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Mathematical Investigation of Transmission of Vaccinated Covid-19 Virus In Tuberculosis Community

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ABSTARCT
Tuberculosis (also known as TB) and coronavirus (also known as COVID-19) are both contagious diseases that continue to harm millions of individuals all over the world each year. However, their incubation periods are quite different, despite the fact that they share symptoms such as coughing, fever and difficultbreathing. Using a set of nonlinear ordinary differential equations, this article presents a mathematical model for the transmission of COVID-19 in a tuberculosis population while the disease is being prevented by vaccination. After that, an analytical investigation of the well-posedness of the suggested co-infection model is carried out by demonstrating the positivity of the solutions. Calculations have also been made to determine the expression of the fundamental reproduction number for co-infection. In order to supplement the outcomes of the analysis, several other simulation situations are graphically executed.

KEYWORDS-*Basic reproduction number, effective contact rate, vaccination rate, recovery rate.*

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I. INTRODUCTION:

The COVID-19 pandemic is as yet killing countless individuals from one side of the planet to the other and finding successful therapies for the disorder has turned into the most troublesome part of the contemporary clinical framework. Tuberculosis, large known as TB, is one more huge gamble to world wellbeing that influences a great many people every year. Coronavirus and tuberculosis (TB) are both infectious sicknesses that attention prevalently on the respiratory framework. Individuals who are tainted with both COVID-19 and TB display side effects that are like each other, like a hack, fever and trouble relaxing. The specific course of transmission of every illness as well as the precaution estimates that can be taken to diminish its effect are unmistakable from each other, regardless of the way that both can be contracted through close contact among ailing and solid people. Individuals who are sound can become tainted with tuberculosis assuming they breathe in the drops that are spread when TB patients who are effectively infectious hack, sniffle or yell. At the point when a contaminated individual hacks, wheezes, breathes out or talks, small spray particles of respiratory drops are delivered very high. These drops can then spread the COVID-19 infection to sound individuals who come into contact with them and permit the infection to enter their bodies through their mouths, noses or eyes. The association between COVID-19 and tuberculosis (TB) is a reason to worry concerning general wellbeing and the co-infection of the two infections happens when an individual is beset with the two sicknesses simultaneously.

The model of transmission co-disease TB in HIV people group that **Lusiana et al. (2017**) created is a powerful framework that contains 10 distinct compartments. They exhibited the sickness free harmony as well as its soundness, the places of endemic balance and the establishment regenerative proportion. Utilizing a Caputo-Fabrizio subsidiary, **Baleanu et al. (2020)** considered a fragmentary request model for the COVID-19 transmission. They had the option to tackle the issue by utilizing the homotopy examination change strategy (HATM) and they likewise gave an answer as focalized series. A SEIR model for COVID-19 was made by **Rezapour et al. (2020)** by utilizing the Caputo subordinate. Through use of the fragmentary Euler method, they had the option to get an estimation of the model's answer. Based on genuine information, their model likewise anticipated the spread of COVID-19 all through Iran and the remainder of the world. **Hezam et al. (2021)** presented a clever unique numerical model structure that is directed by a bunch of differential conditions and that consolidates both the COVID-19 episode and the cholera pestilence. **Tchoumi et al. (2021)** researched the chance of an ideal control situation with a co-disease model for COVID-19 and intestinal sickness. They showed that taking on defensive methods against COVID-19 and jungle fever together could assist with limiting the spread of the illnesses, in contrast with applying every deterrent methodology alone. **Mekonen et al. (2022)** put out utilizing a nonlinear deterministic numerical reenactment to research the expected spread of both tuberculosis and COVID-19 co-infections. Subsequent to figuring the basic multiplication numbers, they

proceeded to talk about the dependability investigation of the balance points of the submodels freely. **Ringa et al. (2022)** explored a shiny new numerical model for COVID-19 and HIV/AIDS to assess the impact of COVID-19 on the movement of HIV as well as the other way around.**Wang et al. (2024)** researched and significant alterations have been observed in pathogen transmission dynamics, host distribution, and human exposure risk. **Phung et al. (2025)** explored the impact of global climate change on the epidemiology of infectious diseases as a critical public health issue.

II. MATHEMATICAL FORMULATION OF THE MODEL:

In this part, we construct the governing numerical model for the codynamics of TB and COVID-19 by parting the absolute populace into nine compartments named as helpless people S. These compartments are totally unrelated with each other. Inert TB tainted people who have no side effects of TB sickness and are not irresistible (L_T), dynamic TB-contaminated people (I_T), COVID-19 tainted people without any side effects however are irresistible $A(t)$, people who have been inoculated against COVID-19 V(t), COVID-19 contaminated people with clinical side effects and are irresistible (I_C), both idle TB and COVID-19 coinfected people $(L_{CT})$and recuperated populace from both TB and COVID-19 (R). Remembering these things, the complete populace at time t, which will be demonstrated by the image $N(t)$can be determined as

$$N(t) = S + L_T + I_T + A + I_C + L_{CT} + I_{CT} + V + R \quad (1)$$

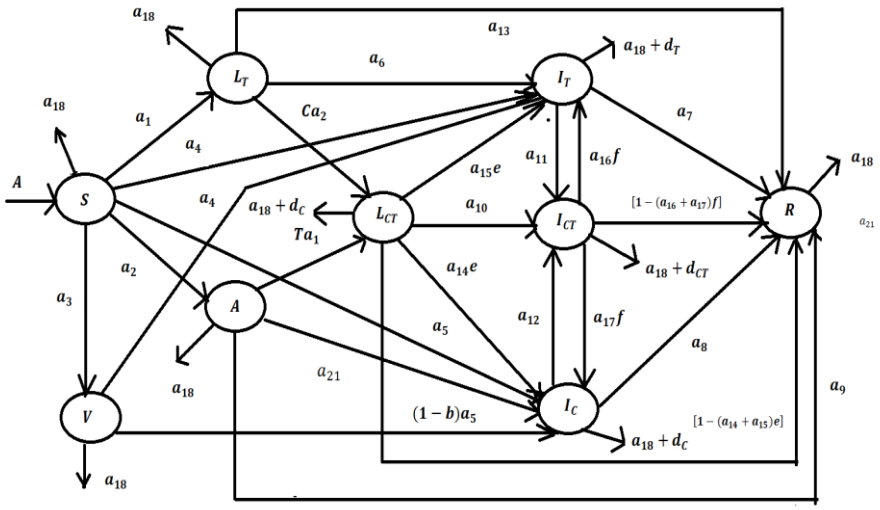


Figure 1- The COVID-19 and tuberculosis co-infection model as shown in a schematic diagram

