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MODELLING THE USE OF THE TRACE-TEST-ISOLATE-TREAT STRATEGY FOR CONTROLLING THE SPREAD OF COVID-19

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ABSTRACT: *During the COVID-19 pandemic that ravaged the entire world between 2019 and 2021, the Trace-Test-Isolate-Treat Strategy was devised as an emergency way of managing the spread of the disease. As the name implies, the Trace-Test-Isolate-Treat Strategy involves identifying those who had contact with an infected person through contact tracing, and subsequent isolation and treatment if confirmed to be infected with the disease. This paper aims to model the transmission dynamics of COVID-19, with the Trace-Test-Isolate-Treat Strategy as a control strategy. To do this, we propose a simple nonlinear system of ordinary differential equations that models COVID-19 dynamics and incorporates the Trace-Test-Isolate-Treat strategy as a way of controlling the spread of the disease. The analysis of the model shows that the disease-free equilibrium is locally asymptotically stable if the reproduction number, R_{eff} is less than one. Furthermore, the model is shown to possess a unique and stable endemic equilibrium if, $R_{eff} > 1$. This confirms the global asymptotic stability of the disease-free equilibrium and the absence of backward bifurcation in the model. Numerical plots show the effectiveness of isolation and treatment of infected persons in reducing the spread of the disease.*

KEYWORDS: Coronavirus; Trace-Test-Isolate-Treat Strategy; disease-free equilibrium; endemic equilibrium; local stability

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INTRODUCTION

Coronaviruses are a group of related zoonotic and RNA viruses that cause diseases in mammals and birds. In humans, these viruses cause respiratory tract infections which can be mild or lethal (Gorbalenya et al., 2020; Brunk, 2020). Mild illness includes some cases of the common cold while more lethal varieties can cause Severe Acute Respiratory Syndrome (SARS) discovered in 2002, Middle-East Respiratory Syndrome (MERS-CoV) discovered in 2012 and Coronavirus Disease 2019 (COVID-19) discovered in 2019 (Abutaleb, 2020; Adebowale et al, 2021). The novel coronavirus disease (COVID-19) is a new strain of coronavirus that has not been previously identified in humans. It was first discovered in December 2019 in Wuhan City, Hubei Province China, and later spread all over the world. On January 30, 2020, the World Health Organization (WHO) declared the COVID-19 outbreak a global health emergency and subsequently declared the disease a global pandemic on March 11, 2020 [Gallegos,2020; Ramzy and McNeil, 2020]. The symptoms of the disease include; headache, fever, chills, sore throat, loss of taste or smell, muscle pain, cough, shortness of breath and breathing difficulties (CDC, 2020). In more severe cases, pneumonia, severe acute respiratory syndrome, Malaise, Diarrhea, Sputum production, kidney failure and death are often associated with the disease(CDC, 2020). The disease can be transmitted from person to person through respiratory droplets from coughing and sneezing (Wu and McGoogan, 2020). Viruses released in respiratory secretions can infect other individuals by direct contact with mucous membranes. There is no officially approved drug for treating those who are infected with the disease. However, treatments are administered to infected persons based on the symptoms manifested by the disease. Fortunately, there have been several WHO-approved vaccines for immunizing interested individuals against the disease. These vaccines, together with non-pharmaceutical protection measures such as wearing face masks and shields, washing hands with soaps or alcohol-based sanitizers in runny water, and maintaining social distancing, among others have helped to control the spread of the disease. Mathematical epidemiologists have not relented in proposing mathematical and statistical models for understanding the transmission dynamics of the disease and incorporating various measures proposed for controlling the spread of the disease (Eikenberry et al., 2020; Ferguson et al., 2020; Hellewell et al., 2020; Musa et al., 2020; Ngonghala et al., 2020).

