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A mathematical model of nonlinear differential equation for controlling global dynamics of coronavirus disease 2019 (COVID-19)

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Abstract---In this paper, we have introduced new mathematical model of Coronavirus Disease (COVID-19) Transmission Model as a system of six nonlinear differential equations to analyze the spread and control of this latest outbreak pandemic disease. This new mathematical model is analysed with the help of optimal control analysis. The main purpose of this optimal control theory which applied to the model is to show the existence of optimal controllers for the nonlinear dynamic system. Based on the assumptions, we also studied and formulate an optimal control model for a coronavirus disease dynamic system in terms of mathematical differential equations in order to focus the effects of prevention and control measures with minimal implementation cost. Then, we established the basic reproduction number R_0 , which makes possible to check whether a prominent infectious disease will continue to spread or not in a susceptible population. The paper was also extended to assess the conditions under which the population will be free of disease. In particular, we focus to include in the mathematical model, quarantine procedure applied to both the infected individuals and to the highly risk of total population, which is expected to be useful. Most importantly, we would like to point out that with the availability of mathematical analysis, the model will have great impact on reducing the spread of such deathly coronavirus disease and can be automatically controlled.

Keywords---basic reproduction number, coronavirus disease, mathematical modeling, nonlinear dynamical systems, optimal control analysis.

Introduction

An outbreak coronavirus (COVID-19) is a deadly infectious disease which becomes one of the most global health concerns to people, to government and to World Health Organization. Coronavirus belong to a group of viruses that infect and causes diseases in human and other animals. It is thought that the virus might be of bat origin, and the transmission of the virus might be linked to a seafood market exposure named as Huanan Seafood Wholesale Market in Wuhan, where sold meat and live animals [22]. The World Health Organization (WHO), China Country Office discovered a case of pneumonia of unknown aetiology, first detected in Wuhan city, Hubei province in China on December 2019 [3][23]. Thereby, the disease is called as coronavirus disease 2019 (COVID-19), and the causative virus was identified as severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2) by International Committee on Taxonomy of Viruses on 11 February, 2020 [23]. This transmitted virus is different from the MERS-CoV, which is first discovered in Saudi Arabia, 2012 [7]. It causes respiratory tract infections which can affect throat, sinuses, airways or lungs. According to the latest report, the symptoms of this coronavirus (COVID-19) include fever, cough, difficulty in breath, tiredness etc. Some patients recovered from the disease with or without special treatment while the severe infected patients caught pneumonia which lead to death. The rapid growth in number of coronavirus cases detected from few to numerous spreads universally within a short time and henceforth, it is considered as one of the most critical pandemic diseases in the current situation. This pandemic disease can spread through direct contact between an infected person and a person. This coronavirus transmission of human-to-human can be in one of the either way by direct transmission through sneezing and coughing or by indirect transmission through contaminated surfaces and devices which is already polluted with the virus, and then touch the nose, mouth, nose and eyes with unwashed hands [6]. In this way, the virus enters the body through the nose, mouth and eyes and then attaches in the airway infects nearby cells starts attacking the body [2]. Thus, it is well instructed to cover mouth and nose with medical masks and avoid touching the face. Many countries have played a role of their responsibility on this public health concerns and are being paid globally to investigate the current outbreak of the coronavirus disease 2019 (COVID-19) with the interests of how many people are infected and suspected, and to reflect the impact of control measures. Besides all these preventive measures, the study of Coronavirus transmission dynamics by mathematical models plays a great role to analyse the spread and control of the disease [4]. Therefore, it is crucial to develop a mathematical model to determine the transmissibility and dynamic of the coronavirus transmission [23]. Many interesting researches have been conducted on this highly global risk of health issue focussing more on mathematical modelling [24,25]. These researches include calculating the basic reproduction number based on next generation matrix [2], sensitivity analysis of cost function [19], using ordinary differential equations [21], optimal control analysis [15], functional mapping [31] and Numerical simulations. However, the model presented in the paper does not include the bat origin and the transmission route from the seafood market to people but rather we emphasized more into the prevention and control measures of coronavirus disease which is highly spread due to certain interventions. For this reason, we present an optimal control problem by introducing it into the

