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OPTIMAL CONTROL OF A NEW CORONA VIRUS MODEL

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Abstract. This study proposes a corona pandemic model that incorporates both reported and unreported cases of virus to be more realistic. In addition, it is advised to employ both preventive measures: vaccination and treatment and applied them at the simultaneously. The optimal controls were characterized with the maximum Pontryagin principle. Finally, the results of the numerical simulations demonstrate the utility of the proposed control mechanisms and this modeling.

Keywords: optimal control; mathematical model; COVID-19; the third dose-corona vaccine.

2020 AMS Subject Classification: 92D30.

1. INTRODUCTION

Nowadays, the term of "COVID19" in the majority of the world's population causes if not panic, at least alarm. In the memory of human beings inhabiting the earth today, there have been various cataclysms, natural disasters and epidemics, but this is the first time humanity has encountered a pandemic of this scale. However, the corona viruses are nothing new for virologists as their characteristics, descriptions and features have long been known to specialists. Nevertheless, this particular strain causing COVID19 has certain differences.

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Corona-viruses are a fairly large list of viruses that can cause an infectious process after entering sensitive human cells, with a wide range of respiratory syndromes of varying severity [1]. They got their name because of the characteristic appearance of the virus particle in electron microscopy-protein spikes frame the virus particle like teeth in a crown. The team of researchers revealed that the genome of the virus isolated from a group of patients with SARS after visiting Wuhan is 89% identical to the bat virus (SARS-like coronavirus isolate bat-SL-CoVZXC21) and 82% to the human virus (SARS-CoV) the epidemic of which occurred in 2002-2004. For this reason, the virus is called SARS-CoV-2. Moreover, the genome of the virus coincides by 96% with the genome of the RaTG13 bat virus [2, 3].

SARS-CoV was not the first coronavirus, it was firstly seen in 1937 as IBV (the avian infectious bronchitis virus) which still causes a lot of trouble for poultry farmers: for example, in an unvaccinated flock of domestic chickens, absolutely all birds get sick, and the mortality rate can reach 60% [4]. 10 years after IBV a second coronavirus was discovered MHZ (the mouse hepatitis virus), and human coronavirus were discovered in the mid-60s of the XX century, yet it has not take so much attention, until the beginning of the XXI century when coronavirus SARS occurred [5, 6]. Coronaviruses come to humans from animals: the 2002-2003 SARS-CoV came from horsehoe bats from which it jumped to musanga, or Malay palm marten, and from musanga to humans [7]. The next wave of coronavirus cases hit the world in 2012, this time it was MERS (Middle East respiratory syndrome). The source of infection was one-humped camels (dromedaries). There were not so many infected people, but the infection turned out to be much more deadly than “SARS”, 40% of those infected died [8]. The first human to human transmission was proven in France by the French Ministry of Social Affairs and Health in 2013. Two years later an outbreak of (MERS-CoV) occurred in South Korea, the virus was introduced by a citizen of the country who returned from the Middle East [9].

The Chinese government reported the first cases of “pneumonia of unknown etiology” in Wuhan on December 31, 2019, but the virus appeared in China a few weeks earlier. In January, the number of cases of infection in China began to increase rapidly, the country imposed quarantine in several major cities. In parallel, the virus began to spread first in different parts

of region (Chinese special administrative regions Hong Kong and Macao, Taiwan, Japan, Korea, Singapore), then the first cases were found in the United States, Australia and Europe (in France, Italy, and Spain). At this point 12 zones were infected with high rates of infection transmission. It has been several weeks since Europe became the epicenter of the epidemic. In this regard, WHO declares a global public health emergency and the number of infected zones keeps increasing and global outbreaks began as Italy, Iran and South Korea see high rates of virus. In 2020 many countries have been infected with the COVID such Kuwait and Bahrain. Hence, on March 11, 2020 the WHO declares the outbreak as a pandemic [10].

Approximately 3 million confirmed infected cases of COVID-19 have been reported across the globe as of late April, 2020 ("COVID-19 Map" 19). Nevertheless, it is assumed that many infections still unreported because of either mildness of symptoms or inexact testing [11]. In April 2, 2020. The (WHO) cited 1.016.128 reported cases of COVID-19 internationally, containing 245175 (6059 died) in USA, 115242 (13915 died) in Italy, 112065 (10348 died) in Spain, 84789 (1109 died) in Germany, 81620 cases (3322 died) in China, 58441 (5380 died) in France, 50468 (3160 died) from Iran, 33718 (2921 died) in the United Kingdom, while the rest of infected cases and moralities belong to 200 other countries. 13 countries measured more than 10000 cases while 38 countries claimed between 1000 and 10000 confirmed cases [12]. On the other hand, the unreported cases are unknown. Thus, a mathematical model was presented in [13] based on reported medical data that helps to give predictions in South Korea, Italy, France and Germany. Then the method was developed in [14]using data generated from the second phase of the epidemic in which it grows exponentially to predict the forward time-line of the epidemic in China, South Korea, Italy, France, Germany and United Kingdom.

Each type of infection takes a certain amount of time to gain a foothold in the body. After that, infectious cells begin to multiply and spread in the human body through the blood, affecting vital organs. In SARS-CoV-2, the incubation period takes an average of 5-6 day, and sometimes it takes up to 14 days. For this reason, most doctors recommend that infected patients go into a two-week quarantine. However, the corona infection is constantly mutating, and it has yet to be studied in detail. The duration of incubation does not always correspond to the norm defined by doctors. Hence there are known cases of such periods: minimum 2 days and maximum 27

days depending on two criteria as the body's defenses and the received dose of SARS-CoV-2 [15, 16].