The following systems of nonlinear differential equations are produced as a consequence as depicted in the flow diagram:

$$\frac{dS}{dt} = A - (a_1 + a_2 + a_3 + a_4 + a_5 + a_{18})S \quad (2)$$

$$\frac{dL_T}{dt} = a_1 S - (Ca_2 + a_6 + a_{13} + a_{18})L_T \quad (3)$$

$$\frac{dI_T}{dt} = a_6 L_T + a_4 S + a_4 V + a_{15} e L_{CT} + a_{16} f I_{CT} - (a_7 + a_{11} + a_{18} + d_T)I_T \quad (4)$$

$$\frac{dA}{dt} = a_2 S - (a_{21} + a_9 + Ta_1 + a_{18})A \quad (5)$$

$$\frac{dI_C}{dt} = a_{14} e L_{CT} + a_5 S + a_{21} A + (a_5 - ba_5)V + a_{17} f I_{CT} - (a_8 + a_{12} + a_{18} + d_C)I_C \quad (6)$$

$$\frac{dL_{CT}}{dt} = Ca_2 L_T + Ta_1 A - (e + a_{10} + a_{18} + d_C)L_{CT} \quad (7)$$

$$\frac{dI_{CT}}{dt} = a_{10} L_{CT} + a_{11} I_T + a_{12} I_C - (f + a_{18} + d_{CT})I_{CT} \quad (8)$$

$$\frac{dV}{dt} = a_3 S - [a_4 + a_5 - ba_5 + a_{18}]V \quad (9)$$

$$\frac{dR}{dt} = a_{13} L_T + a_7 I_T + [f - (a_{16} + a_{17})f]I_{CT} + a_8 I_C + [e - (a_{14} + a_{15})e]L_{CT} + a_9 A - a_{18} R \quad (10)$$

$$a_1 = \frac{a_{19}(I_T + I_{CT})}{N}$$

$$a_2 = \frac{a_{20}(A + I_C + L_{CT} + I_{CT} + V)}{N}$$

Adding equations (2) to (10), we get

$$\frac{dN}{dt} = A - a_{18}N - d_C(L_{CT} + I_C) - d_T I_T - d_{CT} I_{CT} \leq A - a_{18}N \quad (11)$$

Solving equation (11), we get

$$N \leq \frac{A}{a_{18}} + ce^{-a_{18}t} \quad (12)$$

Applying initial condition $N(0) = N_0$ in equation (12), we get

$$N \leq \frac{A}{a_{18}} + \left(N_0 - \frac{A}{a_{18}}\right) e^{-a_{18}t}$$

$$\lim_{t \to \infty} N(t) = \frac{A}{a_{18}} (\text{Carrying Capacity})$$

$$S + L_T + L_{CT} + A + V + I_T + I_{CT} + I_C + R$$

$$\Omega = \left\{S, L_T, L_{CT}, A, V, I_T, I_{CT}, I_C, R \in \Re_+^9; 0 \leq N(t) \leq \frac{A}{a_{18}}\right\}$$

$$S \geq 0, L_T \geq 0, L_{CT} \geq 0, A \geq 0, V \geq 0, I_T \geq 0, I_{CT} \geq 0, I_C \geq 0, R \geq 0$$

Accordingly, the solution is positive in the locale $\mathcal{R}$, and the conditions (2) to (10) are both epidemiologically huge and numerically all around presented. Accordingly, in this situation, we may simply utilize stream made by the model (2) to (10). Besides, the results persevere as the framework proceeds.

The equilibrium point of the co-infection model (2-10) is acquired by addressing the arrangement of condition (13-21):

$$A - (a_1 + a_2 + a_3 + a_4 + a_5 + a_{18})S = 0 \quad (13)$$

$$a_1 S - (Ca_2 + a_6 + a_{13} + a_{18})L_T = 0 \quad (14)$$

$$a_6 L_T + a_4 S + a_4 V + a_{15} e L_{CT} + a_{16} f I_{CT} - (a_7 + a_{11} + a_{18} + d_T)I_T = 0 \quad (15)$$

$$a_2 S - (a_{21} + a_9 + Ta_1 + a_{18})A = 0 \quad (16)$$

$$a_{14} e L_{CT} + a_5 S + a_{21} A + (a_5 - ba_5)V + a_{17} f I_{CT} - (a_8 + a_{12} + a_{18} + d_C)I_C = 0 \quad (17)$$

$$Ca_2 L_T + Ta_1 A - (e + a_{10} + a_{18} + d_C)L_{CT} = 0 \quad (18)$$

$$a_{10} L_{CT} + a_{11} I_T + a_{12} I_C - (f + a_{18} + d_{CT})I_{CT} = 0 \quad (19)$$

$$a_3 S - [a_4 + a_5 - ba_5 + a_{18}]V = 0 \quad (20)$$

$$a_{13} L_T + a_7 I_T + [f - (a_{16} + a_{17})f]I_{CT} + a_8 I_C + [e - (a_{14} + a_{15})e]L_{CT} + a_9 A - a_{18} R = 0 \quad (21)$$

The point at which the system is in a state of disease-free equilibrium, denoted by the symbol (E_0)

$$E_0 = \left(\frac{A}{a_{18}}, 0,0,0,0,0,0,0\right)$$

We utilize the documentation $Y = (L_T, I_T, A, I_C, L_{CT}, I_{CT}, V)$ to mean the vector capabilities

$$\mathcal{F} = \begin{bmatrix} a_1 S \\ 0 \\ a_2 S \\ 0 \\ 0 \\ 0 \\ 0 \end{bmatrix}$$

$$\mathcal{v} = \begin{bmatrix} (Ca_2 + a_6 + a_{13} + a_{18})L_T \\ (a_7 + a_{11} + a_{18} + d_T)I_T - a_6 L_T - a_4 V - a_{15} e L_{CT} - a_{16} f I_{CT} \\ (a_{21} + a_9 + Ta_1 + a_{18})A \\ (a_8 + a_{12} + a_{18} + d_C)I_C + a_{14} e L_{CT} - a_{21} A - (a_5 - ba_5)V - a_{17} f I_{CT} \\ (e + a_{10} + a_{18} + d_C)L_{CT} - Ca_2 L_T - Ta_1 A \\ (f + a_{18} + d_{CT})I_{CT} - a_{10} L_{CT} - a_{11} I_T - a_{12} I_C \\ [a_4 + a_5 - ba_5 + a_{18}]V \end{bmatrix}$$