model of nonlinear differential equations of coronavirus transmission dynamic system with two control variables. Optimal control theory has broad applications in both science and engineering, which is derived from Pontryagin's maximum principle [26] for control policies. Optimal control theory is a powerful mathematical tool to analyse the complex dynamical systems to minimize both the number of infected people and the cost of operation [27]. Although, this is a powerful mathematical model, solving a general nonlinear optimal control problem is a great challenge to control the epidemiology of this outbreak coronavirus disease. In addition, we considered basic reproduction number of estimated values which depend on the model used and values of other parameters. It is considered to be one of the most fundamental epidemiologic metrics and often used to record the contagiousness or transmissibility of infectious disease or quantify the disease severity. The basic reproduction number must be estimated, reported, and applied with great caution in research and practice because it can be easily misrepresented, misapplied and misinterpreted in various ways that would misreport true meaning and value of metrics [10]. From that point of view, we have studied that an outbreak of a coronavirus disease is expected to continue if $R_0 > 1$ and come to an end if $R_0 < 1$, which we considered as a useful aid in the case of dealing with transmission and controlling of infectious coronavirus disease.

Mathematical model framework

In view of the latest outbreak news of coronavirus disease (COVID-19) reported that the disease is spreading around the world, many of the recent applications have been introduced based on mathematical models in order to control like this dangerous infectious disease. The significant role of these mathematical models is to contribute better understanding in the epidemiology of coronavirus disease and other infectious diseases. The main objective of this paper is to describe mathematically, the nonlinear dynamics of the coronavirus infected in a population. This complicated dynamic of nonlinear processes is described by a system of nonlinear differential equations, which focuses on exposure of an infectious disease in a population over time. We formulate and analysed this mathematical model given by a system of nonlinear differential equations in order to extend more knowledge about the dynamics system of how the coronavirus disease is transmitted. In this model, the total number of human populations (N_H) is divided into 9 categories such as Vulnerable people towards coronavirus (C_V), Unprotected people towards outbreak coronavirus or exposed to infectious people directly or indirectly (C_U), Asymptomatic people (C_A), Symptomatic or infected people (C_I), Hospitalized people (C_H), and Recuperate people (C_R). This COVID-19 Transmission Model is introduced based on the model Lee et al [2] to deal with the latest outbreak of Coronavirus disease which is considered as COVID-19. In this model, we do not consider the case of zoonotic transmission although it has been suggested that the coronavirus disease might be originated from bats. This COVID-19 Transmission Model [2] is introduced without the zoonotic case except the primary cases as well as secondary cases of infected people among the vulnerable population in the present situation. We considered that only infectious and hospitalized individuals can infect people and asymptomatic individuals cannot [8]. The represented model illustrates that when a vulnerable people C_V exposed without personal protection or preventive measure turn into exposed or

unprotected people C_U , they get infected C_I . In the meantime, both symptomatic people and asymptomatic people suffer from the virus but asymptomatic people cannot infect others. The carrier symptomatic or infected people C_I can turn into recovery people C_R , being or without being hospitalized C_H .

The following tasks of the model is presented in the form of mathematical terms with the interest of transmission control strategy.

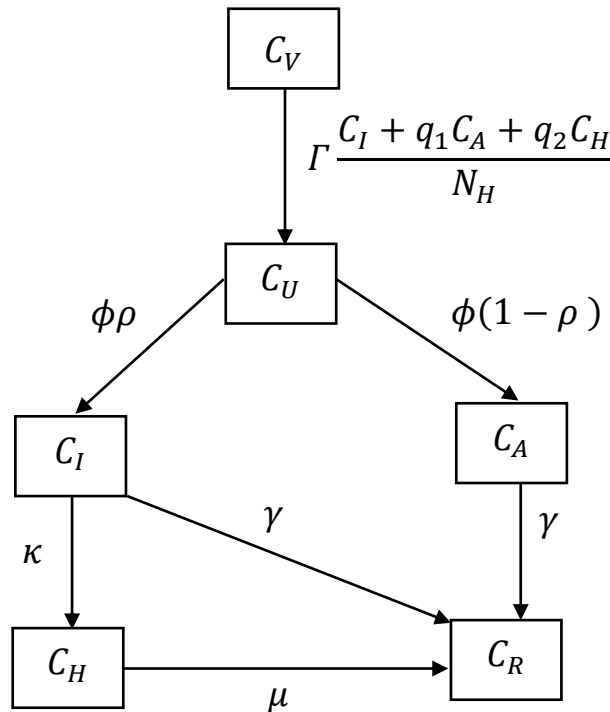


Fig 1: This flow chart represents COVID-19 Transmission Model in the nonlinear dynamic system.

