MATHEMATHICAL MODELING AND OPTIMAL CONTROL ANALYSIS OF COVID-19 PANDEMIC

Debela Etefa

A Thesis Submitted to Department of Applied Mathematics

School of Applied Natural Science

Presented in Partial Fulfillment of the Requirement for the Degree of Master's in Applied Mathematics

Office of Graduate Studies

Adama Science and Technology University

August 4, 2021

Adama, Ethiopia

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Declaration

I hereby declare that this Master Thesis entitled "Mathematical Modeling and Optimal Control Analysis of COVID-19 Pandemic" is my original work. That is, it has not been submitted for the award of any academic degree, diploma or certificate in any other university. All sources of materials that are used for this thesis have been duly acknowledged through citation.

Name of student	Signature	Date

Recommendation

We, the advisors of this thesis, hereby certify that we have read the revised version of the thesis entitled "Mathematical Modeling and Optimal Control Analysis of COVID-19 Pandemic" prepared under our guidance by Debela Etefa submitted in partial fulfillment of the requirements for the degree of Master's of Science in Applied Mathematics. Therefore, we recommend that the submission of revised version of the thesis to the department following the applicable procedures.

Major Advisor	Signature	Date
Co-advisor	Signature	Date

Approval Page

We, the advisors of the thesis entitled "Mathematical Modeling and Optimal Control Analysis of COVID-19 Pandemic" and developed by Debela Etefa, hereby certify that the recommendation and suggestion made by the board of examiners are appropriately incorporated into the final version of the thesis.

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Co-advisor	Signature	Date

We, the undersigned, members of the Board of Examiners of the thesis by Debela Etefa have read and evaluated the thesis entitled "Mathematical Modeling and Optimal Control Analysis of COVID-19 Pandemic" and examined the candidate during open defense. This is, therefore, to certify that the thesis is accepted for partial fulfillment of the requirement of the degree of Master of Science in Applied Mathematics.

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ACRONYMS

COVID-19	Corona Virus Infectious Diseases-2019
EEP	Endemic Equilibrium Point
DFEP	Disease Free Equilibrium Point
MERS-COV	Middle East Respiratory Syndrome Coronavirus
ODE	Ordinary Differential Equations
PMP	Pontryagin Minimum Principle
SARS-COV	Severe Acute Respiratory Syndrome Coronavirus
SARS-COV-2	Severe Acute Respiratory Syndrome Coronavirus-2
WHO	World Health Organization

Abstract

Coronaviruses (CoV) are a large family of viruses that cause illness ranging from the common cold to more severe diseases. This study aims to develop and analyze a mathematical model of COVID-19 transmission dynamics with optimal control. For this, we formulated and analyzed a deterministic mathematical model of five compartments for the transmission dynamics of COVID-19 infection using a system of non-linear ordinary differential equations. These compartments are namely susceptible, exposed, asymptomatic, infected and recovered. We investigated the dynamical behavior of this model and performed the qualitative analysis of the model. The system has two equilibrium points, namely the disease free equilibrium point and the endemic equilibrium point. The basic reproduction number R_0 was calculated using the next-generation matrix and the stability of the equilibrium points were analyzed. From the qualitative analysis, the disease free equilibrium point is both locally and globally stable if $R_0 < 1$, and the endemic equilibrium point is also both locally and globally stable if $R_0 > 1$ under some conditions on the system parameters. Furthermore, sensitivity analysis of the model equation was performed on the key parameters to find out their relative significance and potential impact on the transmission dynamics of COVID-19. Then the optimal control strategy is found by minimizing the number of exposed and infected population taking into account the cost of prevention and treatment. The existence of optimal controls and characterization is established with the help of Pontryagin's Minimum Principle. Finally, numerical simulations of the model equations were carried out using MATLAB R2018b. The findings of this study shows that comprehensive impacts of personal protective and treatment strategies outperform in reducing the COVID-19 infection.

Keywords: Mathematical modeling; SEAIR model; COVID-19; stability analysis; sensitivity analysis; optimal control.

