Covenant Journal of Physical & Life Sciences (CJPL) Vol. 9 No. 1, June 2021
ISSN: *print 2354 - 3574 electronics 2354-3485DOI:*

An Open Access Journal Available Online

Modelling COVID 19 Epidemics: The Role of Social Distancing and Isolation

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Received: 23.10.2020; Accepted: 25.05.2021
Date of Publication: June 2021

Abstract
Coronavirus disease 2019 pandemic, popularly known as the COVID 19 pandemic, was one of the most dreaded pandemics in the history of human epidemiology. It negatively impacted the health and economy of the whole world, leading to a global economy shutdown. This study aims to develop a mathematical model for COVID 19 transmission to investigate the role of social distancing and isolation. Therefore, a mathematical model for COVID 19 incorporating social distancing and isolation of exposed and infectious individuals as controls were formulated. The basic reproduction number, as an epidemic threshold, was computed by the next-generation approach. The model has a globally asymptotically stable disease-free equilibrium whenever the basic reproduction number is less than unity. The numerical results show that whilst COVID 19 can spark a major epidemic in the absence of control. It can be contained with optimum enforcement of rules. The findings of this study reveal that an optimum combination of social distancing and isolation as a control strategy is the most effective and is therefore recommended.
Keywords: COVID 19**,** pandemic, social distancing, isolation

1.0 Introduction

Coronavirus disease 2019 (COVID 19) is a highly infectious disease caused by severe acute respiratory syndrome coronavirus 2 (SARS COV 2). The disease first was identified in December 2019 in Wuhan, the capital city of Hubel, China, and has since spread globally, resulting in a 2019-20 coronavirus pandemic [1,2]. Common symptoms include fever, cough and shortness of

breath. Muscle pain, sputum production, diarrhoea and sore throat are less common [3, 4].

While the majority of cases result in mild symptoms, some progress to pneumonia and multi-organ failure. As of 23 March 2020, the death rate per number of diagnosed cases is 4.4%; however, it ranges from 0.2 to 15%, according to age group and other health problems.

The virus is typically spread during close contact and via respiratory droplets produced when people cough or sneeze. Respiratory droplets may be made during breathing, but they are not considered airborne [5]. It may also spread when one touches a contaminated surface and their face. It is most contagious when people are symptomatic, although spread may be possible before symptoms appear. The virus can live on the surface for up to 72 hours. Time from exposure to onset of symptoms is generally between 2 to 14 days, with an average of 5 days. The standard method of diagnosis is by reverse transcription-polymerase chain reaction from a nasopharyngeal swab. Control and preventive measure for COVID 19 disease are available [6]. These include but not limited to quarantine, symptomatic management and social distancing.

Epidemiological models help to capture infection or disease transmission mechanisms in a population in a mathematical framework to predict the behaviour of the disease spread through the population. Mathematical models have become essential tools in analysing the spread and control of infectious diseases. Understanding the transmission characteristics of infectious diseases in communities, regions and countries in mathematical frameworks can lead to better approaches to decreasing the transmission of these diseases [7].

Due to the exponential spread of COVID-19 worldwide, the need to develop a mathematical model to study the transmission dynamics and spread of these infectious diseases became necessary.

Daniel [8] developed a mathematical model to study the current outbreak of COVID-19 in Nigeria with nonlinear forces of infection. The model studied the impact of the environmental reservoir in the transmission and spread of this disease to humans. Numerical simulation indicated that Nigeria's cumulative number of confirmed cases would reach 55,000 individuals in December 2020 if no mitigation strategies are adopted.

Okuonghae and Omame [9] examined the impact of various non-pharmaceutical control measures (government and personal) on the

population dynamics of the novel coronavirus disease 2019 (COVID-19) in Lagos, Nigeria, using an appropriately formulated mathematical model. They use numerical simulations to show the effect of control measures, specifically the common social distancing, use of face mask and case detection (via contact tracing and subsequent testing) on the dynamics of COVID-19.