In this section, we established the following six-dimensional system of nonlinear differential equations based on the assumptions and the illustration in fig.1[2], which is given by,

$$\begin{aligned}
 C_V(t) &= -\Gamma \frac{C_V(C_I + q_1 C_A + q_2 C_H)}{N_H} \\
 C_U(t) &= \Gamma \frac{C_V(C_I + q_1 C_A + q_2 C_H)}{N_H} - \phi U \\
 C_I(t) &= \phi \rho C_U - (\kappa + \gamma) C_I
 \end{aligned}$$

$$C_A(t) = \phi(1 - \rho)C_U - \gamma C_A \quad (1)$$

$$C_H(t) = \kappa C_I - \mu C_H$$

$$C_R(t) = \gamma C_I + \mu C_H + \gamma C_A$$

With initial conditions $C_V(0) \geq 0$, $C_U(0) \geq 0$, $C_I(0) \geq 0$, $C_A(0) \geq 0$,
 $C_H(0) \geq 0$, $C_R(0) \geq 0$.
 (1a)

Where $N_H = C_V + C_U + C_I + C_A + C_H + C_R$

Here Γ is the rate of transmission from symptomatic infected people C_I to vulnerable people C_V towards outbreak of coronavirus with time t ;
 q_1 and q_2 measures the effectiveness of transmissibility of infection by asymptomatic people C_A with respect to hospitalized people C_H ;
 ϕ is the rate at which an individual set off from unprotected people C_U to symptomatic infectious people C_I ;
 ρ is the proportion of progression unprotected people C_U to symptomatic infectious people C_I , and $(1 - \rho)$ is that of progression to asymptomatic people C_A ;
 κ is the average rate at which symptomatic individuals become hospitalized;
 γ is the rate of recovery without being hospitalized;
 μ is rate of recovery of hospitalized patients.

Based on the above discussion, we defined the variable domain of the model as $\mathcal{U} = \{(C_V, C_U, C_I, C_A, C_H, C_R) \in \mathbb{R}^6 | C_V, C_U, C_I, C_A, C_H, C_R \geq 0\}$ in which all the following parameters $\Gamma, q_1, q_2, \phi, \rho, 1 - \rho, \kappa, \mu$ and γ presented in the model are all positive values. This Coronavirus Transmission model (1) has established two equilibrium points which are given by $(C_V, C_U, C_I, C_A, C_H, C_R) = (0, 0, 0, 0, 0, 0)$ and $(C_V, C_U, C_I, C_A, C_H, C_R) = (C_V, 0, 0, 0, 0, C_R)$. By means of this, we can prove that $\mathcal{U}$ is a positively invariant set with respect to the model under coronavirus dynamic system of nonlinear differential equation (1).

Preposition 1: Let $C_V, C_U, C_I, C_A, C_H, C_R$ be the solution of the system (1) with initial condition (1a) and the closed set $\mathcal{U} = \{(C_V, C_U, C_I, C_A, C_H, C_R) \in \mathbb{R}^6 | C_V, C_U, C_I, C_A, C_H, C_R \geq 0\}$. Then, the set $\mathcal{U}$ is positively invariant under coronavirus dynamic system [21] of nonlinear differential equation (1).

Basic Reproductive Value of R_0

A critical concept in the study of transmission and controlling of infectious coronavirus disease is presented by mathematical model and the dynamic system of this model is characterized by the basic reproductive number [2]. Basic reproductive number is used to defined the number of new cases of coronavirus disease generated by introducing one infected individual into a vulnerable or susceptible population. Basic reproductive number is also known as basic reproductive ratio or simply threshold and is denoted by R_0 [9]. Its effective used is to compute the transmission potential of a disease and is one of the most functional threshold parameters. This threshold condition will allow to discovers how fast a disease can spreads in its initial phase as well as estimate whether a disease will continue to exist or it will die out [2]. Basic reproductive number (R_0)

