Journal of Advanced Research in Applied Sciences and Engineering Technology

Journal homepage:
https://semarakilmu.com.my/journals/index.php/applied_sciences_eng_tech/index
ISSN: 2462-1943

Stability Analysis of the Transmission Model of TB-HIV Co-Dynamics with Vaccination and Treatment

Syamsuddin Toaha[1,*], Sukmawati[1], Kasbawati[1], Firman[1], Wan Zuki Azman Wan Muhamad[2]

[1] Department of Mathematics, Hasanuddin University, Tamalanrea, 90245, Makassar, Indonesia
[2] Institute of Engineering Mathematics, Universiti Malaysia Perlis (UniMAP), 02600 Arau, Perlis, Malaysia

ARTICLE INFO

Article history:
Received 22 March 2024
Received in revised form 18 September 2024
Accepted 4 October 2024
Available online 31 December 2024

Keywords:
TB-HIV co-infection; Vaccination rate; Local stability; Basic reproduction number

ABSTRACT

This study aims to analyse and determine the stability of the equilibrium point of the spread model consists of TB infection, HIV infection, and TB-HIV co-infection disease. This model considers eight compartments, namely unvaccinated susceptible, vaccinated susceptible, exposed, infected with TB, infected with HIV, infected with TB and HIV, treatment, and recovered by considering vaccination and treatment in the compartments as the strategies to manage spread of the diseases. The stability of non-endemic equilibrium point is carried out by determining the basic reproduction number and eigenvalues. Simulation is conducted to investigate effect of vaccination and treatment. By giving appropriate values of parameters and varying values of vaccination rate we found that increasing value of vaccination rate will reduce and eliminate TB infection, HIV infection, and TB-HIV co-infection disease from the population. The curve solutions of the dynamics of each compartment are given to confirm the analytical results.

1. Introduction

One of the problems facing the global community is health. Various efforts have been made to prevent and treat diseases, but the diseases are still not solved. A number of diseases continue to be of global concern, for example kidney disease, breast cancer, and Covid-19 [1-3]. Mathematical models as an approach method and a tool to understand the real phenomena have been widely used not only to understand population dynamics but also spreading of infectious diseases. The problem of spreading infectious diseases in humans is one of the interesting studies in epidemiology and it can be expressed in the form of mathematical models. Some strategies as the efforts in dealing with infectious diseases have been widely discussed by researchers, such as vaccination, immunization, fogging, and treatment [4-8]. The spread of malaria disease has also been studied using an SIR model [9]. The authors have considered the migration factor as an attempt to find out the effect of migration

* *Corresponding author.*
E-mail address: syamsuddint@gmail.com

https://doi.org/10.37934/araset.54.2.143156

from one area to another on dealing with the spread of malaria disease. Vaccination and fogging have been used as strategies to reduce the spread of malaria disease [10].

Tuberculosis is an infectious disease caused by the mycobacterium tuberculosis bacteria that usually affects the lungs. The TB disease can be transmitted through droplets containing bacteria that are inhaled by healthy people. This disease is one of the highest causes of death in the world, along with HIV/AIDS. The phenomenon of TB spread has been studied through modelling by analysing the stability criteria of endemic and non-endemic equilibrium points [11]. Blower, *et al.,* [12] have constructed a theoretical framework to assess the dynamics of TB spread. The study found that it takes one to several hundred years for the spread of TB to fall and reach a stable endemic level. It seems that the decline in TB is simply due to the natural behaviour of an epidemic. Studies of the spread of TB through an SIR model with four compartments that consider time delay and the provision of vaccines to the susceptible compartment have been carried out and found that the provision of vaccines can reduce the number of TB patients [13]. A TB spread model also considered the factors of treatment, migration, and vaccination [14]. The model studied the existence and singularity of solutions as well as the stability of the non-endemic disease point and the basic reproduction number. From the analysis, a threshold value of the vaccination level that causes TB disease to disappear was found. Determining the vaccination level by BCG is still a challenge to be used in eliminating TB from a population.

Tuberculosis was first discovered in developing countries in the early 1980s, along with HIV/AIDS. HIV/AIDS causes a person's immunity to become weak, so the patient cannot fight the tuberculosis bacteria. The HIV/AIDS spread model can be analysed not only using the SEIR model, but can also be expressed in a system of fractional derivatives [15]. Sensitivity analysis and qualitative analysis are used to determine the behaviour of the spread of the disease. From the graphical representation of the sensitivity criteria, a way to reduce the spread of HIV/AIDS in society was found. The dynamics of HIV/AIDS spread considering treatment was analysed using Caputo-Fabrizio and fractal fractional derivatives [16]. From numerical simulations, it was found that the effects of changing the fractional order on the dynamics of the spread of HIV/AIDS. The study of the spread of TB with treatment and drugs conducted by Ozcaglar *et al.,* [17] and found a control strategy for increasing compliance to compartment of treatment, TB-HIV co-infection, and patients.

There are many cases where people with HIV also suffer from TB. This is because patients who are infected with HIV, if not treated properly, will suffer AIDS with immunity slowly weakening and then susceptible to other diseases, such as tuberculosis. Wang *et al.,* [18] considered a spread model of TB-HIV co-infection by involving four compartments. The local and global stability of non-endemic equilibrium points are analysed to understand trajectory behaviour on both diseases and the effects on the disease. To analyse the dynamics of TB-HIV co-infection spread, the model is not only expressed in SEIR variants and some other factors such as vaccination [19], but the model can also be expressed into other forms such as Caputo operator and fractional-derivatives [20,21]. The TB-HIV spread model was developed by making five compartments [22]. The model analysed global stability conditions for endemic and non-endemic equilibrium points. The analysis also found an effective measure to reduce the incidence of TB by 80%. Roeger *et al.,* [23] considered eight compartments in studying the spread of TB-HIV co-infection. Basic reproduction number for the HIV and TB compartments are analysed one by one and then the basic reproduction number for all infected compartments is determined to analyse when TB-HIV co-infection occurs and its dynamics as well as ways to reduce the number of cases of both diseases.

The TB-HIV co-infection disease is still a major health problem in several countries. Anyone can be infected with TB, and people living with HIV are more susceptible to TB disease. Some cases of people living with HIV have a high chance of becoming active TB if they are always around other

people who have active TB. People with HIV who also have latent TB or who are infected with TB can still be cured. Patients who are infected with latent TB and are not treated can develop TB disease in patients with HIV. This is because the immune system is weakened. Untreated TB patients can die. People with HIV and untreated active tuberculosis have a higher risk of death. This model is a development of some models previously studied by the researchers, considering eight compartments with the addition of vaccination and treatment compartments. The influence of the two strategies is analysed analytically and numerically simulated to show the behaviour of the solution curves for each compartment.