CHAPTER 1

INTRODUCTION

1.1 Background of the Study

Coronaviruses are a large family of viruses that are known to cause illness ranging from the common cold to more severe diseases such as severe acute respiratory syndrome (SARS). The severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2) was identified as the cause of a cluster of pneumonia cases in the Chinese city of Wuhan (Chen et al., 2020). This new types of outbreak has been named as the COVID-19 (corona virus disease-2019) and determined as a pandemic by the WHO on January 11, 2020. This coronavirus is a kind of enveloped, single stranded and positive sense virus which belongs to the RNA coronaviridae family (Spaan et al., 1988). The extremely spread of the disease and lack of approved medicine make the disease a challenging problem for public health organizations (Hanscheid et al., 2020; Lee, 2020).

This pandemic has affect billions of people by forming very immense restrictions in their lives, movements, travels (in local, national and international) and social relationships. It has been taken unprecedented measures against to COVID-19, which is caused to many deaths, to intense stress and to changes in life style and forms of work, by the local adminitions and national governments of almost every countries (Çakan, 2020). In lack of any specific drug or therapeutics, social distancing, using mask and hand washing by soap have been recognized as the most commonly utilized preventive measures to control the novel coronavirus diseases (Ferguson et al., 2020). Indeed the outbreaks of COVID-19 has drastically altered the daily life, health of the publics as well the economy. This is one of the main interests for each and everyone how long this situation will continue and when the disease will be under controlled

and the entire world will be returned back to its earlier situation (Çakan, 2020).

The novel coronavirus can cause mild, non-specific symptoms, including fever, cough, shortage of breath, muscle pain and tiredness similar to those caused by SARSCoV and MERS-CoV infections (Gralinski & Menachery, 2020). In more serious cases, it can develop severe pneumonia, acute respiratory distress syndrome, sepsis and septic shock that can lead to death. The virus is transmitted via respiratory droplets produced when an infected person coughing, sneezing and during talking in a social distance less than two meter. The estimated incubation period is 2-14 days, but could be longer (Yang & Wang, 2020). The virus is most contagious when infected people are symptomatic, although can spread before symptoms appear (Rothe et al., 2020). The review given in (Lin et al., 2020) reveals that human coronaviruses such as (SARS, MERS) or endemic human coronaviruses (HCoV) can persist on inanimate surfaces like metal, glass or plastic for up to 9 days at room temperature and the duration of persistence is shorter when a temperature is greater than or equal to 30 $^{\circ}C$. The study also provided strong evidences for the pathogen's environmental survival which can be inactivated by surface disinfection procedures with 62-71% ethanol, 0.5% hydrogen peroxide or 0.1% sodium hypochlorite within 1 minute.

The studies of mathematical modeling play a considerable role in analyzing the factors that may affect spreading of the disease. Here, mathematical epidemiology exists for this purpose. Mathematical methods in epidemiology have a very momentous place in examining the behavioral dynamics of epidemic. Mathematical modeling plays an important role in comprehending and providing useful techniques to predict and analysis the dynamics of infectious disease (LaSale & Lefschetz, 1961). The progression of any outbreak depends on the infectivity of pathogens as well as the available uninfected individuals. For a novel infection, when the transmission dynamics of an epidemiological disease is unknown, mathematical models play a crucial role to estimate the worst and best scenarios. It can also aid in estimating the effect of precautionary measures adopted against disease. With preventive techniques, the main object is to preserve the basic reproduction number R_0 below 1, to control further development of infection, whereas in a mitigation policy, the main object is to indelicate the effect of outbreak (Ferguson et al., 2020).

Many mathematicians worldwide are intensively working on COVID-19, see for example in (Ivorra et al., 2020; Khan & Atangana, 2020; Ndaïrou et al., 2020) and references cited therein. Haileyesus and Getachew (2020) developed a deterministic mathematical model of the pandemic COVID-19 transmission in Ethiopia, which allows transmissions by exposed humans. Çakan (2020) proposed time delayed SEIR epidemic model by taking into account the impact of health care capacity.