can never be measured directly and its values are totally dependent on model structures and assumptions. The basic reproduction number is affected by several factors including biological, social behavioural and environmental which lead to pathogen transmission and accordingly, the value is estimated based on its various types of complex mathematical models. Therefore, R_0 value may vary from disease to disease but also for the same disease in different populations of different regions. For infectious diseases, many complex mathematical models have been proposed by using various methods[14] include the Jacobian matrix, the survival function, calculations from the intrinsic growth rate, existence of the endemic equilibrium, the number of vulnerable at the endemic equilibrium, the average age of infection and the final size equation in order to calculate the basic reproduction number (R_0). Some of these methods have the same results with one another when working with the same model system of nonlinear differential equation [13]. We apply next-generation (infection) matrix of a model to estimate this threshold condition. The necessary computation of the matrices is shown [2,13] below in the interest of determining the basic reproduction number for the given model as,

$$\mathcal{F} = \begin{bmatrix} \Gamma \frac{C_V(C_I + q_1 C_A + q_2 C_H)}{N_H} \\ 0 \\ 0 \\ 0 \end{bmatrix}, \mathcal{V} = \begin{bmatrix} \phi V \\ -\phi \rho C_U + (\kappa + \gamma) C_I \\ -\phi(1 - \rho) C_U + \gamma C_A \\ -\kappa C_I + \mu C_H \end{bmatrix}$$

$$F = \begin{bmatrix} 0 & \Gamma & \Gamma q_1 & \Gamma q_2 \\ 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 \end{bmatrix}, V = \begin{bmatrix} \phi & 0 & 0 & 0 \\ -\phi \rho & \mu + \gamma & 0 & 0 \\ -\phi(1 - \rho) & 0 & \gamma & 0 \\ 0 & -\kappa & 0 & \mu \end{bmatrix}$$

The next generation matrix (M) for the infectious coronavirus disease as proposed in the model is given by

$$M = FV^{-1} = \begin{bmatrix} \frac{\Gamma \rho}{\kappa + \gamma} + \frac{\Gamma \rho \kappa q_2}{\mu(\kappa + \gamma)} + \frac{\Gamma(1 - \rho)q_1}{\gamma} & \frac{\Gamma}{\kappa + \gamma} + \frac{\Gamma \kappa q_2}{\mu(\kappa + \gamma)} & \frac{\Gamma q_1}{\mu} & \frac{\Gamma q_2}{\mu} \\ 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 \end{bmatrix}$$

(2)

Where, $\mathcal{F}$ is the rate of increase of secondary infectious and $\mathcal{V}$ is the rate of the disease progression, recovery and death.

The next generation matrix, $M = FV^{-1}$, a non-negative value, which is obtained at the disease-free equilibrium for the dynamical system. R_0 is the dominant eigen value of the matrix M and therefore, it has a non-negative eigen value, $R_0 = \rho(FV^{-1})$, where ρ is considered as the spectral radius of the next- generation matrix FV^{-1} . Following, we apply the method of the Jacobian matrix of $\mathcal{F}(x)$ and $\mathcal{V}(x)$ and defined it as $F = \left[\frac{\partial \mathcal{F}_i}{\partial x_j} \right]$ and $V = \left[\frac{\partial \mathcal{V}_i}{\partial x_j} \right]$ in order to estimate the

dynamic system at the disease free equilibrium point E_0 , assuming $C_V = N_H$. The basic reproduction number (R_0) is thus calculated by using spectral radius next generation matrix (M) approach for the model of nonlinear differential equations [11] as following:

$$R_0 = \Gamma \frac{\kappa\mu q_1 + \gamma\mu q_1 + \gamma\mu\rho - \kappa\mu q_1\rho - \gamma\mu q_1\rho + \kappa\gamma q_2\rho}{\gamma\mu(\kappa + \gamma)}$$

$$R_0 = \Gamma \left(\frac{\rho}{\kappa + \gamma} + \frac{\rho\kappa q_2}{\mu(\kappa + \gamma)} + \frac{(1 - \rho)q_1}{\gamma} \right) \quad (3)$$

As we have already discussed from the above equation that this basic reproduction number of nonlinear dynamics system which is depends on all these given parameters $\Gamma, q_1, q_2, \rho, \kappa, \mu$ and γ are non-negative values. It is also essential to note that the basic reproduction number R_0 is a dimensionless number, which would have a unit of time^{-1} [20]. The detail dynamic of the coronavirus transmission model is explained by the threshold quantity, R_0 . This threshold quantity is the reproduction number of the nonlinear differential equation model. It is defined as the expected average number of secondary infections that single infectious individual can produced in a vulnerable population. From the above results, we could produce the local stability of disease-free equilibrium indicating the stability of the equilibria of model.