At an early stage, the symptoms of coronavirus are often similar to the main signs of allergies, flu, colds and some other diseases, specially if COVID is mild. Hence, in order to differentiate between the two diseases, patients should pay attention to the duration of the manifestation of these features. If they do not go away for a long time, it is possible that the person is infected with coronavirus [17]. The COVID-19 common symptoms include: high temperature, fatigue, dry cough while other symptoms contain shortness of breath, sore throat, loss of appetite, muscle pain and very few people report diarrhea, nausea, or a runny nose [18]. The transmission factors include air, dust, household items, and food contaminated with the virus. The closer the contact between a healthy person and an infected one, the higher the probability of transmission of infection; thus, medical workers are more likely to get high infection [19].

After the first wave of coronavirus in China, a detailed review of cases from the beginning of the epidemic has appeared. According to the data provided in it, the age groups from 0 to 10 and from 10 to 19 years account for only 1% each. This means that COVID spares the younger generation. The disease occurs in them mostly in a mild form with corresponding symptoms. Some experts believe that the virus is not very dangerous for children. For instance, as of December 2020, there are no known cases of pneumonia or lung damage in a child associated with COVID. However, older people and those who have serious medical problems such as heart disease, diabetes, chronic respiratory diseases, and cancer are more likely to develop serious illness [20, 21].

SARS-CoV-2 has the capacity to escape innate immune responses, as a consequence large copy numbers are produced by the virus in the infected tissues. Treatment of COVID is symptomatic, and the first step to solve the issue of respiratory failure is oxygen therapy. Non-invasive (NIV) and invasive mechanical ventilation (IMV) of the lungs are required in cases of respiratory failure resistant to oxygen therapy. Unfortunately, there is no specific antiviral treatment recommended for this epidemic, yet, there are a number of antiviral drugs used at different stages of the disease [22]; (Hydroxy-)Chloroquine considered as antimalarials, beside

hydroxychloroquine which is utilized as immunomodulatory agent in systemic lupus erythematosus. However, the largest study in [23] approved that hydroxychloroquine on its own or in combination with azithromycin have no crucial influence on patients. Nucleoside analogues are explored as treatment options for COVID-19, preclinical studies have shown that remdesivir an RNA polymerase inhibitor against several RNA viruses as Ebola could be effective for both the prevention and treatment [24, 25]. It was used successfully in January 2020 in a COVID-19 patient. Since, remdesivir has been utilized on a compassionate use basis [26]. There are also Protease inhibitors combining lopinavir and ritonavir which is used in antiretroviral treatment for HIV and suggested for COVID19 infections [27]. Recombinant soluble ACE2 As ACE2 which could prevent inflammation and tissue damage [28]. Another treatment is the convalescent plasma collected from patients who have recovered from an infection, anecdotal application in MERS, SARS, Ebola and Influenza infections supports its use as a neutralizing and immunomodulatory agent [29].

So far, people do not have innate or acquired immunity to the new type of coronavirus SARS-CoV-2, thus, all people on the planet are susceptible to the disease. Mass vaccination has demonstrated its effectiveness in reducing COVID-19 infections among vaccinated groups. Although, preventing vaccinated people from spreading the virus to their household members and close contacts remains open to question. Hypothetically, if a 70 to 80% of people get vaccinated and resistant to COVID-19, herd immunity established conceivably to cease the rest of unvaccinated population from SARS-CoV-2 infection. This theory has been experimentally confirmed in [30]. Various studies have been performed to evaluate Vaccine Effectiveness worldwide: vaccines against SARS-CoV-2 have been expanding extensively through divers technical routes, along with the traditional inactivated vaccine, DNA vaccine, viral vector vaccine, mRNA vaccine, and recombinant protein vaccine. Among studies that have been effectuated to prove the Vaccine Effectiveness of heterologous prime booster vaccination is made in Brazil, exploiting an inactivated vaccine and an mRNA vaccine booster. Results have shown that VE of the two-dose regimen resistant to either infection or severe outcomes declined for all ages; whereas, vaccine-induced antibodies enhanced remarkably when an mRNA booster dose fulfilled the two-dose of inactivated vaccine [31]

However, the cross-protection of new current vaccines resistant to emerging COVID-19 variants has been considered as the recent global concern; SARS-CoV-2 accumulates mutations at about the same rate as the causative agent of influenza, with new characteristics as rapid transmission, virulence, and immune escape. The strain of Alpha variant detected in South-Eastern England in September 2020, characterized by its upraised transmissibility, beside preliminary studies that suggest an increase in mortality. Mechanistic demonstration correlate this high transmission characteristic with higher nasopharyngeal viral load combined with lengthened viral shedding; howbeit, Monel et al asserts that alpha variant does not develop neither viral RNA content nor lengthened viral shedding [32]. The delta variant, because of several mutations, turned out to be the most contagious and caused the rise of a new wave of COVID-19. The first discovery of delta strain was in October 2020 in India, and by the beginning of July 2021, WHO recorded the delta strain in 98 countries [33]. The last contagious variant of SARS-CoV2 appeared at the end of 2021 in southern Africa. The Omicron variant differed from previous strains by a huge number of mutations and it quickly spread around the planet. The organization of this paper is as follows. In Sect. 2, we formulate the optimal control problem and we use the Pontryagin's Maximum principle w to characterize it. In Sect. 3, we give the numerical method and the simulation results. Finally, we draw conclusions in Sect. 4.

2. Presentation of the Model

We are proposing a new S, I, I_r, I_u, R, D model, that will allow us without controls to divide the population total into six categories:

S : is the number of individuals susceptible to virus infection at a specific time t;

I: is the number of asymptomatic infectious individuals at a specific time t;

I_r: is the number of reported symptomatic infectious individuals (i.e., ,symptomatic infectious showing severe symptoms) at a specific time t;

I_u: is the number of unreported symptomatic infectious individuals (i.e., symptomatic infectious with mild symptoms) at time t;

R: Recovered, which means, individuals who were previously infected and treated.