Iboi et al. [10] developed a mathematical model for understanding the transmission dynamics and control of COVID-19 in Nigeria. Their model, which was parametrised using COVID-19 data published in Nigeria Centre for Disease Control (NCDC), was used to assess the community-wide impact of various control and mitigation strategies in the entire Nigeria nation. From the results, they stated that, for the worst-case scenario where social distancing, lockdown and other community transmission reduction measures are not implemented, Nigeria would have recorded a devastatingly high COVID-19 mortality by April 2021.

Ivorra et al. [11] developed a mathematical model for the spread of the coronavirus disease 2019 (COVID-19) by taking into account the known unique characteristics of the diseases, as the existence of undetected infectious cases and the different sanitary and infectiousness conditions of hospitalised people. The results of different scenarios show how the different values of the percentage of detected cases would have changed the global magnitude of COVID-19 in China.

The plan of this paper is as follows. The model formulation is done in section 2. The model analysis is done in section 3. Numerical computation and results are presented in section 4. Discussion of results and conclusive remarks are passed in sections 5 and 6, respectively.

2. Model Formulation

This model subdivides the human population $N(t)$ into six compartments of susceptible $S(t)$, exposed $E(t)$, infectious $I(t)$, socially distanced $S_1(t)$ isolated $I_S(t)$ and recovered $R(t)$, humans. So that;

$$N(t) = S(t) + E(t) + I(t) + S_1(t) + I_S(t) + R(t) \quad (1)$$

2.1. Basic Assumptions

The following are the assumptions of the existing model by Zou and Zhang [12]:

(i) The population is homogeneous and randomly mixing,

(ii) Exit out of the population is by COVID 19-related mortality only.

The variables and parameters used in the model are defined in Table 1.

2.2 Susceptible, Exposed, Infected, Social Distanced, Isolated and Recovered Populations

The population of susceptible humans S, are reduced by infection, following contact with infected humans (at the rate β). The exposed population is further reduced as a result of social distancing (at the rate ε_1). These definitions give the following expression for the rate of change of the susceptible human population.

$$\frac{dS}{dt} = -\beta S\frac{I}{N} - \varepsilon_1 S$$

The population of Exposed (latent) humans E is generated following infection (at the rate β). They are decreased as a result of progression into the infectious class (at the rate σ), isolation (at the rate ε_2) so that

$$\frac{dE}{dt} = \beta S\frac{I}{N} - (\sigma + \varepsilon_2)E$$

Infectious humans I are generated due to progression into the infected class from the latent class (at the rate σ). It is diminished by recovery (at the rate γ), isolation (at the rate ε_3), and disease-induced death (at the rate d), so that

$$\frac{dI}{dt} = \sigma E - (\gamma + \varepsilon_3 + d)I$$

Social Distanced population S_1 is generated via social distancing (at the rate ε_1. Hence,

$$\frac{dS_1}{dt} = \varepsilon_1 S$$

The population of Isolated humans I_S are generated (at the rates ε_2 and ε_3). It is diminished by recovery (at the rate γ_1) and disease-induced death (at the rate d_1), so that

$$\frac{dI_S}{dt} = \varepsilon_2 E + \varepsilon_3 I - (\gamma_1 + d_1)I_S$$

The population of recovered humans R are generated are (at the rates γ and γ_1). Thus,

$$\frac{\mathrm{dR}}{\mathrm{dt}} = \gamma I + \gamma_1 I_S$$

The above assumptions and derivatives lead to the following system of ordinary differential equations:

