0.85
5	α_S	0.8	16	φ_S	0.9
6	α_{MS}	0.3	17	φ_V	0.1
7	σ	0.5	18	κ	0.2
8	d_S	0.1	19	a	0.1
9	d_{MS}	0.12	20	b	0.5
10	d_M	0.1	21	c	0.1
11	ε	0.5			

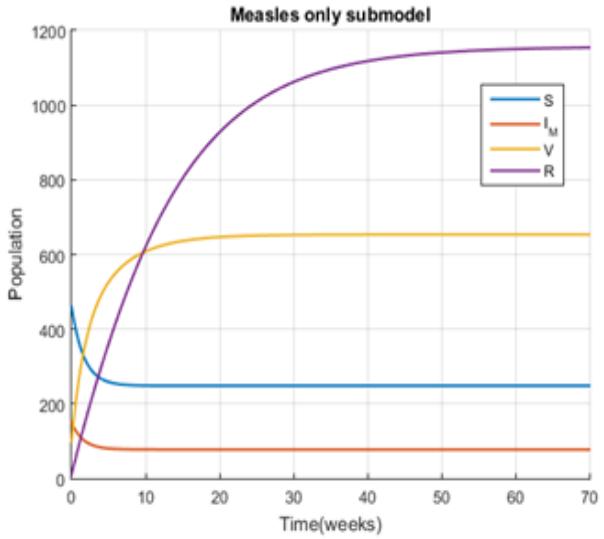
The initial values used in obtaining the solution of the model are given below,

$$N(0) = 1000, 200 < S(0) < 500, 0 < I_S(0) < 200, I_M(0) = 150, I_{MS}(0) = 150, L_S(0) = 100,$$
$$50 < T(0) \leq 100, V(0) = 100 \text{and} R(0) = 10$$

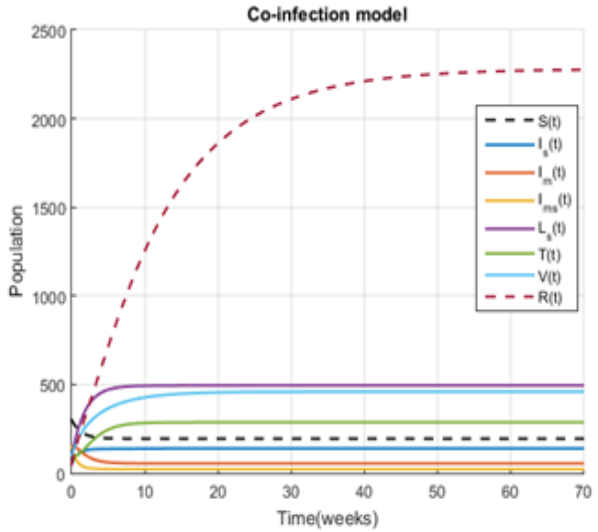
ISSN No. 2454-6194 | DOI: 10.51584/IJRIAS |Volume X Issue II February 2025



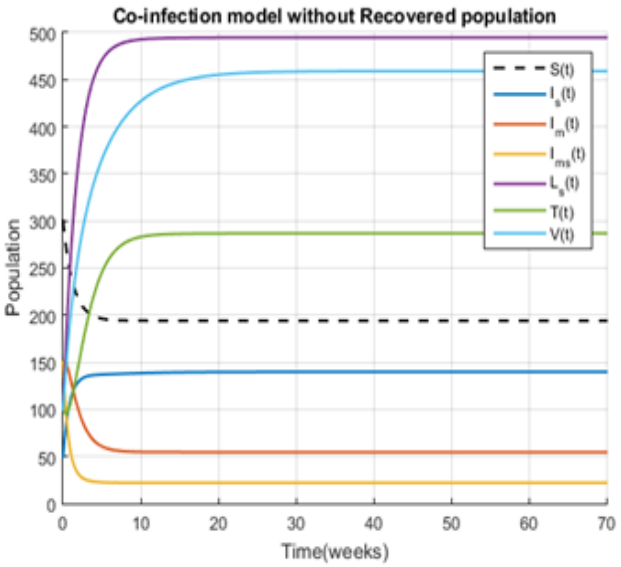
(a)



(b)

