

Mathematical Modeling of COVID-19 Transmission with Mass Testing and Contact Tracing

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Abstract: Corona virus disease or COVID-19 is an infectious disease whose etiological agent has been identified as a novel corona virus known as Severe Acute Respiratory Syndrome Corona virus 2 (SARS CoV 2). Symptoms of the disease include fever, fatigue, loss of smell and taste, dry cough and breathing difficulties in severe cases. The disease is mainly transmitted through discharge from the nose or mouth when an infectious person coughs or sneezes. In this paper, we used a 5-compartmental model incorporating isolation of positive cases to investigate the effect of mass testing and contact tracing on the transmission of COVID-19. The stability analysis of the model showed that the disease-free equilibrium was asymptotically stable when the basic reproduction number is less than unity. Further we performed the sensitivity analysis of the model. The purpose of the sensitivity analysis was to compare the impact of the mass testing to that of contact tracing with the aim of advising the disease control practitioners on the best strategy to stop community transmission in time of limited resources. The results of this analysis showed that mass testing with case isolation had greater impact on community transmission as compared to contact tracing. These results were validated by the use of the numerical simulation of the model. As the number of cases continue to surge and the health facilities get overwhelmed therefore, the health control practitioners need to adopt a control strategy that has the greatest impact on community transmission. The results obtained in this manuscript showed that mass testing followed by case isolation reduced the value of the basic reproduction number much more than contact tracing and is therefore a better strategy in combating community transmission of the disease.

Keywords; COVID-19, SARS Coronavirus 2, contact tracing, mass testing, sensitivity analysis, equilibrium, stability

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List of Symbols and Notations.

β	Disease transmission rate
σ	Progression rate from exposed to infectious compartments
ω	Proportion of individuals isolated through contact tracing
α	Proportion of individuals isolated through mass testing
γ_1	Recovery rate of infectious population
γ_2	Recovery rate of Isolated individuals
μ	Per capita natural mortality rate
d	Per capita Disease mortality rate
r	Birth rate
R_0	Basic Reproduction Number
K	Next Generation Matrix
S	Proportion of susceptible population
E	Proportion of Exposed population
I	Proportion of Infectious population
T	Proportion of Isolated population
R	Proportion of Recovered population.

I. Introduction

On December 31st 2019, health authorities in China notified World Health Organization (WHO) about a cluster of a viral Pneumonia of unknown etiology in Wuhan, Hubei province in China [11]. An investigation was launched and the etiological agent was identified as a novel coronavirus which was named Severe Acute Respiratory Syndrome Coronavirus 2 (SARS CoV 2) and the disease it caused was named Corona Virus Disease 2019 (COVID-19) [5]. On 30th January 2020, WHO declared the outbreak as a public health emergency of international concern (PHEIC) [12] and advised countries to prepare for containment measures. On 11th March

2020 the outbreak was named a global pandemic after Italy, Japan, South Korea and Iran reported a surge in the cases of COVID-19 [13]. The disease quickly spread to many countries around the world and as of 20th July 2020, there were more than 14,741,000 confirmed COVID-19 positive cases and more than 610,000 deaths associated with the disease in 213 countries and territories around the world and two international conveyances [14]. As a preventive measure, countries around the world have canceled major events, closed schools and universities and advised people to work from home whenever possible. These measures are broadly referred to as social distancing and are aimed at slowing down the transmission of the disease [1]. A number of research papers have been published for COVID-19 epidemic. [15] used a 5-compartmental model that incorporated the virus in the environment. Their model showed that the basic reproduction number comprised of three parts of which the transmission from the exposed to susceptible population played the major role in the disease transmission. The analysis of the model showed that the disease-free equilibrium was globally asymptotically stable when the basic reproduction number was less than one while endemic equilibrium was stable when the basic reproduction number was greater than one. The authors used the data of the reported cases in Wuhan from 23rd January 2020 to 10th February 2020 to estimate the parameters of the model. Simulation results showed that the epidemic would peak and then the infection level would decrease and approach an endemic state in the long run. [7] used an 8-compartmental model to investigate the transmission dynamics of the disease. They further performed sensitivity analysis to investigate the contribution of the model parameters to the transmission of COVID-19. The analysis of their model showed that all model parameters contributed to the transmission of the disease. [9] used a deterministic model incorporating clinical progression of the disease, the individual epidemiological status and intervention measures. The authors found that the control reproductive number could be as high as 6.47, and that intervention strategies such as intensive contact tracing followed by quarantine and isolation could effectively reduce the control reproduction number and the risk of transmission of the disease. The study by [8] used a 10-compartmental model incorporating asymptomatic carriers and waning of immunity after recovery. They used the model to assess the effect of lock-down on the transmission of COVID-19 in India. Their model results showed that lock-down could slow down the spread of the disease and delay the peak but the total number of cases in the long run would remain the same. This could however give time for the government to prepare effective policies and set-up medical facilities in preparation for the surge in the number of infections. The authors further proposed a lock-down strategy which would be implemented periodically for seven days and then the economy re-opened for five days to allow the economy to recover before another lock-down is imposed. They noted that locking down the economy would keep the transmission rate low, but keeping the economy shut for a long time would lead the economic depression which would increase the rate of unemployment. [1] used a modified SEIR model incorporating social distancing parameter to estimate transmission of COVID-19. The social distancing parameter was allowed to vary from 0 (total lock-down) to 1 (homogeneous mixing of the population). The results of the model analysis showed that social distancing had the potential to reduce the transmission from the polynomial to linear form. In this paper, we use a SEIR model that incorporates isolation of positive cases to investigate the effect of mass testing and contact tracing to the transmission of COVID-19.