2.3 Model Equation

$$\frac{dS}{dt} = -\beta S\frac{I}{N} - \varepsilon_1 S \quad (2)$$

$$\frac{dE}{dt} = \beta S\frac{I}{N} - (\sigma + \varepsilon_2)E \quad (3)$$

$$\frac{dI}{dt} = \sigma E - (\gamma + \varepsilon_3 + d)I \quad (4)$$

$$\frac{dS_1}{dt} = \varepsilon_1 S \quad (5)$$

$$\frac{dI_S}{dt} = \varepsilon_2 E + \varepsilon_3 I - (\gamma_1 + d_1)I_S \quad (6)$$

$$\frac{\mathrm{dR}}{\mathrm{dt}} = \gamma I + \gamma_1 I_S \quad (7)$$

$$S \geq 0, E \geq 0, I \geq 0, S_1 \geq 0, Q \geq 0, R \geq 0 \quad (8)$$

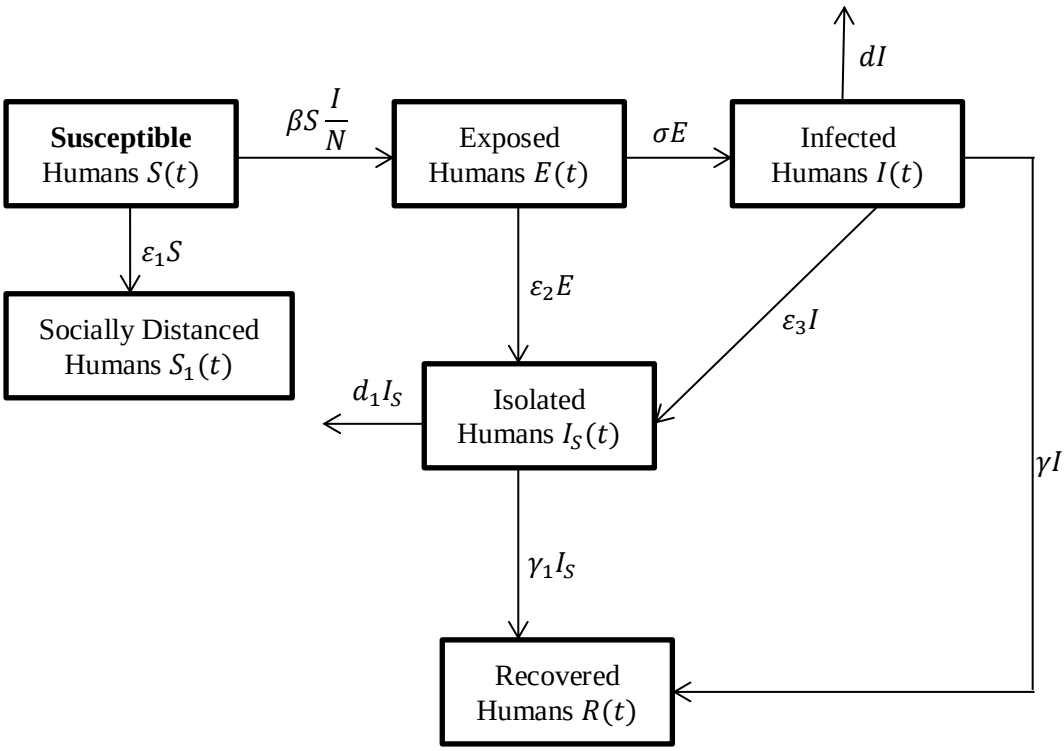

Figure 1: Schematic description of the mathematical model

Table 1: Variables and Parameters used in the model and their description

Variable/Parameter	Description
$S(t)$	The number of susceptible hosts at time t
$E(t)$	The number of latent hosts at time t
$I(t)$	The number of infectious human hosts at time t
$S_1(t)$	The number of the socially distanced human population at time t
$I_S(t)$	The number of isolated human hosts at time t
$R(t)$	The number of recovered humans at time t
β	Infection transmission rate
ε_1	Social distancing rate
ε_2	The isolation rate of exposed humans
ε_3	The isolation rate of infected humans
σ	Progression rate to infectious class
d	COVID-19 mortality rate of infected humans
d_1	The COVID-19 mortality rate of isolated humans
γ	Recovery rate of infected humans with COVID-19
γ_1	The recovery rate of isolated humans with COVID-19

For the prevalence of the disease, it is necessary to model in terms of the proportion of susceptible, exposed, infected, social distanced, isolated and recovered compartments.

