SENSITIVITY AND STABILITY ANALYSES OF COVID-19 AND TUBERCULOSIS CO-INFECTION DYNAMICS IN THE PRESENCE OF DISEASE RELAPSE

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Global public health in a chaotic world: The role of modeling & data science

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Abstract

Active Tuberculosis (TB) remains a major risk factor to increase the spread of Covid-19 in any community. Until date, the co-infection of Covid-19 and TB continue to result in untimely yet preventable deaths of its victims. Covid-19 had an exponential increase in cases between October 2023 and January 2024, attaining a growth factor of 6.53, having recorded a gradual decline in previous years. This research investigated cases of reinfection with Covid-19 by people who have previously recovered or have been vaccinated against it. It is estimated that one-third of the world's population are infected with latent TB. Moreover, the emergent prevalence of Covid-19 resulted in drastic decline of the diagnosis and treatment of TB. This study presents a novel and robust deterministic co-infection model for the duo. Mono-infection models for the transmission, prevention and control dynamics of TB and Covid-19 were also developed.

Covid-19

In late December 2019, Covid-19 caused by the new SARS-CoV-2, broke out in Wuhan city of China. Contracted when an individual comes in close direct contact with an infected person or there respiratory droplets. The SARS-CoV-2 is established in the URT consisting of the nose and throat. Risk factors for higher severity rate and consequently higher mortality rate for Covid-19 are pre-existing disease e.g TB, cancer, people aged ≥ 60, non-vaccinated, pregnant women etc.

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Tuberculosis

TB is an infectious disease caused by bacillus MTB. Pulmonary TB attacks the lungs while extra-pulmonary TB affect other body parts like the CNS, brain, spine, or kidneys of people with weak immune systems and children. TB is the 10th leading cause of death worldwide since 2007 and the main cause of death from a single infectious agent, ranking above HIV/AIDS (Schlüter et al., 2021). Treatment of TB via multiple antibiotics do not remove tubercle bacilli, the causative agent. Recovered individuals are classified as low-risk latent individuals who can get re-infected due to relapse.

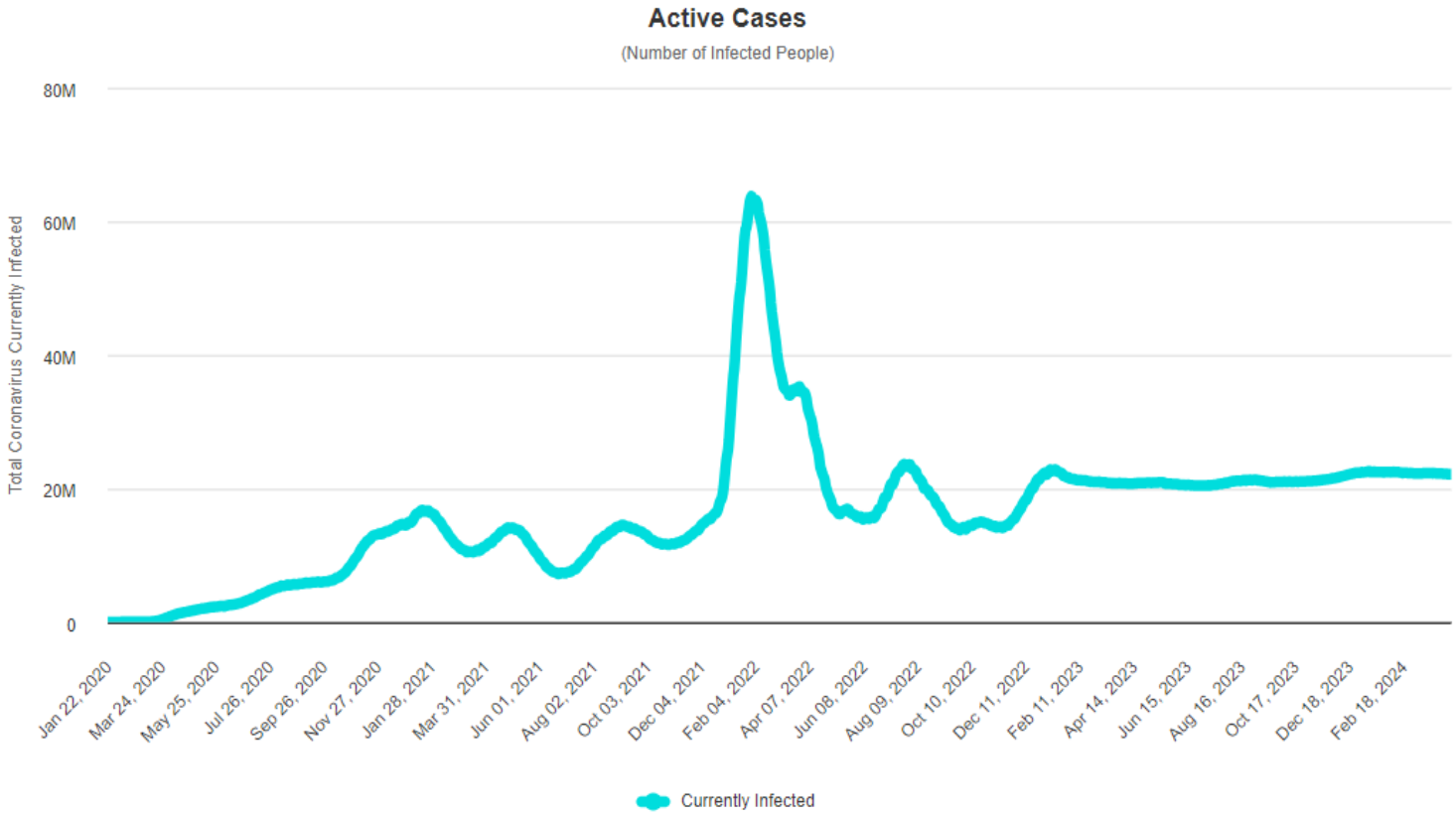

Figure 1: Active COVID-19 Cases Globally: Jan. 2020 - April 2024 (Worldometers, 2024)

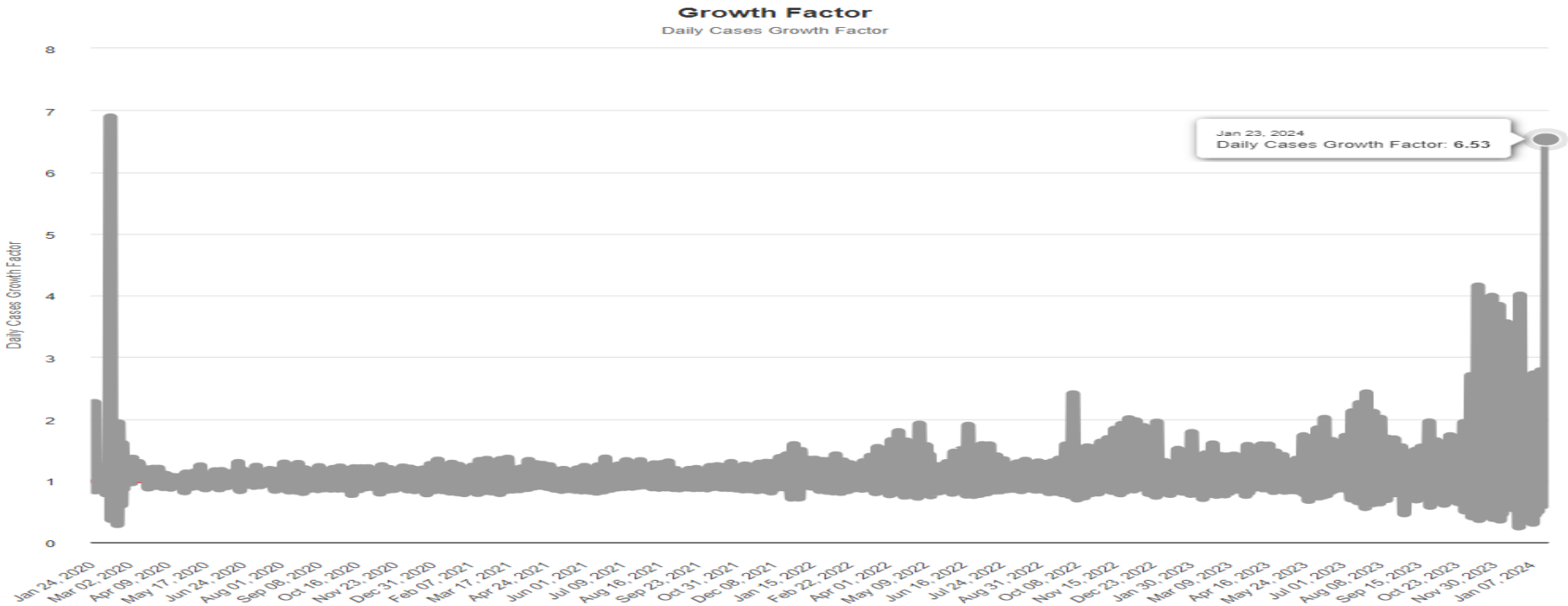

Figure 2: Growth Factor of Daily New Cases of Covid-19 Worldwide: Jan. 2020-Jan. 2024 (Worldometers, 2024)

Growth Factor

Figure 2 shows the growth factor of Covid-19 globally from 2020 to 2024 indicating an exponential increase between October 2023 and January 2024. Growth factor is the factor by which a quantity multiplies itself over time. The formula used is every day's new cases divided by new cases on the previous day.