II. Mathematical Formulation

In this paper, we model the transmission of novel SARS corona virus 2 using five compartments of susceptible (S), Exposed (E), Infectious(I), Isolated (T) and recovered (R) individuals. All individuals in the population are initially susceptible to the disease until an infectious individual is introduced into the population at a time t_0 . The transmission of the disease occurs when a susceptible individual interacts with an infectious individual. The force of infection (λ) which is the rate at which new infections are generated is given by the law of mass action. The law says that for a population in which individuals mix homogeneously, the rate of interaction between two subsets is directly proportional to the products of the number of individuals in each subset concerned [6]. Thus

$$\lambda = \beta SI$$

where $\beta = c \cdot p(i)$ and c is the contact rate while $p(i)$ is the probability of transmission in any given contact. We assume that the recovery rate which is the inverse of the infectious period is a constant.

We further assume that there are no vertical transmission and therefore all births enter the susceptible class (S). The flow chart for the model is shown in figure 1 below.

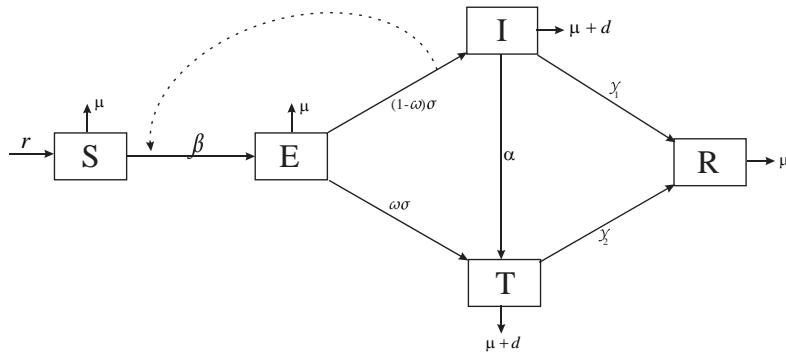


Figure 1: COVID-19 Transmission Model with both Contact Tracing and Mass Testing

In this model an individual is initially susceptible to the disease and upon interacting with an infectious individual the susceptible individual contracts the disease and enters the class E of exposed individuals. The individuals in this class have contracted the disease but their viral load is low and are not transmitting it to other individuals. As the viral load increases, the exposed individuals will start shedding the virus and enter the infectious class/compartment (I).

Upon finding an infectious individual in the population, the disease surveillance team activates contact tracing to trace all possible contacts that could have resulted to transmission of the disease and isolate them if found positive for COVID-19. Through contact tracing which is followed by testing, the exposed individuals are isolated from the rest of the population at a rate ω . The isolated individuals enter the compartment T. Individuals in this compartment do not interact with the rest of the population and therefore do not pose any risk of disease transmission to the rest of the population. However, because it is not possible to trace all contacts to a particular positive case, some exposed individuals remain in the population and progress to the infectious compartment I after a mean incubation period of $\frac{1}{\sigma}$ days. A large number of these individuals are asymptomatic and do not show any sign of the disease, however a small number develop symptoms and visit the health facility where they are tested and isolated upon testing positive for COVID-19. In addition, the disease surveillance team conducts mass testing to identify the positive cases in the population and isolates them at a rate α . The model assumes that individuals recovering from the disease acquire life long immunity from further infections. This generates the class R of recovered individuals.