Sensitivity analysis of transmission model:

The major significant of sensitivity analysis is to indicate how much the parameters of model play an important role in the transmission dynamics of coronavirus disease (COVID-19) and highlighted the most sensitive parameters Γ and κ , which are presented in the model [19]. Simple formulas are determined in terms of the basic reproduction number R_0 for the sensitivity indices which permit to recognize the variations in model parameters for the disease-free reproduction number and for the infected population in the endemic equilibrium state [18]. The main advantage of this sensitivity index in an epidemiological model is to predict the dominant factors which is connected with a certain intervention that affects the coronavirus disease among the population to a great extent. Sensitivities parameters of Γ, κ are expressed through basic reproduction number R_0 as [2] follows;

$$S_\Gamma = \frac{\partial R_0}{\partial \Gamma} \frac{\partial \Gamma}{\partial R_0} = 1,$$

$$S_\kappa = \frac{\partial R_0}{\partial \kappa} \frac{\partial \kappa}{\partial R_0} = \frac{\kappa\rho \left(\gamma q_2 - \frac{1}{(\kappa + \gamma)^2} \right)}{\frac{\rho}{(\kappa + \gamma)} - \frac{q_2(\rho - 1)}{\gamma} + \frac{\kappa q_2 \rho}{\mu(\kappa + \gamma)}}$$

In the sensitivity indices, the value of basic reproduction number R_0 can be minimize by reducing Γ and increasing κ . The control variables $0 \leq w_1(t) \leq 1$ and $0 \leq w_2(t) \leq 1$ represents the number of interventions at time t to minimize the contact rate Γ and to add hospitalization rate κ of suspected cases to minimize the spread of coronavirus disease. When the approach of this control measures

changes some of parameter values in the Coronavirus Transmission Model, then we need to know the consequences results the changes occur on R_0 for the control of transmission. If the estimated reproduction number is approaching to one, then the control and treatment measures are implemented with this value of R_0 that it is possible to eradicate the disease in short time. The fact of this is that an increase in the transmission rate will increase the spread of the coronavirus disease in a vulnerable human population. The basic work of this basic reproduction number is to evaluate transmission capability of a coronavirus disease and it is equally important for evaluating control alternatives to stop the spread of infection from an initially disease-free population. It is to focus on the control efforts of the infectious human and the contaminated environment [19]. There are three possibilities exist which indicate certain criteria of transmission of coronavirus disease in a dynamical system based on the value of R_0 which includes [21],

- i. If $R_0 < 1$, indicates disease-free equilibrium in which the infected individual can spread more than one, the disease will reduce and finally cease.
- ii. If $R_0 = 1$, a single infected individual causes one new infection, the disease will remain active and steady but there won't be an outbreak of coronavirus disease.
- iii. If $R_0 > 1$, shows an endemic equilibrium exists in the human population, in which the infected individual can spread more than one among vulnerable population that may lead to an outbreak of coronavirus disease.

Mathematical model analysis with an optimal control characterization:

Optimal control theory is of the one most substantial mathematical tool to implement in the complex dynamical systems with control strategy in order to minimize the number of infected people and to lessen the cost of function [15]. Generally, optimal control is a set of differential equations determine the paths of the control variables which reduce the cost function while implementing the control law for a dynamic system. Recently, optimal control has been successfully applied to many of epidemiological problems [16]. Optimal control problems are mainly are nonlinear in nature and therefore cannot have simple analytical solutions like the linear system. For that consequence, we have to employ numerical methods to solve optimal control problems. In this paper, we designed an optimal control model in order to obtain optimal prevention with minimal implementation cost for the transmission dynamics of COVID-19 in a vulnerable population. The model of equation (1) is transform into new model by adding two control variables $w_1(t), w_2(t)$ which is now considered as an optimal problem,

$$\begin{aligned}
 C_V(t) &= -\Gamma[1 - w_1(t)] \frac{C_V(C_I + q_1 C_A + q_2 C_H)}{N_H} \\
 C_U(t) &= \Gamma[1 - w_1(t)] \frac{C_V(C_I + q_1 C_A + q_2 C_H)}{N_H} - \phi U \\
 C_I(t) &= \phi \rho C_U - \gamma C_I - \kappa [1 + \lambda w_2(t)] C_I \\
 C_A(t) &= \phi(1 - \rho) C_U - \gamma C_A \\
 C_H(t) &= \kappa [1 + \lambda w_2(t)] C_I - \mu C_H \\
 C_R(t) &= \gamma C_I + \mu C_H + \gamma C_A
 \end{aligned}
 \tag{4}$$