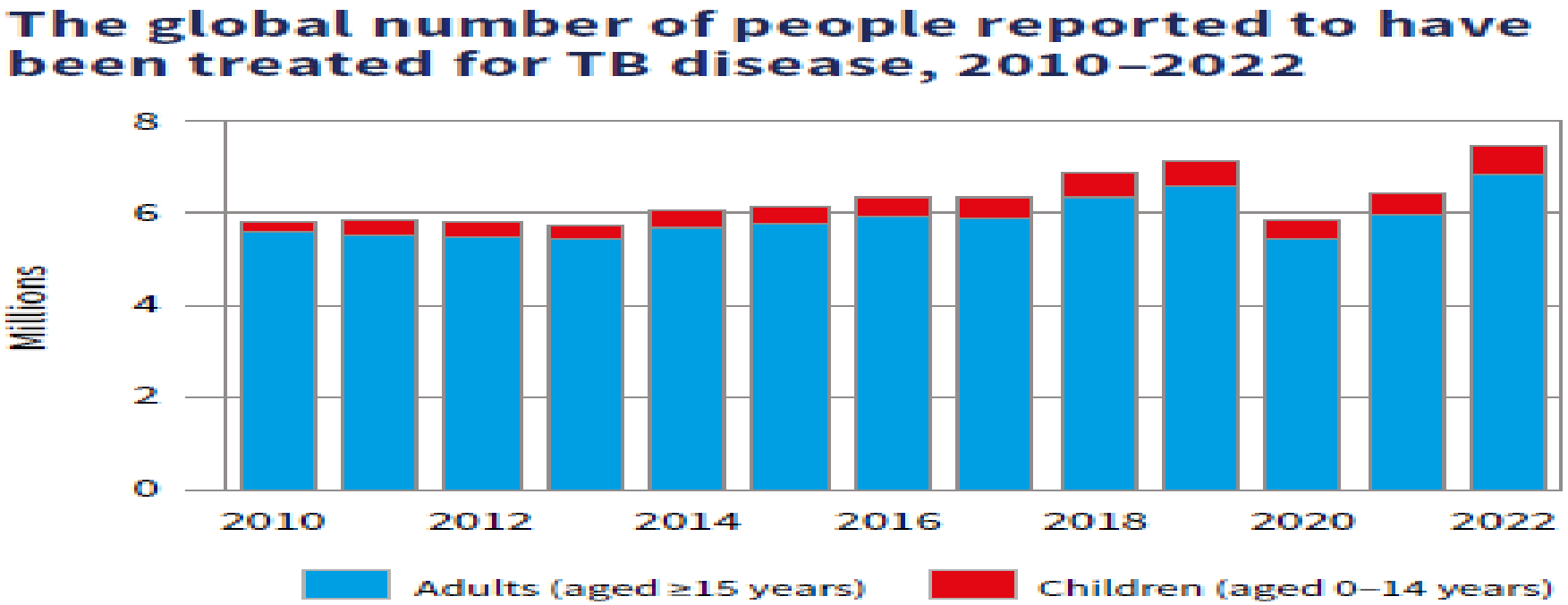

Figure 3: The Global Number of People treated for TB Disease, 2010–2022 (World Health Organization, 2023)

Global TB Treatment

Figure 3 shows the global number of People treated for TB between 2010 and 2022 indicating a decline in the years 2020 and 2021 associated with the emergent prevalence and chaotic spread of Covid-19.

Co-infection of Covid-19 and TB

1. Higher rates of co-infection between Covid-19 and other respiratory pathogens like MTB are experienced compared to co-infection with other diseases. TB and SARS-CoV-2 have the same route of infection, respiratory organs including the lungs, thus potentiating their effect on each other and mutually accelerating there progression to a critical stage (Tadolini et al., 2020):
2. According to Khurana & Aggarwal (2020), both TB and Covid-19 diseases spread in overcrowded areas with poor and undernourished population and both via respiratory droplets resulting in simultaneous co-infection with 12.3% mortality. Unprecedented nature of Covid-19 unmasks subtle active cases of TB infections which have not been previously diagnosed, responsible for hidden transmission.

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2. According to Khurana & Aggarwal (2020), both TB and Covid-19 diseases spread in overcrowded areas with poor and undernourished population and both via respiratory droplets resulting in simultaneous co-infection with 12.3% mortality. Unprecedented nature of Covid-19 unmasks subtle active cases of TB infections which have not been previously diagnosed, responsible for hidden transmission.
3. In the first-ever global cohort of TB patients co-infected with COVID-19 recruited by the Global Tuberculosis Network (GTN) in 8 countries and 3 continents, it was contained that out of the 49 patients reviewed, 26 had TB before COVID-19, 14 had COVID-19 first and 9 had both diseases diagnosed within the same week, 4 on the same day (Tadolini et al., 2020).
4. In a case study analyses of the co-infection of TB and Covid-19 by Stochino et al. (2020), among the 24 in-patients diagnosed with active TB in Sondrio province, northern Italy, 20 cases of co-infection with Covid-19 was identified.

Disease Modeling

We employed the compartmental disease modeling approach. Each compartment of the model is made up of mutually exclusive time-dependent sub-population consisting of individuals with the same disease status. The total human population is classified into 12 mutually exclusive compartments.

Table 1: The Model's State Variables

Variables	Description
$S(t)$	Susceptible Population
$I_C(t)$	Covid-19 Infected Population
$I_L(t)$	Latent TB Infected Population
$I_A(t)$	Active TB Infected Population
$I_{CL}(t)$	Co- infected with Covid-19 and Latent TB Population
$I_{CA}(t)$	Co-Infected with Covid-19 and Active TB Population
$R_C(t)$	Covid-19 Recovered Population
$R_T(t)$	TB Recovered Population
$R_{CT}(t)$	Covid-19 and TB Co-Recovered Population
$V_C(t)$	Covid-19 Vaccinated Population
$V_T(t)$	TB Vaccinated Population
$V_{CT}(t)$	Covid-19 and TB Co-Vaccinated Population

Parameters	Description
Λ	Recruitment rate into the susceptible population by birth or immigrat
μ	Natural death rate
δ_C	Covid-19 induced death rate
δ_T	TB induced death rate
β_C	Covid-19 effectual contact/transmission rate
β_T	TB effectual contact/transmission rate
λ_C	Force of infection associated with Covid-19
λ_T	Force of infection associated with TB
ν_C	Covid-19 vaccination rate
ν_T	TB vaccination rate
ω_C	Rate of loss of immunity for Covid-19 vaccinated class
ω_T	Rate of loss of immunity for TB vaccinated class
θ_C	Rate of loss of immunity for Covid-19 recovered class
θ_T	Rate of loss of immunity for TB recovered class
γ_C	Recovery rate via treatment for Covid-19
γ_T	Recovery rate via treatment for TB
ρ_1	Rate of progression from latent TB to active TB
ρ_2	Rate of progression from co-infected (latent TB) to co-infected (activ

The Covid-19 and TB Co-infection Model

$$\frac{dS}{dt} = \Lambda - (\nu_C + \nu_T + \lambda_C + \lambda_T)S + \omega_C V_C + \omega_T V_T + \theta_C R_C + \theta_T R_T - \mu S, \tag{1}$$

$$\frac{dI_C}{dt} = \lambda_C(S + V_T) - \lambda_T I_C - \gamma_C I_C - (\delta_C + \mu)I_C, \tag{2}$$

$$\frac{dI_L}{dt} = \lambda_T(S + V_C) - \lambda_C I_L - \rho_1 I_L - \mu I_L, \tag{3}$$

$$\frac{dI_A}{dt} = \rho_1 I_L - \lambda_C I_A - \gamma_T I_A - (\delta_T + \mu)I_A, \tag{4}$$

$$\frac{dI_{CL}}{dt} = \lambda_T I_C + \lambda_C I_L - \rho_2 I_{CL} - \gamma_C I_{CL} - (\delta_C + \mu)I_{CL}, \tag{5}$$

$$\frac{dI_{CA}}{dt} = \lambda_C I_A + \rho_2 I_{CL} - (\gamma_C + \gamma_T)I_{CA} - (\delta_C + \delta_T + \mu)I_{CA}, \tag{6}$$

$$\frac{dR_C}{dt} = \gamma_C I_C + \gamma_C I_{CL} + \gamma_C I_{CA} + \theta_T R_{CT} - \theta_C R_C - \gamma_T R_C - (\delta_T + \mu)R_C, \tag{7}$$

$$\frac{dR_T}{dt} = \gamma_T I_A + \gamma_T I_{CA} + \theta_C R_{CT} - \theta_T R_T - \gamma_C R_T - (\delta_C + \mu)R_T, \tag{8}$$

$$\frac{dR_{CT}}{dt} = \gamma_T R_C + \gamma_C R_T - (\theta_C + \theta_T)R_{CT} - \mu R_{CT}, \tag{9}$$

$$\frac{dV_C}{dt} = \nu_C S - \lambda_T V_C - \nu_T V_C + \omega_T V_{CT} - \omega_C V_C - \mu V_C, \tag{10}$$

$$\frac{dV_T}{dt} = \nu_T S - \lambda_C V_T - \nu_C V_T + \omega_C V_{CT} - \omega_T V_T - \mu V_T, \tag{11}$$

$$\frac{dV_{CT}}{dt} = \nu_T V_C + \nu_C V_T - (\omega_C + \omega_T)V_{CT} - \mu V_{CT}. \tag{12}$$

Satisfying the initial conditions; $\{(S, I_C, I_L, I_A, I_{CL}, I_{CA}, R_C, R_T, R_{CT}, V_C, V_T, V_{CT}) \in R_+^{12} : S_0 \geq 0, I_{C0} \geq 0, I_{L0} \geq 0, I_{A0} \geq$