The Mathematical model for the system is given by

$$\begin{aligned} \frac{dS}{dt} &= r - \mu S - \beta SI \\ \frac{dE}{dt} &= \beta SI - (\mu + \sigma)E \\ \frac{dI}{dt} &= (1 - \omega)\sigma E - (\mu + d + \gamma_1 + \alpha)I \\ \frac{dT}{dt} &= \omega\sigma E + \alpha I - (\mu + d + \gamma_2)T \\ \frac{dR}{dt} &= \gamma_1 I + \gamma_2 T - \mu R \end{aligned} \quad (1)$$

2.1 Equilibrium Analysis

A point $x = x_e$ is said to be an equilibrium point of a non-autonomous system

$$\frac{d}{dt}x(t) = f(t, x)$$

whenever $x(t)$ is a state vector if and only if the state vector is unchanging at that point i.e $\frac{d}{dt}x(t) = 0$ and therefore the equilibrium point of the system will satisfy the equation $f(t, x_e) = 0$

For the system 1 above, the equilibrium points are obtained by solving the equations

$$r - \mu S - \beta SI = 0 \quad (2)$$

$$\beta SI - (\mu + \sigma)E = 0 \quad (2)$$

$$(1 - \omega)\sigma E - (\mu + d + \gamma_1 + \alpha)I = 0 \quad (3)$$

$$\omega\sigma E + \alpha I - (\mu + d + \gamma_2)T = 0$$

$$\gamma_1 I + \gamma_2 T - \mu R = 0$$

From equation 3 we have

$$E = \frac{\mu+d+\gamma_1+\alpha}{(1-\omega)\sigma} \quad (4)$$

Substituting equation 4 into equation 2 and simplifying, we get

$$\left[\beta S - \frac{(\mu + \sigma)(\mu + d + \gamma_1 + \alpha)}{(1 - \omega)\sigma} \right] I = 0$$

Thus either $I = 0$ or

$$S = \frac{(\mu + \sigma)(\mu + d + \gamma_1 + \alpha)}{(1 - \omega)\beta\sigma}$$

The system therefore has two equilibrium points

- i) The Disease Free equilibrium (DFE) given by

$$(S^0, E^0, I^0, T^0, R^0) = \left(\frac{r}{\mu}, 0, 0, 0, 0 \right)$$

- ii) The Endemic Equilibrium Point (EEP) given by $(S^*, E^*, I^*, T^*, R^*)$

where

$$\begin{aligned} S^* &= \frac{(\mu + \sigma)(\mu + d + \gamma_1 + \alpha)}{(1 - \omega)\beta\sigma} \\ E^* &= \frac{(1 - \omega)\beta r \sigma - (\mu + \sigma)(\mu + d + \gamma_1 + \alpha)}{(1 - \omega)(\mu + \sigma)\beta\sigma} \\ I^* &= \frac{(1 - \omega)\sigma}{(\mu + \sigma)(\mu + d + \gamma_1 + \alpha)} - \frac{\mu}{\beta} \\ T^* &= \frac{\omega\sigma E^* - \alpha I^*}{\mu + d + \gamma_2} \\ R^* &= \frac{\gamma_1 I^* + \gamma_2 T^*}{\mu} \end{aligned}$$

2.1.1 Basic Reproduction Number

The basic reproduction number denoted by (R_0) is defined as the average number of secondary cases resulting from an index case in a completely susceptible population[10]. The value of R_0 is usually useful to provide insights in the design of the control methods for emerging epidemics. Generally when $R_0 > 1$ then on average each positive case will generate more than one other case during the period of infectiousness and this implies that the pathogen will invade the population. If on the other hand $R_0 < 1$ then on average each case will on average generate less than one other case during it's period of infectiousness. This would imply that the number of infected individuals in the population will decay as a function of time and therefore the epidemic would not occur. To find the basic reproduction number, we shall employ the method described in [2] where R_0 is defined as the spectral radius of the next generation matrix. The next generation matrix is constructed by first identifying those equations in the system that describe the generation of new infections and the changes in state. This system of equations is referred to as the infected sub-system. The infected sub-system is then linearised over the disease free equilibrium. The right hand side of the resulting system is then split into the transmission matrix (T) and the transition matrix V. Where T in a non-negative matrix and V is a non-singular M-Matrix. The next generation matrix (K) is then defined as $K = TV^{-1}$ and $R_0 = \rho(K)$ [2].