Where the control variable $w_1(t)$ represents the number of interventions among the vulnerable population towards coronavirus infectious disease which is required to minimize human contact (quarantine) rate at time t . After quarantine, the contact rate of people in vulnerable population would be $1 - w_1(t)$, in that case $w_1(t)$ is indicating the level of successful prevention efforts while the other control variable $w_2(t)$ represents the necessary treatment contribute to the infected humans after hospitalized. It is considered that $w_2(t)$ encourage the hospitalization rate increase as soon as the case confirmed and λ is a rate constant proportional to $w_2(t)$. It is clearly suggested that we can depend on these time dependent control variables to reduce the number of infections of coronavirus disease as well as minimizing the cost of precaution measures [2].

The significant cause of this optimal control problem is to surveillance on reducing the number of contacts and directed infected individuals as hospitalized individuals with preventive measures will minimize the number of infected cases as well as the cost functional, which is expressed as,

$$J(w_1, w_2) = \int_0^T \left\{ D_1 C_I(t) + D_2 C_A(t) + D_3 C_H(t) + \frac{E_1}{2} w_1^2(t) + \frac{E_2}{2} w_2^2(t) \right\} dt \quad (5)$$

This objective functional J , is subject to the differential equation (4) of nonlinear dynamic system, where the quantities D_1, D_2 , and D_3 are term as the weight constants of the symptomatic infectious class, asymptomatic class and hospitalized individuals respectively and E_1 and E_2 are weight coefficients constants which represent the charge amount. These specific terms $\frac{1}{2} E_1 w_1^2$ and $\frac{1}{2} E_2 w_2^2$ represents a detailed account of charges arise when an infected individual spread COVID-19 to a vulnerable or susceptible population through unprotected contact and treatment charge of hospitalized patients in order to minimize the rate of infected individuals, respectively. The main purpose of this paper is to minimize the number of infected human and the cost of applying the control non-negative values w_1 and w_2 with the given objective functional J which is expressed as, $J(w_1, w_2)$. We used this objective functional J to investigate the optimal level of efforts that would be needed to control this coronavirus disease.

We apply this optimal control functions w_1^*, w_2^* satisfying the Lagrange Formulation such that $J(w_1^*, w_2^*) = \min\{J(w_1, w_2) | (w_1, w_2) \in \mathcal{W}\}$ subject to nonlinear dynamic system (4), where the admissible control set is given by $\mathcal{W} = \{w_1(t), w_2(t) | w_1(t), w_2(t)\}$ is Lebesgue measurable on $[0, T]$, with $0 \leq w_1(t), w_2(t) \leq 1$, where T is the final time. This basic framework of an optimal control problem is to establish the existence of the optimal control [17] and to identify the optimal control through the optimality system equation (6).

Existence of an Optimal Control in a Nonlinear Dynamic System:

We defined the Lagrange corresponding to the Hamiltonian for the optimal control which is derived from Pontryagin's Maximum Principle provides the necessary and sufficient conditions for an optimum which needs to be satisfied as follows;

$$\mathcal{H}\{(X(t), \mathcal{W}(t), \Lambda(t))\}$$

$$\begin{aligned}
&= D_1 C_I(t) + D_2 C_A(t) + D_3 C_H(t) + \frac{E_1}{2} w_1^2(t) + \frac{E_2}{2} w_2^2(t) + \Lambda(t) \left(\frac{dX(t)}{dt} \right)^T \\
&= D_1 C_I(t) + D_2 C_A(t) + D_3 C_H(t) + \frac{E_1}{2} w_1^2(t) + \frac{E_2}{2} w_2^2(t) + \chi_1 C_V(t) + \chi_2 C_U(t) + \chi_3 C_A(t) \\
&\quad + \chi_4 C_I(t) + \chi_5 C_H(t) + \chi_6 C_R(t) \\
&= D_1 C_I(t) + D_2 C_A(t) + D_3 C_H(t) + \frac{E_1}{2} w_1^2(t) + \frac{E_2}{2} w_2^2(t) \\
&\quad + \chi_1 \left\{ -\Gamma[1 - w_1(t)] \frac{C_V(C_I + q_1 C_A + q_2 C_H)}{N_H} \right\} \\
&\quad + \chi_2 \left\{ \Gamma[1 - w_1(t)] \frac{C_V(C_I + q_1 C_A + q_2 C_H)}{N_H} - \phi U \right\} \\
&\quad + \chi_3 \{ \phi \rho C_U - \gamma C_I - \kappa [1 + \lambda w_2(t)] C_I \} + \chi_4 \{ \phi(1 - \rho) C_U - \gamma C_A \} \\
&\quad + \chi_5 \{ \kappa [1 + \lambda w_2(t)] C_I - \mu C_H \} + \chi_6 \{ \gamma C_I + \mu C_H + \gamma C_A \}
\end{aligned} \tag{6}$$