The Trace-Test-Isolate-Treat strategy has been considered an effective way of reducing the spread of COVID-19. The implementation of this COVID-19 control strategy involves tracing those who have physical contact with a confirmed infected person. Those who are successfully traced are kept in a temporary isolation facility or self-isolation for a period equivalent to the incubation period of the disease. At the end of the temporary isolation, those who test positive for the disease are kept in a main isolation facility where they receive treatment until they recover or die due to the disease. In this work, we model the Trace-Test-Isolate-Treat strategy into the transmission dynamics of COVID-19 as a control strategy and determine its effectiveness in reducing the spread of the disease.

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Formation of the Model

The model we propose is a system of nonlinear ordinary differential equations which describes the transmission dynamics and control of coronavirus disease (COVID-19). The total human population under study is divided into eight (8) compartments/classes namely, the susceptible (S), those with protection against the disease (P), those who have contact with an infected person, but are not traced (T_N), infectious (I), those that have contact with the infectious persons, traced and isolated (T), those whose status is confirmed positive, and are isolated (Q), and those that have recovered from the disease (R), and the deceased (D).

With adequate awareness about the disease and its modes of spread being created, we assume that a certain proportion, δ of the susceptible class adopts protection measures against the disease. Under the Trace-Test-Isolate-Treat Strategy, when those without protection have contact with an infectious person, I, contact tracing is activated to identify them. Let $\alpha c I(t) S(t)$ be the number of persons in the susceptible class that have contact with infectious persons, where c is the rate at which contacts are made, and α is the probability of transmission of the virus during contact. The proportion, κ who are not traced moves into the compartment, T_N. In this compartment, the fraction, q_1 who is not infected with the virus moves into the protection compartment, P, while the fraction, β, who is infected with the virus moves into the infectious class, I. A proportion ν_2 of the infectious class with visible symptoms are quarantined in class Q, while the proportions ν_1 and τ_1 who are not quarantined recover naturally or die due to the disease, respectively. On the other hand, the proportion $(1-\kappa)$ who are traced (T) is kept in an isolation facility for 14 days; the incubation period of the disease. At the expiration of the incubation period, tests are re-conducted to determine their infection status. At this stage, the proportion, q_2 whose status is confirmed positive are kept in the main isolation compartment Q, where they receive medical attention until they recover from the disease at the rate q_3 or die due to the disease at the rate, τ_2, while the proportion, q_0 of T whose status are confirmed negative embraces protection from the disease. We assume that those in the infectious compartments, I and Q cannot die naturally, but due to complications from the disease infection. However, all other compartments except compartment, D benefit from the natural death which occurs at the rate, μ_1. In the management and control of COVID-19, the importance of prompt and proper burial or disposal of the deceased cannot be over-emphasized. Hence, we include in compartment, D, the rate, μ_2 at which the deceased is buried or disposed of.