Consider the system 1 above, then the infected sub-system is given by

$$X_1 = \beta SI - (\mu + \sigma)E$$

$$X_2 = (1 - \omega)\sigma E - (\mu + d + \gamma_1 + \alpha)I$$

From which

$$DX = \begin{pmatrix} -(\mu + \sigma) & \beta S \\ (1 - \omega)\sigma & -(\mu + d + \alpha + \gamma_1) \end{pmatrix}$$

At DFE, $S = \frac{r}{\mu}$, substituting this value, we get the Jacobian matrix (J)

$$J = \begin{pmatrix} -(\mu + \sigma) & \frac{\beta r}{\mu} \\ (1 - \omega)\sigma & -(\mu + d + \alpha + \gamma_1) \end{pmatrix}$$

$$= T - V$$

$$\text{where } T = \begin{pmatrix} 0 & \frac{\beta r}{\mu} \\ (1 - \omega)\sigma & 0 \end{pmatrix}$$

$$\text{and } V = \begin{pmatrix} \mu + \sigma & 0 \\ 0 & \mu + d + \alpha + \gamma_1 \end{pmatrix}$$

The next generation matrix (K) becomes

$$K = TV^{-1} = \begin{pmatrix} 0 & \frac{\beta r}{\mu(\mu + d + \alpha + \gamma_1)} \\ \frac{(1-\omega)\sigma}{\mu + \sigma} & 0 \end{pmatrix}$$

From which

$$R_0 = \rho(K) = \sqrt{\frac{\beta r \sigma (1-\omega)}{\mu(\mu+\sigma)(\mu+d+\alpha+\gamma_1)}} \quad (5)$$

2.2 Stability Analysis

The analysis of the stability of equilibrium points seeks to answer three fundamental questions

- i) Does a constant solution of the system exist and if so what happens to the trajectories of the solution near this constant solution i.e. do the trajectories point towards the constant solution or away from it?
- ii) What happens to the solution of the system as time approaches infinity?
- iii) Do the solutions of the system oscillate or not?

We say that the equilibrium point is stable if the trajectories of the solution near the equilibrium point points towards the equilibrium point else the equilibrium point is unstable.

2.2.1 Stability Analysis for the Disease Free Equilibrium

To determine the stability of the disease free equilibrium, we first find the Jacobian matrix of the system(1). The Jacobian matrix is then linearized at the disease free equilibrium. The linearized system has a solution of the form $X(t) = \exp(\lambda t)$. where $X(t)$ is the state vector and λ is the Eigen value of the Jacobian matrix. Thus if the spectral radius of the Jacobian matrix is less than zero then $X(t)$ will be a monotonically decreasing function and will approach zero as t approaches infinity hence the Disease Free Equilibrium will be asymptotically stable.

The Jacobian matrix of the system (1) is given by

$$J = \begin{pmatrix} -\beta I - \mu & 0 & -\beta S & 0 & 0 \\ \beta I & -(\mu + \sigma) & \beta S & 0 & 0 \\ 0 & (1 - \omega)\sigma & -(\mu + d + \gamma_1 + \alpha) & 0 & 0 \\ 0 & \omega\sigma & \alpha & -(\mu + d + \gamma_2) & 0 \\ 0 & 0 & \gamma_1 & \gamma_2 & -\mu \end{pmatrix}$$

At DFE, $I = 0$ and $S = \frac{r}{\mu}$. Substituting back, we get

$$J_{DFE} = \begin{pmatrix} -\mu & 0 & -\frac{\beta r}{\mu} & 0 & 0 \\ 0 & -(\mu + \sigma) & \frac{\beta r}{\mu} & 0 & 0 \\ 0 & (1 - \omega)\sigma & -(\mu + d + \gamma_1 + \alpha) & 0 & 0 \\ 0 & \omega\sigma & \alpha & -(\mu + d + \gamma_2) & 0 \\ 0 & 0 & \gamma_1 & \gamma_2 & -\mu \end{pmatrix}$$

The characteristic equation becomes

$$\begin{vmatrix} -\mu - \lambda & 0 & -\frac{\beta r}{\mu} & 0 & 0 \\ 0 & -(\mu + \sigma) - \lambda & \frac{\beta r}{\mu} & 0 & 0 \\ 0 & (1 - \omega)\sigma & -(\mu + d + \gamma_1 + \alpha) - \lambda & 0 & 0 \\ 0 & \omega\sigma & \alpha & -(\mu + d + \gamma_2) - \lambda & 0 \\ 0 & 0 & \gamma_1 & \gamma_2 & -\mu - \lambda \end{vmatrix} = 0$$

Thus we get the Eigen values

$$\lambda_{1,2} = -\mu,$$

$$\lambda_3 = -(\mu + d + \gamma_2)$$

$$\lambda_4 = \frac{-\Theta - \sqrt{\Theta^2 - 4((\mu + \sigma)(\mu + d + \gamma_1 + \alpha) - \frac{\beta r \sigma (1-\omega)}{\mu})}}{2}$$

and

$$\lambda_5 = \frac{-\Theta + \sqrt{\Theta^2 - 4((\mu + \sigma)(\mu + d + \gamma_1 + \alpha) - \frac{\beta r \sigma (1-\omega)}{\mu})}}{2}$$