Optimal control theory is an area of mathematics that is used extensively in controlling the spread of infection diseases. It is a powerful mathematical tool that can be used to make decisions involving complex biological situation (Fleming & Rishel, 2012). Mathematical models with optimal control have played a major role in increasing our understanding of the dynamics of infectious diseases and also to investigate the optimal use of intervention strategies to mitigate the spreads of infectious diseases. It has become a valuable tool in the analysis of infectious disease dynamics and to support the development of control strategies. Optimal control theory has been applied to various mathematical models for studying the transmission dynamics of COVID-19 for example, see in (Chernet et al., 2020; Haileyesus & Getachew, 2020; Legesse & Shiferaw, 2020) and references cited therein. It deals with the problem of finding a control law for a given system such that a certain optimality criterion is achieved with minimum implementation cost. A control problem includes a cost functional that is a function of state and control variables. An optimal control is a set of differential equations describing the paths of the control variables that minimize the cost function.
In the present thesis we analyzed the transmission dynamics COVID-19 using mathematical model with real data from Ethiopia by classifying the populations into susceptible, exposed, asymptomatic infected, symptomatic infected and recovered with appropriate assumptions. Then we extended the model to optimal control and present optimal intervention techniques.

1.2 Statement of the Problem

Coronavirus disease 2019 (COVID-19) pandemic which began in Wuhan city is now the problem of the world.

Globally, COVID-19 is affecting above 223 countries. According to WHO data, the total confirmed cases are 147,539,302 and the reported deaths due the disease is 3,116,444 deaths

up to April 27, 2021.

In Africa, COVID-19 case was first reported in Egypt on 14 February 2020. Then it addressed all the African countries. Initially, the disease was confined to capital cities, and gradually a significant number of countries in Africa are now reporting the cases in multiple provinces. Also, WHO report shows 3,285,051 total confirmed cases and 82,102 confirmed deaths are reported in Africa up to April 27, 2021.

In Ethiopia the first confirmed case of COVID-19 was on 13 March 2020, in capital city of Ethiopia, Addis Ababa. Up to April 27, 2021, the total reported confirmed cases and death reported due to COVID-19 in Ethiopia respectively are 253,120, and 3,570 (WHO et al., 2020).

Mathematical models for COVID-19 infection can provide better insights into the dynamics of virus and may play a significant role in designing better control strategies. Many mathematical models have been developed to study the pandemic of COVID-19. Çakan (2020) proposed time delayed SEIR epidemic model with compartments consisting of Susceptible (S) against to the disease COVID-19, Exposed (E) to the coronavirus, Infectious (I) and Recovered (R) individuals by taking into account the impact of health care capacity. But they did not consider the asymptomatic (infectious individuals who are not show symptoms of the disease). Thus, in this thesis we have developed new mathematical models with optimal control based on (Çakan, 2020) by introducing asymptomatic, induced death rate due to asymptomatic compartment (μ_2) and apply it to predict the tends of epidemic and its control strategies with out time delay. After modeling, the existence and stability criteria of the equilibria in terms of the basic reproduction number is determined. Sensitivity analysis of the model equation was performed on the key parameters to find out their relative significance and potential impact on the transmission dynamics of COVID-19. Finally, the proposed model parameters are fitted with real data from Ethiopia.

1.3 Objective of the Study

1.3.1 General Objective

The general objective of this study is to develop and analyze a mathematical model of COVID-19 transmission dynamics with optimal control.

1.3.2 Specific Objectives

The specific objectives of the study are to:

- develop COVID-19 transmission dynamics model,
- analyze the qualitative behavior of the model,
- extend the developed model in to optimal control system,
- analyze the impact of each control strategies on controling COVID 19.

1.4 Significant of the Study

A well studied and organized research report on COVID-19 will provide strong information on how to design appropriate control and preventive measures in order to bring a long term solution. Thus, the outcome of this study are helpful to:

- predict the dynamic analysis of COVID-19 pandemic.
- improve decision making at strategical level and adds advantage of interpret the situation of the coronavirus disease.
- motivate other researchers for further study and mathematical analysis.

1.5 Operational Definition of Technical Terms

The following epidemiological terms are defined for later use.

Epidemic is the rapid spread of disease to a large number of people in a given population within a short period of time.

In epidemiology, an infection is said to be **endemic** in a population when that infection is constantly maintained at a baseline level in a geographic area without external inputs.

A **pandemic** is an epidemic of an infectious disease that has spread across a large region, for instance multiple continents or worldwide, affecting a substantial number of people.