D: is the number of individuals deceased due to an infection at a specific time t;

Individuals in the asymptomatic infected compartment that can spread the coronavirus with

transmission rate β while being in contact with susceptibles which can transformed into an active disease with symptomatic infections at a rate α but on two categories: the symptomatic infectious with severe symptoms and with mild symptoms, the first with rate α_r and the second with rate α_u . Treatment of the reported symptomatic infectious individuals at rate ν_r which represent the rate of recovery is fixed at $1/21\text{day}^{-1}$, corresponding to an average duration of infection of 21 day, the immunity for unreported symptomatic infectious (though here it also accounts for the infrequent natural recovery) at rate τu that represents the rate of recovery. Unfortunately, the recovered individuals can revert back to susceptible class at rate ρ. The total of population N, in this model is not assumed to be constant, so the logistic growth that systems grow exponentially until the inherent carrying capacity of the system is approached, at which time the rate of growth slows and eventually saturates.

Therefore we obtain the following system

$$
(1)\qquad \begin{cases}
S(t+1) = S(t) + r\left(1-\frac{N(t)}{K}\right)N(t) - \frac{\beta S(t)I(t)}{N(t)} - \frac{\beta_U S(t)I_U(t)}{N(t)} - \mu S(t) + \rho R(t), \\
I(t+1) = I(t) + \frac{\beta S(t)I(t)}{N(t)} + \frac{\beta_U S(t)I_u(t)}{N} - \alpha I(t) - \mu I(t), \\
I_r(t+1) = I_r(t) + \alpha_r I(t) - \tau_r I_r(t) - (\mu+\delta_r) I_r(t) \\
I_u(t+1) = I_u(t) + \alpha_u I(t) - \tau_U I_u(t) - (\mu+\delta_u) I_u(t) \\
R(t+1) = R(t) + \tau_r I_r(t) + \tau_u I_u(t) - \mu R(t) - \rho R(t). \\
D(t+1) = D(t) + \delta_r I_r(t) + \delta_u I_u(t).
\end{cases}
$$

$t \in \{0,\cdots,T-1\}$, $S(0) \geq 0, I(0) \geq 0, I_r(0) \geq 0, I_u(0) \geq 0, R(0) \geq 0$ and $D(0) \geq 0$ are the given initial states. The meanings of the parameters considered in the model is given in Tab. 1 .

TABLE 1. **The meanings of the parameters considered in the model**

Paramter	Meaning
β	Transmission rate due to asymptomatic infection I
β_u	Transmission rate due to unreported infectious I_u
r	Natural birth rate constant
K	Loading capacity
μ	Natural death rate
δ_r	Mortality rate due to asymptomatic infections I
δ_u	Mortality rate due to unreported symptomatic infected I_u
α_r	Rate at which asymptomatic infecteds become overtly symptomatic
α_u	Rate at which asymptomatic infectees become unreported symptomatic
f	Fraction of asymptomatic infectious who become symptomatically infectious
τ_r	Recovery rates for inpatients
τ_u	Outpatient recovery rate
ρ	Rate at which recovered individuals lose their immunity and return to the susceptible class
N	Total number of population

3. THE OPTIMAL CONTROL PROBLEM

3.1. Presentation of the controls. The model includes control variables representing treatment and vaccination measures, which are continuously implemented during a considered period of disease treatment: We now consider the Coronavirus model and introduce tow control functions v and u our goal is reducing the number of susceptible individuals S and infected individuals I_r during the times steps $t = 0$ to T and also minimizing the the cost of treatment. Then, the controlled discrete time mathematical model is given as follows.

$$
(2)\quad \begin{cases}
S(t+1) = S(t) + r\left(1 - \frac{N(t)}{K}\right)N(t) - \frac{\beta}{N(t)}S(t)I(t) - \frac{\beta_u}{N(t)}S(t)I_u(t) + \rho R(t) - (v(t)+\mu)S(t) \\
I(t+1) = I(t) + \frac{\beta S(t)I(t)}{N(t)} + \frac{\beta_u S(t)I_u(t)}{N(t)} - (\alpha+\mu)I(t)\Big) \\
I_r(t+1) = I_r(t) + \alpha_r I(t) - \tau_r I_r(t) - (u(t)+\mu+\delta_r)I_r(t) \\
I_u(t+1) = I_u(t) + \alpha_u I(t) - (\tau_u+\mu+\delta_u)I_u(t) \\
R(t+1) = R(t) + \tau_r I_r(t) + \tau_u I_u(t) + v(t)S(t) + u(t)Ir(t) + (\rho-\mu)R(t). \\
D(t+1) = D(t) + \delta_r I_r(t) + \delta_u I_u(t).
\end{cases}
$$

with $t \in \{0, \cdots, T-1\}$, $S(0) \geq 0, I(0) \geq 0, I_r(0) \geq 0, I_u(0) \geq 0, R(0) \geq 0$ and $D(0) \geq 0$ are the given initial states.

3.2. Objective Functional. Our plan is to reduce the number of unvaccinated patients with three doses and maximize the number of recovered patients with minimal cost. Therefore, the problem is to minimize the objective functional given by

$$J(u,v) = AS(T) + FI_r(T) - BR(T) + \sum_{t=0}^{T-1} \left(AS(t) + FI_r(t) - BR(t) + \frac{1}{2}Cv^2(t) + \frac{1}{2}Eu^2(t) \right) \tag{3}$$

where A, B, F are positive parameters and $C > 0$, $E > 0$ are the weight constants of the controls, $u = (u_0, \cdots, u_{T-1})$,$v = (v_0, \cdots, v_{T-1})$ and T is the final time of our control strategy. Our goal is to minimize the number of susceptible individuals and the number of reported infected I_r, minimizing the cost of implementing controls and increasing the number of recovered individuals. This means that we are searching for optimal controls u^* and v^* such that

$$J(u^*, v^*) = min\{J(u,v)/u \in \mathscr{U}, v \in \mathscr{V}\} \tag{4}$$

where $\mathscr{U}$ and $\mathscr{V}$ are the control sets defined by

$$\mathscr{U} = \{u/U_{\min} \leq u(i) \leq U_{\max}, i = 0, ..., T-1\} \tag{5}$$

$$\mathscr{V} = \{v/V_{\min} \leq v(i) \leq V_{\max}, i = 0, ..., T-1\} \tag{6}$$

3.3. Sufficient conditions. The sufficient condition of existence of an optimal control (u^*, v^*) for the problem (2) and (4) is derived from the following theorem.