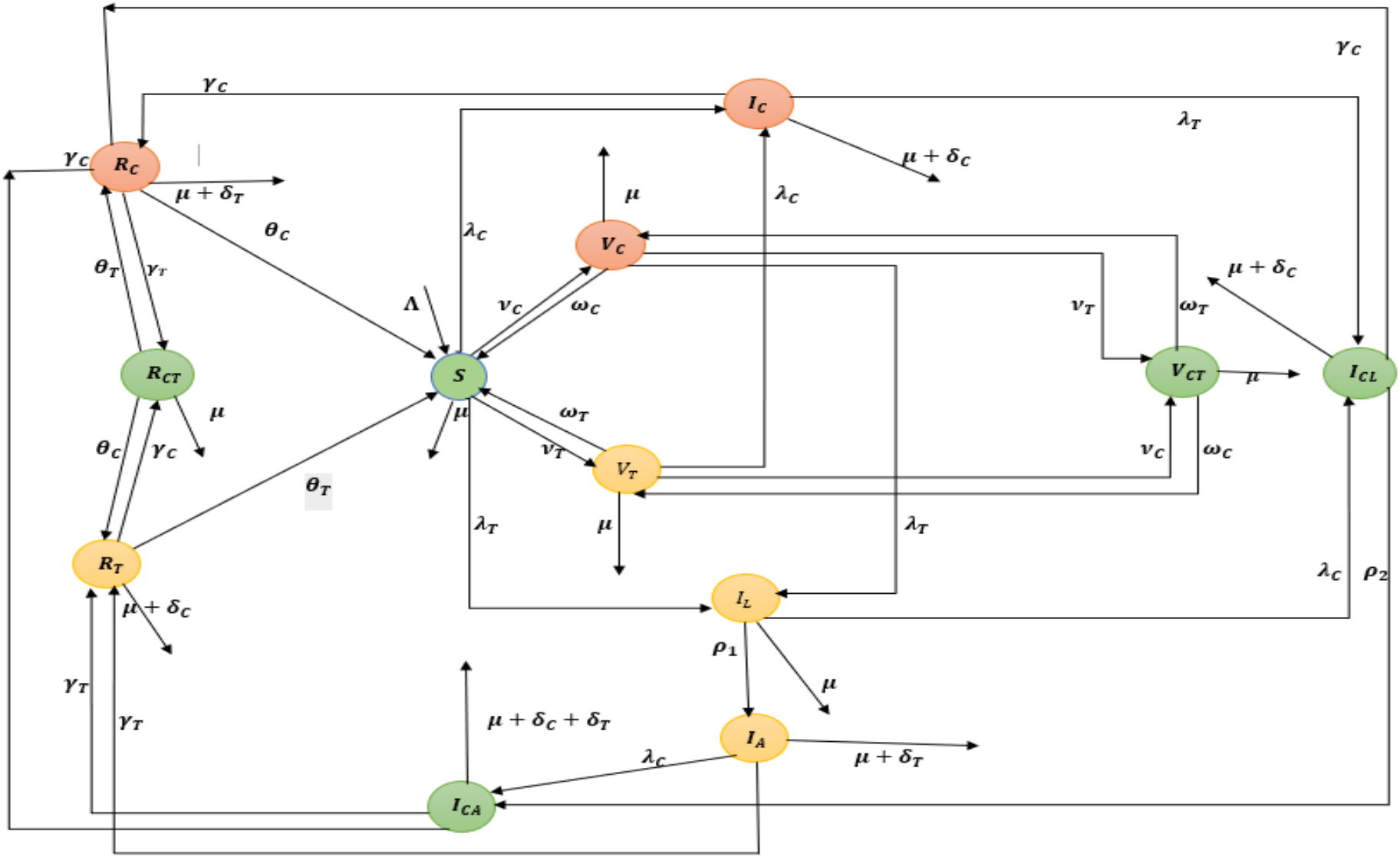


Figure 4: Flow Diagram for the Covid-19 and TB Co-infection Model

The Covid-19 Model

$$\frac{dS}{dt} = \Lambda - \nu_C S - \lambda_1 S + \omega_C V_C + \theta_C R_C - \mu S, \tag{13}$$

$$\frac{dI_C}{dt} = \lambda_1 S - \gamma_C I_C - (\delta_C + \mu) I_C, \tag{14}$$

$$\frac{dR_C}{dt} = \gamma_C I_C - \theta_C R_C - \mu R_C, \tag{15}$$

$$\frac{dV_C}{dt} = \nu_C S - \omega_C V_C - \mu V_C. \tag{16}$$

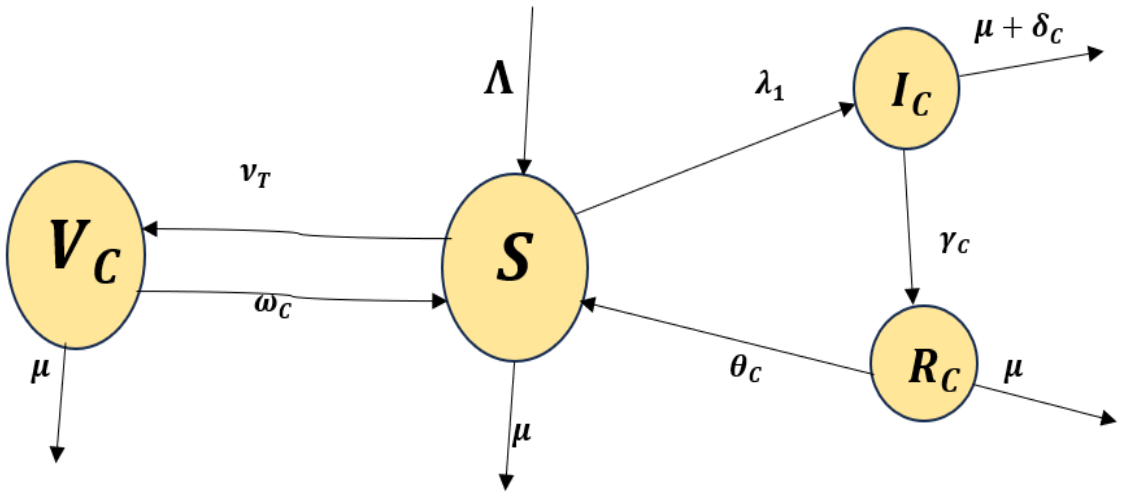


Figure 5: Flow Diagram for the Covid-19 Model

The TB Model

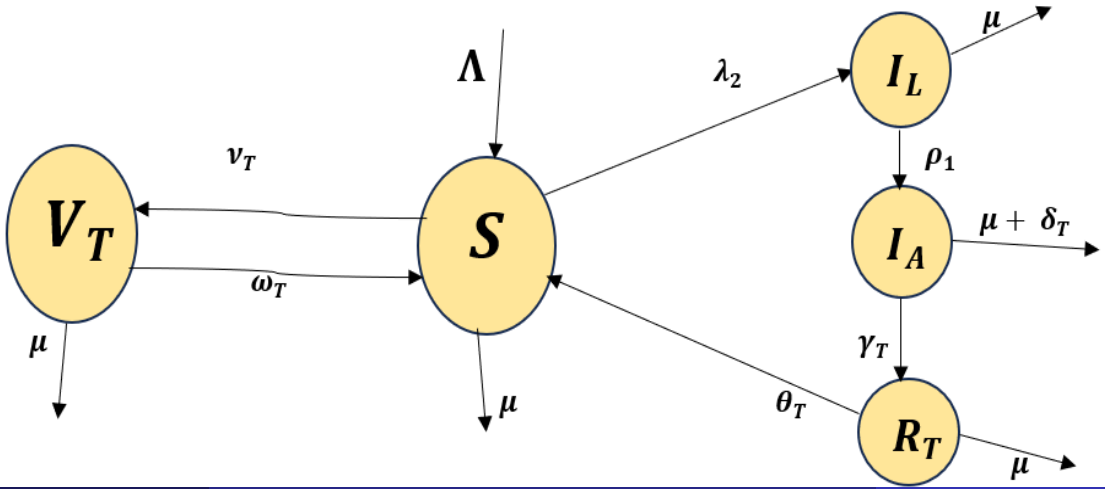
$$\frac{dS}{dt} = \Lambda - \nu_T S - \lambda_2 S + \omega_T V_T + \theta_T R_T - \mu S, \tag{17}$$

$$\frac{dI_L}{dt} = \lambda_2 S - \rho_1 I_L - \mu I_L, \tag{18}$$

$$\frac{dI_A}{dt} = \rho_1 I_L - \gamma_T I_A - (\delta_T + \mu) I_A, \tag{19}$$

$$\frac{dR_T}{dt} = \gamma_T I_A - \theta_T R_T - \mu R_T, \tag{20}$$

$$\frac{dV_T}{dt} = \nu_T S - \omega_T V_T - \mu V_T. \tag{21}$$



Invariant/Bounded Region of Solution

$$\frac{dN(t)}{dt} = \Lambda - \mu N(t) - \delta_C(I_C + I_{CL} + I_{CA} + R_T) - \delta_T(I_A + I_{CA} + R_C) \tag{22}$$

$$\leq \Lambda - \mu N(t) \tag{23}$$

$$\Longrightarrow \int \frac{dN(t)}{\Lambda - \mu N(t)} \leq \int dt \tag{24}$$

Thus,

$$\ln(\Lambda - \mu N(t)) \geq -(\mu t + C)$$

$$\Longrightarrow (\Lambda - \mu N(t)) \geq Ae^{-\mu t}$$

where $A = e^{-C}$ is a constant.
At $t = 0$, $N(0) = N_0 \geq 0$

$$\therefore (\Lambda - \mu N_0) \geq A$$

Accordingly,

$$(\Lambda - \mu N(t)) \geq (\Lambda - \mu N_0)e^{-\mu t}$$

$$-\mu N(t) \geq -\Lambda + (\Lambda - \mu N_0)e^{-\mu t}$$

$$\Longrightarrow N(t) \to \frac{\Lambda}{\mu} \quad as \quad t \to \infty$$

Thus, $N(t) \in [N_0, \frac{\Lambda}{\mu}]$.
Hence, the feasible set of the solution of the model equations enter and remain in the region:

$$\Omega = \{(S, I_C, I_L, I_A, I_{CL}, I_{CA}, R_C, R_T, R_{CT}, V_C, V_T, V_{CT}) \in R_+^{12} : N(t) \leq \frac{\Lambda}{\mu}\} \tag{25}$$

Positivity of Solution: The Positivity Theorem (Tilahun et al., 2018).

"The solution of a model equations remain positive for future time if the respective initial values of the model's state variables are all positive".

Proof:

$$\frac{dS}{dt} = \Lambda - (\nu_C + \nu_T)S - \lambda_C S - \lambda_T S + \omega_C V_C + \omega_T V_T + \theta_C R_C + \theta_T R_T - \mu S$$

$$\geq -(\nu_C + \nu_T + \lambda_C + \lambda_T + \mu)S.$$

Thus,

$$\int \frac{dS}{S} \geq -\int (\nu_C + \nu_T + \lambda_C + \lambda_T + \mu)dt$$

$$\ln S(t) \geq -A(t) + C$$

$$S(t) \geq Be^{-A(t)},$$

where $A(t) = \int(\nu_C + \nu_T + \lambda_C + \lambda_T + \mu)dt$, C is a constant of integration.
At $t = 0, S_0 > 0$
$\therefore S(t = 0) = S_0 \geq B$

$$S(t) \geq S_0 e^{-A(t)} \tag{26}$$

$$\geq 0 \forall t \geq 0.$$

Parameter Estimation We estimated the values of the Covid-19 model's parameters based on real data-sets of COVID-19 in Nigeria according to NCDC (2024) and Corona virus pandemic weekly trends (Worldometers, 2024). The average life expectancy (ALE) of Nigerians for the year 2024 is 56.05 (Macrotrends, 2024). Hence, the natural death rate of individuals was calculated by taking the reciprocal of the ALE (in weeks), that is;

$$\mu = \frac{1}{56.05 \times 52} = 0.0003431$$

The disease induced death rate $= \frac{totaldeath}{totalcases} = \frac{3155}{267188} = 0.01180817$ (Worldometers, 2024). The recovery rate via treatment $= \frac{totaltreated}{totalcases} = \frac{3}{5} = 0.6$ (NCDC, 2024). The recruitment rate (by birth or immigration) is the ratio of the population growth to total population , given by (NCDC, 2024) as:
$\Lambda = \frac{5{,}347{,}585}{229{,}152{,}217} = 0.023336$