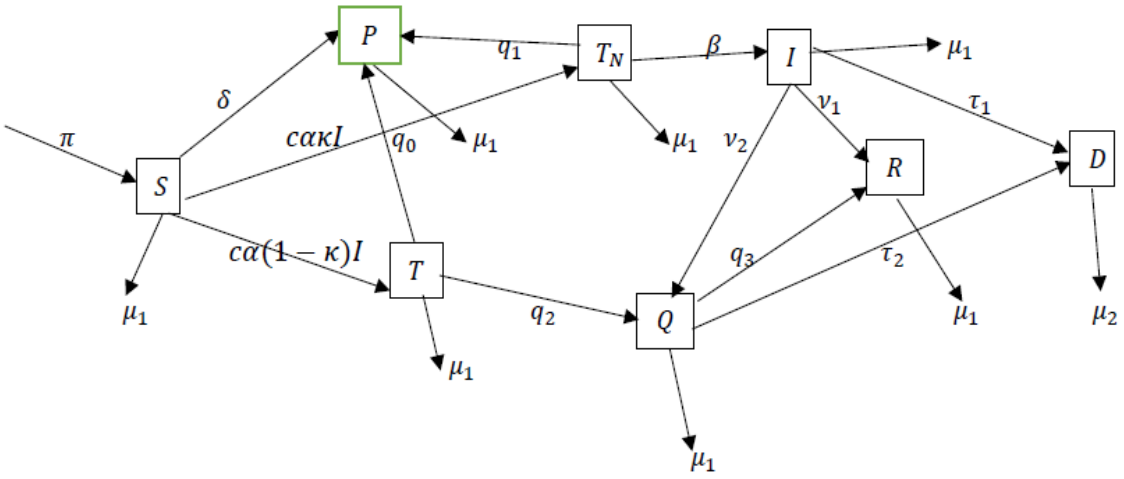

Figure 1: Flow Diagram for the Disease Transmission and Control

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Following the assumptions on the transmission dynamics and control of COVID-19, with the disease flow diagram (figure 1), we obtain the system of nonlinear ordinary differential equations

$$\begin{aligned}
\frac{dS}{dt} &= \pi - c\alpha\kappa IS - c\alpha(1-\kappa)IS - (\delta + \mu_1)\,S \\
\frac{dP}{dt} &= \delta S + q_0 T + q_1 T_N - \mu_1 P \\
\frac{dT_N}{dt} &= c\alpha\kappa SI - (q_1 + \beta + \mu_1)T_N \\
\frac{dT}{dt} &= \alpha c(1-\kappa)SI - (q_0 + q_2 + \mu_1)T \qquad (1) \\
\frac{dI}{dt} &= \beta T_N - (\tau_1 + v_1 + v_2 + \mu_1)I \\
\frac{dQ}{dt} &= q_2 T + v_2 I - (\tau_2 + q_3 + \mu_1)Q \\
\frac{dR}{dt} &= v_1 I + q_3 Q - \mu_1 R \\
\frac{dD}{dt} &= \tau_1 I + \tau_2 Q \; - \mu_2 D
\end{aligned}$$

with the initial solutions$S(0) = S_0, P(0) = P_0, T_N(0) = T_{N0}, I(0) = I_0, T(0) = T_0, Q(0) = Q_{I0}, R(0) = R_0, D(0) = D_0$. We assume that a unique bounded solution to the model system exists in the domain Ω described as $\Omega = \left\{S, P, T_N, I, T, Q,\ R, D \in R_+^8 | S + P + T_N + I + T + Q + R + D \leq \frac{\pi}{\mu_1}\right\}$

Table 1: Description of Parameters used in this Model

Parameter	***Meaning***
π	Recruitment rate of Humans into the susceptible class
α	Probability of transmission of the virus from infected persons during contact
c	The rate at which contacts are made between infected and uninfected persons
κ	The proportion of those who have contact with infected persons who are traced
μ_1	Natural death rate of humans
β	Incubation rate of coronavirus
q_0	Proportion of the traced that are not infected

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q_2	Proportion of the traced that are infected
τ_1	The proportion of the infected humans that die due to the infection
τ_2	Proportion of the isolated humans that die due to the infection
v_1	Proportion of infected humans that recover without treatment
v_2	Proportion of infected humans that are isolated
μ_2	Rate of burial of deceased persons
δ	Proportion of susceptible class that protect themselves
q_1	Proportion of those not traced that are not infected
q_3	Proportion of those isolated that recover after treatment

MODEL ANALYSIS

Local Stability Analysis of the Disease-Free Equilibrium

The disease-free equilibrium, $E_0 = \left(\frac{\pi}{\delta+\mu_1}, \frac{\delta\pi}{\mu_1(\delta+\mu_1)}, 0,0,0,0,0,0\right)$ is locally asymptotically stable if all the eigenvalues of the Jacobian matrix of (1) are all negative or have negative real parts. If at least one eigenvalue has a positive real part, E_0 is unstable.