Adding equations (2) – (7) gives the rate of change of the total population:

$$\frac{dN}{dt} = -\beta S\frac{I}{N} - \varepsilon_1 S + \beta S\frac{I}{N} - (\sigma + \varepsilon_2)E + \sigma E - (\gamma + \varepsilon_3 + d)I + \varepsilon_1 S + \varepsilon_2 E + \varepsilon_3 I - (\gamma_1 + d_2)I_S + yI + y_1 I_S$$

$$\frac{dN}{dt} = -dI - d_1 I_S \quad (9)$$

We now define the proportion for each compartment as follows:

$$s = \frac{S}{N}, e = \frac{E}{N}, i = \frac{I}{N}, s_1 = \frac{S_1}{N}, i_S = \frac{Q}{N}, \text{and } r = \frac{R}{N},$$

So that

$$s + e + i + s_1 + i_S + r = 1 \Longrightarrow s = 1 - e - i - s_1 - i_S - r$$

The system (2) – (7) expressed in terms of proportion is given below:

$$\frac{ds}{dt} = -\beta si - \varepsilon_1 s \quad (10)$$

$$\frac{de}{dt} = \beta si - \sigma e - \varepsilon_2 e \quad (11)$$

$$\frac{di}{dt} = \sigma e - (\gamma + d + \varepsilon_3)i \quad (12)$$

$$\frac{ds_1}{dt} = \varepsilon_1 s \quad (13)$$

$$\frac{di_S}{dt} = \varepsilon_2 e + \varepsilon_3 i - (\gamma_1 + d_1)i_S \quad (14)$$

$$\frac{dr}{dt} = \gamma i + \gamma_1 i_S \quad (15)$$

$$s \geq 0, e \geq 0, i \geq 0, s_1 \geq 0, i_S \geq 0, r \geq 0 \quad (16)$$

2.4 Invariant Region

The rate of change of the human population in proportion is given by

$$\frac{dn}{dt} = -\beta si - \varepsilon_1 s + \beta si - \sigma e - \varepsilon_2 e + \sigma e - (\gamma + d + \varepsilon_3)i + \varepsilon_1 s + \varepsilon_2 e + \varepsilon_3 i - (\gamma_1 + d_1)i_S + \gamma i + \gamma_1 i_S$$

$$\frac{dn}{dt} = -di - d_1 i_S$$

In the absence of infection, it is clear that

$$\frac{dn}{dt} \leq 0 \quad (17)$$

Applying the theorem of differential inequality by Birkhof and Rota [13] on equation (17), we obtain

$$0 \leq n(t) \leq 1 \; as \; t \to \infty$$

Thus the region

$$\Omega = \{(s, e, i, s_1, i_S, r) \in \mathbb{R}^6_+ : s + e + i + s_1 + i_S + r \leq 1\}$$

is positively invariant.

In this region, the model can be considered as being epidemiological and mathematically well-posed. Thus every solution of the basic model with initial conditions in Ω remains in Ω for all $t > 0$.

3. Model Analysis

The model (10) – (15) has a disease-free equilibrium (DFE) given by

$$\boldsymbol{\Omega_0} = (s, e, i, s_1, i_S, r) = (1,0,0,0,0,0) \quad (18)$$

We will use the disease-free equilibrium state and the next generation operator method to compute the basic reproduction number R_0.