Table 2: Table of Values for the Model's Parameters

Parameters	**Values**	**Sources**
Λ	0.0233363	Estimated
μ	0.0003431	Estimated
δ_C	0.0118081	Estimated
β_C	0.0005944	Adeosun et al. (2022)
ν_C	0.20	Assumed
γ_C	0.60	Estimated
ω_C	0.050	Adeosun et al. (2022)
θ_C	0.010	Adeosun et al. (2022)
δ_T	0.1060	Jajarmi et al. (2019)
β_T	0.006	Mekonen & Obsu (2022)
ν_T	0.50	Rwezaura et al. (2022)
γ_T	0.516	Mekonen & Obsu (2022)
ω_T	0.02	Estimated
θ_T	0.0005	Bandekar & Ghosh (2022)
ρ_1	0.020	Colijn et al. (2009)

Disease Free Equilibrium (DFE)

A DFE is a state in which a studied population remains in the absence of the disease(s). The DFE point was obtained by analyzing the models' parameters at the point where the population remains in the absence of the disease.

$$E_{C0} = (S^*, 0, 0, V_C^*)$$

satisfying $\frac{dS}{dt} = \frac{dI_C}{dt} = \frac{dR_C}{dt} = \frac{dV_C}{dt} = 0$ and $I_C = R_C = 0$ and;

$$E_{T0} = (S^*, 0, 0, 0, V_T^*)$$

satisfying $\frac{dS}{dt} = \frac{dI_L}{dt} = \frac{dI_A}{dt} = \frac{dR_T}{dt} = \frac{dV_t}{dt} = 0$ and $I_L = I_A = R_T = 0$
The DFE points were obtained as:

$$E_{C0} = (\frac{\Lambda}{\mu}H, 0, 0, \frac{\Lambda}{\mu}H^*) \tag{27}$$

$H = \frac{(\mu+\omega_C)}{(\mu+\omega_C+\nu_C)}, S^* = \frac{\Lambda}{\mu}$ iff $H = 1$ and this $\implies \nu_C = 0$ and $V_C = 0$.

$$E_{T0} = (\frac{\Lambda}{\mu}K, 0, 0, 0, \frac{\Lambda}{\mu}K^*); K = \frac{(\mu + \omega_T)}{(\mu + \omega_T + \nu_T)} \tag{28}$$

Local Stability Analyses of the DFE

The next-generation matrix approach defines R_e as the spectral radius, the maximum of the absolute values of the eigenvalues, of the next generation matrix FV^{-1} of the system. If the effective reproduction number $R_e < 1$, then the DFE is locally asymptotically stable and unstable if $R_e > 1$.

$$F = \begin{pmatrix} \beta_C S^* & 0 \\ 0 & 0 \end{pmatrix} and V = \begin{pmatrix} (\gamma_C + \delta_C + \mu) & 0 \\ -\gamma_C & (\theta_C + \mu) \end{pmatrix}$$

$$V^{-1} = \frac{1}{|V|} \begin{pmatrix} (\theta_C + \mu) & -\gamma_C \\ 0 & (\gamma_C + \delta_C + \mu) \end{pmatrix}$$

$G = FV^{-1} = \begin{pmatrix} \frac{\beta_C S^*}{(\gamma_C+\delta_C+\mu)} & 0 \\ 0 & 0 \end{pmatrix}$, eigen values $\lambda_C = [0, \frac{\beta_C S^*}{(\gamma_C+\delta_C+\mu)}]$

$R_0^C = \frac{\beta_C S^*}{(\gamma_C+\delta_C+\mu)}$, $R_0^T = \frac{\beta_T S^* \rho_1}{(\delta_T+\gamma_T+\mu)(\rho_1+\mu)}$

$R_e = R_0^C X = 0.488809434806727$ and $R_e = R_0^T X = 0.034299221768125 6$

Global Stability Analyses of the DFE

We employed the generalized method of constructing Lyapunov functions given by Yusuf (2021). Define $V_T(t, S, I_L, I_A, R_T, V_T) = C_1 I_L + C_2 I_A; \quad C_1, C_2 > 0.$

$$\begin{aligned} \frac{dV_T}{dt} &= C_1 I_L' + C_2 I_A' \\ &= C_1(\beta_T I_A S - (\rho_1 + \mu) I_L) + C_2(\rho_1 I_L - (\gamma_T + \delta_T + \mu) I_A) \end{aligned}$$

$$= (C_1 \beta_T S - C_2(\gamma_T + \delta_T + \mu)) I_A + (C_2 \rho_1 - C_1(\rho_1 + \mu)) I_L \tag{29}$$

Substituting $C_1 = \frac{\rho_1}{\rho_1 + \mu}$ and $C_2 = 1$ in (29), we obtained;

$$V_T' = (\frac{\rho_1}{(\rho_1 + \mu)} \beta_T S - (\gamma_T + \delta_T + \mu)) I_A$$

$$< 0; \quad R_0^T < 1 \implies \frac{\rho_1}{(\rho_1 + \mu)} \beta_T S - (\gamma_T + \delta_T + \mu) < 0$$

$V_T' = 0$ iff $I_A = 0$. Therefore, the function V_T is strictly Lyapunov at the DFE point according to the LaSalle's invariance principle (La Salle, 1976) and hence E_0^T is globally asymptotically stable.

Endemic Equilibrium Point (EEP)

(Brown et al., 2006)

The EEP for the models were obtained by solving for all state variables of each model, while equating there derivatives with respect to time as zero. Basically, a model shall have an endemic equilibrium if the algebraic system derived from the model by setting all derivatives to zero, has a solution in which each state variable is strictly positive.

Cont'd....

$E_C^* = (S^*, I_C^*, R_C^*, V_C^*)$ and $E_T^* = (S^*, I_L^*, I_A^*, R_T^*, V_T^*)$, are positive state solutions of the models satisfying $\frac{dS}{dt} = \frac{dI_C}{dt} = \frac{dR_C}{dt} = \frac{dV_C}{dt} = 0$ and $\frac{dS}{dt} = \frac{dI_L}{dt} = \frac{dI_A}{dt} = \frac{dR_T}{dt} = \frac{dV_T}{dt} = 0$

$S^* = \frac{(\gamma_C+\delta_C+\mu)}{\beta_C} > 0,\ V_C^* = \frac{\nu_C(\gamma_C+\delta_C+\mu)}{\beta_C(\omega_C+\mu)} > 0,$

$I_C^* = \frac{(\theta_C+\mu)}{B\gamma_C}[\Lambda - \frac{\mu}{H\beta_C}(\gamma_C + \delta_C + \mu)] > 0$ and $R_C^* = \frac{\Lambda - \frac{\mu}{H\beta_C}(\gamma_C+\delta_C+\mu)}{B} > 0$ if $[\Lambda - \frac{\mu}{H\beta_C}(\gamma_C + \delta_C + \mu)] > 0$

The expressions for the state equations are positive provided $R_0^C = \frac{\Lambda H\beta_C}{\mu(\gamma_C+\delta_C+\mu)} > 1$ and $R_0^T = \frac{\beta_T S^* \rho_1}{(\delta_T+\gamma_T+\mu)(\rho_1+\mu)} > 1$

There exists unique endemic equilibria for the models provided $R_0^C, R_0^T > 1$.

Stability of the EEP

We defined an appropriate Lyapunov function for the TB model at E_T^* as:

$$L_T(S, I_L, I_A, R_C.V_C) = \frac{1}{2}[(S-S^*)+(I_L-I_L^*)+(I_A-I_A^*)+(R_T-R_T^*)+(V_T-V_T^*)]^2 \tag{30}$$

$$\frac{dL_t}{dt} = (N_T - N_T^*) \times \frac{dN_T}{dt}.$$

$$= (N_T - (\frac{\Lambda}{\mu R_0^T} + I_A^* B_C)) \times (\Lambda - \mu N_T - \delta_T I_A)$$

$$\leq (N_T - \frac{\Lambda}{\mu})(\Lambda - \mu N_T)$$

$$\leq -\frac{(\Lambda - \mu N_T)^2}{\mu} \leq 0 \tag{31}$$

Since $I_A > 0$ and $R_0^T > 1$ at E_T^*.
Therefore, for $R_0^T > 1$, the endemic equilibrium point E_T^* exists and the function L_T is strictly Lyapunov function. This implies that E_T^* is globally asymptotically stable.

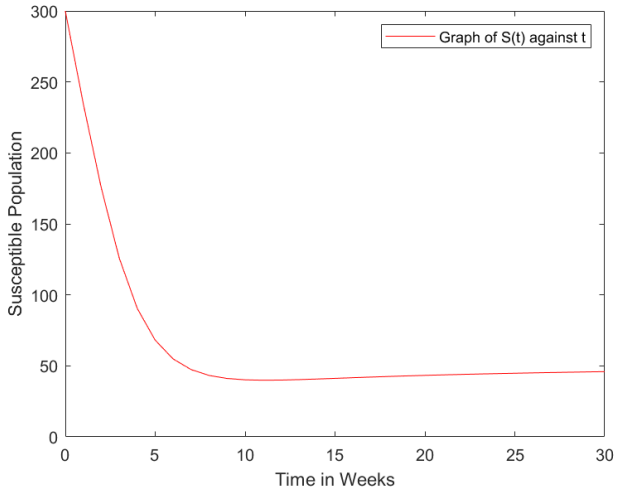
Sensitivity Analyses

To determine the exact impact of each parameter contained in R_e. The normalized forward sensitivity index of R_e with respect to a parameter p: $\Gamma_p^{R_e} = \frac{\partial R_e}{R_e} \div \frac{\partial p}{p}$

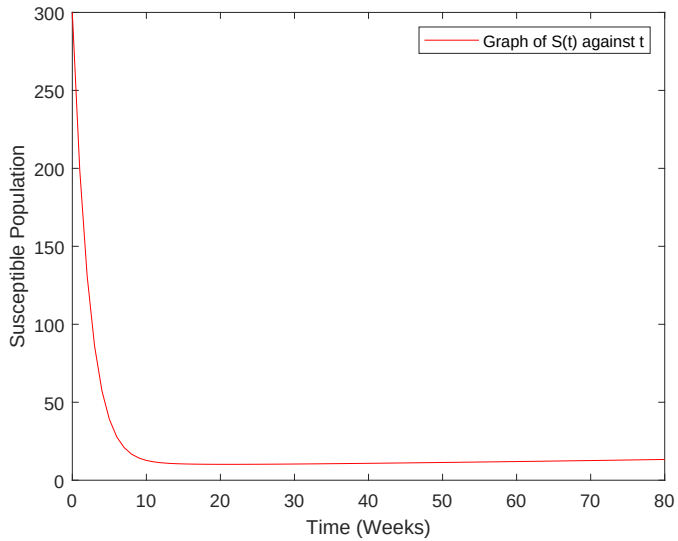
Table 3: Sensitivity Indices for the Basic Reproduction Numbers

Parameters	**Signs**	**Values**
Λ	$+$	1
β_C	$+$	1
μ	-	0.2446653
ω_C	$+$	0.1978857
ν_C	-	0.9540073
γ_C	-	0.97814180
δ_C	-	0.0210713
β_T	$+$	1
ρ_1	$+$	0.0038064
ω_T	$+$	0.8297130
ν_T	-	0.9882296
γ_T	-	0.7628824
δ_T	-	0.2365526
μ	-	0.8458547

Numerical Simulations The system of ODEs was solved numerically by implementing the fourth order Runge Kutta algorithm on MATLAB subroutine.