Theorem 1. *There exists an optimal control $(u^*, v^*) \in \mathscr{U} \times \mathscr{V}$ such that*

$$J(u^*, v^*) = min\{J(u,v)/u \in \mathscr{U}, v \in \mathscr{V}\}$$

subjected to the control system 2 with initial conditions.

Proof. Given that the parameters of the system are bounded and there exist a finite number of time steps, S, I, I_r, I_u, R and D are uniformly bounded for any (u,v) in the control set $\mathscr{U} \times \mathscr{V}$, so $J(u,v)$ is also bounded for any $(u,v) \in \mathscr{U} \times \mathscr{V}$. This implies that $\inf_{(u,v)\in\mathscr{U}\times\mathscr{V}} J(u,v)$ is finite, and there exists a sequence $(u^n, v^n) \in \mathscr{U} \times \mathscr{V}$ such as that

$$\lim_{n\to+\infty} J(u^n,v^n) = \inf_{(u,v)\in\mathscr{U}\times\mathscr{V}} J(u,v)$$

and corresponding sequences of states S,I,I_r,I_u,R and D . Since there is a finite number of uniformly bounded sequences, then there exists $(u^*,v^*)\in\mathscr{U}\times\mathscr{V}$ and S^*,I^*,I_r^* ,I_u^* and R^* such as, over a sequence $(u^n,v^n)\to(u^*,v^*)$, $S^n\to S^*$, $I^n\to I^*$, $I_r^n\to I_r^*$, $I_r^n\to I_u^*$, $R^n\to R^*$ and $D^n\to D^*$. Finally, as a result of the finite dimensional structure of the system 2 and the objective function $J(u,v)$, we obtain that (u^*,v^*) is an optimal control with corresponding statesS^*, I^*, I_r^* ,I_u^* and R^*. Which complete the proof.

□

3.4. Necessary conditions. We now have the Hamiltonian H in time step t, given by

(7)

$$\begin{aligned}
H(t) =& AS(t)+Fl(t)-BR(t)+\frac{1}{2}Cv^2(t)+\frac{1}{2}Eu^2(t)\\
&+\lambda_{1,t+1}\left[S(t)+r\left(1-\frac{N(t)}{K}\right)N(t)-\frac{S(t)}{N(t)}\left(\beta l(t)+\beta_u I_u(t)\right)+\rho R(t)-\left(v(t)+\mu S(t)\right)\right]\\
&+\lambda_{2,t+1}\left[l(t)+\frac{S(t)}{N(t)}\left(\beta l(t)+\beta_u I_u(t)\right)-(\alpha+\mu)I(t))\right]\\
&+\lambda_{3,t+1}\left[I_r(t)+\alpha_r l(t)-\tau_r I_r(t)-\left(u(t)+\mu+\delta_r\right)I_r(t)\right]\\
&+\lambda_{4,t+1}\left[I_u(t)+\alpha_u I(t)-\left(\tau_u+\mu+\delta_u\right)I_u(t)\right]\\
&+\lambda_{5,t+1}\left[R(t)+\tau_r I_r(t)+\tau_u I_u(t)+v(t)S(t)+u(t)I_r(t)+(\rho-\mu)R(t)\right]\\
&+\lambda_{6,t+1}\left[D(t)+\delta_r I_r(t)+\delta_u I_u(t)\right]
\end{aligned}$$

Theorem 2. *Given optimal controls u^*, v^* and solutions S^*,E^*,T^*,P^*,J^*,K^* ,$R^*,Y^*$and W^* of corresponding state system 2, there exists ζ_i^j, $i=0...N-1$, $j=1,2,\cdots,9$, the adjoint variables that satisfy the following equations*

$$\begin{aligned}
\lambda_{1,t} =& A+\left(1-\mu+r-2\frac{r}{K}N(t)\right)\lambda_{1,t+1}+\frac{1}{N(t)^2}\left(N(t)-S(t)\right)\left(\beta I(t)+\beta_u I_u(t)\right)\\
&\left(\lambda_{2,t+1}-\lambda_{1,t+1}\right)+v(t)\left(\lambda_{5,t+1}-\lambda_{1,t+1}\right)\\
\lambda_{2,t} =& F+(1-\mu)\lambda_{2,t+1}+\frac{1}{N(t)^2}\left(\beta S(t)\left(N(t)-I(t)\right)-\beta_u S(t)I_u(t)\right)\left(\lambda_{2,t+1}-\lambda_{1,t+1}\right)\\
&+\alpha_r\left(\lambda_{3,t+1}-\lambda_{2,t+1}\right)+\alpha_u\left(\lambda_{4,t+1}-\lambda_{2,t+1}\right)+\left(r-2\frac{r}{K}N(t)\right)\lambda_{1,t+1}
\end{aligned}$$

$$\lambda_{3,t} = (1-\mu-\delta_r)\,\lambda_{3,t+1} + \left(\tau_r + u(t)\left(\lambda_{5,t+1}-\lambda_{3,t+1}\right) + \left(r - 2\frac{r}{K}N(t)\right)\lambda_{1,t+1}\right.$$