3.1 **Basic Reproduction Number R_0**

For the recipe on computation of basic reproduction number, (see [14,15,16,17]). Let the non-negative matrix, F, of new infection terms and the M-matrix, V, of transfer terms associated with the model (10) – (15) are given respectively, by

$$F = \begin{pmatrix} 0 & \beta \\ 0 & 0 \end{pmatrix}$$

and

$$V = \begin{pmatrix} \sigma + \varepsilon_2 & 0 \\ -\sigma & \gamma + d + \varepsilon_3 \end{pmatrix}$$

so that

Now

$$V^{-1} = \begin{pmatrix} \frac{1}{\sigma+\varepsilon_2} & 0 \\ \frac{\sigma}{(\sigma+\varepsilon_2)(\gamma+d+\varepsilon_3)} & \frac{1}{\gamma+d+\varepsilon_3} \end{pmatrix}$$

$$FV^{-1} = \begin{pmatrix} \frac{\beta\sigma}{(\sigma+\varepsilon_2)(\gamma+d+\varepsilon_3)} & \frac{\beta}{(\gamma+d+\varepsilon_3} \\ 0 & 0 \end{pmatrix}.$$

The dominant eigenvalue of $FV^{-1} = \begin{pmatrix} \frac{\beta\sigma}{(\sigma+\varepsilon_2)(\gamma+d+\varepsilon_3)} & \frac{\beta}{(\gamma+d+\varepsilon_3} \\ 0 & 0 \end{pmatrix}$ is given by

$\lambda = \frac{\beta\sigma}{(\sigma+\varepsilon_2)(\gamma+d+\varepsilon_3)}$

and therefore, the basic reproduction number is given by

$$R_0 = \frac{\beta\sigma}{(\sigma+\varepsilon_2)(\gamma+d+\varepsilon_3)}. \qquad (19)$$

3.2. Local Stability of Disease Free Equilibrium (DFE) State

We investigate the local stability of the disease-free (DFE) state by evaluating the associated Jacobian of equations (10) – (15) at the DFE state. The Jacobian matrix J for the system (10) – (15), evaluated at the disease-free equilibrium, $\boldsymbol{\Omega_0}$ is given by

$$J(\Omega_0) = \begin{pmatrix} -\varepsilon_1 & 0 & -\beta & 0 & 0 \\ 0 & -(\sigma+\varepsilon_2) & \beta & 0 & 0 \\ 0 & \sigma & -(\gamma+d+\varepsilon_3) & 0 & 0 \\ \varepsilon_1 & 0 & 0 & 0 & 0 \\ 0 & \varepsilon_2 & \varepsilon_3 & 0 & -(\gamma_1+d_1) \\ 0 & 0 & \gamma & 0 & \gamma_1 \end{pmatrix} \qquad (20)$$

The disease-free equilibrium is locally asymptotically stable if and only if all of the eigenvalues of the Jacobian matrix J have a negative

real part [18]. The eigenvalues can be determined by solving the characteristic equation $|J - \lambda I| = 0$ The eigenvalues are given by

$$(0-\lambda)(-(\gamma+d_1)-\lambda)(0-\lambda)(-\varepsilon-\lambda)[(-(\sigma+\varepsilon_2)-\lambda)(-(\gamma+d+\varepsilon_3)-\lambda) - \beta\sigma] = 0$$

$$(0-\lambda)(-(\gamma+d_1)-\lambda)(0-\lambda)(-\varepsilon-\lambda)[(\sigma+\varepsilon_2)(\gamma+d+\varepsilon_3)+\lambda(\sigma+\varepsilon_2) + \lambda(\gamma+d+\varepsilon_3)+\lambda^2-\beta\sigma] = 0$$

that is

$$(0-\lambda)(-(\gamma+d_1)-\lambda)(0-\lambda)(-\varepsilon-\lambda)[\lambda^2+\lambda(\sigma+\varepsilon_2+\gamma+d+\varepsilon_3)+(\sigma+\varepsilon_2)(\gamma+d+\varepsilon_3)-\beta\sigma] = 0 \quad (21)$$

Then

$\lambda = 0$ (twice), $\lambda = -(\gamma + d_1)$, $\lambda = -\varepsilon$,

and

$$\left[\lambda^2+\lambda(\sigma+\varepsilon_2+\gamma+d+\varepsilon_3)+(\sigma+\varepsilon_2)(\gamma+d+\varepsilon_3)-\beta\sigma\right] = 0 \quad (22)$$