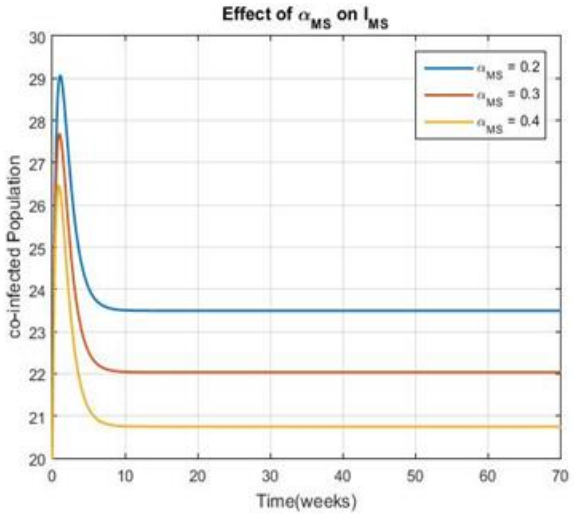


(c)

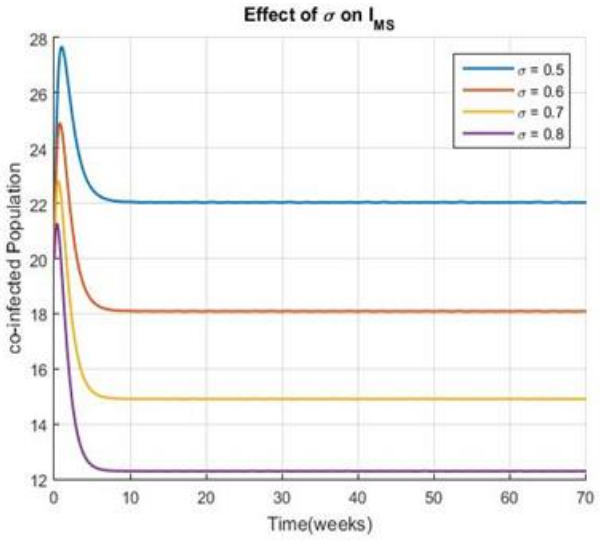


(d)

Impact of Treatment and Vaccination on the Co-Infected Population



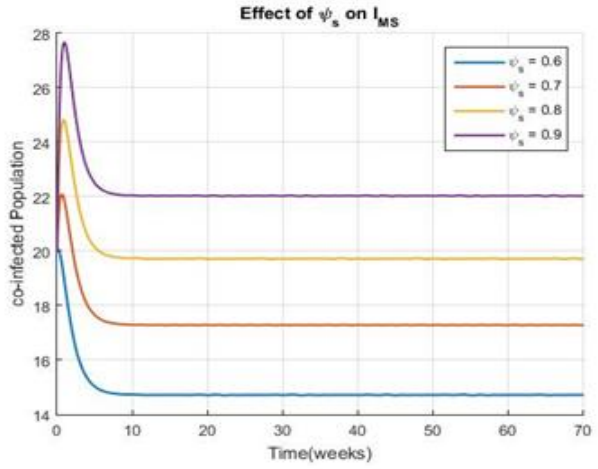
(a)



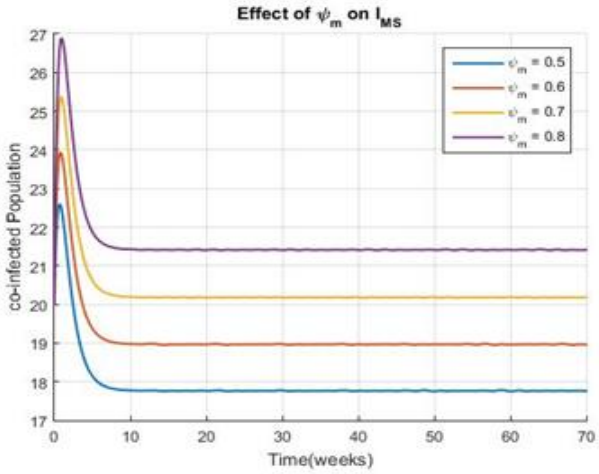
(b)