2. Formulation of a Model for the Spread of TB-HIV Co-Infection Diseases

A model describing the spread of TB disease in terms of the SEIR type has been developed [12,17]. A development of model is introduced to model co-dynamics of TB and HIV. The total population is divided into eight compartments. The infected class is divided into three compartments, namely infectious with TB ($\boldsymbol{I_T}$), HIV infectious ($\boldsymbol{I_H}$) and TB-HIV co-infection ($\boldsymbol{I_{TH}}$). Individuals in the newborn class were considered healthy and susceptible and then moved to the unvaccinated susceptible ($\boldsymbol{S_u}$) and vaccinated susceptible ($\boldsymbol{S_v}$) with birth rate $\boldsymbol{\pi}$. Individuals in the $\boldsymbol{S_v}$ susceptible compartment were vaccinated and became immune. This vaccine can weaken the bacteria in the body so that the individual does not get sick and then move to compartment $\boldsymbol{E}$ which is exposed but not yet categorized as an infected with TB and HIV at a rate $\boldsymbol{(1-\sigma)\beta_v S_v I_T}$, where $\boldsymbol{\sigma}$ is the effectiveness rate of the vaccination. The individual may also move to compartment $\boldsymbol{R}$ or recovered at a rate of $\boldsymbol{\varphi}$.

The individuals in the susceptible compartment S_u are not vaccinated, so that their immunity becomes weak and moves to the compartments E, I_T, I_H, and I_{TH} at the rate of $q\beta_1 S_u I_T$, $(1-q)\beta_1 S_u I_T$, $q\beta_2 S_u I_H$, and $\beta_3 S_u I_{TH}$ respectively. The constants β_1, β_2, and β_3 indicate the average contact that occurs between healthy individuals who are exposed and TB infected, HIV infected, and infected with TB-HIV. Individual in compartment infected with TB can be handled by treatment because the main symptom is still mild such as continuous cough can occur for three weeks or more. Based on these complaints, the individuals can be categorized to be an infected with TB. Before a patient suffering from TB is treated first to prevent infection, so the individuals can move to compartment T or treatment at a rate of $\omega_1 I_T$.

The compartment I_H or HIV infected can be handled by treatment because the diagnosis of HIV usually does not appear immediately when someone is newly infected with HIV and with the same symptoms of flu that appear for 1-2 weeks after HIV infection occurs. Before infection occurs, prevention is carried out and individuals move to compartment T or treatment at a rate of $\omega_2 I_{TH}$. After giving a treatment, the individual can move to the compartment R or recovered naturally at a rate of τ. It is also assumed that the individuals in the recovered or cured compartment are not re-infected with TB and HIV disease, or co-infected with TB-HIV. Based on the above assumptions, the dynamics of TB and HIV spread in compartments is shown in Figure 1 below.

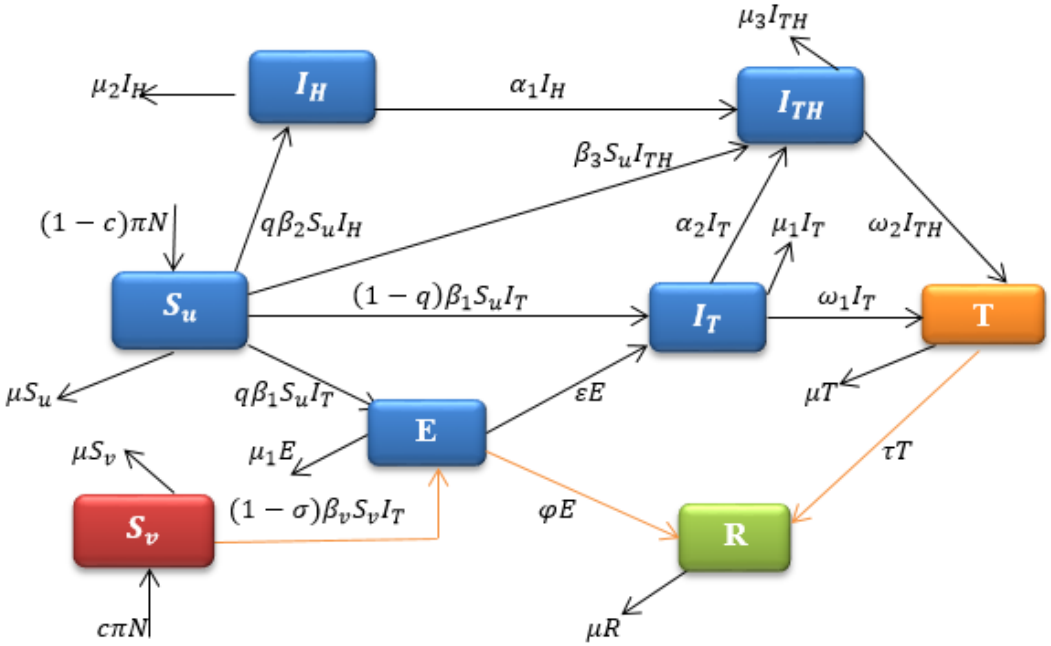


Fig. 1. Spread dynamics of TB-HIV co-infection diseases with vaccination and treatment

Based on the given assumptions and the spread flow shown in Figure 1, the dynamics of the spread of TB-HIV co-infection diseases with vaccination and treatment is given by the following system of differential Eq. (1) below.

$$\begin{aligned}
\frac{dS_u}{dt} &= (1-c)\pi N - \beta_1 S_u I_T - q\beta_2 S_u I_H - \beta_3 S_u I_{TH} - \mu S_u \\
\frac{dS_v}{dt} &= c\pi N - (1-\sigma)\beta_v S_v I_T - \mu S_v \\
\frac{dE}{dt} &= q\beta_1 S_u I_T + (1-\sigma)\beta_v S_v I_T - (\varphi + \varepsilon + \mu_1)E \\
\frac{dI_T}{dt} &= (1-q)\beta_1 S_u I_T + \varepsilon E - (\alpha_2 + \omega_1 + \mu_1)I_T \\
\frac{dI_H}{dt} &= q\beta_2 S_u I_H - (\alpha_1 + \mu_2)I_H \\
\frac{dI_{TH}}{dt} &= \alpha_1 I_H + \alpha_2 I_T + (\beta_3 S_u - \omega_2 - \mu_3)I_{TH} \\
\frac{dT}{dt} &= \omega_1 I_T + \omega_2 I_{TH} - (\tau + \mu)T \\
\frac{dR}{dt} &= \varphi E + \tau T - \mu R.
\end{aligned} \tag{1}$$

The total of population is denoted as $N = S_u + S_v + E + I_T + I_H + I_{TH} + T + R$. The initial state of each compartment at time $t = 0$ are symbolized as $S_u(0) = S_{(u0)}$, $S_v(0) = S_{(v0)}$, $E(0) = E_{(0)}$, $I_T(0) = I_{(T0)}$, $I_H(0) = I_{(H0)}$ $I_{TH}(0) = I_{(TH0)}$, $T(0) = T_{(0)}$, and $R(0) = R_{(0)}$. The notations $\frac{dS_u}{dt}$, $\frac{dS_v}{dt}$, $\frac{dE}{dt}$, $\frac{dI_T}{dt}$, $\frac{dI_H}{dt}$, $\frac{dI_{TH}}{dt}$, $\frac{dT}{dt}$ and $\frac{dR}{dt}$ indicate the growth rate for compartments susceptible without vaccination, susceptible with vaccination, exposed, infected with TB, infected with HIV, infected with TB-HIV, treated, and recovered. The parameters used in the model are assumed to be positive.