$$\lambda_{4,t} = (1-\mu-\delta_u)\,\lambda_{4,t+1} + \frac{1}{N(t)^2}\left(\beta_u S(t)N(t) - I_u(t) - \beta_u S(t) I_u(t)\right)\left(\lambda_{2,t+1}-\lambda_{1,t+1}\right)$$
$$+ \tau_u\left(\lambda_{5,t+1}-\lambda_{4,t+1}\right) + \left(r - 2\frac{r}{K}N(t)\right)\lambda_{1,t+1}$$

$$\lambda_{5,t} = -B + (1-\mu)\lambda_{5,t+1} + \rho\left(\lambda_{1,t+1}-\lambda_{5,t+1}\right) + \left(r - 2\frac{r}{K}N(t)\right)\lambda_{1,t+1}$$

$$\lambda_{6,t} = \lambda_{6,t+1} + \left(r - 2\frac{r}{K}N(t)\right)\lambda_{1,t+1}.$$

with the conditions of transversality at time N

$$\lambda_1(T) = A, \lambda_2(T) = F, \lambda_3(T) = 0, \lambda_4(T) = 0 \quad \lambda_5(T) = -B, \text{ and } \lambda_6(T) = 0$$

In addition, for $i = 0, 1, \cdots, T-1$ *we obtain the optimal control* (u^*, v^*) *as*

$$\begin{aligned} \mathrm{u}^*(t) &= \min\left[U_{\max}, \max\left(U_{\min}, \frac{1}{E}\left(\lambda_{3,t+1}-\lambda_{5,t+1}\right) I_r(t)\right)\right] \\ \mathrm{v}^*(t) &= \min\left[V_{\max}, \max\left(V_{\min}, \frac{1}{C}\left(\lambda_{1,t+1}-\lambda_{5,t+1}\right) S(t)\right)\right] \end{aligned} \tag{8}$$

Proof. The Hamiltonian H_i at time step t is obtained by 7. For $t = 0, \cdots, N-1$, the adjoint equations and transversality conditions can be derived by using the discrete-time Pontryagin maximum principle given in [34, 35, 36] as follows

$$\begin{aligned} \Delta\lambda_{1,t} &= \frac{\partial H(t)}{\partial S(t)}, & \lambda_{1,T} &= A \\ \Delta\lambda_{2,t} &= \frac{\partial H(t)}{\partial I(t)}, & \lambda_{2,T} &= F \\ \Delta\lambda_{3,t} &= \frac{\partial H(t)}{\partial I_r(t)}, & \lambda_{3,T} &= 0 \\ \Delta\lambda_{4,t} &= \frac{\partial H(t)}{\partial I_u(t)}, & \lambda_{4,T} &= 0 \\ \Delta\lambda_{5,t} &= \frac{\partial H(t)}{\partial R(t)}, & \lambda_{5,T} &= -B \\ \Delta\lambda_{6,t} &= \frac{\partial H(t)}{\partial D(t)}, & \lambda_{6,T} &= 0 \end{aligned}$$

For $i = 0, \cdots, N-1$, the optimal controls (u^*, v^*) can be determined from the optimality conditions

$$\begin{cases} \frac{\partial H(t)}{\partial v(t)} = Cv(t) - S(t)\lambda_{1,t+1} + S(t)\lambda_{5,t+1} = 0 \\ \frac{\partial H(t)}{\partial u(t)} = Eu(t) - I_r(t)\lambda_{3,t+1} + I_r(t)\lambda_{5,t+1} = 0 \end{cases}$$

thus, we obtain

$$u(t) = \frac{1}{E}\left(\lambda_{3,t+1} - \lambda_{5,t+1}\right) I_r(t)$$
$$v(t) = \frac{1}{C}\left(\lambda_{1,t+1} - \lambda_{5,t+1}\right) S(t) \tag{9}$$

By the bounds in $\mathscr{U}$ *and* $\mathscr{V}$ of the controls, it is simple to obtain u and v in the form of 8. □

4. Numerical Simulation and Discussion

In this section we present numerical simulations for the optimization problem given above. Writing the program in MATLAB, we simulate the work using different data. The optimization systems are solved using a discrete iterative process that converges after an appropriate test similar to FBSM. First, the state system is solved with the initial assumption forward in time, and then the adjoint system is solved backward in time due to the transversality conditions. Next, we update our optimal control values with the state and co-state resources that were derived in the previous steps. Finally, we run the previous steps until the standard tolerance is reached.

4.1. Strategy one: Vaccination.

We use only optimum control $v(t)$.

This control strategy, which is based on vaccinating the susceptible population with many vaccines, has demonstrated a remarkable efficiency in reducing the number of cases that have been reported and the numbers of deaths caused by the disease, as shown in Figures (1) and (3).