The Jacobian matrices of $\mathcal{F}$ and $\mathcal{v}$ at the disease free equilibrium point (E_0) are, respectively,

$$F = \begin{bmatrix} 0 & a_{19} & 0 & 0 & 0 & a_{19} & 0 \\ 0 & 0 & 0 & 0 & 0 & 0 & 0 \\ 0 & 0 & a_{20} & a_{20} & a_{20} & 0 & a_{20} \\ 0 & 0 & 0 & 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 & 0 & 0 & 0 \end{bmatrix}$$

$$a_1 = \frac{a_{19}(I_T + I_{CT})}{N}$$

$$a_2 = \frac{a_{20}(A + I_C + L_{CT} + I_{CT} + V)}{N}$$

$$V = \begin{bmatrix} k_1 & 0 & 0 & 0 & 0 & 0 & 0 \\ -a_6 & k_2 & 0 & 0 & -a_{15}e & -a_{16}f & -a_4 \\ 0 & 0 & k_3 & 0 & 0 & 0 & 0 \\ 0 & 0 & -a_6 & k_4 & -a_{14}e & -a_{17}f & k_6 \\ 0 & 0 & 0 & 0 & k_5 & 0 & 0 \\ 0 & -a_{11} & 0 & -a_{12} & -a_{10} & k_6 & 0 \\ 0 & 0 & 0 & 0 & 0 & 0 & k_7 \end{bmatrix}$$

$k_1 = a_6 + a_{13} + a_{18}, k_2 = a_7 + a_{11} + a_{18} + d_T, k_3 = a_6 + a_9 + a_{18} k_4 = a_8 + a_{12} + a_{18} + d_C,$
$k_5 = e + a_{10} + a_{18} + d_C,$

$$k_6 = f + a_{18} + d_{CT},$$

$$k_7 = a_5 - ba_5, k_8 = a_4 + a_5 - ba_5 + a_{18}$$

FV^{-1}

$$= \begin{bmatrix} \frac{a_{19}a_6}{k_1k_2} + \frac{a_{19}a_{11}a_6k_4}{Pk_1k_2} & \frac{a_{19}}{k_2} + \frac{a_{19}a_{11}k_4}{Pk_2} & \frac{a_{19}a_{12}a_{21}}{Pk_3} & \frac{a_{19}a_{12}}{P} & 0 & \frac{a_{19}k_4}{P} & -\frac{a_{19}a_4}{k_2k_7} - \frac{a_{19}k_6a_{12}}{Pk_7} \\ 0 & 0 & 0 & 0 & 0 & 0 & 0 \\ 0 & 0 & \frac{a_{20}}{k_3} + \frac{a_{20}a_{21}}{k_3k_4} & \frac{a_{20}}{k_4} & \frac{a_{20}a_{14}e}{k_4} + a_{20} & 0 & -\frac{a_{20}k_6(k_6k_4 - a_{12}a_{17}f) + a_{17}fk_6a_{12}}{k_4Pk_7} \\ 0 & 0 & 0 & 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 & 0 & 0 & 0 \end{bmatrix}$$

$$+ \frac{a_{20}}{k_7}$$

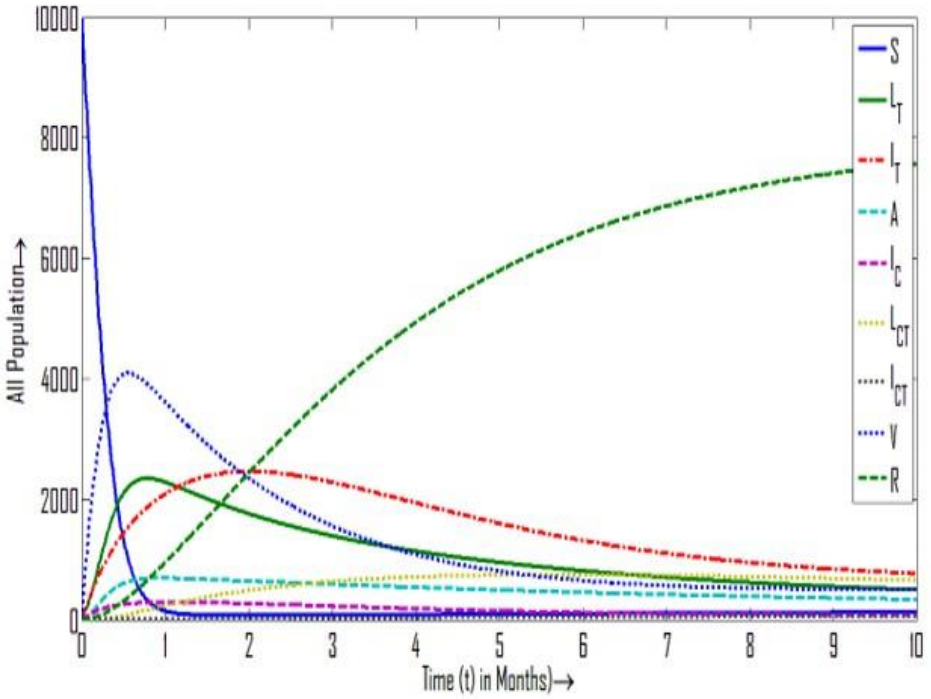
Where $P = (k_6k_4 - a_{12}a_{17}f)$

Subsequently, basic reproduction number (R_{CT}) of the co-infection model (2-10) is given by