3. Stability Analysis of the Model

The constructed TB-HIV co-infection spread disease model is analysed focusing on the existence and stability of endemic and non-endemic equilibrium points. For simplification, the model Eq. (1) is normalized and suppose that $x_1 = \frac{S_u}{N},\ x_2 = \frac{S_v}{N}, x_3 = \frac{E}{N}, x_4 = \frac{I_T}{N}, x_5 = \frac{I_H}{N}, x_6 = \frac{I_{TH}}{N}, x_7 = \frac{T}{N}$, and $x_8 = \frac{R}{N}$. Therefore, the model Eq. (1) is then rewritten in the form

$$\begin{aligned}
\frac{dx_1}{dt} &= (1-c)\pi - \beta_1 x_1 x_4 - q\beta_2 x_1 x_5 - \beta_3 x_1 x_6 - \mu x_1 \\
\frac{dx_2}{dt} &= c\pi - (1-\sigma)\beta_v x_2 x_4 - \mu x_2 \\
\frac{dx_3}{dt} &= q\beta_1 x_1 x_4 + (1-\sigma)\beta_v x_2 x_4 - (\varphi + \varepsilon + \mu_1)x_3 \\
\frac{dx_4}{dt} &= (1-q)\beta_1 x_1 x_4 + \varepsilon x_3 - (\alpha_2 + \omega_1 + \mu_1)x_4 \\
\frac{dx_5}{dt} &= q\beta_2 x_1 x_5 - (\alpha_1 + \mu_2)x_5 \\
\frac{dx_6}{dt} &= \alpha_1 x_5 + \alpha_2 x_4 + (\beta_3 x_1 - \omega_2 - \mu_3)x_6 \\
\frac{dx_7}{dt} &= \omega_1 x_4 + \omega_2 x_6 - (\tau + \mu)x_7 \\
\frac{dx_8}{dt} &= \varphi x_3 + \tau x_7 - \mu x_8.
\end{aligned} \tag{2}$$

The equilibrium condition of the model occurs when the growths of all compartments are zero. The endemic and non-endemic equilibrium points can be determined by setting $\frac{dx_1}{dt} = \frac{dx_2}{dt} = \frac{dx_3}{dt} = \frac{dx_4}{dt} = \frac{dx_5}{dt} = \frac{dx_6}{dt} = \frac{dx_7}{dt} = \frac{dx_8}{dt} = 0$ and then solving the system of equations simultaneously. To obtain the non-endemic equilibrium point, which means that there is no spread of disease, the compartments with infection should be set to be zero. Thus, we have $x_3 = 0,\ x_4 = 0, x_5 = 0, x_6 = 0, x_7 = 0,\ x_8 = 0$. Substituting $x_3 = x_4 = x_5 = x_6 = x_7 = x_8 = 0$ into the system of equations gives $x_{1_0} = \frac{(1-c)\pi}{\mu}$ and $x_{2_0} = \frac{c\pi}{\mu}$. Therefore, the non-endemic equilibrium point is written as $T_0 = \left(x_{1_0},\ x_{2_0},\ x_{3_0},\ x_{4_0},\ x_{5_0},\ x_{6_0},\ x_{7_0},\ x_{8_0}\right) = \left(\frac{(1-c)\pi}{\mu},\ \frac{c\pi}{\mu},\ 0,0,0,0,0,0\right)$.

The TB-HIV co-infection disease model includes the compartments of susceptible without vaccination, susceptible with vaccination, exposed, infected without treatment, infected with treatment, and recovered. Following standard methods, the infected and exposed individuals are grouped. Let *Y* be a group that includes susceptible without vaccination, susceptible with vaccination, exposed, infected with treatment, and recovered. While the other compartments are grouped in ***Z*** which includes infected individuals. Then we have $Y = (x_1, x_2, x_3, x_7, x_8)$ and $Z = (x_4, x_5, x_6)$.

Suppose that

$$\begin{pmatrix} \frac{dx_4}{dt} \\ \frac{dx_5}{dt} \\ \frac{dx_6}{dt} \end{pmatrix} = \begin{pmatrix} (1-q)\beta_1 x_1 x_4 + \varepsilon x_3 - (\alpha_2 + \omega_1 + \mu_1)x_4 \\ q\beta_2 x_1 x_5 - (\alpha_1 + \mu_2)x_5 \\ \alpha_1 x_5 + \alpha_2 x_4 + (\beta_3 x_1 - \omega_2 - \mu_3)x_6 \end{pmatrix}. \tag{3}$$

The non-endemic equilibrium points in group Y is written as $Y^* = \left(x_{1_0}, x_{2_0}, x_{3_0}, x_{7_0}, x_{8_0}\right) = \left(\frac{(1-c)\pi}{\mu}, \frac{c\pi}{\mu}, 0, 0, 0\right)$. Substituting Y^* into Eq. (3) gives

$$\boldsymbol{h}(Y^*, Z) = \begin{pmatrix} \frac{(1-q)\beta_1(1-c)\pi}{\mu} x_4 - (\alpha_2 + \omega_1 + \mu_1)x_4 \\ \frac{q\beta_2(1-c)\pi}{\mu} x_5 - (\alpha_1 + \mu_2)x_5 \\ \alpha_1 x_5 + \alpha_2 x_4 + \left(\frac{\beta_3(1-c)\pi}{\mu} - \omega_2 - \mu_3\right) x_6 \end{pmatrix}. \quad (4)$$

Apply partial derivatives of $\boldsymbol{h}(Y^*, Z)$ with respect to $Z = (x_4, x_5, x_6)$ to get

$$\frac{\partial \boldsymbol{h}(Y^*, Z)}{\partial Z} = \begin{pmatrix} \frac{(1-q)\beta_1(1-c)\pi}{\mu} - (\alpha_2 + \omega_1 + \mu_1) & 0 & 0 \\ 0 & \frac{q\beta_2(1-c)\pi}{\mu} - (\alpha_1 + \mu_2) & 0 \\ \alpha_2 & \alpha_1 & \frac{\beta_3(1-c)\pi}{\mu} - \omega_2 - \mu_3 \end{pmatrix}.$$

Thus, we have matrix *A* as follows,

$$A = \begin{pmatrix} \frac{(1-q)\beta_1(1-c)\pi}{\mu} - (\alpha_2 + \omega_1 + \mu_1) & 0 & 0 \\ 0 & \frac{q\beta_2(1-c)\pi}{\mu} - (\alpha_1 + \mu_2) & 0 \\ \alpha_2 & \alpha_1 & \frac{\beta_3(1-c)\pi}{\mu} - \omega_2 - \mu_3 \end{pmatrix}. \quad (5)$$

If the matrix A is decomposed in terms of $\boldsymbol{F} - \boldsymbol{V}$ where $\boldsymbol{F}$ is a positive definite matrix and $\boldsymbol{V}$ is a diagonal matrix, we get

$$\boldsymbol{F} = \begin{pmatrix} \frac{(1-q)\beta_1(1-c)\pi}{\mu} & 0 & 0 \\ 0 & \frac{q\beta_2(1-c)\pi}{\mu} & 0 \\ \alpha_2 & \alpha_1 & \frac{\beta_3(1-c)\pi}{\mu} \end{pmatrix}, \text{ and } \boldsymbol{V} = \begin{pmatrix} \alpha_2 + \omega_1 + \mu_1 & 0 & 0 \\ 0 & \alpha_1 + \mu_2 & 0 \\ 0 & 0 & \omega_2 + \mu_3 \end{pmatrix}.$$