Four eigenvalues are negative. Now equation of the submatrix J_1, where equation (22) is the characteristic

$$J_1 = \begin{pmatrix} -(\sigma+\varepsilon_2) & \beta \\ \sigma & -(\gamma+d+\varepsilon_3) \end{pmatrix} \quad (23)$$

If the trace of $J_1 < 0$ and the $\det(J_1) > 0$ then the eigenvalues are negative
The trace of $J_1 = -(\sigma + \varepsilon_2 + \gamma + d + \varepsilon_3) < 0$ (24)

and $det(J_1) = (\sigma+\varepsilon_2)(\gamma+d+\varepsilon_3) - \beta\sigma > 0$ (25)

That is,

$$1 - \frac{\beta\sigma}{(\sigma+\varepsilon_2)(\gamma+d+\varepsilon_3)} > 0 \quad (26)$$

$$1 - R_0 > 0 \quad \text{if} \quad R_0 < 1$$

Thus we proved the following lemma.

Lemma 1: The DFEs of the model (10) – (15), given by Ω_0, locally asymptotically stable (LAS) if $R_0 < 1$ and ε_0 is unstable if $R_0 > 1$.

3.3 Global Asymptotical Stability (GAS) of Disease Free Equilibrium (DFE) State

Theorem 1: The DFE of model (10) – (15), given by Ω_0 is GAS whenever $R_0 \leq 1$.

Proof Consider the Lyapunov function

$$F = e + i,$$

with Lyapunov derivative (where a prime represents differentiation with respect to t)

$$\begin{aligned} F' &= \beta si - \sigma e - \varepsilon_2 e \ + \sigma e - (\gamma + d + \ \varepsilon_3)i \\ &= [\beta - (\gamma + d + \ \varepsilon_3)]i + [\sigma - (\varepsilon_2 + \ \sigma)]e \\ &= \ [\beta - (\gamma + d + \ \varepsilon_3)]i + [\sigma - (\varepsilon_2 + \ \sigma)]\frac{\beta i}{\sigma + \varepsilon_2} \\ &= \ [\beta - (\gamma + d + \ \varepsilon_3)]i + [\frac{\sigma\beta}{(\sigma+\varepsilon_2)} - \beta]i \\ &= \ \left[\frac{\sigma\beta}{(\sigma+\varepsilon_2)} - (\gamma + d + \ \varepsilon_3)\right] i \\ &= (\gamma + d + \ \varepsilon_3)i[\frac{\sigma\beta}{(\sigma+\varepsilon_2)(\gamma+d+\ \varepsilon_3)} - 1] \\ &= (\gamma + d + \ \varepsilon_3)i[R_0 - 1] \\ &\leq 0 \text{ for } \ R_0 \leq 1 \end{aligned}$$

4. Numerical Simulation and Results

For our numerical simulations, we make use of the parameter values in Table2.

Table 2: Baseline Parameter values for equations (9) – (14)

Parameter	Value	Source	Parameter	Value	Source
$S(0)$	15000	*assumed*	ε_2	$0-1$	*variable*
$E(0)$	2	*assumed*	ε_3	$0-1$	*variable*
$I(0)$	2	*assumed*	σ	$1/5.2$	[20]
$S_1(0)$	0	*assumed*	γ	$1/7$	[21]
$I_S(0)$	0	*assumed*	d	0.044	[10]
$R(0)$	0	*assumed*	γ_1	$1/7$	[21]
β	0.6321	[19]	d_1	0.02	*estimated*
ε_1	$0-1$	*variable*			