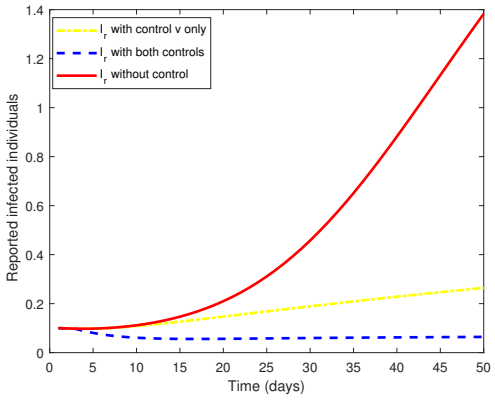

FIGURE 1. Reported infected individuals with and without the control v

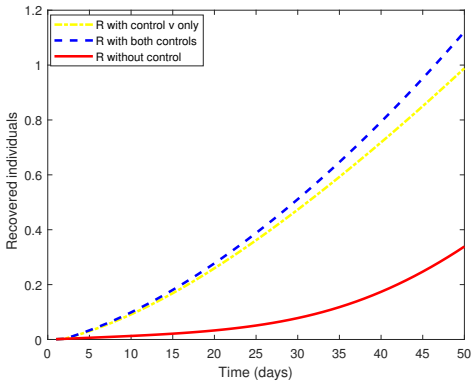

FIGURE 2. Recovered individuals with and without the control v

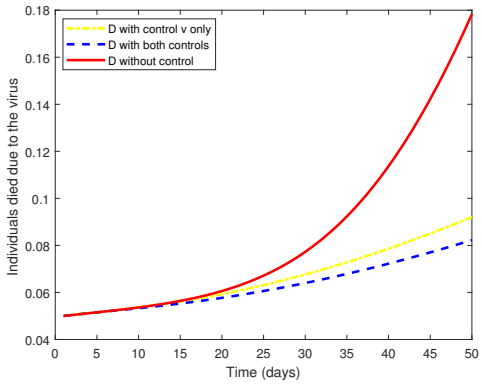

FIGURE 3. Individuals died due to the virus with and without the control v

4.2. Strategy two: Treatment. We use only optimum control $u(t)$.

According to figure (5) , this control technique has demonstrated a remarkable efficiency in increasing the number of recovered individuals, and according to figures (4) and (6), this strategy has decreased the number of reported infected individuals and the numbers of deaths caused by the virus. This technique is based on the treatment of reported infected individuals with health problems due to the corona virus.

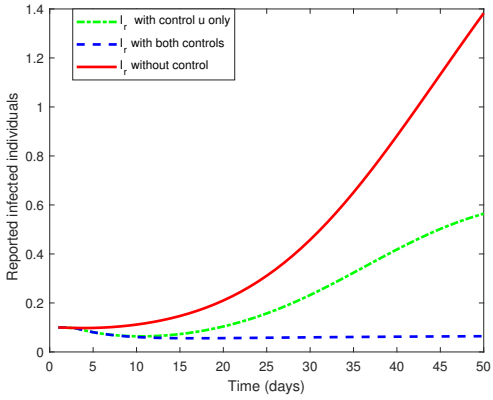

FIGURE 4. Reported infected individuals with and without the control u

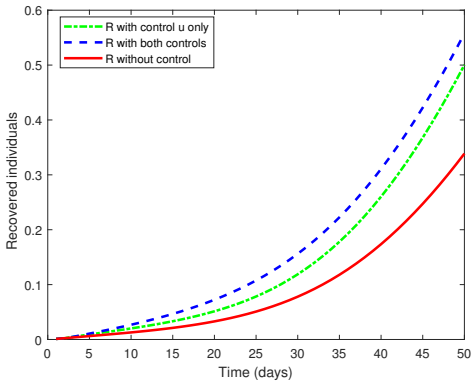

FIGURE 5. Recovered individuals with and without the control u

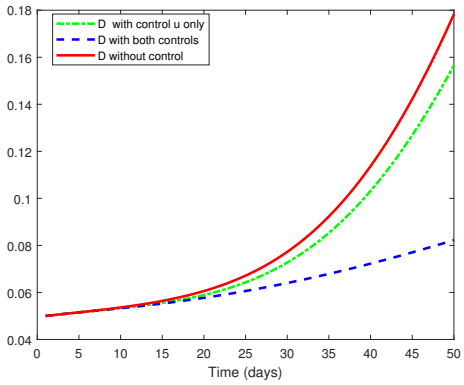

FIGURE 6. Individuals died due to the virus with and without the control u

4.3. Strategy three:Awareness of the importance vaccination and treatment. We combine the optimal controls $u(t)$ and $v(t)$.

Our final technique is the simultaneous application of the previous two strategies, and it has produced good results. In fact, the number of infected individuals is significantly reduced in Figures (8), (10), and (9). Figure (11) shows a rise in recovered individuals, whereas Figure (12) shows a decline in disease outbreak deaths.