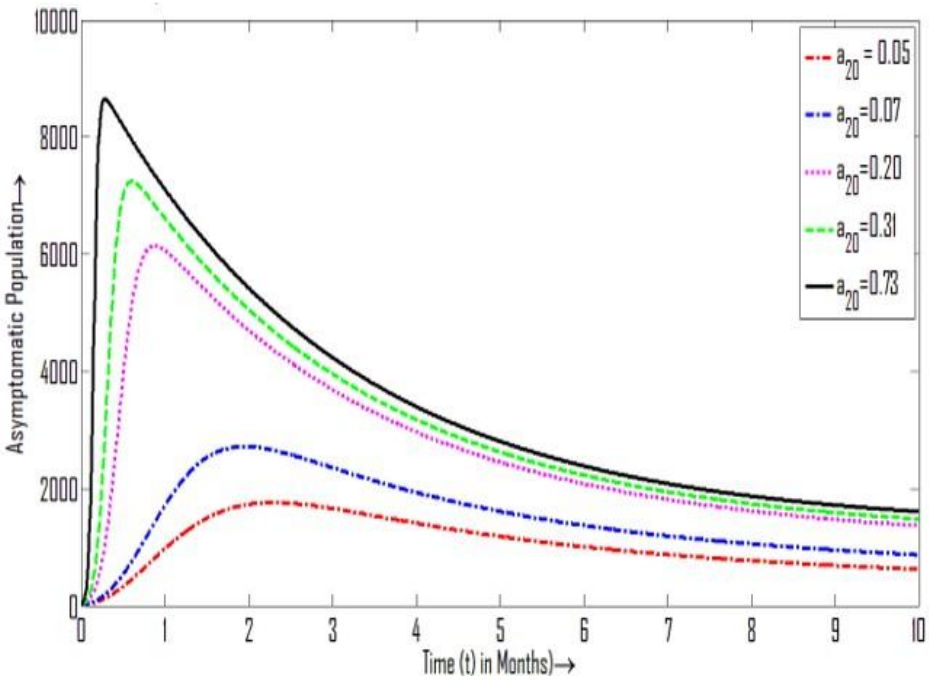
$$R_{CT} = max\left\{\frac{a_{19}a_6}{k_1k_2} + \frac{a_{19}a_{11}a_6k_4}{Pk_1k_2}, \frac{a_{20}}{k_3} + \frac{a_{20}a_{21}}{k_3k_4}\right\} \quad (22)$$

III. RESULTS AND DISCUSSION:

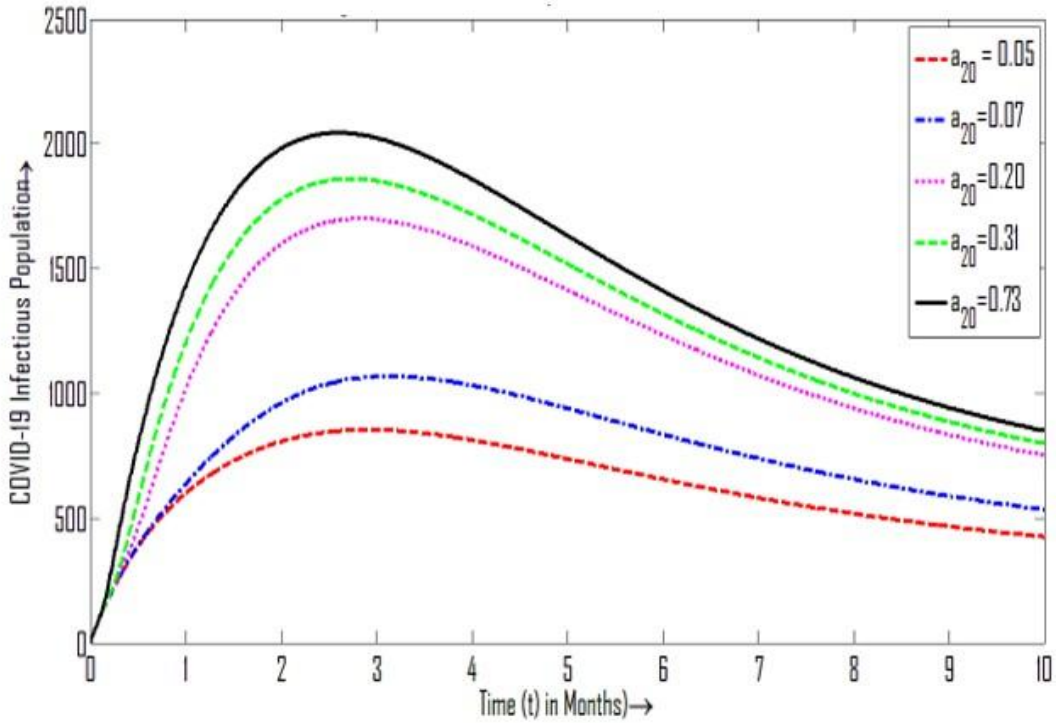
Graph 1: Variation in all population with time t



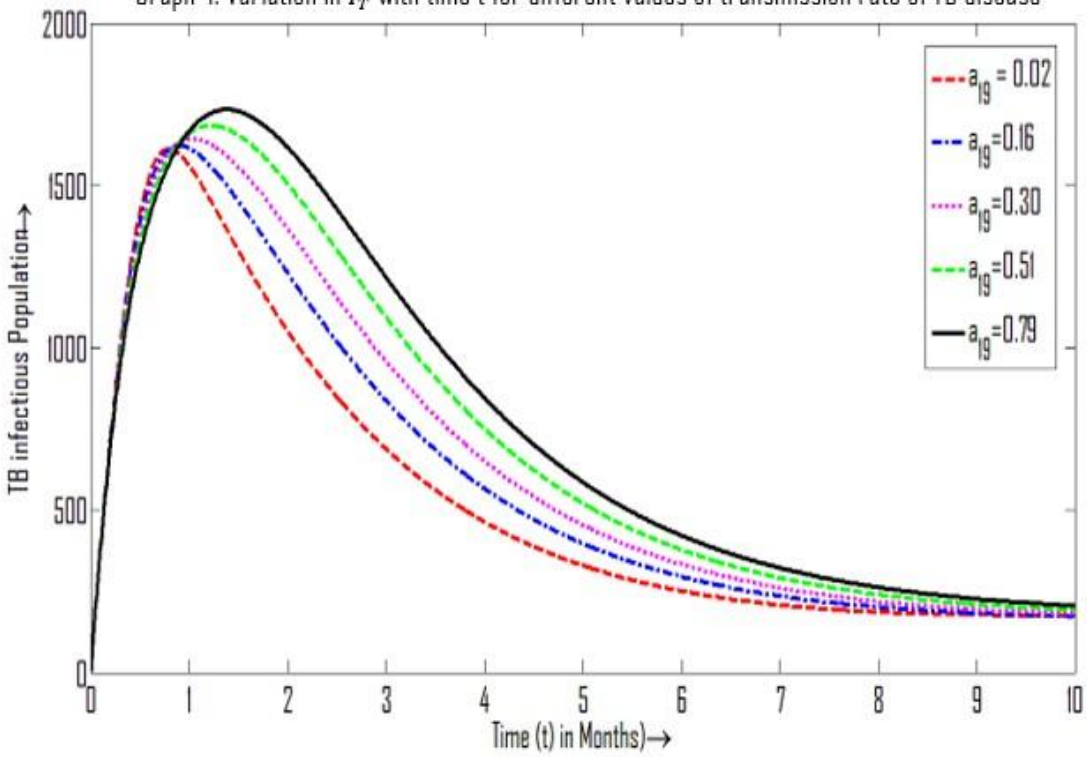
Graph 2: Variation in A(t) with time t for different values of effective contact rate for COVID-19 disease