The inverse of matrix $\boldsymbol{V}$ is written as

$$\boldsymbol{V^{-1}} = \begin{pmatrix} \frac{1}{\alpha_2 + \omega_1 + \mu_1} & 0 & 0 \\ 0 & \frac{1}{\alpha_1 + \mu_2} & 0 \\ 0 & 0 & \frac{1}{\omega_2 + \mu_3} \end{pmatrix}.$$

From matrices $\boldsymbol{F}$ and $\boldsymbol{V^{-1}}$, the next generation matrix is determined by the matrix

$$\boldsymbol{FV^{-1}} = \begin{pmatrix} \frac{(1-q)\beta_1(1-c)\pi}{\mu(\alpha_2 + \omega_1 + \mu_1)} & 0 & 0 \\ 0 & \frac{q\beta_2(1-c)\pi}{\mu(\alpha_1 + \mu_2)} & 0 \\ \frac{\alpha_2}{\alpha_2 + \omega_1 + \mu_1} & \frac{\alpha_1}{\alpha_1 + \mu_2} & \frac{\beta_3(1-c)\pi}{\mu(\omega_2 + \mu_3)} \end{pmatrix}.$$

The eigenvalues from the next generation matrix are found by solving the characteristic equation $f(\lambda) = \left|(\boldsymbol{FV^{-1}} - \lambda \boldsymbol{I})\right| = 0$, where

$$f(\lambda) = \begin{vmatrix} \frac{(1-q)\beta_1(1-c)\pi}{\mu(\alpha_2+\omega_1+\mu_1)} - \lambda & 0 & 0 \\ 0 & \frac{q\beta_2(1-c)\pi}{\mu(\alpha_1+\mu_2)} - \lambda & 0 \\ \frac{\alpha_2}{\alpha_2+\omega_1+\mu_1} & \frac{\alpha_1}{\alpha_1+\mu_2} & \frac{\beta_3(1-c)\pi}{\mu(\omega_2+\mu_3)} - \lambda \end{vmatrix},$$

that is

$$\left(\frac{(1-q)\beta_1(1-c)\pi}{\mu(\alpha_2+\omega_1+\mu_1)} - \lambda\right)\left(\frac{q\beta_2(1-c)\pi}{\mu(\alpha_1+\mu_2)} - \lambda\right)\left(\frac{\beta_3(1-c)\pi}{\mu(\omega_2+\mu_3)} - \lambda\right) = 0. \quad (6)$$

The roots of characteristic Eq. (6) are $\lambda_1 = \frac{(1-q)\beta_1(1-c)\pi}{\mu(\alpha_2+\omega_1+\mu_1)}$, $\lambda_2 = \frac{q\beta_2(1-c)\pi}{\mu(\alpha_1+\mu_2)}$, and $\lambda_3 = \frac{\beta_3(1-c)\pi}{\mu(\omega_2+\mu_3)}$. We can write $\mathcal{R}_1 = \frac{(1-q)\beta_1(1-c)\pi}{\mu(\alpha_2+\omega_1+\mu_1)}$, $\mathcal{R}_2 = \frac{q\beta_2(1-c)\pi}{\mu(\alpha_1+\mu_2)}$, and $\mathcal{R}_3 = \frac{\beta_3(1-c)\pi}{\mu(\omega_2+\mu_3)}$, then we have $\mathcal{R}_0 = \max\{\mathcal{R}_1, \mathcal{R}_2, \mathcal{R}_3\}$.

The endemic equilibrium point occurs when TB and HIV are spreading in the population. This situation occurs when the infected compartments are always positive. To obtain the endemic equilibrium point we assume that $x_3 > 0$, $x_4 > 0$, and $x_5 > 0$ which implies that $x_6, x_7, x_8 > 0$. Therefore, we reach the equilibrium point $T_1 = \left(x_{1_1}, x_{2_1}, x_{3_1}, x_{4_1}, x_{5_1}, x_{6_1}, x_{7_1}, x_{8_1}\right)$. With the appropriate values of the parameters, the endemic equilibrium point will occur. The endemic equilibrium point is quite difficult to get analytically because the model is more complex with high dimensions. The existence and stability of endemic and non-endemic equilibrium points are determined by evaluating the value of the basic reproduction number $\mathcal{R}_0$. The eigenvalue method is also used to confirm the results obtained using the basic reproduction number.

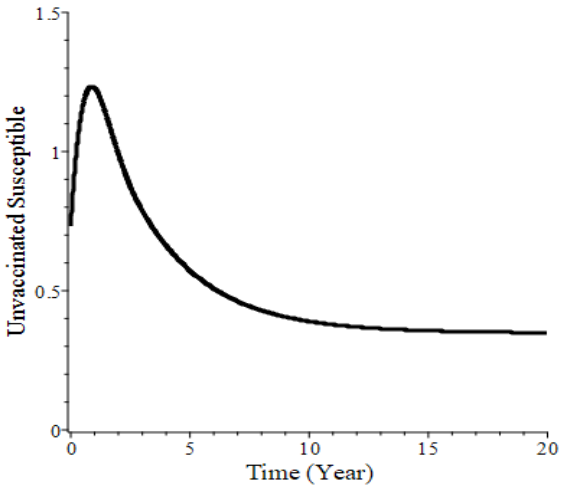
4. Numerical simulations

Numerical simulations are performed to confirm the existence of endemic and non-endemic equilibrium points and to determine the stability of each equilibrium point. This simulation is done to confirm that the non-endemic equilibrium point T_0 is stable when $\mathcal{R}_1, \mathcal{R}_2, \mathcal{R}_3 < 1$, otherwise it becomes unstable when $\mathcal{R}_1, \mathcal{R}_2, \mathcal{R}_3 > 1$. When the non-endemic equilibrium point is unstable, the endemic equilibrium point appears and becomes stable. The dynamics of each compartment with various values of vaccination and treatment are shown in the given figures. In addition, this simulation is conducted to show the effects of vaccination rate (c) and effectiveness of vaccination (σ) on the rate of spread disease in the population. Simulations on the model of TB-HIV co-infection disease are carried out with some values of dominant parameters that affect the behaviour of the compartments in the model.

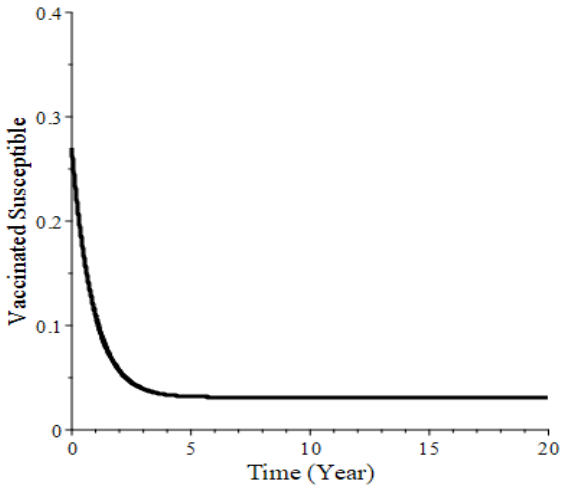
Table 1
Parameter values of related to the TB-HIV co-infection disease spread model