Our numerical results are shown in Figures 2 through 5

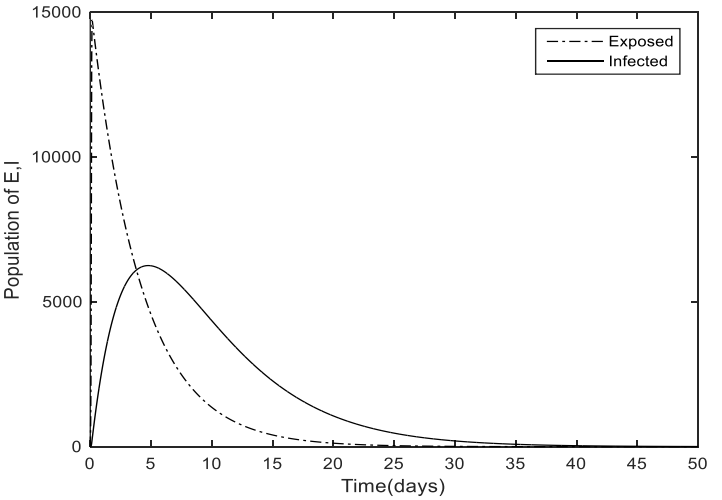

Figure 2: Graph of COVID-19 in exposed and infected population over time without control measures $(\varepsilon_1 = \varepsilon_2 = \varepsilon_3 = 0,\ R_0 = 2.993)$.

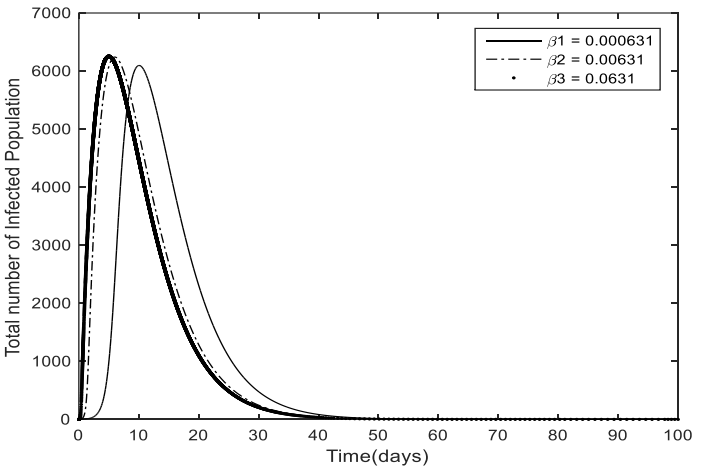

Figure 3: Graph of infected individuals with COVID-19 varying infection transmission rates ($\beta = 0.000631, R_0 = 0.0025;\ \beta = 0.006321, R_0 = 0.023;\ \beta = 0.06321, R_0 = 0.2994$) without controls.

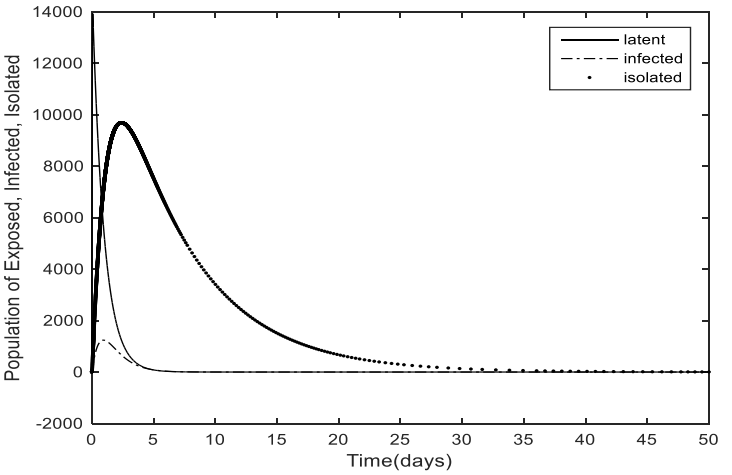

Figure 4: Graph of exposed, infected and isolated individuals with COVID-19 with controls ($(\varepsilon_1 = 0.9,\ \varepsilon_2 = 0.8,\ \varepsilon_3 = 0.9, R_0 = 0.13206)$. Other parameter values are as stated in Table 2