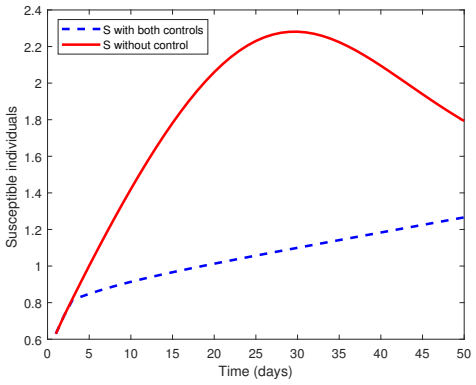

FIGURE 7. Susceptible individuals with and without both controls

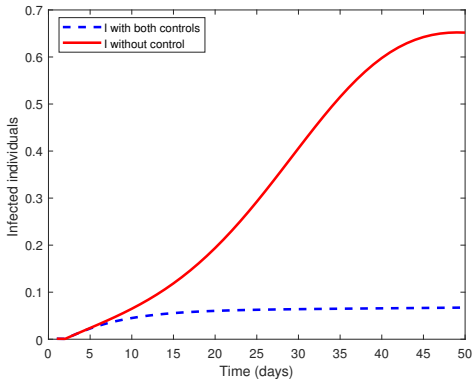

FIGURE 8. Infected individuals with and without both controls

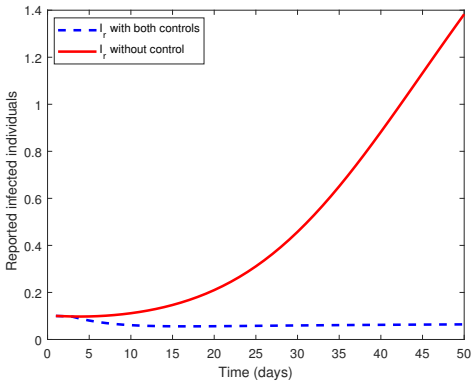

FIGURE 9. Reported infected individuals with and without both controls

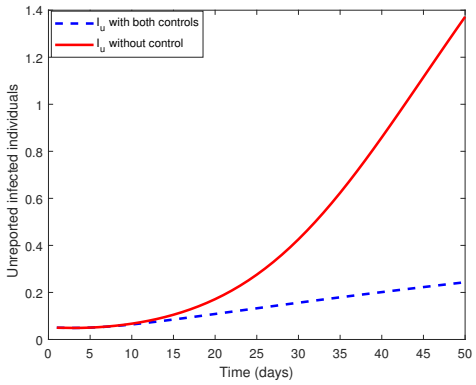

FIGURE 10. Unreported infected individuals with and without both controls

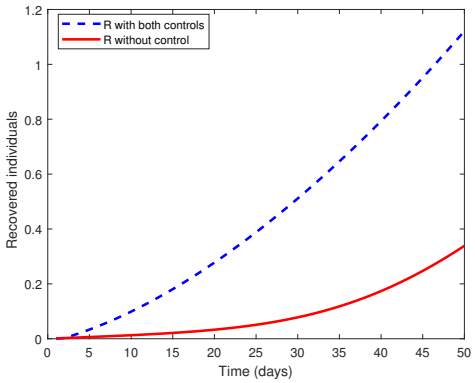

FIGURE 11. Recovered individuals with and without both controls

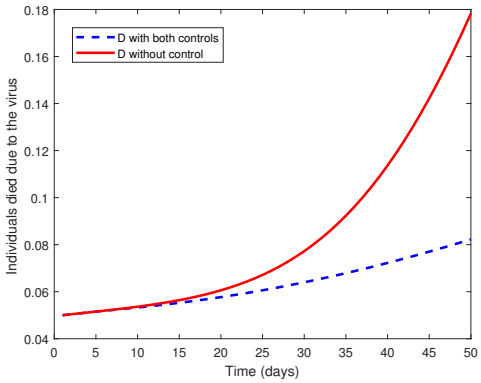

FIGURE 12. Individuals died due to the virus with and without both controls

5. CONCLUSION

This article proposes a more realistic corona pandemic model that takes into account both reported and unreported cases of disease. Additionally, the simultaneous use of the two control strategies of vaccination and treatment is suggested. Finally, the results of the numerical simulations supported the previous theoretical findings.

CONFLICT OF INTERESTS

The authors declare that there is no conflict of interests.

REFERENCES

[1] N.N. Chathappady House, S. Palissery, H. Sebastian, Corona viruses: A review on SARS, MERS and COVID-19, Microbiol. Insights. 14 (2021), 117863612110024. https://doi.org/10.1177/117863612110 02481.

[2] K. Dhama, S. Khan, R. Tiwari, et al. Coronavirus disease 2019–COVID-19, Clin. Microbiol. Rev. 33 (2020), e00028-20. https://doi.org/10.1128/cmr.00028-20.

[3] W. Zhang, Covid-19: from basics to clinical practice, World Scientific Publishing, Hackensack, 2020.

[4] F. Awad, R. Chhabra, M. Baylis, K. Ganapathy, An overview of infectious bronchitis virus in chickens, World's Poultry Sci. J. 70 (2014), 375–384. https://doi.org/10.1017/s0043933914000385.

[5] V. Saceleanu, M.S. Moreanu, R.A. Covache-Busuioc, et al. SARS-COV-2 – the pandemic of the XXI century, clinical manifestations - neurological implications, J. Med. Life. 15 (2022), 319–327. https://doi.org/10.251 22/jml-2020-0151.

[6] S.C. Keane, D.P. Giedroc, Solution structure of mouse hepatitis virus (MHV) nsp3a and determinants of the interaction with MHV nucleocapsid (N) protein, J. Virol. 87 (2013), 3502–3515. https://doi.org/10.1128/jvi. 03112-12.

[7] A. Zeidler, T.M. Karpinski, SARS-CoV, MERS-CoV, SARS-CoV-2 comparison of three emerging coronaviruses, Jundishapur J. Microbiol. 13 (2020), e103744. https://doi.org/10.5812/jjm.103744.

[8] E.I. Azhar, D.S.C. Hui, Z.A. Memish, et al. The middle east respiratory syndrome (MERS), Infect. Dis. Clinics North Amer. 33 (2019), 891–905. https://doi.org/10.1016/j.idc.2019.08.001.

[9] S.Y. Cho, J.M. Kang, Y.E. Ha, et al. MERS-CoV outbreak following a single patient exposure in an emergency room in South Korea: an epidemiological outbreak study, The Lancet. 388 (2016), 994–1001. https://doi.org/10.1016/s0140-6736(16)30623-7.

[10] R.S. Sneed, K. Key, S. Bailey, et al. Social and psychological consequences of the COVID-19 pandemic in African-American communities: Lessons from Michigan, Psychol. Trauma: Theory Res. Pract. Policy. 12 (2020), 446–448. https://doi.org/10.1037/tra0000881.

[11] C.C. Chow, J.C. Chang, R.C. Gerkin, et al. Global prediction of unreported SARS-CoV2 infection from observed COVID-19 cases, MedRxiv. (2020). https://doi.org/10.1101/2020.04.29.20083485.

[12] I. Madabhavi, M. Sarkar, N. Kadakol, COVID-19: A review, Monaldi Arch. Chest Dis. 90 (2020), 1298. https://doi.org/10.4081/monaldi.2020.1298.

[13] Z. Liu, P. Magal, O. Seydi, et al. Understanding unreported cases in the COVID-19 epidemic outbreak in Wuhan, China, and the importance of major public health interventions, Biology. 9 (2020), 50. https://doi.or g/10.3390/biology9030050.

[14] Z. Liu, P. Magal, G. Webb, Predicting the number of reported and unreported cases for the COVID-19 epidemics in China, South Korea, Italy, France, Germany and United Kingdom, J. Theor. Biol. 509 (2021), 110501. https://doi.org/10.1016/j.jtbi.2020.110501.