The Jacobian matrix of (1) is;

$$J(E_0) = [-(\delta + \mu_1)\ 0\ 0\ 0\ c\alpha\kappa S^0\ 0\ 0\ 0\ \delta\ -\mu_1\ 0\ 0\ 0\ 0\ 0\ 0\ 0\ 0\ -C_1\ 0\ c\alpha\kappa S^0\ 0\ 0\ 0\ 0\ 0\ 0$$
$$-C_2\ c\alpha(1-\kappa)S^0\ 0\ 0\ 0\ 0\ 0\ \beta\ 0\ -C_3\ 0\ 0\ 0\ 0\ 0\ 0\ q_2\ v_2$$
$$-(\tau_2+q_3)\ 0\ 0\ 0\ 0\ 0\ 0\ v_1\ q_3\ -\mu_1\ 0\ 0\ 0\ 0\ 0\ \tau_1\ \tau_2\ 0\ -\mu_2\ ]$$

where $C_1 = (q_1 + \beta + \mu_1), C_2 = (q_0 + q_2 + \mu_1), C_3 = (\tau_1 + v_1 + v_2 + \mu_1)$.

The eigenvalues of $J(E_0)$ are $-\mu_1, -\mu_1, -\mu_2, -(\delta + \mu_1), -(\tau_2 + q_3 + \mu_1)$, and the roots of the cubic equation;

$$-\lambda_3 - [C_1 + C_2 + C_3]\lambda_2 - [C_1C_2 + C_2C_3 + C_1C_3(1 - R_{eff})]\lambda - C_1C_3(1 - R_{eff}) = 0 \quad (2)$$

where $R_{eff} = \frac{\beta c\alpha\kappa\pi}{(\delta+\mu_1)(q_1+\beta+\mu_1)(\tau_1+v_1+v_2+\mu_1)}$ is called the effective reproduction number of COVID-19. It is the average number of persons that can be infected with COVID-19 when an index case of the disease is introduced in a disease-free population, in the presence of this control strategy. Using Descartes's rule of signs, we see that all the roots of (2) will be negative if $R_{eff} < 1$. Therefore, E_0 is locally asymptotically stable if $R_{eff} < 1$.

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3.2 Existence of Endemic Equilibrium and its Local Stability

Let $E_1 = (S^*, P^*, T_N^*, T^*, I^*, Q^*, R^*)$ be the endemic equilibrium of the model equation (1), where $S^* = \frac{\pi}{(\delta+\mu_1)+c\alpha\kappa I^*}$, $P^* = \frac{\delta S^* + q_0 T^* + q_1 T_N^*}{\mu_1}$, $T_N^* = \frac{c\alpha\kappa S^* I^*}{q_1+\beta+\mu_1}$, $I^* = \frac{\beta T_N^*}{\tau_1+v_1+v_2}$, $T^* = \frac{c\alpha(1-\kappa)S^* I^*}{q_0+q_2+\mu_1}$, $Q^* = \frac{q_2 T^* + v_2 I^*}{\tau_2+q_3+\mu_1}$, $R^* = \frac{v_1 I^* + q_3 Q^*}{\mu_1}$, $D^* = \frac{\tau_1 I^* + \tau_2 Q^*}{\mu_2}$. That is, E_1 is the solution to the system of equations;

$$\pi - c\alpha\kappa I S^* - c\alpha(1-\kappa)I^* S^* - (\delta + \mu_1)S^* = 0 \quad (3)$$

$$\delta S^* + q_0 T^* + q_1 T_N^* - \mu_1 P^* = 0 \quad (4)$$

$$c\alpha\kappa S^* I^* - (\beta + q_1 + \mu_1)T_N^* = 0 \quad (5)$$

$$\alpha c(1-\kappa)S^* I^* - (q_0 + q_2 + \mu_1)T^* = 0 \quad (6)$$

$$\beta T_N^* - (\tau_1 + v_1 + v_2 + \mu_1)I^* = 0 \quad (7)$$

$$q_2 T^* + v_2 I^* - (\tau_2 + q_3 + \mu_1)Q^* = 0 \quad (8)$$

$$v_1 I^* + q_3 Q^* - \mu_1 R^* = 0 \quad (9)$$

$$\tau_1 I^* + \tau_2 Q^* - \mu_2 D^* = 0 \quad (10)$$

Substituting the endemic equilibrium points into (7) equations gives

$$\frac{\beta c\alpha\kappa\pi I^*}{(\beta + q_1 + \mu_1)\left(c\alpha\kappa I^* + (\delta + \mu_1)\right)} - (\tau_1 + v_1 + v_2 + \mu_1)I^* = 0$$