ISSN No. 2454-6194 | DOI: 10.51584/IJRIAS |Volume X Issue II February 2025

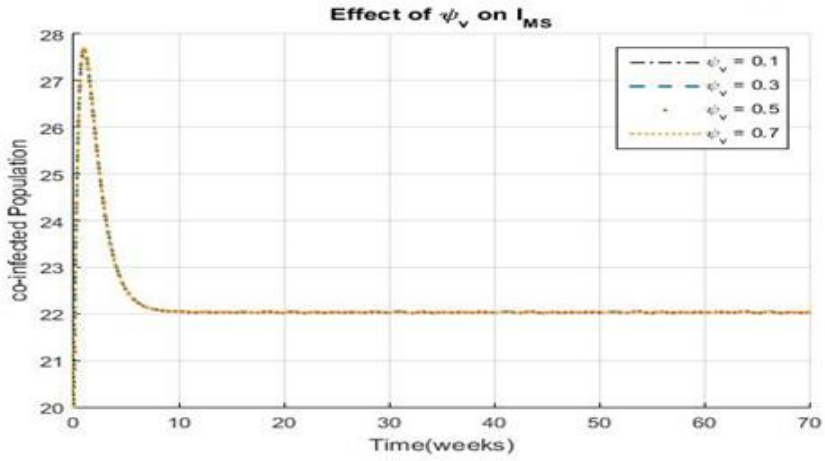
Effect of Contact Rate on the Co-Infected Population



(a)



(b)



(c)

DISCUSSION

In line with the graphical results in section 4.0, it was observed that;

Figure 4.1: Time series plot of the (a) Syphilis only model (b) measles only model (c) co-infection model and (d) co-infection model without recovered population.

The time plot solution given in figure 4.2 shows that whenever the combined treatment rate α_{MS} of the syphilis and measles co-infected individuals increases, the number of co-infected individuals decreases.

Figure 4.2: Time series plot of the co-infected population (a) with different treatment rate (b) with different vaccination rate.

Similarly, whenever the vaccination rate is increased, i.e. more persons are added to the vaccinated compartment the co-infected compartment decreases. This is because more persons recover from the measles vaccine without contact with syphilis-infected individuals.

Figure 4.3: Time series plot of the co-infected population (a) with different susceptible to syphilis contact rate (b) with different susceptible to measles contact rate (c) with different vaccinated to syphilis infected contact rate.

Figure 4.3 shows that whenever there is greater contact between susceptible individuals and syphilis infected individuals, and susceptible individuals and measles infected individuals the co-infected compartment

ISSN No. 2454-6194 | DOI: 10.51584/IJRIAS |Volume X Issue II February 2025

increases in number. However, the contact rate between the measles vaccinated individuals and syphilis infected class does not affect the co-infected class as seen in figure 4.3(c).

CONCLUSION

In this paper, we formulated a mathematical model to study the transmission pattern of secondary syphilis and measles co-infection. Due to the introduction of immigration factor, the disease free equilibrium did not exist. Through analytical studies, we determined the endemic equilibrium point through which we established the stability of the secondary syphilis and measles sub-models and the coinfection model.

We went further to numerically simulate the results of the proposed model and obtained the time series plots for each sub-model and the coinfection model. We observed that the numerical results agreed with our analytical findings.

We also established the sensitivity of the parameters $\alpha_{MS}, \sigma, \varphi_M, \varphi_S$ and φ_V and observed while an increase in all parameters considered increased the co-infected class φ_V did not show any effect on co-infected class.