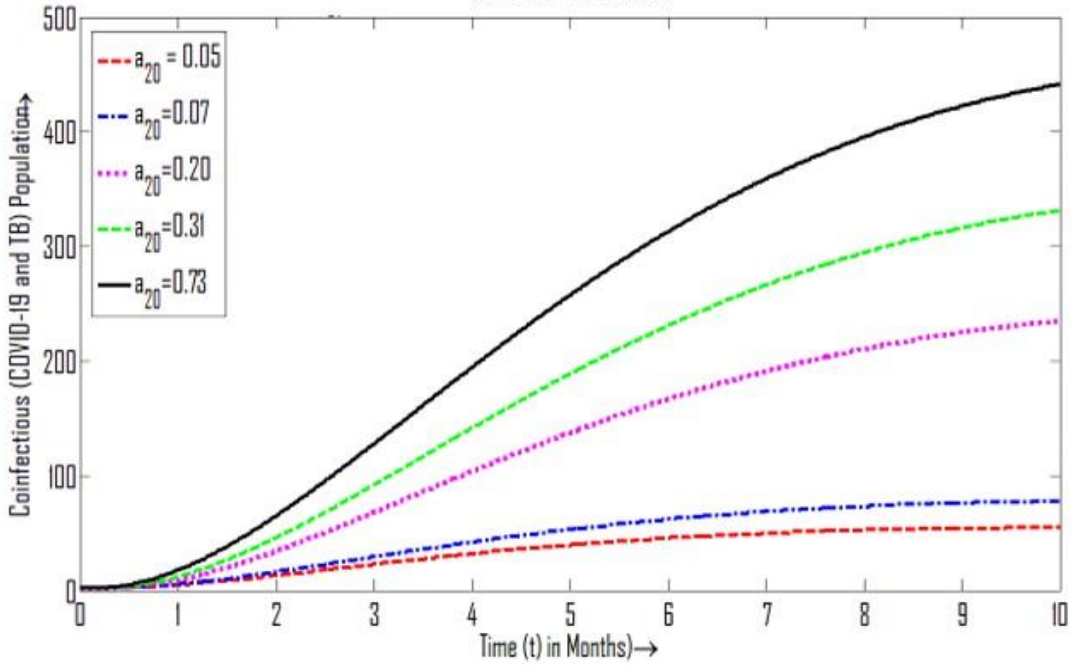
Graph 3: Variation in Ic(t) with time t for different values of effective contact rate for COVID-19



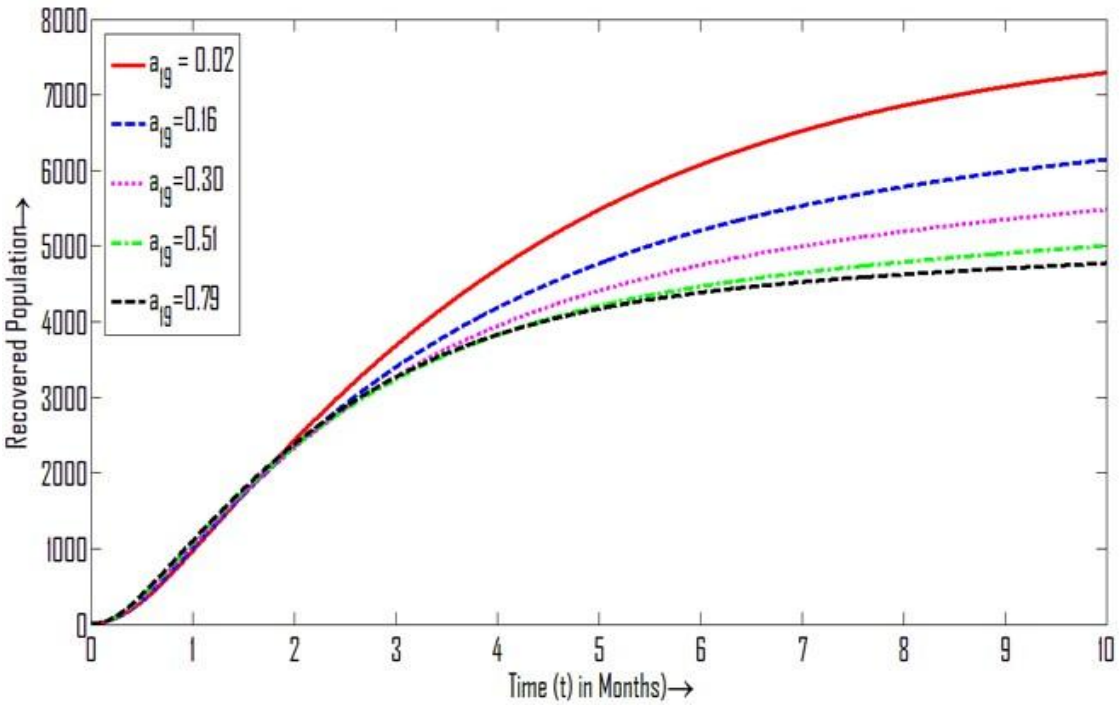
Graph 4: Variation in I_T with time t for different values of transmission rate of TB disease