Parameters	Description	Values	References
π	Natural birth rate	0.027-1.33	[24]
μ	Natural death rate	1.001	Assumed
μ_1	Death rate caused by TB disease	0.3	[24]
μ_2	Death rate caused by HIV disease	0.3	Assumed
μ_3	Death rate caused by TB and HIV	0.4	Assumed
c	Vaccination rate	0.01-0.9	[24]
σ	Vaccination effectiveness level	0.01	Assumed
β_v	Transmission rate due to contact between vaccinated susceptible or healthy and exposed	0.35	[24]
β_1	Average contact that occurs between susceptible and TB infected	1.5-1.9	Assumed
β_2	Average contact that occurs between susceptible and HIV infected	1.5-1.9	Assumed
β_3	Average contact that occurs between susceptible and TB-HIV infected	1.5	Assumed
q	Level of disease transmission	0.5	[24]
α_1	Average contact that occurs between HIV infected and TB infected	0.03-0.003	Assumed
α_2	Average contact that occurs between TB infected and HIV infected	0.03-0.003	Assumed
ω_1	Transition rate from TB infected to treated	1	Assumed
ω_2	Transition rate from TB-HIV infected treated	1	Assumed
φ	Transition rate from exposed to recovered	0.03	Assumed
ε	Transition rate from exposed to TB infected	0.0003	[24]
τ	Treatment rate	0.03	Assumed

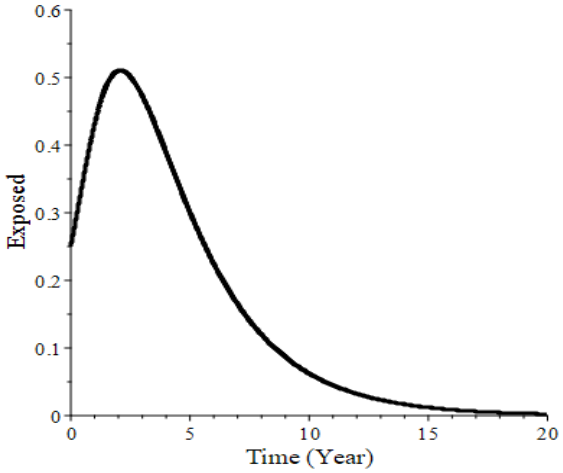
To plot the solution curves of the compartments, we take the initial conditions as $S_u(0) = 0.73$, $S_v(0) = 0.27$, $E(0) = 0.25$, $I_T(0) = 0.32$, $I_H(0) = 0.32$, $T(0) = 0.15$, and $R(0) = 0.10$. The parameter values used in the simulation are $\beta_1 = 1.9$, $\beta_2 = 1.9$, $I_{TH}(0) = 1.554$, $\beta_3 = 1.5$, $\beta_v = 0.35$, $c = 0.01$, $\sigma = 0.01$, $\omega_1 = 1$, $\omega_2 = 1$, $\pi = 1.33$, $\mu = 1.001$, $\mu_1 = 0.3$, $\mu_2 = 0.3$, $\mu_3 = 0.4$, $q = 0.5$, $\alpha_1 = 0.03$, $\alpha_2 = 0.03$, $\varepsilon = 0.0003$, $\varphi = 0.03$, and $\tau = 0.03$ with appropriate units. Then we have a non-endemic equilibrium point $T_0 = (3.1071, 0.0314, 0, 0, 0, 0, 0, 0)$ with eigenvalues $\lambda_1 = -1.001$, $\lambda_2 = -1.0010$, $\lambda_3 = -1.0001$, $\lambda_4 = -1.0310$, $\lambda_5 = 3.2606$, $\lambda_6 = -0.3307$, $\lambda_7 = 1.7222$, and $\lambda_8 = 2.6217$. Since $\mathcal{R}_1 = 1.2496$, $\mathcal{R}_2 = 1.2622$, and $\mathcal{R}_3 = 1.9930$, we get $\mathcal{R}_0 = 1.9930$. From the basic reproduction number and the values of eigenvalues, we know that the non-endemic equilibrium point T_0 is not stable. This means that with the given parameter values, the non-endemic case will occur and the TB-HIV co-infection disease will remain in the population. The solution curves of the compartments are shown in Figure 2.


Unvaccinated Susceptible
Time (Year)

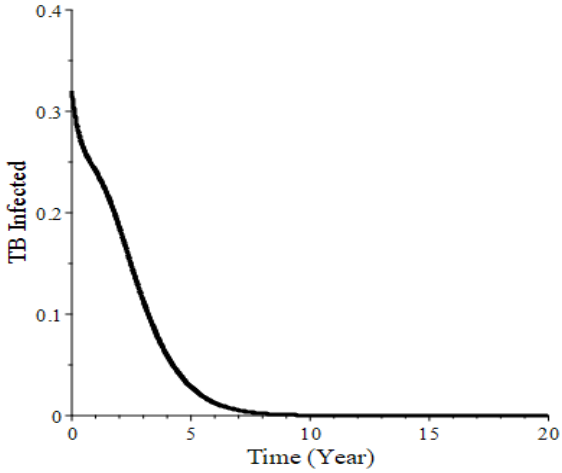
(a)


Vaccinated Susceptible
Time (Year)

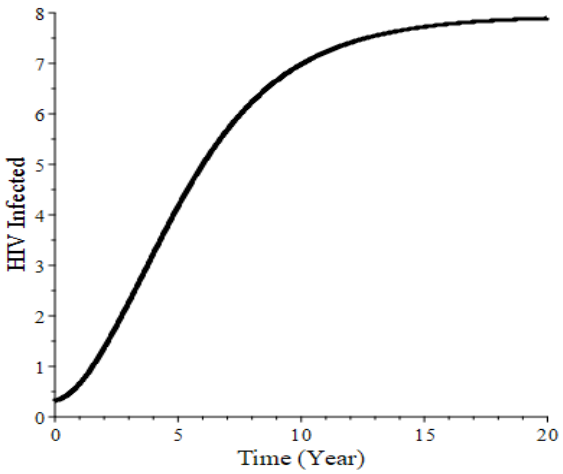
(b)


Exposed
Time (Year)

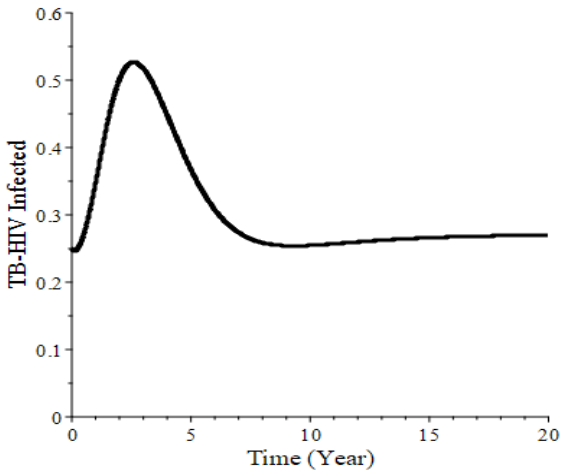
(c)


TB Infected
Time (Year)