which simplifies to give

$$-c\alpha\kappa(\beta + q_1 + \mu_1)(\tau_1 + v_1 + v_2 + \mu_1)I^{*2} + (\delta + \mu_1)(\beta + q_1 + \mu_1)(\tau_1 + v_1 + v_2 + \mu_1)\left[R_{eff} - 1\right]I^* = 0 \quad (11)$$

The trivial solutions, $I^* = 0$, to (11) corresponds to the disease-free equilibrium, which is locally asymptotically stable when $R_{eff} < 1$. The second solution, $I^* = \frac{\delta+\mu_1}{c\alpha\kappa}\left(R_{eff} - 1\right)$ is positive if $R_{eff} > 1$. This shows that a unique endemic equilibrium of the model exists only if $R_{eff} > 1$. If we linearize the model system around the endemic equilibrium, E_1, we get the Jacobian matrix;

$$J(E_1) = \begin{bmatrix} -A_1 & 0 & 0 & 0 & -c\alpha S^* & 0 & 0 & 0 & \delta & -\mu_1 & q_1 & q_0 & 0 & 0 & 0 & 0 & c\alpha\kappa I^* & 0 \\ & -A_2 & 0 & c\alpha\kappa S^0 & 0 & 0 & 0 & c\alpha(1-\kappa)I^* & 0 & 0 & -A_3 & c\alpha(1-\kappa)S^0 & 0 & 0 & 0 & 0 & 0 & \beta & 0 \\ & & -A_4 & 0 & 0 & 0 & 0 & 0 & 0 & q_2 & v_2 & -(\tau_2 + q_3 + \mu_1) & 0 & 0 & 0 & 0 & 0 & v_1 & q_3 \\ & & & -\mu_1 & 0 & 0 & 0 & 0 & 0 & \tau_1 & \tau_2 & 0 & -\mu_2 & \end{bmatrix}$$

where,

$$A_1 = c\alpha I^* + (\delta + \mu_1), A_2 = \beta + q_1 + \mu_1, A_3 = q_0 + q_2 + \mu_1, A_4 = \tau_1 + v_1 + v_2 + \mu_1.$$

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The eigenvalues of $J(E_1)$ are $-\mu_1, -\mu_1, -\mu_2, -(\tau_2 + q_3 + \mu_1), -(q_0 + q_2 + \mu_1)$ and the roots of the cubic equation

$$-\lambda^3 - \theta_1\lambda^2 - \theta_2\lambda - \theta_3 = 0. \quad (12)$$

where

$\theta_1 = ((c\alpha I^* + (\delta + \mu_1)) + (\beta + q_1 + \mu_1) + (\tau_1 + v_1 + v_2 + \mu_1)),$

$\theta_2 = ((c\alpha I^* + (\delta + \mu_1))(\beta + q_1 + \mu_1) + (c\alpha I^* + (\delta + \mu_1))(\tau_1 + v_1 + v_2 + \mu_1) + (\beta + q_1 + \mu_1)(\tau_1 + v_1 + v_2 + \mu_1)),$

$\theta_3 = ((c\alpha I^* + (\delta + \mu_1))(\beta + q_1 + \mu_1)(\tau_1 + v_1 + v_2 + \mu_1)) + \beta c_2 \alpha_2 \kappa S^* I^*.$

All the coefficients of (12) are negative since $S^* > 0, I^* > 0$. Therefore, all the eigenvalues of $J(E_1)$ are negative or have a negative real part. Since E_1 does not exist when $R_{eff} \leq 1$, we conclude that the endemic equilibrium, E_1 is locally asymptotically stable if $R_{eff} > 1$. The existence of a unique endemic equilibrium, and its local asymptotic stability when $R_{eff} > 1$, assures that there is no backward bifurcation in the model. Therefore, the disease-free equilibrium is globally asymptotically stable when $R_{eff} < 1$.