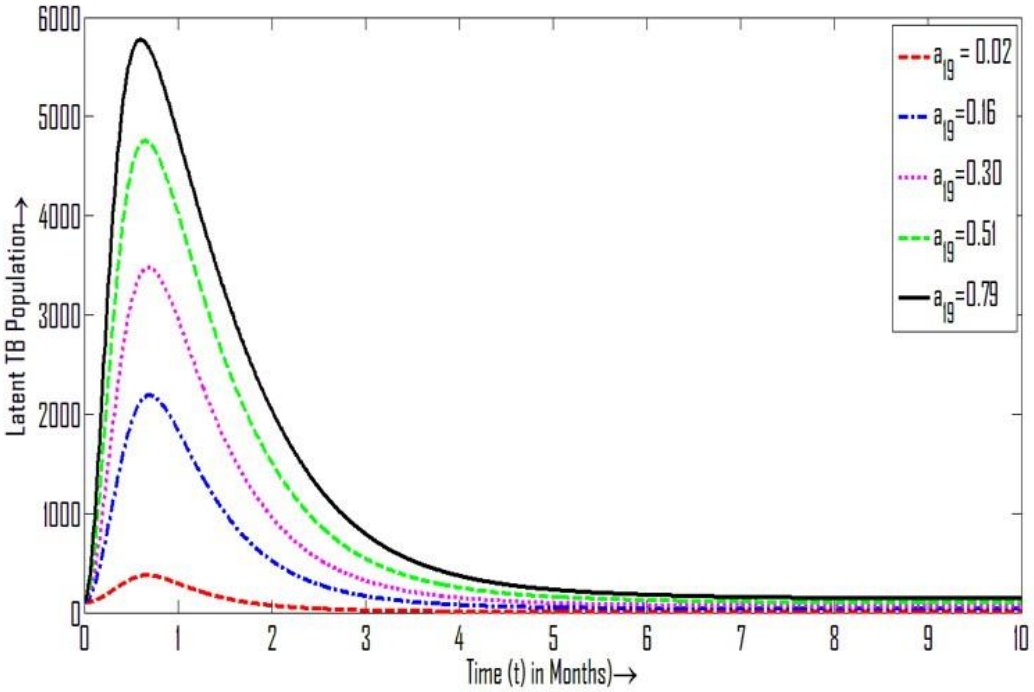
Graph 5: Variation in I_{CT} (t) with time t for different values of effective contact rate for COVID-19 disease



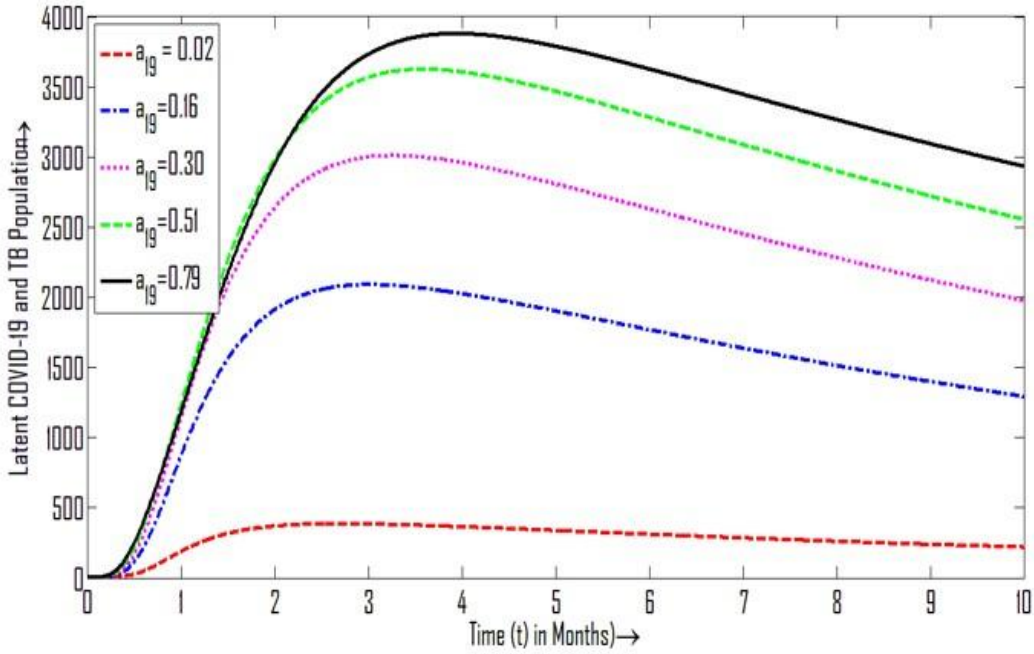
Graph 6: Variation in R(t) with time t for different values of transmission rate of TB disease



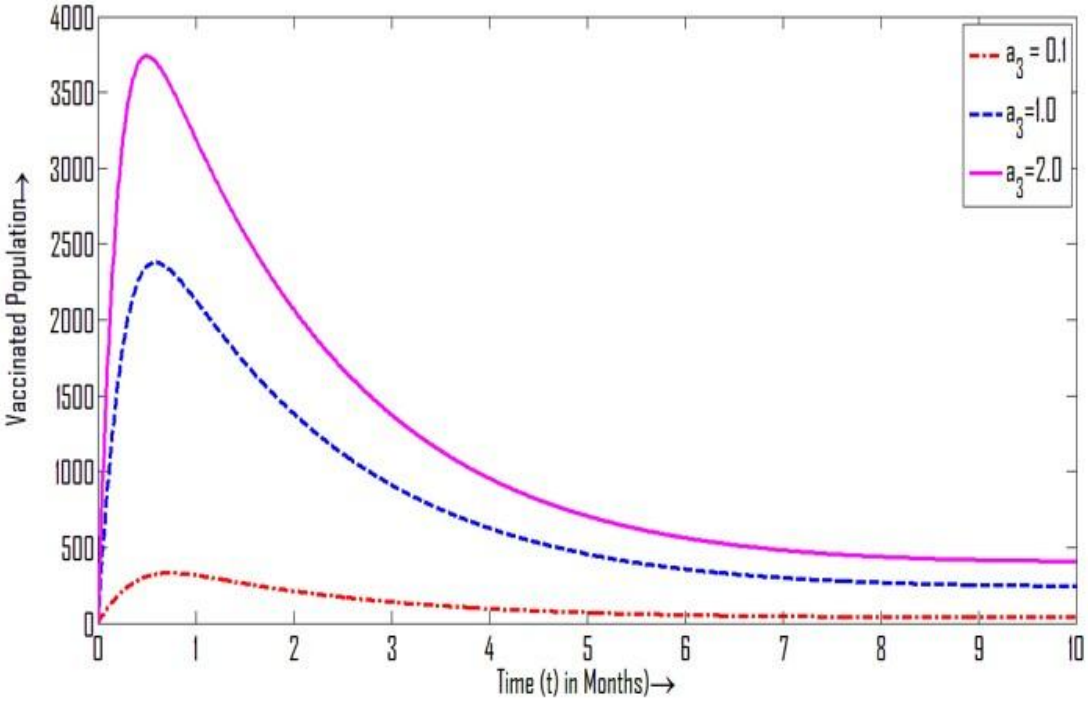
Graph 7: Variation in I_T (t) with time t for different values of transmission rate of TB disease