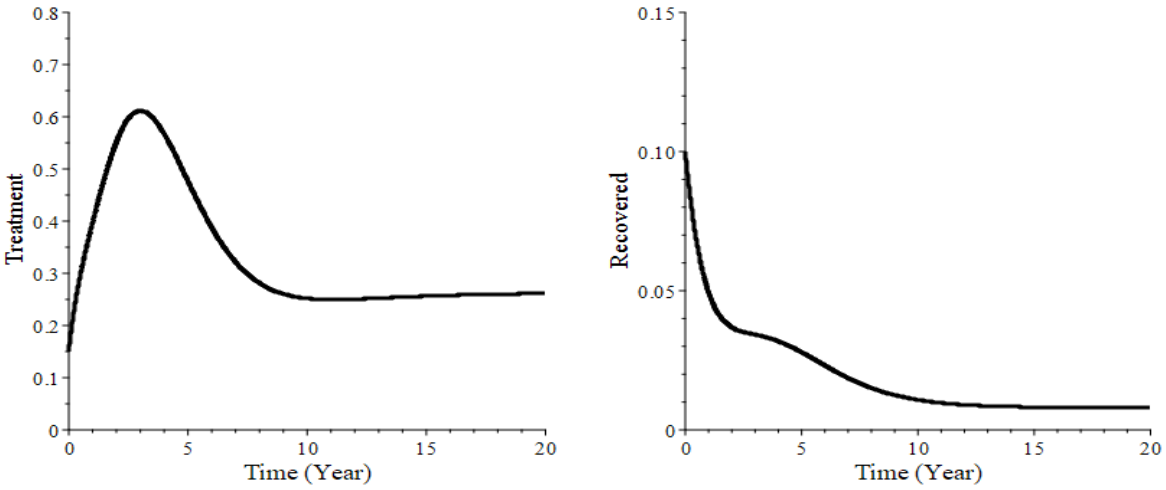
(d)


HIV Infected
Time (Year)

(e)


TB-HIV Infected
Time (Year)

(f)

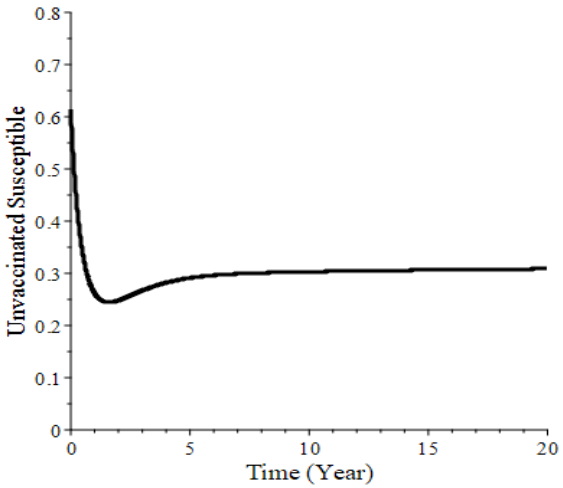


(g) (h)

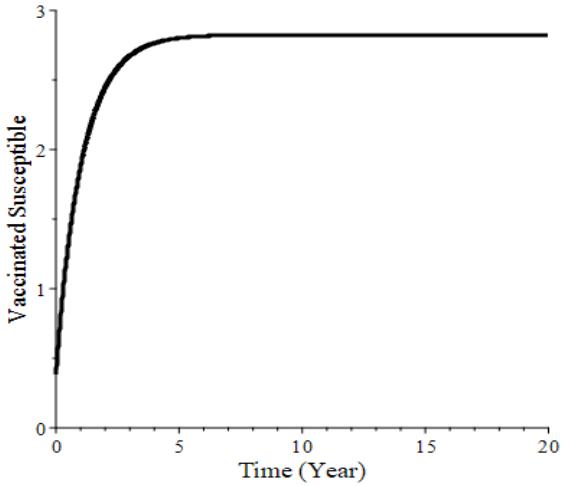
Fig. 2. Solution curves of all compartments for endemic case

Figures 2(a) and 2(b) show that the number of individuals in the unvaccinated and vaccinated susceptible compartments will reach the equilibrium point, the two compartments will always exist. While Figures 2(c) and 2(d) show that the number of individuals in the exposed and TB infected compartments will go to zero. The exposed individuals will die out, and TB infected individuals will also disappear from the population. Although TB infected will disappear, individuals infected with HIV, TB-HIV co-infected, treated, and recovered will not tend to zero. Individuals in the HIV infected and TB-HIV co-infected compartments will remain coexist and still occur endemically, Figures 2(e), 2(f), 2(g) and 2h).

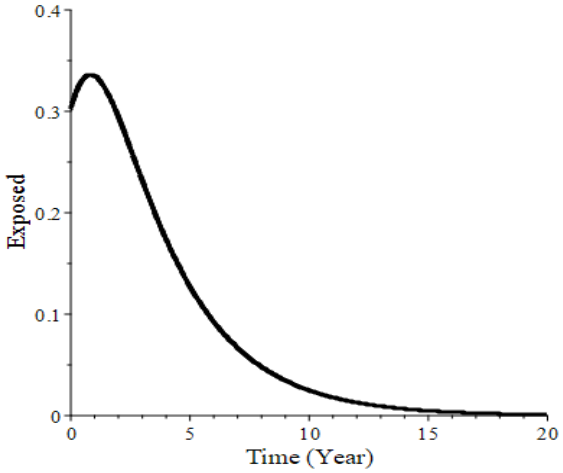
In the next simulation, we take the values of vaccination rate is quite high, which is expected to reduce the infection rate. We take the parameter values as $\beta_1 = 1.5$, $\beta_2 = 1.5$, $\beta_3 = 1.5$, $\beta_v = 0.35$, $c = 0.9$, $\sigma = 0.0001$, $\omega_1 = 1$, $\omega_2 = 1$, $\pi = 0.1$, $\mu = 1.001$, $\mu_1 = 0.3$, $\mu_2 = 0.3$, $\mu_3 = 0.3$, $q = 0.5$, $\alpha_1 = 0.0003$, $\alpha_2 = 0.0003$, $\varepsilon = 0.0003$, $\varphi = 0.03$, and $\tau = 0.03$ with appropriate units. From the given parameter values, we get the non-endemic equilibrium point $T_0 = (0.314, 2.825, 0, 0, 0, 0, 0, 0)$ and from which we get the eigenvalues $\lambda_1 = -1.001$, $\lambda_2 = -1.001$, $\lambda_3 = -1.001$, $\lambda_4 = -1.001$, $\lambda_5 = -0.929$, $\lambda_6 = -0.338$, $\lambda_7 = -1.065$, and $\lambda_8 = -0.065$. We also have $\mathcal{R}_1, \mathcal{R}_2, \mathcal{R}_3 < 1$, where $\mathcal{R}_1 = 0.0020$, $\mathcal{R}_2 = 0.0202$, and $\mathcal{R}_3 = 0.0405$. Therefore, we have $\mathcal{R}_0 = 0.0405$. Since $\mathcal{R}_0 < 1$ and the real part of all eigenvalues are negative, then the non-endemic equilibrium point is locally asymptotically stable. This means that there is no more endemic after tens year and the population will be free from the TB and HIV diseases. The solution curves of each compartment are plotted in Figure 3.