Numerical Solution of the Model

The numerical solution to the model is presented in this section. With the help of MATLAB ode45, the model is solved using the initial solution$S_0 = 150, P_0 = 100, T_0 = 50, T_{N0} = 50, I_0 = 0, Q_0 = 30, R_0 = 20, D_0 = 12$, and the parameter values as shown in Table 2. The numerical solution (figure 2-figure 5) shows the trajectories of the disease in the compartments of the population of interest.

Table 2: Parameter Values used in this model

Parameter	***Value***	***Parameter***	***Value***
π	500	τ_1	0.1
α	0.5	τ_2	0.001
c	0.175	v_1	0.35
κ	0.5	v_2	0.25
μ_1	0.00003	μ_2	0.75
β	0.25	δ	0.025
q_0	0.05	q_1	0.017
q_2	0.275	q_3	0.15

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In Figure 2, we have the graph of traced humans and those that are not traced. The graph shows that the two compartments are equal for a very short period. However, the number of those that are not traced grows higher than the number that are traced. The number of persons that are not traced outnumbered those that are traced because of more contacts that are made by those that are not traced. In Figure 3, the graph shows at any point in time *t*, the number of infected persons isolated is always higher than the number of infected persons that are not isolated. Figure 4 shows that increasing the rate at which infected persons are isolated, helps to reduce the number of infected persons in the population. In the same way, as shown in Figure 5, isolation of infected persons helps to reduce the number of deaths due to the disease.