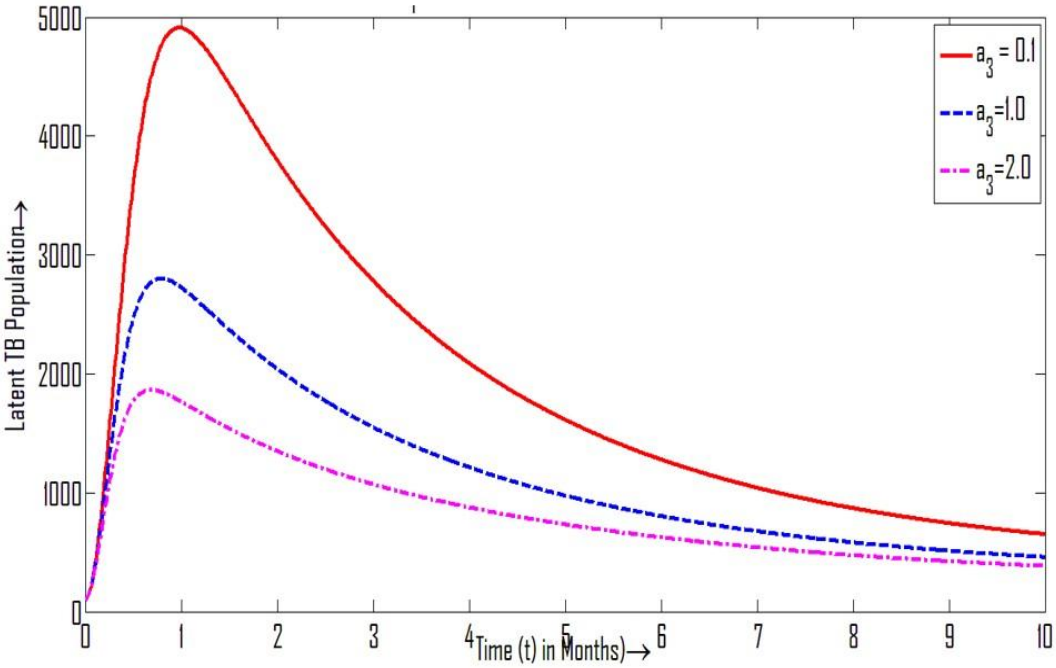
Graph 8: Variation in I_{CT} (t) with time t for different values of transmission rate of TB disease



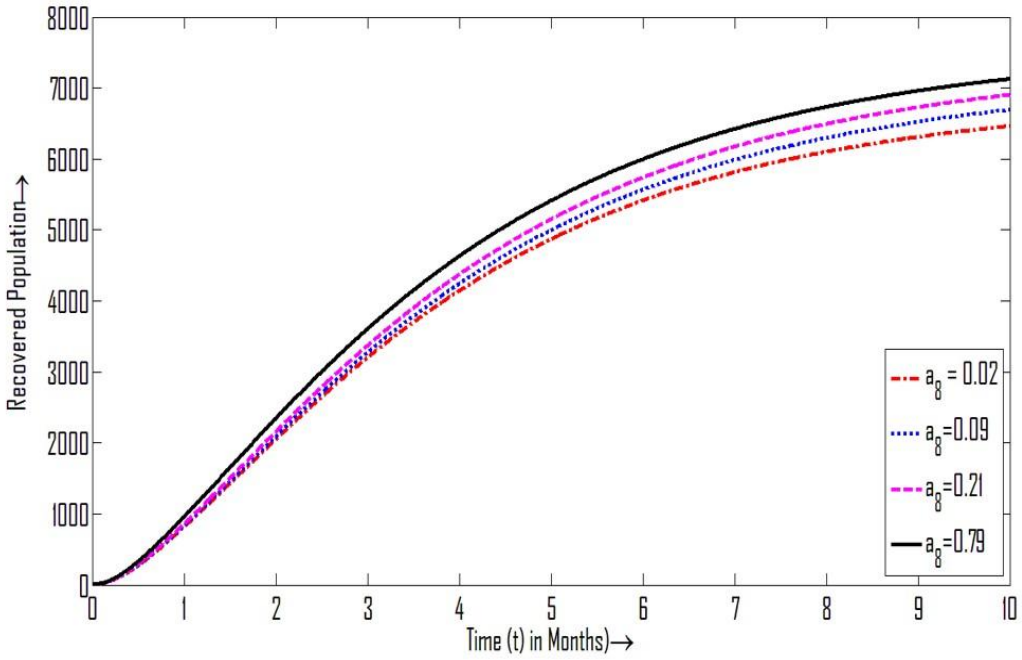
Graph 9: Variation in V(t) with time t for different values of COVID-19 vaccination rate



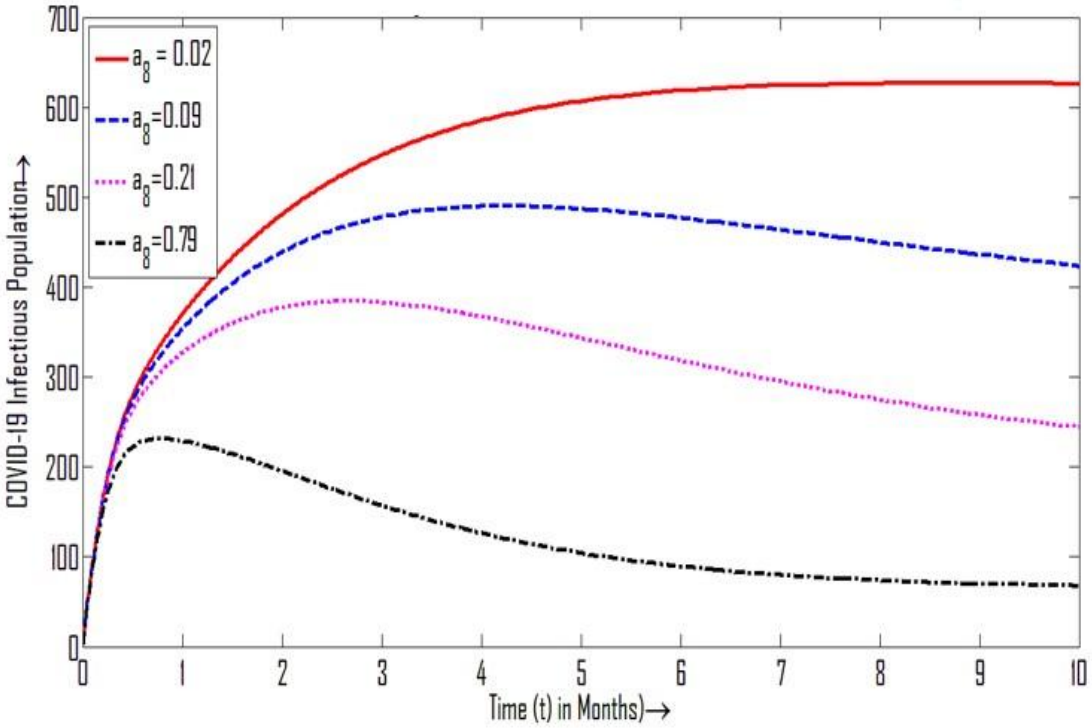
Graph 10: Variation in L_T (t) with time t for different values of COVID-19 vaccination rate