Unvaccinated Susceptible
Time (Year)

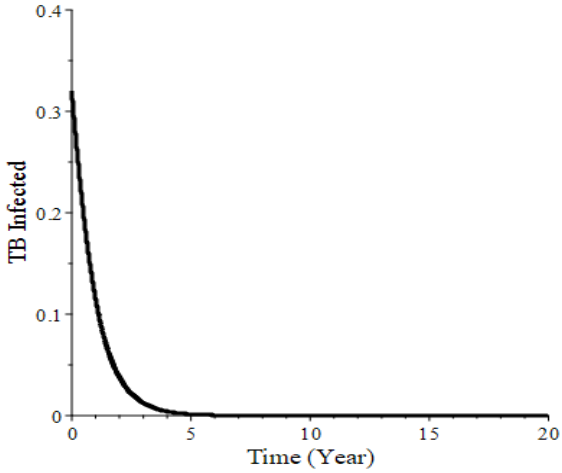
(a)


Vaccinated Susceptible
Time (Year)

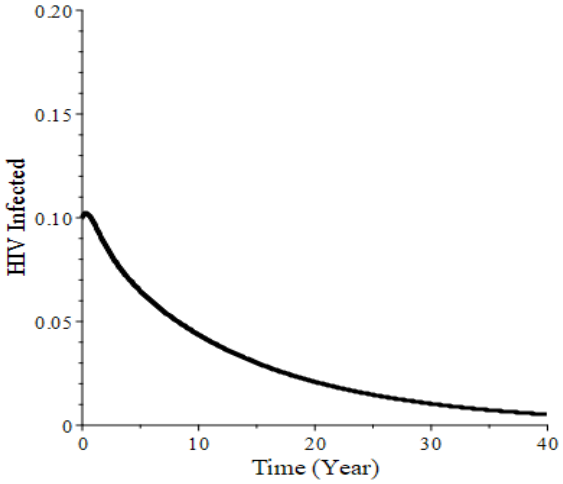
(b)


Exposed
Time (Year)

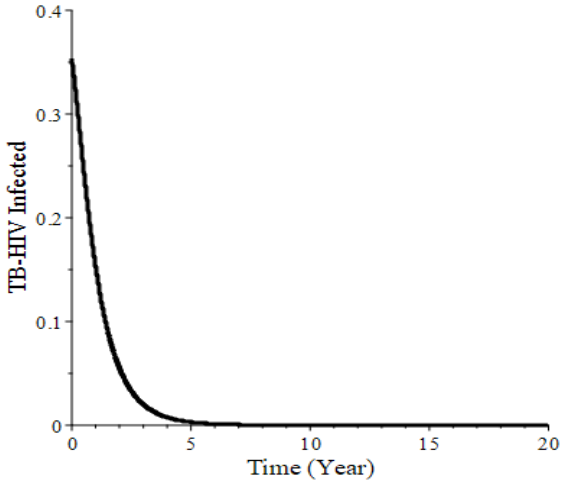
(c)


TB Infected
Time (Year)

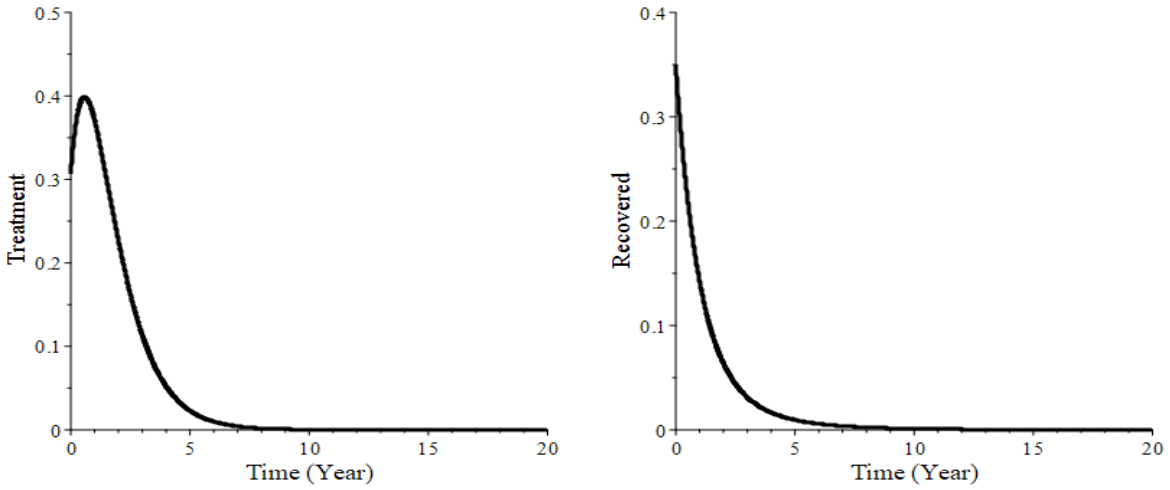
(d)


HIV Infected
Time (Year)

(e)


TB-HIV Infected
Time (Year)

(f)



(g) (h)

Fig. 3. Solution curves of each compartment for non-endemic case

Figures 3(a) and 3(b) show that the number of individuals in the unvaccinated and vaccinated susceptible compartments will move towards the equilibrium point, both compartments always exist. The equilibrium value for compartment S_u decreases while the equilibrium value for compartment S_v increases compared to Figure 2(a) and 2(b) This is because in the second simulation there is an increase in the vaccination level. While Figures 3(c) to 3(h) show that the number of individuals in the exposed, TB infected, HIV infected, TB-HIV co-infected, treatment and recovered compartments will go to zero, there will be no more endemic in the population. This shows the effectiveness of vaccine administration, which can turn the endemic state into non-endemic by increasing the vaccination level in the susceptible compartment.

5. Conclusion

A spread model consisting of tuberculosis, HIV, and TB-HIV with eight compartments has been developed, taking into account the vaccination of the susceptible compartment and the addition of the treatment compartment. The existence and stability of non-endemic equilibrium points are analysed using the method of eigenvalues and the determination of basic reproduction number $(\mathcal{R}_0)$. The influence of vaccination and treatment on the spread of the disease is simulated by varying the vaccination rate. In the first simulation, a low vaccination rate is given, and in the second simulation, a relatively high vaccination rate is given, while the other parameter values are unchanged. When the value of vaccination rate is sufficiently low $(c = 0.01)$, an unstable non-endemic equilibrium point is obtained. Individuals in compartments I_H, I_{TH}, *T*, and *R* will not tend to zero. This means that endemicity is still occurring in these compartments.

In the second simulation, a fairly high value of vaccination rate $(c = 0.9)$ was given and a stable non-endemic equilibrium point is obtained. Individuals in the compartments I_T I_H, I_{TH}, *T*, and *R* will tend to zero, which means that there is no more endemic occurrence. The TB and HIV infection will disappear from the population after ten years. By increasing the vaccination rate, the endemic state becomes non-endemic. Treatment does not give a significant effect on the spread of TB and HIV disease. Increasing the vaccine rate also has the effect of increasing the value of equilibrium point for compartment S_v at the non-endemic equilibrium point, while decreasing the value of equilibrium point for S_u at the non-endemic equilibrium point. In addition, increasing the vaccination rate will decrease the value of the basic reproduction number. This means that vaccination can help reduce

the rate of spread of TB infection, HIV infection, and TB-HIV co-infection disease and population will be free from endemic cases.

Acknowledgement
This research was not funded by any grant.