Where $\Theta = 2\mu + \sigma + d + \gamma_1 + \alpha$

we note that $Re\{\lambda_{1,2,3,4}\} < 0$, thus for stability of the DFE, then $Re\{\lambda_5\} < 0$ or

$$(\mu + \sigma)(\mu + d + \gamma_1 + \alpha) - \frac{\beta r \sigma (1-\omega)}{\mu} > 0$$

from which

$$\frac{\beta r \sigma (1-\omega)}{\mu(\mu + \sigma)(\mu + d + \alpha + \gamma_1)} < 1$$

From the foregoing analysis, we note that the disease free equilibrium is asymptotically stable if and only if the basic reproduction number is less than unity.

2.3 Sensitivity Analysis

In order to determine the optimal control strategy, the knowledge of the relative importance of the different factors responsible for the disease transmission is important. Normally the disease transmission is related to the basic reproduction number (R_0) such that a large value of R_0 is an indicator of the disease which is difficult to control. The purpose of the sensitivity analysis is to determine the parameters that have the greatest impact on R_0 . Sensitivity of the parameters affecting the basic reproduction number is measured by two factors;

- i) The sensitivity index which is defined as the rate of change of R_0 with respect to the parameter of interest. A positive sensitivity index will indicate that R_0 increases with the increasing value of the parameter considered while a negative value will indicate that R_0 decreases as the parameter value increases [3].
- ii) The Elasticity index which is defined as the relative change of the basic reproduction number with respect to the parameter of interest. The elasticity index of R_0 with respect to the parameter τ is denoted by $\Upsilon_\tau^{R_0}$ and defined by [3]

$$\Upsilon_\tau^{R_0} = \frac{\tau}{R_0} \frac{\partial R_0}{\partial \tau}$$

The magnitude of the elasticity index is a measure of the impact of the parameter being considered to the basic reproduction number. A large value of the parameter therefore is an indicator of a parameter that has a greater impact on the basic reproduction number and which should be targeted when designing the disease control strategy.

In this research work we compare the impact of isolation through contact tracing and mass testing i.e. the parameters ω and α respectively by computing the elasticity indices with respect to these two parameters. Differentiating R_0 (equation 5) with respect to ω we get

$$\frac{\partial R_0}{\partial \omega} = -\frac{1}{2} \sqrt{\frac{\beta r \sigma}{\mu(1-\omega)(\mu+\sigma)(\mu+d+\gamma_1+\alpha)}}$$

Thus increasing the parameter ω will decrease the basic reproduction number. We now find the elasticity index with respect to ω

$$\begin{aligned} \Upsilon_\omega^{R_0} &= \frac{\omega}{R_0} \frac{\partial R_0}{\partial \omega} \\ &= \frac{\omega}{R_0} \times \left(-\frac{1}{2} \sqrt{\frac{\beta r \sigma}{\mu(1-\omega)(\mu+\sigma)(\mu+d+\gamma_1+\alpha)}} \right) \\ &= -\frac{\omega}{2(1-\omega)} \end{aligned}$$

$$\text{and } |\Upsilon_\omega^{R_0}| = \frac{\omega}{2(1-\omega)}$$

Similarly Differentiating R_0 (equation 5) with respect to α we get

$$\frac{\partial R_0}{\partial \alpha} = -\frac{1}{2} \sqrt{\frac{\beta r \sigma (1-\omega)}{\mu(\mu+\sigma)(\mu+d+\gamma_1+\alpha)^3}}$$

While the elasticity index is given by

$$\Upsilon_\alpha^{R_0} = \frac{\alpha}{R_0} \frac{\partial R_0}{\partial \alpha}$$

$$\begin{aligned}
 &= \frac{\alpha}{R_0} \times \left(-\frac{1}{2} \sqrt{\frac{\beta r \sigma (1 - \omega)}{\mu(\mu + \sigma)(\mu + d + \gamma_1 + \alpha)^3}} \right) \\
 &= \frac{-\alpha}{2(\mu + d + \gamma_1 + \alpha)} \\
 \text{and } |\Upsilon_{\alpha}^{R_0}| &= \frac{\alpha}{2(\mu + d + \gamma_1 + \alpha)}
 \end{aligned}$$

We note that $\Upsilon_{\alpha}^{R_0} < 0$ thus R_0 will decrease with increasing value of α .