[15] C. Leung, The difference in the incubation period of 2019 novel coronavirus (SARS-CoV-2) infection between travelers to Hubei and nontravelers: The need for a longer quarantine period, Infect. Control Hosp. Epidemiol. 41 (2020), 594–596. https://doi.org/10.1017/ice.2020.81.

[16] X. Jiang, S. Rayner, M. Luo, Does SARS-CoV-2 has a longer incubation period than SARS and MERS?, J. Med. Virol. 92 (2020), 476–478. https://doi.org/10.1002/jmv.25708.

[17] C.I. Paules, H.D. Marston, A.S. Fauci, Coronavirus infections-More than just the common cold, JAMA. 323 (2020), 707-708. https://doi.org/10.1001/jama.2020.0757.

[18] B.M. Clemency, R. Varughese, D.K. Scheafer, et al. Symptom criteria for COVID-19 testing of heath care workers, Acad. Emerg. Med. 27 (2020), 469–474. https://doi.org/10.1111/acem.14009.

[19] M. Delikhoon, M.I. Guzman, R. Nabizadeh, et al. Modes of transmission of severe acute respiratory syndrome-coronavirus-2 (SARS-CoV-2) and factors influencing on the airborne transmission: A review, Int. J. Environ. Res. Public Health. 18 (2021), 395. https://doi.org/10.3390/ijerph18020395.

[20] S. Rehman, T. Majeed, M.A. Ansari, et al. Current scenario of COVID-19 in pediatric age group and physiology of immune and thymus response, Saudi J. Biol. Sci. 27 (2020), 2567–2573. https://doi.org/10.1016/j.sjbs.2020.05.024.

[21] N.M. Mustafa, L. A Selim, Characterisation of COVID-19 pandemic in paediatric age group: A systematic review and meta-analysis, J. Clinic. Virol. 128 (2020), 104395. https://doi.org/10.1016/j.jcv.2020.104395.

[22] D. Popov, Treatment of COVID-19 infection. A rationale for current and future pharmacological approach, EC Pulmonol. Respir. Med. 9 (2020), 38-58.

[23] J. Magagnoli, S. Narendran, F. Pereira, et al. Outcomes of hydroxychloroquine usage in United States veterans hospitalized with COVID-19, Med. 1 (2020), 114-127.e3. https://doi.org/10.1016/j.medj.2020.06.001.

[24] D. Siegel, H.C. Hui, E. Doerffler, et al. Discovery and synthesis of a phosphoramidate prodrug of a pyrrolo[2,1-f][triazin-4-amino] adenine C-nucleoside (GS-5734) for the treatment of Ebola and emerging viruses, J. Med. Chem. 60 (2017), 1648–1661. https://doi.org/10.1021/acs.jmedchem.6b01594.

[25] M. Wang, R. Cao, L. Zhang, et al. Remdesivir and chloroquine effectively inhibit the recently emerged novel coronavirus (2019-nCoV) in vitro, Cell Res. 30 (2020), 269–271. https://doi.org/10.1038/s41422-020-0282-0.

[26] M.L. Holshue, C. DeBolt, S. Lindquist, et al. First case of 2019 novel coronavirus in the United States, N. Engl. J. Med. 382 (2020), 929–936. https://doi.org/10.1056/nejmoa2001191.

[27] J. Shuter, Lopinavir/ritonavir in the treatment of HIV-1 infection: a review, Therap. Clinic. Risk Manage. 4 (2008), 1023–1033. https://doi.org/10.2147/tcrm.s3285.

[28] D. Batlle, J. Wysocki, K. Satchell, Soluble angiotensin-converting enzyme 2: a potential approach for coronavirus infection therapy?, Clinic. Sci. 134 (2020), 543–545. https://doi.org/10.1042/cs20200163.

[29] J. Mair-Jenkins, M. Saavedra-Campos, J.K. Baillie, et al. The effectiveness of convalescent plasma and hyperimmune immunoglobulin for the treatment of severe acute respiratory infections of viral etiology: a systematic review and exploratory meta-analysis, J. Infect. Dis. 211 (2014), 80–90. https://doi.org/10.1093/infdis/jiu396.

[30] J. Salo, M. Hägg, M. Kortelainen, et al. The indirect effect of mRNA-based COVID-19 vaccination on healthcare workers' unvaccinated household members, Nat. Commun. 13 (2022), 1162. https://doi.org/10.1038/s41467-022-28825-4.

[31] T. Cerqueira-Silva, S.V. Katikireddi, V. de Araujo Oliveira, et al. Vaccine effectiveness of heterologous CoronaVac plus BNT162b2 in Brazil, Nat. Med. 28 (2022), 838–843. https://doi.org/10.1038/s41591-022-01701-w.

[32] W.S. Hart, E. Miller, N.J. Andrews, et al. Generation time of the alpha and delta SARS-CoV-2 variants: an epidemiological analysis, Lancet Infect. Dis. 22 (2022), 603–610. https://doi.org/10.1016/s1473-3099(22)00001-9.

[33] K. Kupferschmidt, M. Wadman, Delta variant triggers new phase in the pandemic, Science. 372 (2021), 1375–1376. https://doi.org/10.1126/science.372.6549.1375.

[34] R. Bouajaji, H. Laarabi, M. Rachik, Optimal control strategy for a discrete time epidemic models of mycobacterium tuberculosis infections, Commun. Math. Biol. Neurosci. 2020 (2020), 15. https://doi.org/10.28919/cmbn/4328.

[35] M. Lafif, I. Khaloufi, Y. Benfatah, et al. A mathematical SIR model on the spread of infectious diseases considering human immunity, Commun. Math. Biol. Neurosci. 2022 (2022), 69. https://doi.org/10.28919/cmbn/7552.

[36] H. Laarabi, M. Rachik, O. El Kahlaoui, et al. Optimal vaccination strategies of an sir epidemic model with a saturated treatment, Univ. J. Appl. Math. 1 (2013), 185-191. https://doi.org/10.13189/ujam.2013.010305.