References

[1] Halim, Ahmad Ashraf Abdul, Vijayasarveswari Veeraperumal, Allan Melvin Andrew, Mohd Najib Mohd Yasin, Mohd Zamri Zahir Ahmad, Kabir Hossain, Bifta Sama Bari, and Fatinnabila Kamal. "UWB-based early breast cancer existence prediction using artificial intelligence for large data set." *Journal of Advanced Research in Applied Sciences and Engineering Technology* 29, no. 2 (2023): 81-90. https://doi.org/10.37934/araset.29.2.8190

[2] Bakeri, Iffah Sahira, Siti Rashidah Hanum Abd Wahab, and Adi Irfan Che Ani. "The Technology Adaptation Measures to Reduce Impacts of Covid-19 Pandemic on the Construction Industry." *Journal of Advanced Research in Applied Sciences and Engineering Technology* 31, no. 1 (2023): 34-52. https://doi.org/10.37934/araset.31.1.3452

[3] Deepika, J., P. Selvaraju, Mahesh Kumar Thota, Mohit Tiwari, Dunde Venu, K. Manjulaadevi, and N. Geetha Lakshmi. "Efficient classification of kidney disease detection using Heterogeneous Modified Artificial Neural Network and Fruit Fly Optimization Algorithm." *Journal of Advanced Research in Applied Sciences and Engineering Technology* 31, no. 3 (2023): 1-12. https://doi.org/10.37934/araset.31.3.112

[4] Brauer, Fred, Carlos Castillo-Chavez, and Carlos Castillo-Chavez. *Mathematical models in population biology and epidemiology*. Vol. 2, no. 40. New York: springer, 2012. https://doi.org/10.1007/978-1-4614-1686-9

[5] Kalu, A. U., and S. C. Inyama. "Mathematical model of the role of vaccination and treatment on the transmission dynamics of tuberculosis." *Gen. Math. Notes* 11, no. 1 (2012): 10-23.

[6] Wiraningsih, Eti Dwi, W. L. Aryati, Syamsuddin Toaha, and Suzanne Lenhart. "Optimal control for SEIR rabies model between dogs and human with vaccination effect in dogs." In *Proceedings of the 6th IMT-GT Conference on Mathematics, Statistics and its Applications (ICMSA2010) Universiti Tunku Abdul Rahman, Kuala Lumpur, Malaysia*, vol. 6, pp. 1161-1175. 2010.

[7] Wiraningsih, Eti Dwi, Folashade Agusto, Lina Aryati, S. Lenhart, S. Toaha, and W. Govaerts. "Stability analysis of rabies model with vaccination effect and culling in dogs." *Applied Mathematical Sciences* 9, no. 77-80 (2015): 3805-3817. https://doi.org/10.12988/ams.2015.53197

[8] Muin, R. M., and S. Toaha. "Effect of vaccination and treatment on the MSEICR model of the transmission of hepatitis B virus." In *Journal of Physics: Conference Series*, vol. 1341, no. 6, p. 062031. IOP Publishing, 2019. https://doi.org/10.1088/1742-6596/1341/6/062031

[9] Beay, Lazarus Kalvein, Kasbawati Kasbawati, and Syamsuddin Toaha. "Effects of human and mosquito migrations on the dynamical behavior of the spread of malaria." In *AIP Conference Proceedings*, vol. 1825, no. 1. AIP Publishing, 2017. https://doi.org/10.1063/1.4978975

[10] Hartati, H., and S. Toaha. "Stability analysis of SEISEIR-SEI modelling on the dynamics of spread dengue fever with vaccination and insecticide." In *Journal of Physics: Conference Series*, vol. 1341, no. 6, p. 062033. IOP Publishing, 2019. https://doi.org/10.1088/1742-6596/1341/6/062033

[11] Egbetade, S. A., M. O. Ibrahim, and A. O. Babatunde. "Mathematical Analysis Of A Tuberculosis Epidemic Model." *International Refereed Journal of Engineering and Science* 1 (2012): 23-26.

[12] Blower, Sally M., Angela R. Mclean, Travis C. Porco, Peter M. Small, Philip C. Hopewell, Melissa A. Sanchez, and Andrew R. Moss. "The intrinsic transmission dynamics of tuberculosis epidemics." *Nature medicine* 1, no. 8 (1995): 815-821. https://doi.org/10.1038/nm0895-815

[13] Iskandar, Taufiq, Natasya Ayuningtia Chaniago, Said Munzir, Vera Halfiani, and Marwan Ramli. "Mathematical model of tuberculosis epidemic with recovery time delay." In *AIP Conference Proceedings*, vol. 1913, no. 1. AIP Publishing, 2017. https://doi.org/10.1063/1.5016655

[14] Egbetade, S. A., and M. O. Ibrahim. "Modelling the Impact of BCG vaccines on tuberculosis epidemics." *Journal of Mathematical Modelling and Application* 9, no. 1 (2014): 49-55.

[15] Jamil, Saba, Muhammad Farman, and Ali Akgül. "Qualitative and quantitative analysis of a fractal fractional HIV/AIDS model." *Alexandria Engineering Journal* 76 (2023): 167-177. https://doi.org/10.1016/j.aej.2023.06.021

[16] Farman, Muhammad, Ali Akgül, Merve Taştan Tekin, Muhammad Mannan Akram, Aqeel Ahmad, Emad E. Mahmoud, and Ibrahim S. Yahia. "Fractal fractional-order derivative for HIV/AIDS model with Mittag-Leffler kernel." *Alexandria Engineering Journal* 61, no. 12 (2022): 10965-10980. https://doi.org/10.1016/j.aej.2022.04.030

[17] Ozcaglar, Cagri, Amina Shabbeer, Scott L. Vandenberg, Bülent Yener, and Kristin P. Bennett. "Epidemiological models of Mycobacterium tuberculosis complex infections." *Mathematical biosciences* 236, no. 2 (2012): 77-96. https://doi.org/10.1016/j.mbs.2012.02.003

[18] Wang, Xiaoyan, Junyuan Yang, and Fengqin Zhang. "Dynamic of a TB-HIV coinfection epidemic model with latent age." *Journal of Applied Mathematics* 2013 (2013). https://doi.org/10.1155/2013/429567

[19] King, L. and S. Ahuja. "TB and HIV Coinfection: Current Trend, Diagnosis and Treatment Update." *Physician's Research Network*, New York, (2006).

[20] Xu, Changjin, Zixin Liu, Yicheng Pang, Ali Akgül, and Dumitru Baleanu. "Dynamics of HIV-TB coinfection model using classical and Caputo piecewise operator: A dynamic approach with real data from South-East Asia, European and American regions." *Chaos, Solitons & Fractals* 165 (2022): 112879. https://doi.org/10.1016/j.chaos.2022.112879

[21] Liu, Xuan, Shabir Ahmad, Mati ur Rahman, Yasir Nadeem, and Ali Akgül. "Analysis of a TB and HIV co-infection model under Mittag-Leffler fractal-fractional derivative." *Physica Scripta* 97, no. 5 (2022): 054011. https://doi.org/10.1088/1402-4896/ac645e

[22] Guo, Zhong-Kai, Hong Xiang, and Hai-Feng Huo. "Analysis of an age-structured tuberculosis model with treatment and relapse." *Journal of Mathematical Biology* 82 (2021): 1-37. https://doi.org/10.1007/s00285-021-01595-1

[23] Roeger, Lih-Ing W., Zhilan Feng, and Carlos Castillo-Chavez. "Modeling TB and HIV co-infections." *Mathematical Biosciences & Engineering* 6, no. 4 (2009): 815-837. https://doi.org/10.3934/mbe.2009.6.815

[24] Green, Chris W. "HIV dan TB." *Jakarta Pusat: Yayasan Spiritia* (2016).