III. Results and Discussion

3.1 Elasticity Indices

In this section, we present the elasticity indices and the corresponding values of the basic reproduction numbers obtained by varying the mass testing and contact tracing parameters. We use the parameter values $\mu = 0.01429$ per year [6], $r = 0.0384$ per year [4], $d = 0.28045$ per 1,000, $\beta = 0.287$, $\sigma = \frac{1}{5}$ and $\gamma_1 = \gamma_2 = \frac{1}{20}$. The parameters $\beta, \gamma_1, \gamma_2, \sigma$ and d were estimated using the data reported in Kenya between 13th March 2020 and 5th May 2020 [16]. Using these values and assuming no isolation (i.e $\alpha = \omega = 0$), we get $R_0 = 3.9145$.

Table 1 gives the values of the elasticity indices and the corresponding values of R_0 for suitably chosen values of α and ω .

α	$\Upsilon_{\alpha}^{R_0}$	R_0
0.00	-	3.9145
0.01	-0.0829	3.5754
0.05	-0.2492	2.7724
0.08	-0.3069	2.4324
0.10	-0.3326	2.2649
0.12	-0.3523	2.1277
0.15	-0.3744	1.9619

a) $\omega = 0$

ω	$\Upsilon_{\omega}^{R_0}$	R_0
0.00	-	3.9145
0.01	-0.0051	3.8949
0.05	-0.0263	3.8154
0.08	-0.0435	3.7547
0.10	-0.0556	3.7136
0.12	-0.0682	3.6722
0.15	-0.0882	3.6090

b) $\alpha = 0$

Table 1: The Elasticity Indices and the corresponding values of R_0 for suitably chosen values of α and ω

From the data in table 1(a) and table 1 (b), we observe that before isolation measures are introduced $R_0 = 3.9145$. From table 1(a) we note that when mass testing with case isolation is introduced resulting to isolation of 1 % ($\alpha = 0.01$) of the infectious cases, then the value of R_0 decreased to 3.5754. On increasing the value of α , the value of R_0 continued to decrease and when $\alpha = 0.15$ then the elasticity index was -0.3744 and the value of R_0 reduced to 1.9619. The data in table 1(b) on the other hand shows that introducing contact tracing with case isolation resulting to isolation of 1 % ($\omega = 0.01$) of the positive cases, the value of R_0 decreased to 3.8949. Further we note that R_0 decreases with increasing ω and when $\omega = 0.15$, then the value of the elasticity index was -0.0682 and $R_0 = 3.6090$. By comparing the data in tables 1(a) and 1(b) therefore, we note that although contact tracing is a good method of mitigating COVID-19, mass testing with case isolation had a greater impact on the value of R_0 and is therefore much more effective in stopping community transmission of the virus. During the times of limited resources therefore, the disease surveillance team should put more resources on mass testing with the aim of isolating the infectious individuals in the population, rather than focusing more on the contact tracing which is likely to get more of the exposed individuals.

As the number of positive cases increases, the health care facilities tend to become overwhelmed. It is therefore prudent that the disease surveillance team choose the most optimal strategy to mitigate the spread of COVID-19. The results of this analysis shows that mass testing has a greater impact in stopping community transmission than contact tracing and therefore as the health facilities becomes overwhelmed as the cases increase, the disease surveillance team should do more of mass testing and aim to isolate only the infectious cases.

3.2 Numerical Results

In this section we present the results of the numerical simulation of the model. We consider a population of 1,000,000 individuals and use the initial conditions $I_0 = 100, E_0 = 100, T_0 = 0, R_0 = 0$ and $S_0 = 999,800$. Using these values the results of the model are as shown in figure 2. The results of the numerical simulation shows that if there is no isolation, then the peak will be attained on the 80th day with more than 400,000 individuals contracting the disease.

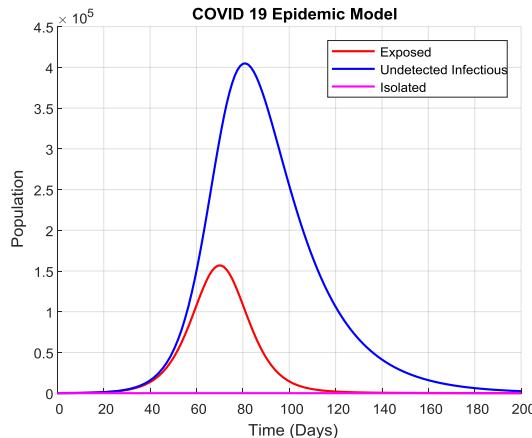


Figure 2: Transmission dynamics for SARS corona virus 2 with no isolation. In this case the peak is attained on the 80th day with more than 40% of the population getting infected.