(a) Covid-19 Profile



(b) TB Profile

Figure 7: Susceptible Population against Time

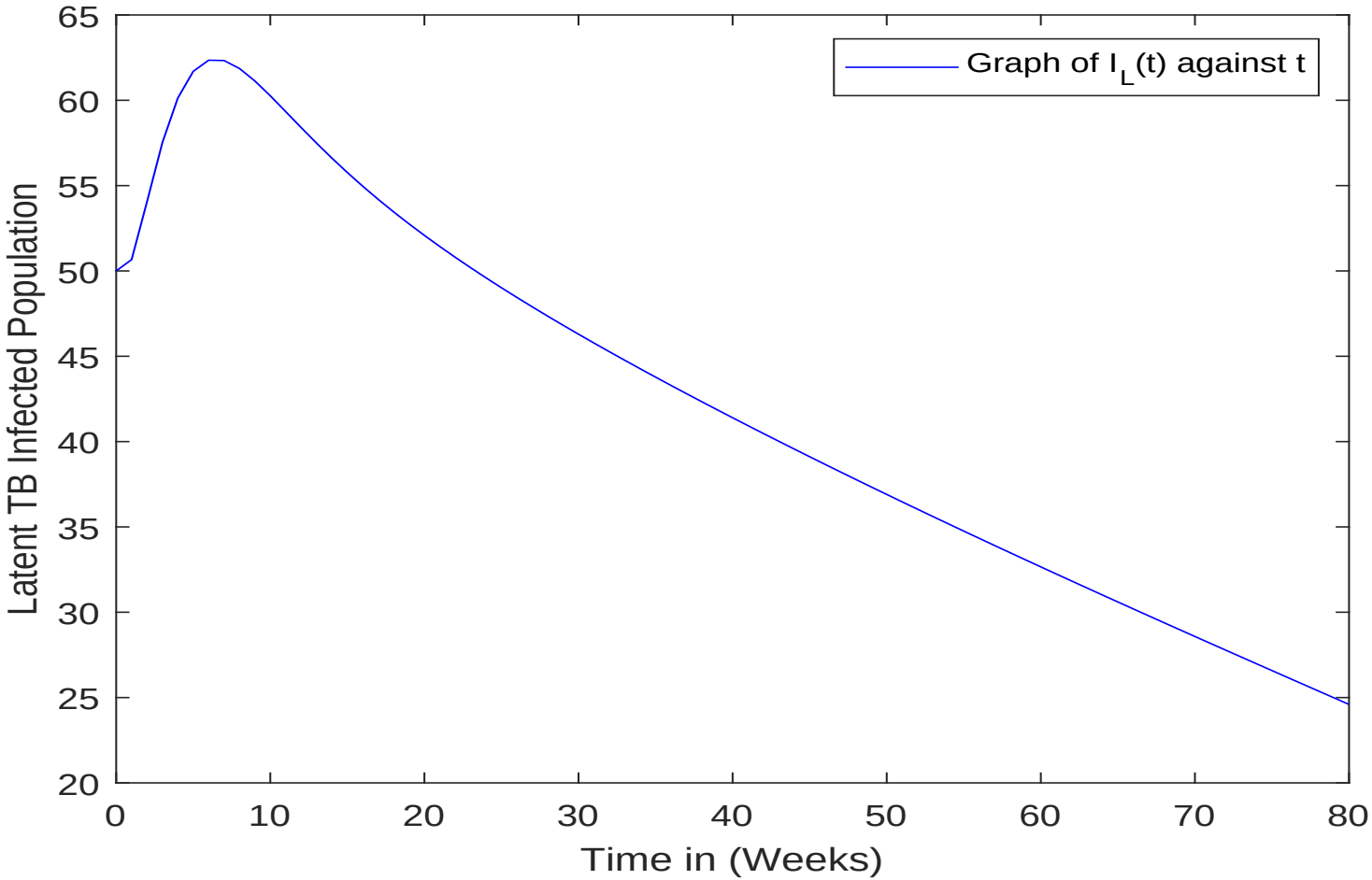
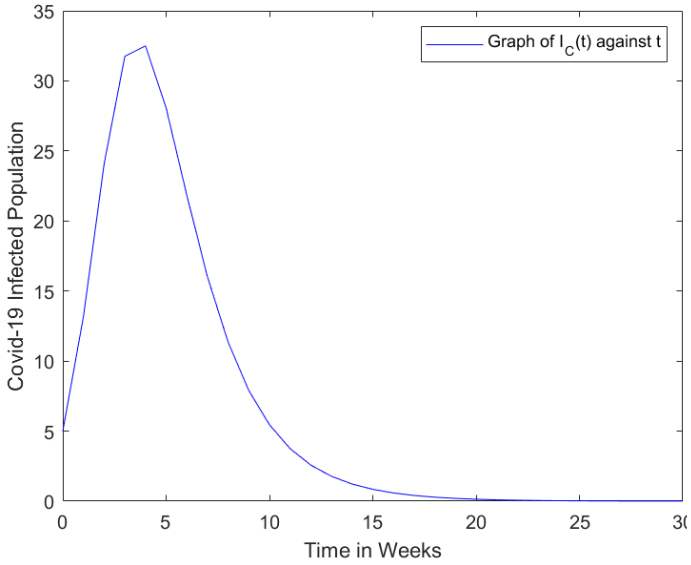
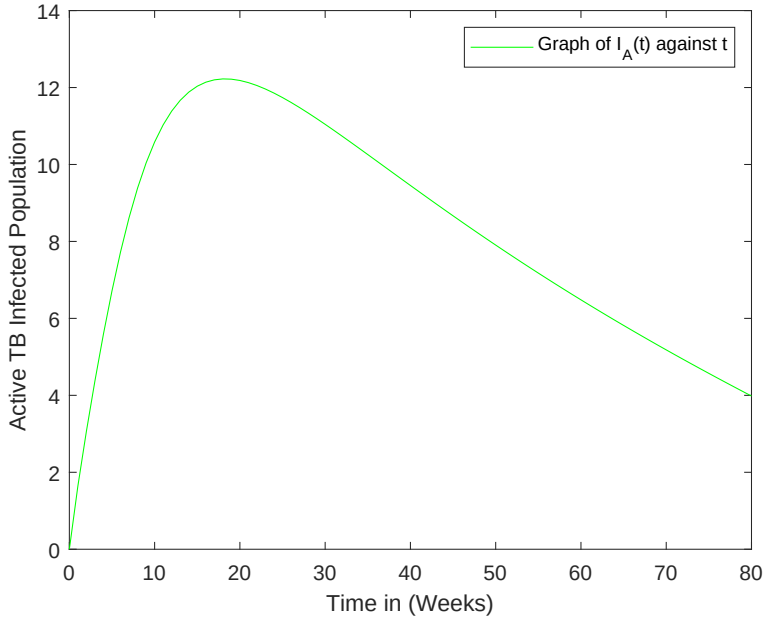