Graph 11: Variation in R(t) with time t for different values of recovery rate from COVID-19 vaccination rate



Graph 12: Variation in I_C(t) with time t for different values of recovery rate from COVID-19



In this part of the article, we carry out numerical solutions of the co-infection model. The ode45 solver in MATLAB is used to integrate the answers to the system equations after they have been solved. Here, the numerical solutions to the co-infection model are shown (2-10). In order to accomplish this, we make use of the starting values of the state variables for the co-infection model, which are as follows:

$$S(0) = 10000, L_T(0) = 100, I_T(0) = 3, A(0) = 10, I_C(0) = 3$$

$$L_{CT}(0) = 2, I_{CT}(0) = 2, V(0) = 3, R(0) = 3$$

and the values for all of the parameters are shown in Table 1. Table 1 contains the parameter values that were used in the plotting of the time series graphs for the numerical solutions to the co-infection model (2)-(10). These graphs are numbered (1)-(12). A graph depicting the change in total population as a function of time has been provided (1). We have demonstrated, via the use of graph (2)-(8) that the influence of contact rates of the disease with infected compartments of system (2-10). As a result, we have reached the conclusion that the states I_T, I_C, L_{CT} and I_{CT} all increase as the transmission coefficients are raised. Graphs (9) and (10) respectively indicate the impact that the COVID-19 vaccination rate has had on the prevalence of latent TB as well as the population that has been vaccinated against it. It has been noted that as the vaccination rate of COVID-19 rises, the proportion of vaccinated individuals rises while the proportion of latent individuals falls. The influence that recovery rate has on both the recovered population and the population infected with COVID-19 is depicted in graphs (11) and (12) respectively. It has been demonstrated that a rise in the COVID-19 recovery rate will result in a rise in the number of individuals in the recovered class while simultaneously resulting in a fall in the number of COVID-19 infectious class.

Table1: Numerical values of parameter for sensitivity analysis

S. No.	Symbol	Meaning	Numerical Value	Source
1	A	The rate at which susceptible individuals are recruited into the population	500	Assumed
2	a_1	TB's infectious force	0.3425	Assumed
3	a_2	COVID-19's ability to infect	0.1175	Assumed
4	a_2	The immunization rate for COVID-19	2	Assumed
5	a_4	The rate at which persons who are both susceptible and vaccinated become infected with tuberculosis in a given compartment	0.4	Assumed
6	a_5	The rate at which individuals who are sensitive to COVID-19 make their way into infected compartments	0.1	Assumed
7	a_6	individuals who have been exposed to tuberculosis but have not yet developed the disease	0.25	Assumed

8	a_7	Rate of recovery for patients afflicted with tuberculosis	0.516	Assumed
9	a_8	Rates of recovery for individuals infected with COVID-19	0.5	Assumed
10	a_9	The recovery rate of those persons who were exposed to COVID-19	0.05	Mekonen et al.(2021)
11	a_{10}	Transfer rate of persons who have been exposed to both TB and COVID-19 to those who are co-infected	0.02	Assumed
12	a_{11}	Rate of COVID-19 infection among TB patients and those infected with TB	0.001	Assumed
13	a_{12}	Rate of tuberculosis infection among those who were infected with COVID-19	0.002	Assumed
14	a_{13}	Recovery rate of patients who are latently infected with tuberculosis	0.09	Silva and Torres (2015)
15	a_{14}	Rates of individuals L_{CT} who have recovered from TB	0.2	Assumed
16	a_{15}	Recovery rate of people who tested positive for L_{CT} from COVID-19	0.8	Assumed
17	a_{16}	TB recovery rate of patients who are L_{CT} infected	0.04	Assumed
18	a_{17}	Recovery rate of COVID-19 in persons tested by L_{CT}	0.6	Assumed
19	a_{18}	The individuals' rates of death due to natural causes	0.0477	Mekonen et .(2021)
20	a_{19}	The rate at which the TB disease is spread	0.6	Ullah et al. (2020)

21	a_{20}	The rate of COVID-19 transmission	0.659	Mekonen et al. (2021)
22	C	Rate at which persons who have been exposed to TB get exposed to COVID-19	0.25	Assumed
23	T	TB exposure risk for COVID-19 asymptomatic persons	0.03	Assumed
24	d_1	Rate of fatalities caused by the COVID-19 virus	0.023	Mekonen et al.(2021)
25	d_2	The mortality rate attributable to TB germs	0.01	Ullah et al. (2020)
26	d_3	The death rate as a result of simultaneous infection with both diseases	0.2	Assumed
27	f	Exit rates from the coinfected L_{CT} group	0.003	Assumed
28	e	Individuals' departure from the L_{CT} class	0.01	Assumed

IV. CONCLUDING REMARKS:

In the current investigation, a nonlinear deterministic mathematical modelling for the co-infection of tuberculosis and COVID-19 is proposed in order to investigate the possibility that these diseases may continue to spread. The biological relevance of the model can be demonstrated by demonstrating the existence of positive solutions inside a particular region. In addition, there is a stable endemic equilibrium point that may be found for reproduction numbers that are higher than one. In order to supplement the analytical results, a variety of simulation situations were run and it was found that they were in good agreement with each other. In addition, the results of the simulation show that an increase in the contact rate made the co-infection of both diseases significantly worse. On the other hand, the spread of co-infection diseases could be reduced by reducing the effective contact rate and increasing the number of treatments.

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