Figure 3(a) shows the results of the model when contact tracing is introduced tracking 5% of the exposed individuals with no mass testing. In figure 3(b), mass testing is introduced at a lower rate tracking 5% of the infectious cases in the population and with no contact tracing. As can be seen from figure 3(a) and 3(b) mass testing combined with case isolation results to much lower infections as compared to contact tracing.

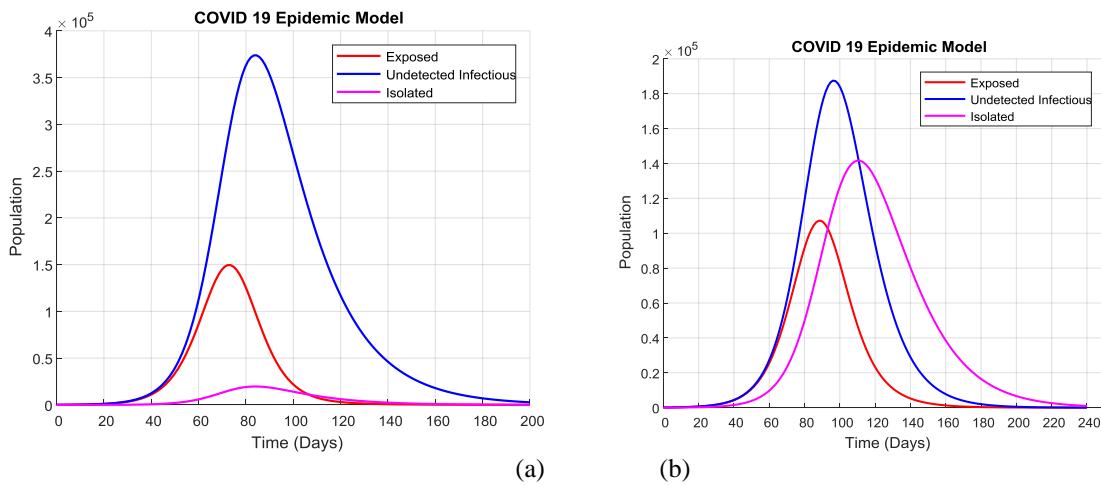


Figure 3: Transmission dynamics for SARS corona virus 2 with (a) $\omega = 5\%$ and $\alpha = 0$ (b) $\omega = 0\%$ and $\alpha = 5\%$

Figures 4, 5 and 6 shows the results of the model with contact tracing (a) and mass testing (b), from the graphs it is observed that mass testing combined with case isolation results to lower infection than contact tracing.

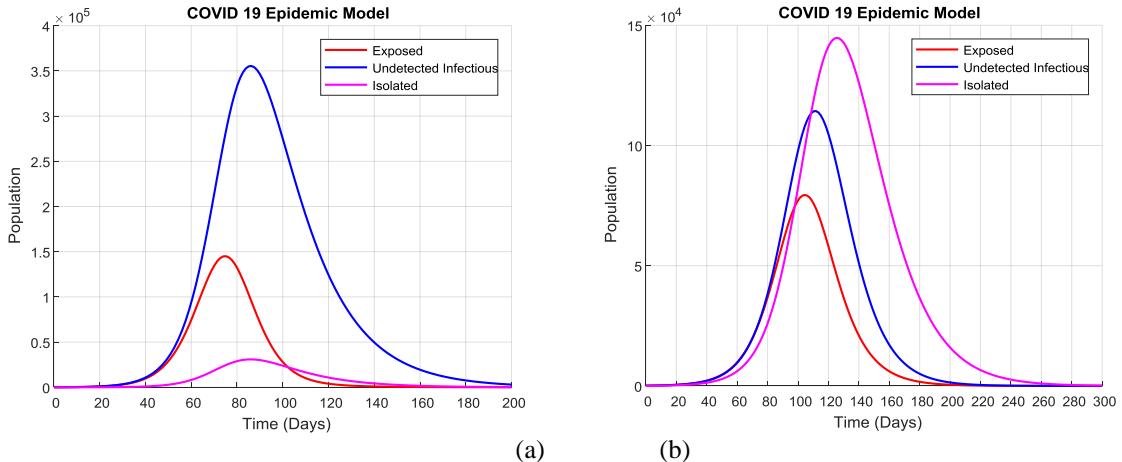


Figure 4: Transmission dynamics for SARS corona virus 2 with (a) $\omega = 8\%$ and $\alpha = 0$ (b) $\omega = 0\%$ and