Figure 8: Latent TB Infected Population against Time

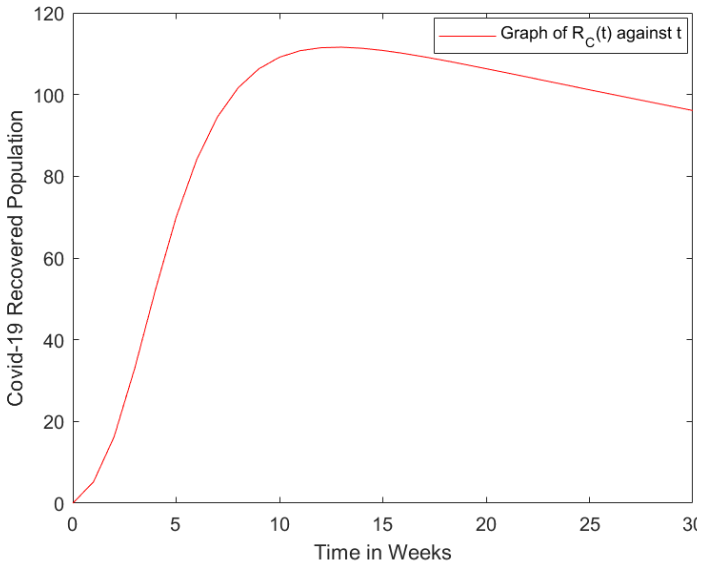


(a) Covid-19 Profile

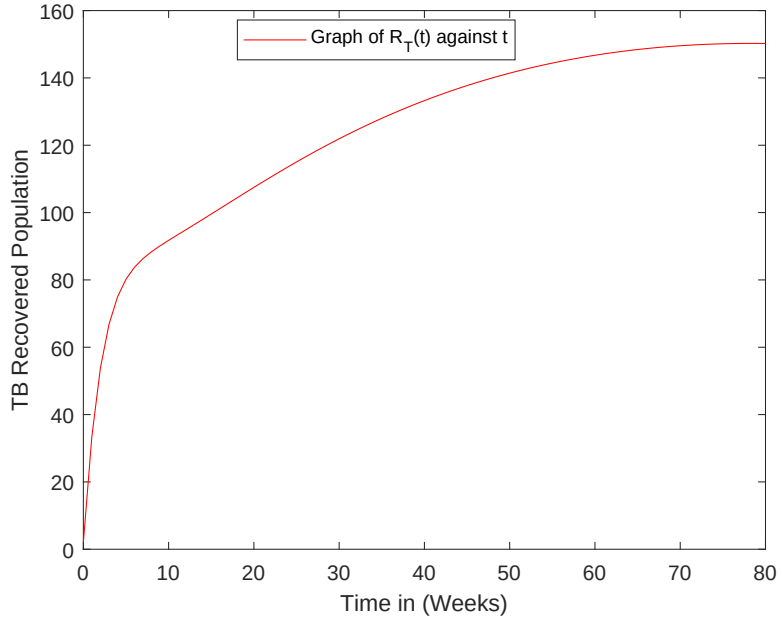


(b) TB Profile

Figure 9: Infected Population against Time

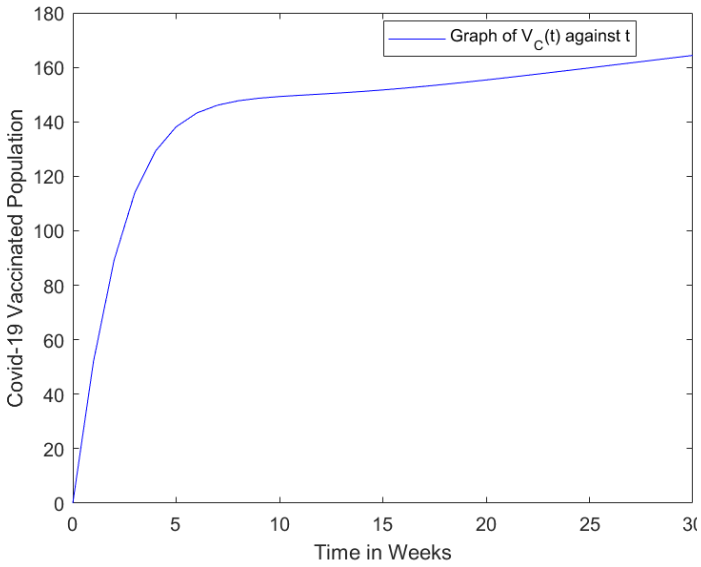


(a) Covid-19 Profile

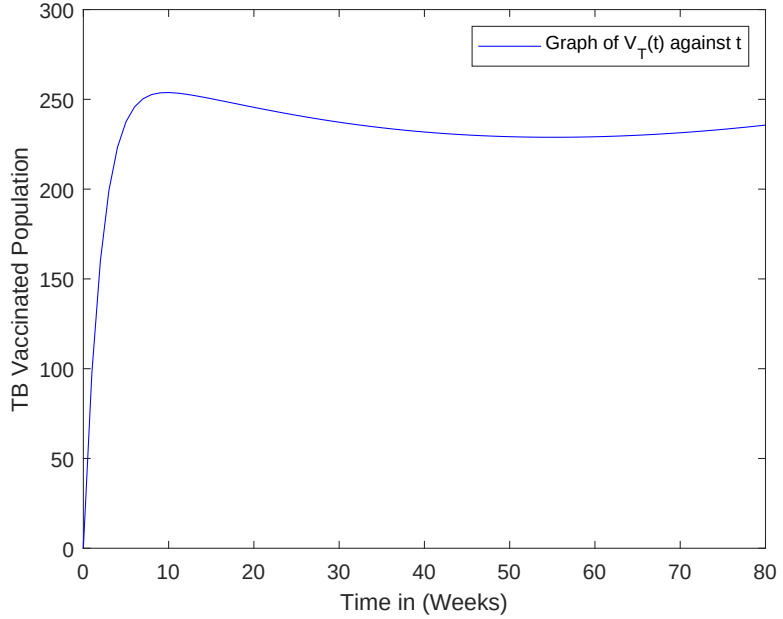


(b) TB Profile

Figure 10: Recovered Population against Time



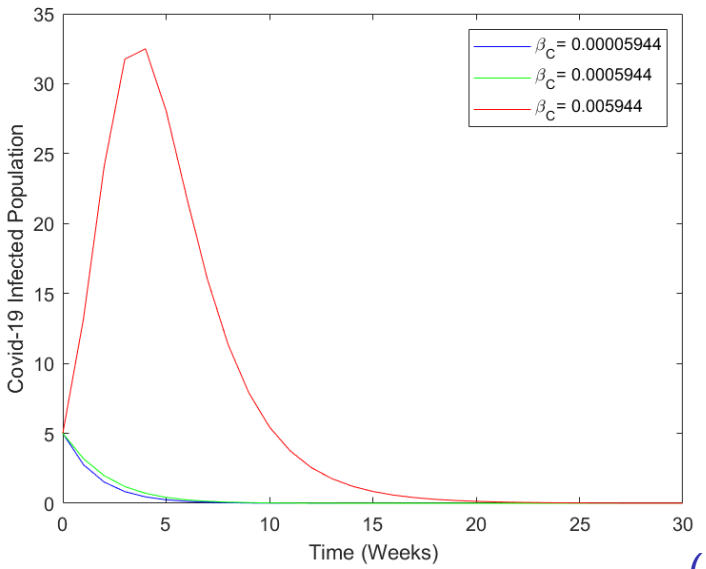
(a) Covid-19 Profile



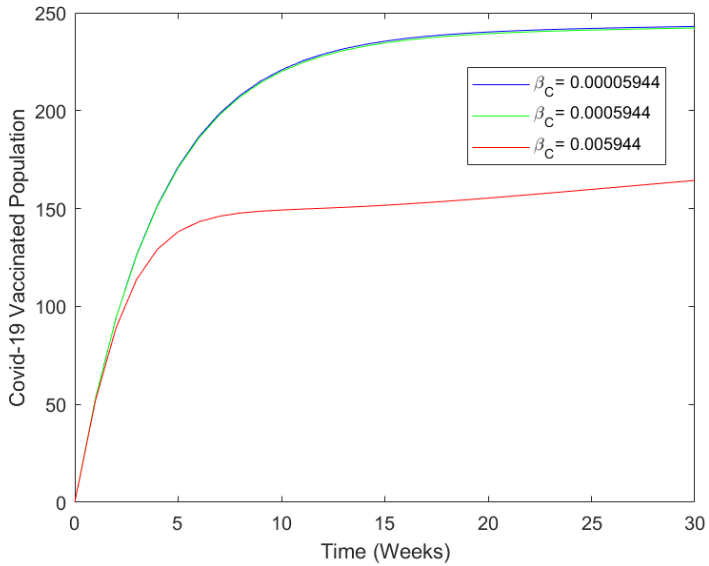
(b) TB Profile

Figure 11: Vaccinated Population against Time

Numerical Simulation: Variation of the Covid-19 Parameters

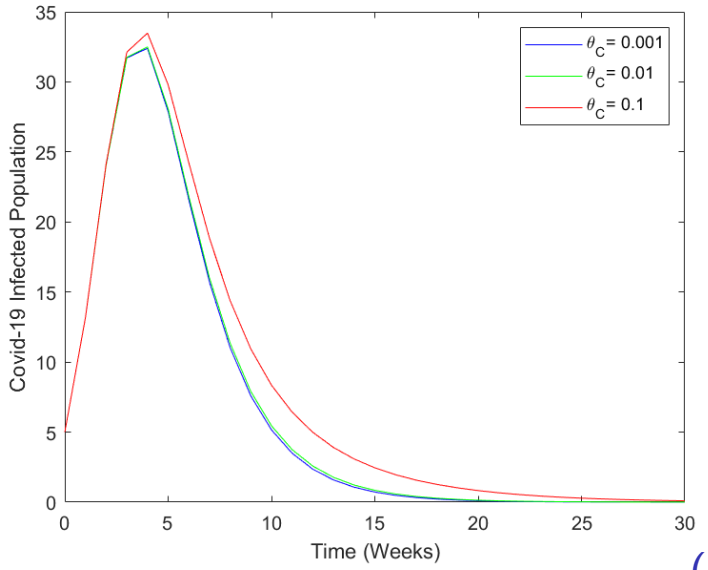


(a) Infected Profile

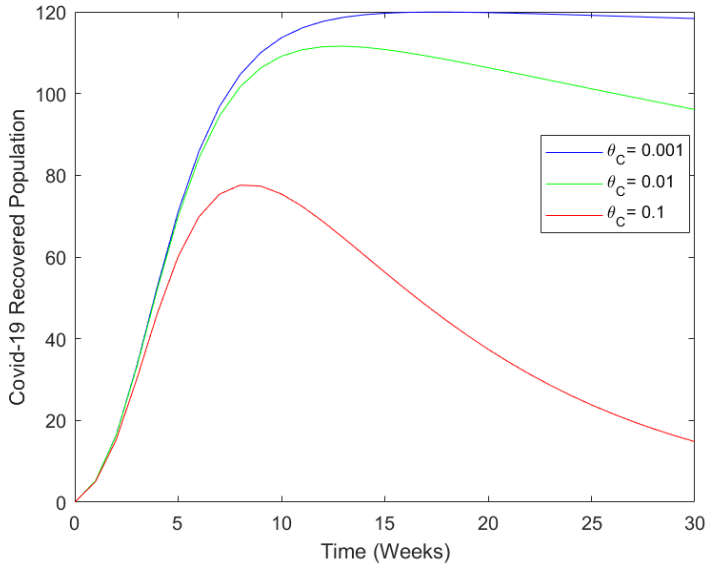


(b) Vaccinated Profile

Figure 12: Effects of Covid-19 Contact Rate

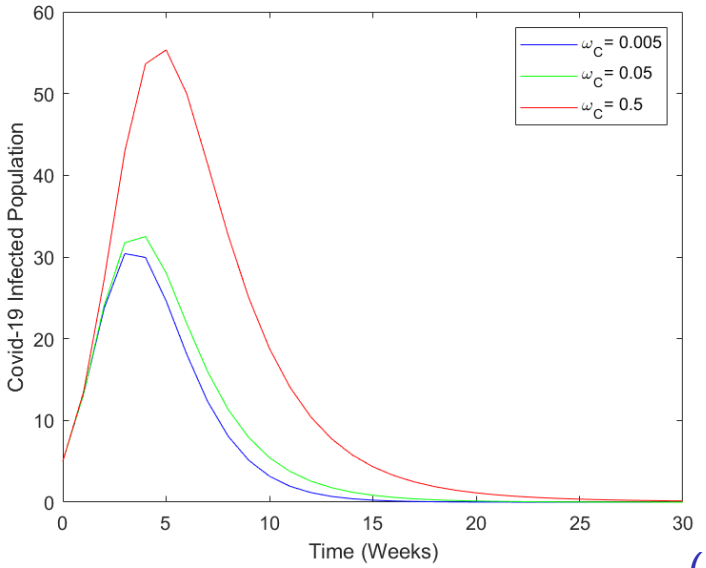


(a) Infected Profile

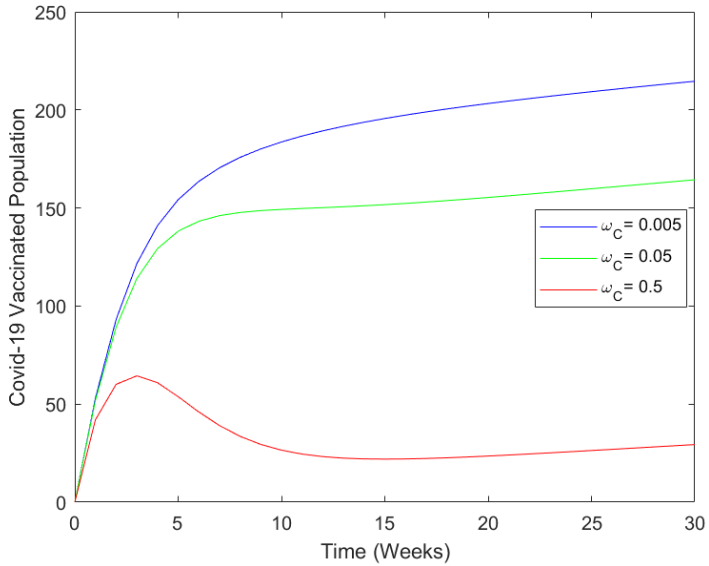


(b) Recovered Profile

Figure 13: Effects of Disease Relapse on Covid-19

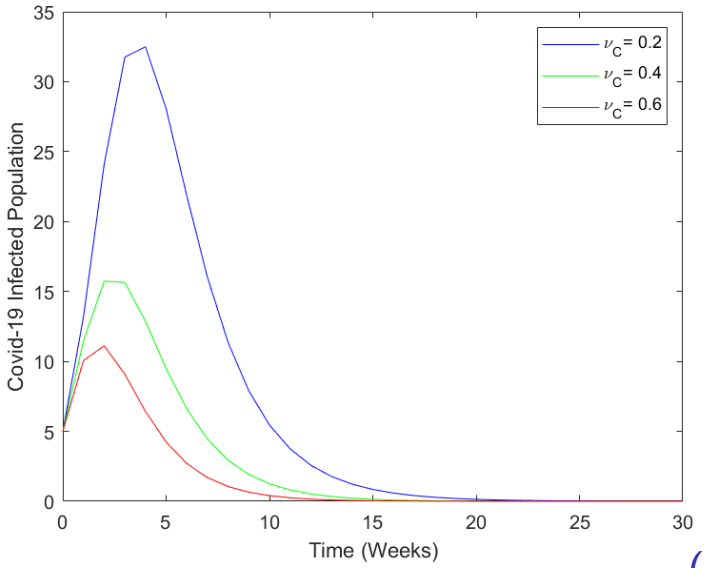


(a) Infected Profile

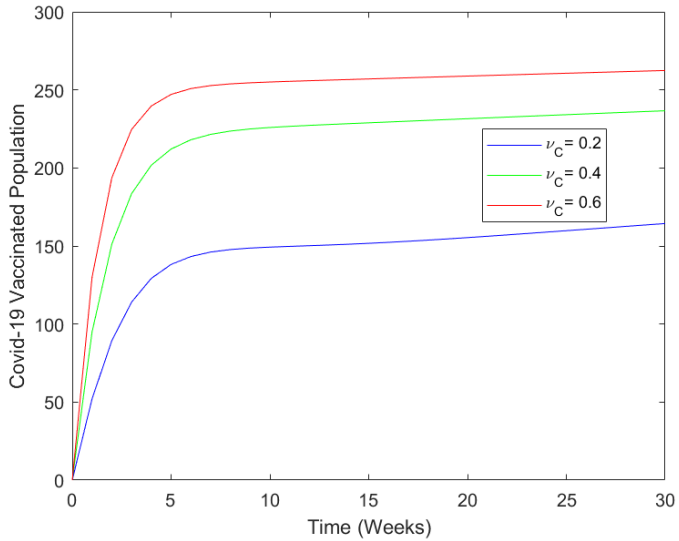


(b) Vaccinated Profile

Figure 14: Effects of Immunity Wane after Vaccination on Covid-19

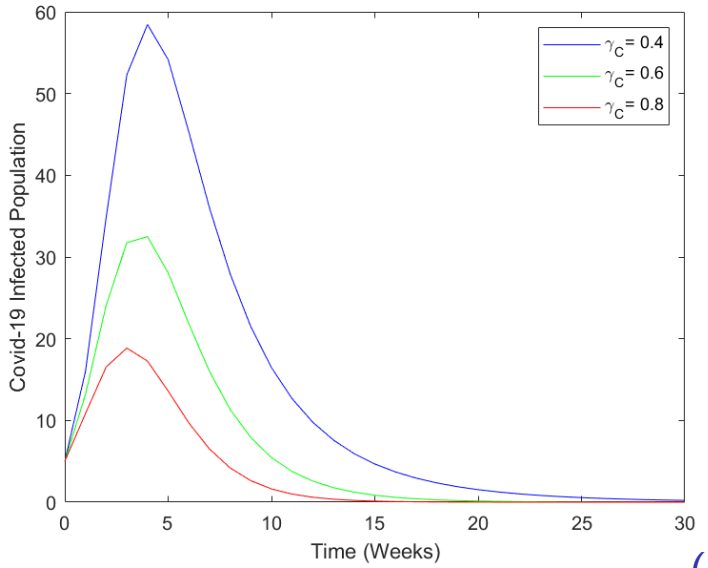


(a) Infected profile