REFERENCES

1. Kretzchmar, M., & Wallinga, J. (2010). Mathematical models in infectious disease epidemiology. Modern infectious disease epidemiology: concepts, methods, mathematical models and Public Health, 209-221.
2. Dietz, K.; & Heesterbeek, J.A.P. (2002). Daniel's Bernoullis Epidemiological Model Revisited. Mathematical Biosciences, 180(1-2), 1-21.
3. Kermack, W.O. & McKendrick, A.G. (1927). A contribution to the mathematical theory of epidemics. Proceedings of the royal society of London. Series A, containing papers of a mathematical and physical character, 115(772), 700-721.
4. Mkhatshwa, T., & Mummert, A. (2010). Modeling super-spreading events for infectious diseases: case study SARS arxiv preprint arxiv:1007.0908.
5. Fenichel, E.P., Castillo-Chavez, C.; Ceddia, M.G.; Chowell, G.; Parra, P.A.G.; Hickling, G.J.; & Villalobos, C. (2011). Adaptive human behavior in epidemiological models. Proceedings of the National Academy of Sciences, 108(15), 6306-6311.
6. Keeling, M.J.; Danou, L.; Vernon, M.C. & House, T.A. (2010). Individual identity and movement network for disease metapopulations. Proceedings of the national academy of sciences, 107(19), 8866-8870.
7. Codling, E.A.; Plank, M.J.; & Benhamou, S. (2008) Random walk models in Biology Journal of the Royal Society Interface, 5(25), 813-834.
8. Gumel, A.M.; Lubuma, J.; Sharomi, O.; & Terefe, Y. (2918). Mathematics of a sex structured model for syphilis transmission dynamics. Mathematical method in the Applied Sciences, 41(18), 8488-8513.
9. Sand-Roy, C.M.; Shuai, Z.; & Van den Driessche, P. (2016). A mathematical model of syphilis transmission in an MSM population. Mathematical biosciences, 277,59-70.
10. Iboi, E.; & Okuonghae, D. (2016). Population dynamic of a mathematical model for syphilis. Applied mathematical modeling, 40(5-6), 3573-3590.
11. Tuite, A.R.; Fisman, D.N.; & Mishra, S. (2013). Screen more or screen more often? Using mathematical models to inform syphilis control strategies. BMC Public Health, 13(1), 1-9.
12. Momoh, A. A.; Bala, Y., Washachi, D.J., & Delthie, D. (2021). Mathematical Analysis and optimal control interventions for sex structured syphilis model with three stages of infection and loss of immunity. Advances in Difference Equations, 2021 (1), 1 – 26.
13. Teklu, S.W.; & Mekonnin, T.T. (2021). HIV/AIDs pneumonia coinfection model with treatment at each infection stage: Mathematical analysis and numerical simulation. Journal of Applied Mathematics (2021), 1-21.
14. Rahmayani, S.A.; Aldila, D.; & Handari, B.D. (2021). Cost-effectiveness analysis on measles transmission with vaccination and treatment intervention. AIMS Mathematics, 6(11), 12491-12527.

ISSN No. 2454-6194 | DOI: 10.51584/IJRIAS |Volume X Issue II February 2025

15. Getahun, M.; Beyene, B.; Ademe, A.; Teshome, B.; Tetera, M.; Afe work, A.; … & Asha, A. (2017). Epidemiology of Laboratory confirmed measles virus cases in the Southern nations of Ethiopia, 2007-2014. BMC infectious diseases, 17(1), 1-8.
16. Nchasi, G.; Paul, I.K.; Sospeter, S.B.; Mallya, M.R.; Ruaichi, J., & Malunga, J. (2022). Measles outbreak in sub-saharan Africa amidst Covid-19: a rising concern, efforts, challenges, and future recommendations. Annuals of medicine and surgery, 81, 104264.
17. Unicef, W. (2022). WHO warn of perfect storm of conditions for measles outbreaks, Affecting children WHO and UNICEF, Manhattan, NY, USA.
18. Gans, H., Maldonado, Y.A., & Kaplan, S.L. (2018). Measles: Epidemiology and transmission.
19. Momoh, A.A.; Ibrahim, M.O., Uwanta, I.J. & Manga, S.B. (2013). Mathematical model for control of measles epidemiology. International Journal of pure and Applied Mathematics, 87(5), 707-718.
20. Edward, S.; Raymond, K.E., Gabriel, K.T., Nestory, F., Model for control and elimination of the transmission dynamics of measles. Applied and computational mathematics, 4(6), 396-408.
21. Scam, F.M., & Nas, H. (2022). Mathematical analysis of SLIPR infectious model without vaccination: a case study of measles outbreaks. Annuals of mathematical modeling, 2(2), 67-75.
22. Mutuguta J.W., Rotich, T., & Chepkwony, I. (2019). Mathematical modeling of the Transmission Dynamics of measles under the effect of vaccination.
23. Tilahum, G.T.; & Alemneh, H.T. (2021). Mathematical modeling and optimal control analysis of Covid-19 in Ethiopia Journal of Interdisciplinary Mathematics 24(8), 2101-2120.
24. Xui, Y.; Ruan, X. & Xiao, Y. (2021). Measles dynamics on network models with optimal control strategies. Advances in Difference Equations, 2021(1), 1-18.
25. Pokharel, A.; Adhikari, K., Gautam, R., Uprety, K.N., & Vaidya, N.K. (2022). Modeling transmission dynamics of measles in Nepal and its control with monitored vaccination program. Mathematical Biosciences and Engineering, 19(8).