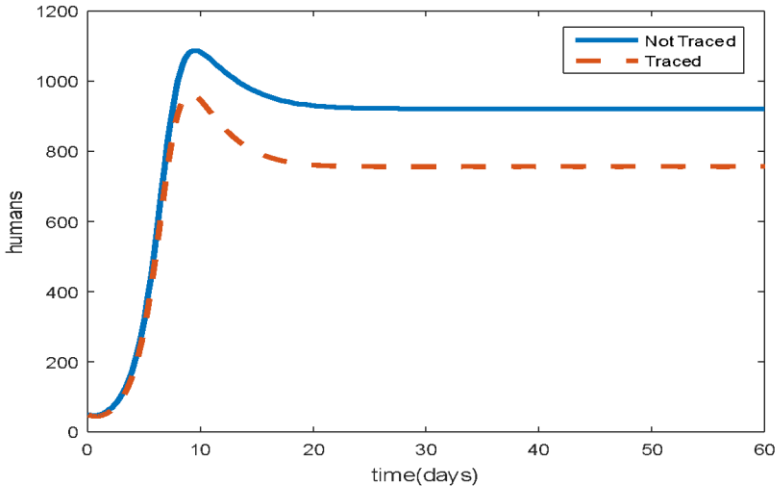

Figure 2: Number of persons traced and not traced at time t

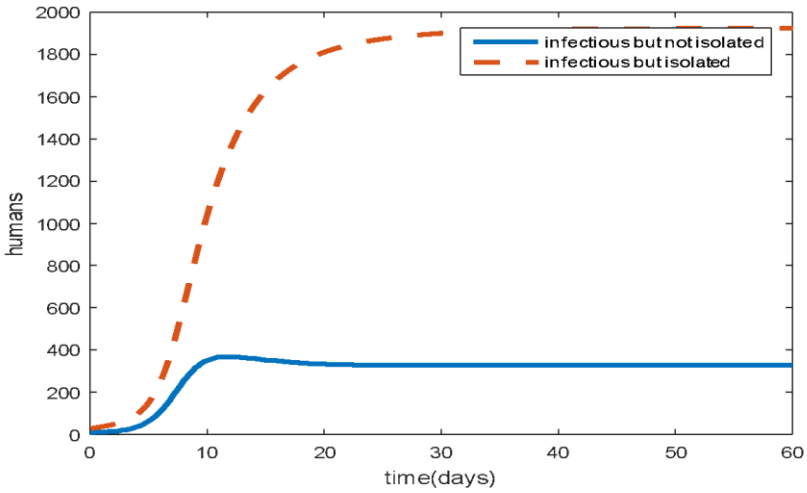

Figure 3: Number of infectious persons isolated and not isolated at time t

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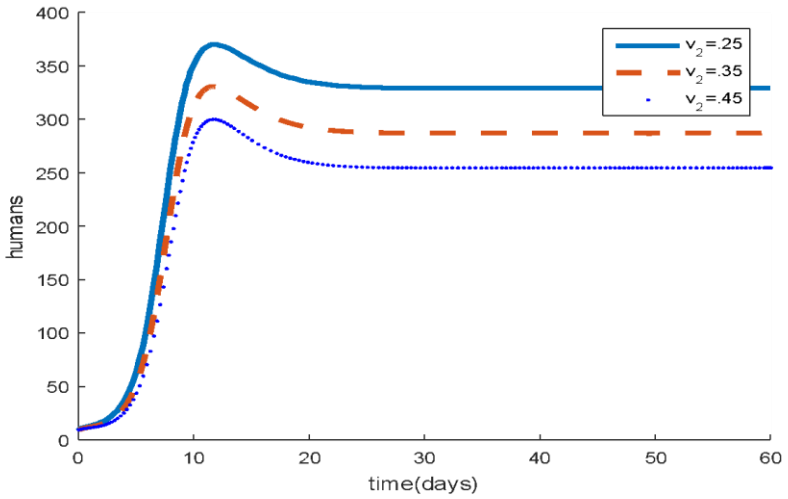

Figure 4: Effect of Isolation on the Number of Infected Persons

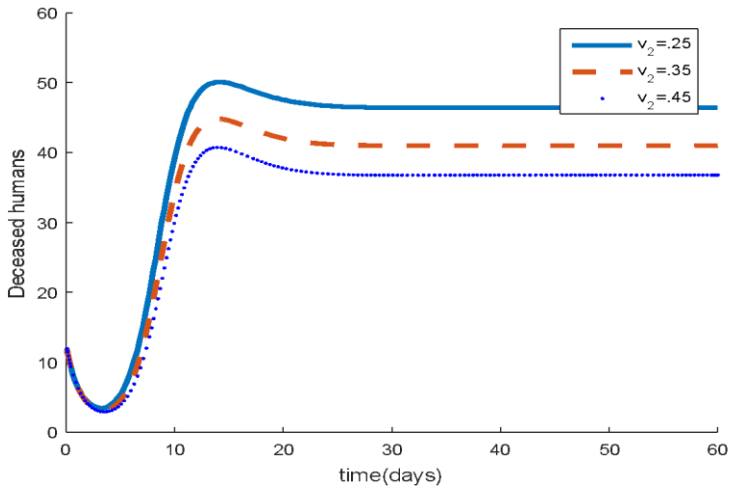

Figure 5: Effect of Isolation on the Number of Deceased Persons

SUMMARY AND CONCLUSION

In this paper, we have proposed a mathematical model which implements the Trace-Test-Isolate-Treat strategy for managing the spread of COVID-19. The model is a deterministic system of nonlinear ordinary differential equations which describes the transmission dynamics of COVID-19 in an 8-compartmental human population. In the stability analysis of the disease-free and endemic equilibrium of the model, we have that the disease-free equilibrium is both locally and globally asymptotically stable when $R_{eff} < 1$, while the model has a unique endemic equilibrium when $R_{eff} > 1$, which is locally asymptotically stable if $R_{eff} > 1$. The importance of contact tracing, testing, isolating, and treatment of infected persons in the management of COVID-19 and other related infections cannot be overemphasized. The Trace-Test-Isolate-Treat Strategy has proved to be an effective way of handling outbreaks of infectious viral diseases such as coronavirus disease.

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