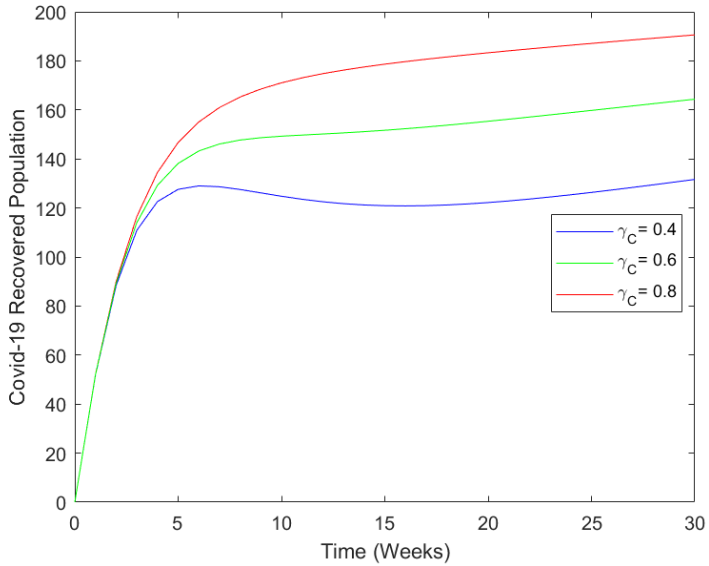


(b) Vaccinated Profile

Figure 15: Effects of Vaccination Rate on Covid-19



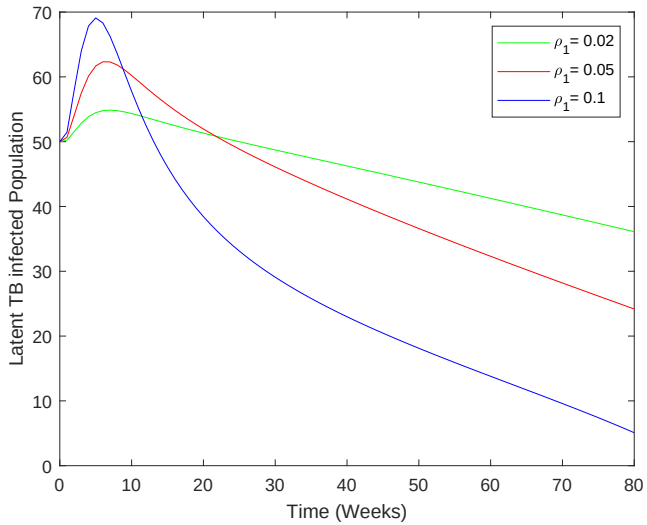
(a) Infected profile



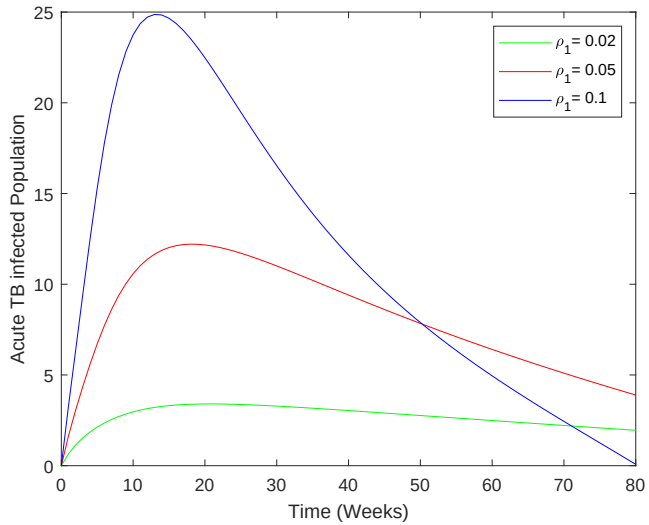
(b) Recovered Profile

Figure 16: Effects of Treatment Rate on Covid-19

Numerical Simulation: Variation of the TB Parameters

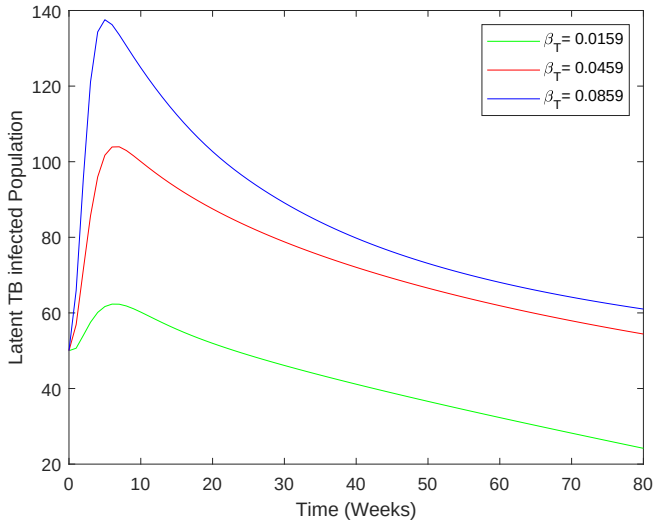


(a) Latent profile

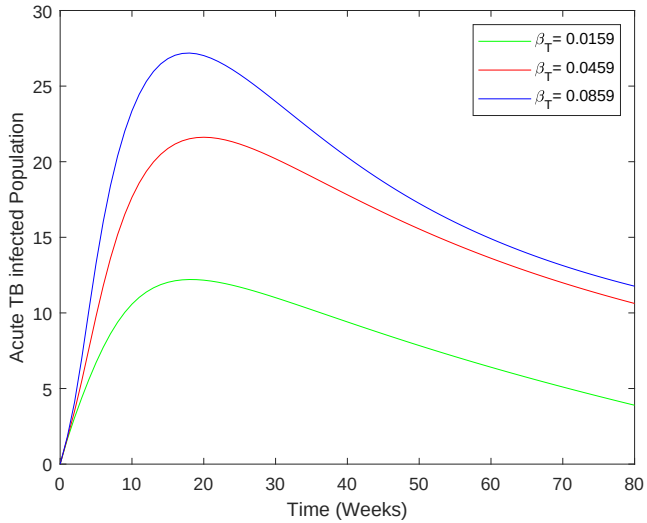


(b) Infected Profile

Figure 17: Effects of progression rate from latent to active TB

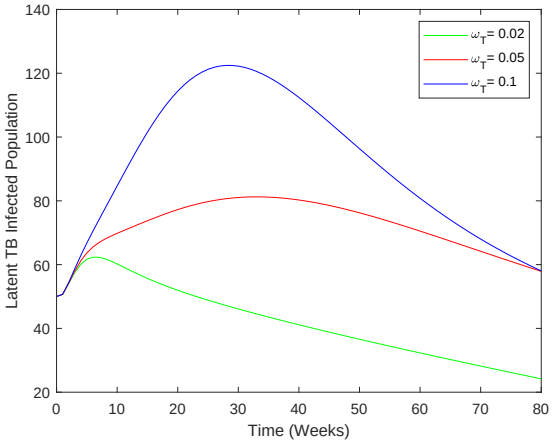


(a) Latent Profile

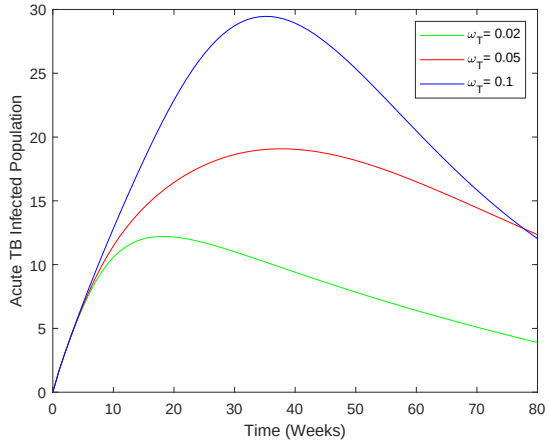


(b) Infected Profile

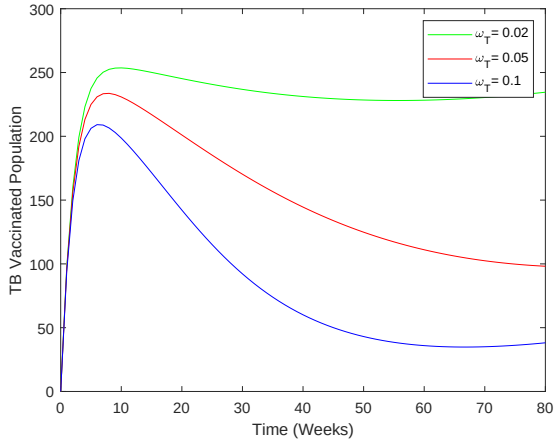
Figure 18: Effects of TB contact Rate



(a) Latent profile

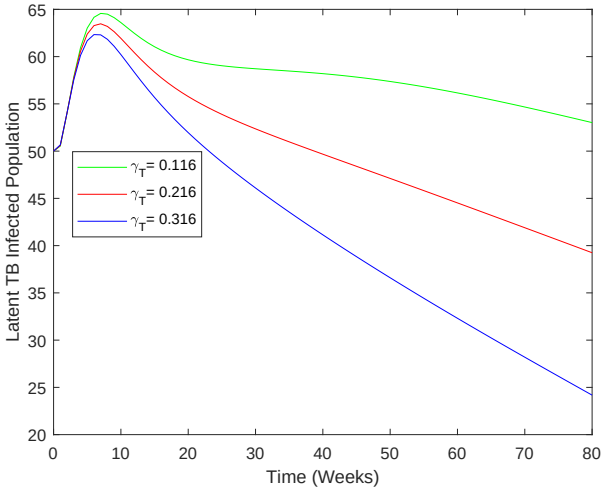


(b) Infected Profile

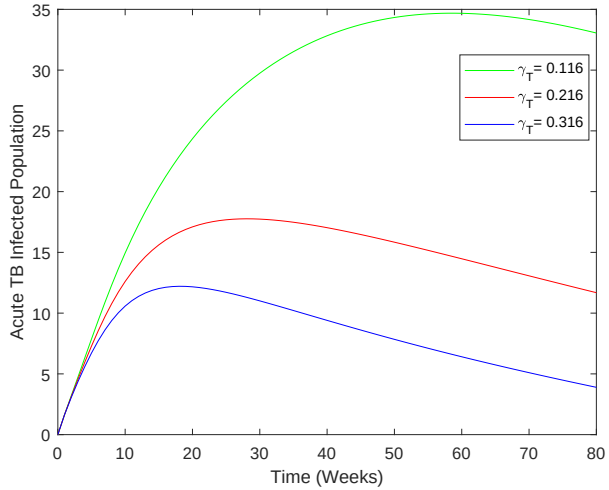


(c) Vaccinated Profile

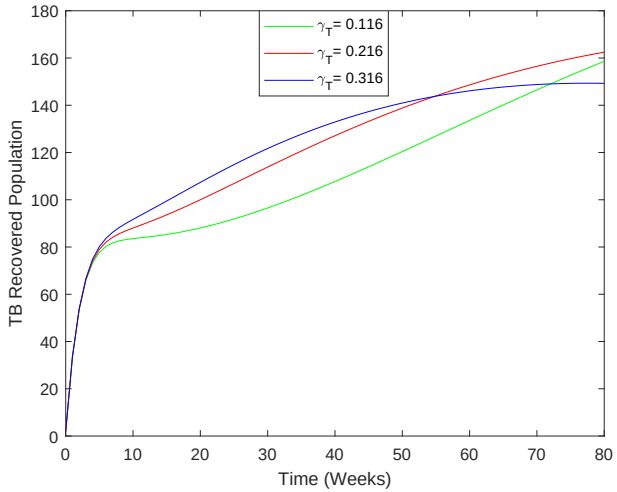
Figure 19: Effects of Immunity Wane on TB



(a) Latent profile

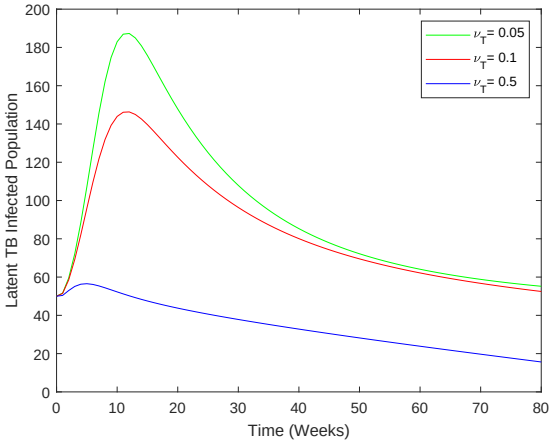


(b) Infected Profile

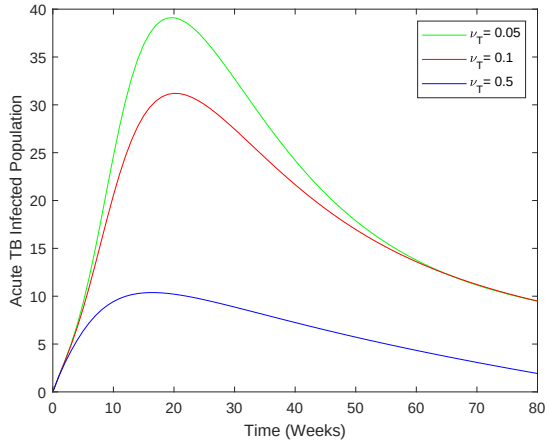


(c) Recovered Profile

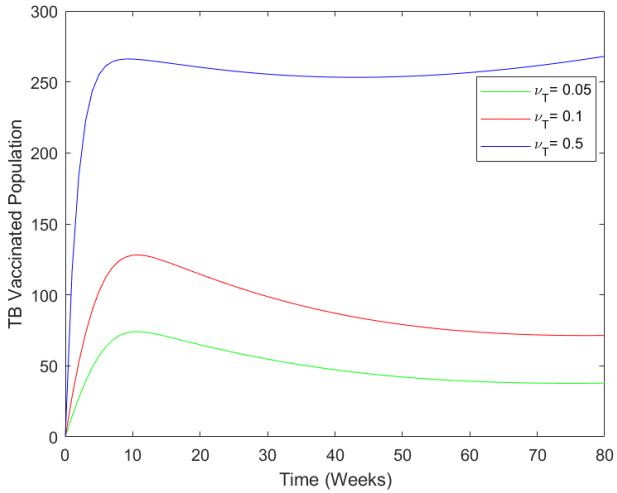
Figure 20: Effects of Treatment on TB



(a) Latent profile



(b) Infected Profile



(c) Vaccinated Profile

Figure 21: Effects of Vaccination on TB

Conclusion and Recommendations

1. Establish the effectiveness of mathematical modeling in predicting future trends and possible controls for infectious disease in general and Covid-19 and TB in particular.
2. Presents a very comprehensive and robust co-infection model for Covid-19 and Tuberculosis and also mono-infection models.
3. Results of the stability analyses shows a stable DFE for Covid-19 and TB suggesting that the diseases can be well managed if necessary implementations are made.
4. Sensitivity analyses show that recruitment and contact/transmission rates are the most sensitive parameter to increase the spread of the diseases while vaccination and treatment rates are the most sensitive to decrease the spread.
5. The simulation results show that the infected population approaches zero but didn't converge on zero; hence the need for an OCP is necessary to obtain a control solution.
6. We recommend awareness on efficacy of vaccinations for Covid-19 and TB
7. Point of care diagnosis is highly advised for quick, easily accessible and accurate diagnosis followed by treatment to prevent high contact rate.


Thank You For
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