$$\alpha = 8\%$$

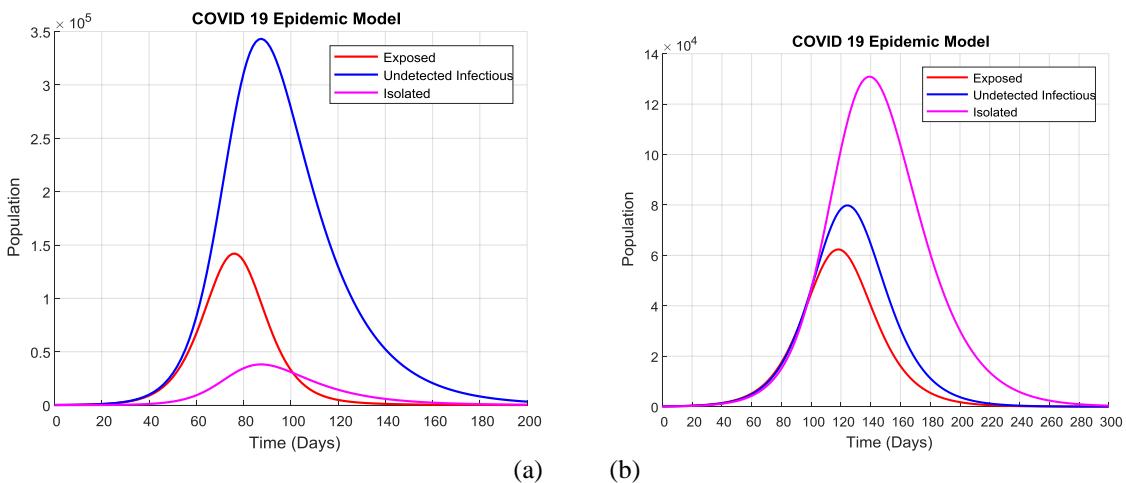


Figure 5: Transmission dynamics for SARS corona virus 2 with (a) $\omega = 10\%$ and $\alpha = 0$ (b) $\omega = 0\%$ and $\alpha = 10\%$

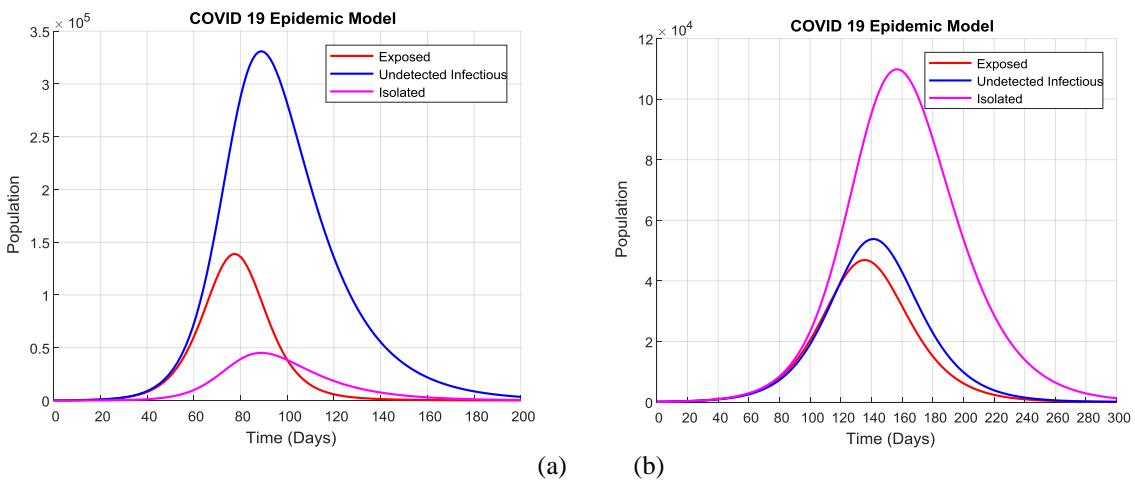


Figure 6: Transmission dynamics for SARS corona virus 2 with (a) $\omega = 12\%$ and $\alpha = 0$ (b) $\omega = 0\%$ and $\alpha = 12\%$

IV. Conclusion

This research was designed to study and compare the effect of contact tracing and mass testing to community transmission of COVID-19 using mathematical modeling. The results of the model analysis showed that the model has a unique disease free equilibrium which is asymptotically stable when $R_0 < 1$ and unstable otherwise. We further carried out sensitivity analysis of the model. The results of the sensitivity analysis showed that mass testing combined with case isolation is a more effective method in combating community transmission as compared to contact tracing. As the number of cases continue to increase and the health facilities get overwhelmed therefore, the health control practitioners need to adopt a control strategy that has the greatest impact on community transmission. The results obtained in this manuscript showed that mass testing followed by case isolation reduced the value of the basic reproduction number much more than contact tracing and is therefore a better strategy in combating community transmission of COVID-19.

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