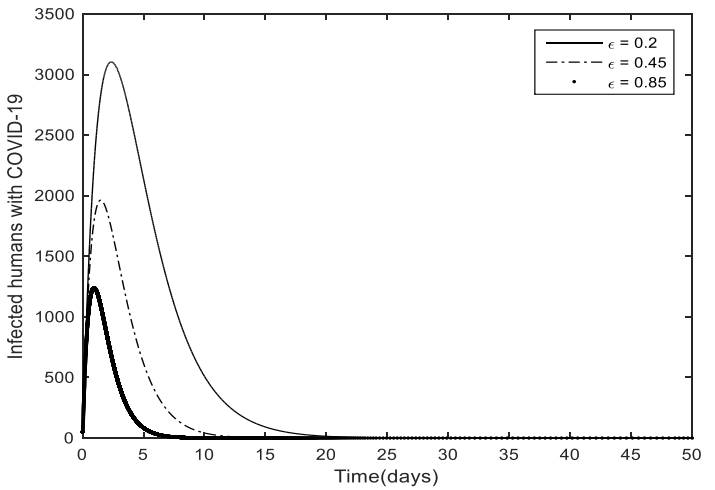

Figure 5: Effect of isolation of individuals with COVID-19. ($\varepsilon = 0.2, R_0 = 0.8414$; $\varepsilon = 0.45, R_0 = 0.3342$; $\varepsilon = 0.85, R_0 = 0.1320$). Other parameter values are given in Table 2.

5 Discussion on the Numerical Results

We presented a deterministic model for COVID-19 incorporating social distancing and isolation of exposed and infected individuals. The results are analytical and numerical.

The theoretical analysis showed there exists a region where the model

is epidemiological meaningful and mathematically well-posed. The COVID-19 model has a globally asymptotically stable (GAS) disease-free equilibrium (DFE) whenever the basic reproduction number, R_0, is less than unity. The basic reproduction number, given by $R_0 = \frac{\beta\sigma}{(\sigma+\varepsilon_2)(\gamma+d+\varepsilon_3)}$ is an epidemic threshold which determines whether the disease can spread or not. For $R_0 < 1$, the disease cannot invade the population but for $R_0 > 1$, the disease can spread.

The numerical results are based on the numerical simulations presented in Figure 2 to Figure 5.

Figure 2 reveals an increasing prevalence of COVID-19 without control strategies. It was observed that the infection increased to about 45% of the population within 5-10 days of the outbreak. Also, Lemma 1, with $R_0 = 2.993 > 0$ shows that infection persists in the population without control measures.

Figure 3 shows the increasing prevalence of COVID-19 with increasing infection transmission rates ($\beta = 0.000831;\ 0.00631;\ 0.0631$) in the absence of control strategies. With the basic reproduction number, $R_0 = 0.0025; 0.023; 0.2994 < 1$ in each case, shows the convergence of the solution profile to the disease-free equilibrium (DFE), consistent with Lemma 1 and Theorem 1. Thus for an effective preventive strategy (such as using prophylaxis, hand sanitiser), effort should reduce the infection transmission rate.

In Figure 4, it was observed that infected humans would decline few days after infection when control strategies are applied. With the basic reproduction number, $R_0 = 0.13206$, the solution profile converges to the disease-free equilibrium.

Figure 5 shows a decreasing prevalence of COVID-19 infection with an increasing isolation rate ($\varepsilon = 0.2, 0.45, 0.85$) and social distancing. Thus an effective combination of isolation of infected individuals and social distancing as control strategies is essential for control and eradication of COVID-19.

6. Conclusion

A deterministic model for COVID-19 incorporating social distancing and isolation of exposed and infectious individuals as control strategies is presented and analysed. The study shows the following:

1. The disease-free equilibrium of the COVID-19 model is shown to be globally asymptotically stable whenever the basic reproduction number is less than unity.
2. The study's findings suggest that an optimum combination of isolation and social distancing is the most

effective strategy for the COVID 19 pandemic.

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