Where $\chi_j (j = 1, 2, 3, 4, 5, 6)$ are the adjoint variables and the state variables for the dynamics system of coronavirus outbreak are denoted by $X(t) = C_V(t), C_U(t), C_A(t), C_I(t), C_H(t), C_R(t)$.

Theorem V(a): There exists an optimal control $w^* = (w_1^*, w_2^*) \in \mathcal{W}$ such that $J(w_1^*, w_2^*) = \min\{J(w_1, w_2) | (w_1, w_2) \in \mathcal{W}\}$ subject to the control nonlinear dynamic system (4) with the initial condition at $t = 0$ [15].

Conclusion

This tremendous Coronavirus outbreak is one of the top lists of high-priority threats to human health under World Health Organization since 31st December 2019[3]. An ongoing threat coronavirus (COVID-19) causes respiratory disease that is primarily characterized by cough, fever and shortness of breath and eventually associated with severe pneumonia creates an outbreak in Wuhan, China and rapidly spread throughout the world. This threatening life situation of novel coronavirus infections became the spotlight and panic attack to many countries. As a result, many scientists and researchers tend to do their best research in different ways to bring out with the best solutions for this outbreak of novel coronavirus. In particular, we intend to present the mathematical model for the prevention and treatment of infected individuals with a quarantine procedure. In this paper, we described the presented mathematical model as Coronavirus (COVID-19) Transmission Model 2019 along with optimal control analysis and R_0 was obtained based on Next Generation Matrix (NGM) to estimate the transmissibility of the SARS-CoV-2. The significant role of these mathematical models has been applied to many real-world problems, which helps in understanding the epidemiology of coronavirus disease [27] and many other infectious diseases like measles, influenza, polio, HIV disease and Ebola virus disease [10]. From an epidemiological point of view, this mathematical modeling approach is the standard way to study the dynamical behaviour of infectious diseases in populations. As a result, we propose and analyze a mathematical model given by a system of nonlinear differential equations to acquire significant achievements against infectious disease [16]. The analyses of this Coronavirus (COVID-19) Transmission Model is to determine the possible benefits of these control strategies through optimal control theory and basic reproduction number.

Optimal control analysis is of the most effective control method which we can apply successfully, to minimize the spread of a disease with minimum cost. At the time same, we consider the basic reproductive number R_0 in order to indicate whether the disease will persist or disappear for this widespread of coronavirus disease in a population [2]. The most difficult tasks is the approximation of model parameters in mathematical modelling. The proposed mathematical model (1) establishes mathematical relationships among the six different sub-populations and enable for the change of individuals between sub-populations [29]. It is believed that introducing all these effective control measures at the onset of the outbreak will decrease the number of initially infected people and thus require less expenditure on controlling of this outbreak as a whole. We provide useful information with reference to the present dynamics and control of coronavirus disease, which can be established by analysing the best suitable epidemiological models. Although, we describe new insights into the dynamics and control intervention strategies for coronavirus disease, effective control measures still remain a great challenge. In any case of outbreak, there will be great difficult to manage without effective control measures. In this latest endemic prevention scenario, the most affordable and best way to control the spread of outbreak coronavirus diseases is concentrating on medical mask intervention when there is a limited budget for interventions. In this paper, we mentioned about the necessity of fixing the model to real data so that it will be practically useful in controlling the spread of the coronavirus [29]. Although, this optimal control theory results in optimal strategies to reduce the infection of coronavirus disease, it is not efficient to predict the long-term dynamics of the disease as a whole [28]. Eventually, it is important to highlight the fact that our main interest is to govern the state of process under which the population will be free of disease.

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