1.6 Mathematical Preliminary

In this section, we state some theorems and give the definitions of important concepts for later use in this study. The aim is to clarify terminologies and results that are utilized in the subsequent chapters.

1.6.1 Linearizion and the Jacobian

In most of the systems of real world problem, it becomes apparent that nearly all systems are non-linear, including the model we are examining. However, most of the theory that has been developed by mathematicians governing the behavior of systems of differential equations, especially stability, is centered upon linear systems. Thus, in order to further understand the behavior of a non-linear system it is first crucial to linearize the system. Essentially, this process approximates a non-linear system in a linear manner near the values around which a linear approximation occurs.

In a neighborhood of the equilibria we can make a linear approximation to determine the local character of the paths (Lukes & DL, 1982). This technique allows the stability of the system at the equilibria to be determined and provides a starting point for global investigations of solutions. The goal of this stability analysis is to perturb the system from equilibrium and study the behavior of the system. Thus, we will look to see if the solutions move towards or away from equilibrium. In order to linearize the system, we must compute the Jacobian matrix of the system. The Jacobian is the matrix of the partial derivatives of each function with respect to each variable. Essentially, the Jacobian provides a linear approximation of a system at any given value (Layek, 2015).

1.6.2 Routh-Hurwitz Criteria

The linear stability of a system of differential equations:

$$\frac{dX}{dt} = AX$$

where, $X = (x_1, x_2, ..., x_n)$ is determined by the roots of the characteristic polynomial, A is the Jacobian matrix of the linearized system. The solution of the system is obtained by setting $X = x_0 e^{\lambda t}$. Where x_0 is a constant vector to be determined, λ is the eigenvalue of A. The

solution $X = x_0 e^{\lambda t}$ (the equilibrium point) is locally stable if all the roots of the characteristic polynomial:

$$P(\lambda) = \lambda^n + a_1\lambda^{n-1} + a_2\lambda^{n-2} + ... + a_{n-1}\lambda + a_n = 0$$

lie in the left hand complex plane that is $Re(\lambda) < 0$ for all roots λ of characteristic polynomial. Now consider the polynomial

$$\lambda^n + a_1\lambda^{n-1} + a_2\lambda^{n-2} + ... + a_{n-1}\lambda + a_n = 0$$

where all the coefficients $a_1, a_2, ..., a_n$ are real and $a_n \neq 0$. The necessary and sufficient condition for all the roots of the characteristic polynomial equation to have $Re(\lambda) < 0$ is the Routh-Hurwitz conditions(Merkin, 1997). These Routh-Hurwitz condition are with $a_n > 0$,

$$D_1 = a_1 > 0$$

$$\det(D_2) = \begin{vmatrix} a_1 & 1 \\ a_3 & a_2 \end{vmatrix} = a_1a_2 - a_3 > 0$$

$$\det(D_3) = \begin{vmatrix} a_1 & 1 & 0 \\ a_3 & a_2 & a_1 \\ 0 & 0 & a_3 \end{vmatrix} = a_1a_2a_3 - a_3^2 > 0$$

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$$\det(D_n) = \begin{vmatrix} a_1 & a_3 & a_5 & . & . & . \\ 1 & a_2 & a_4 & . & . & . \\ 0 & a_1 & a_3 & . & . & . \\ . & & & & & \\ . & & & & & \\ .0 & 0 & 0 & . & . & . & a_k \end{vmatrix} > 0, \text{ for k =1, 2, 3, ... ,n.}$$

1.6.3 Method of Computing Basic Reproduction Number

The basic reproduction number, which is denoted by R_0, is the average number of new cases (infections), that one infected case will generate during its entire infectious life time. The basic reproduction number is an important non-dimensional quantity in epidemiology

as it sets the threshold in the study of a disease both for predicting its outbreak and for evaluating its control strategies (Diekmann et al., 1990). Thus, whether a disease becomes persistent or dies out in a community depends on the value of the reproduction number R_0 . If $R_0 < 1$ it means that every infectious individual will cause less than one secondary infection which is impossible and hence the disease will die out and when $R_0 > 1$ every infectious individual will cause more than one secondary infection and hence the disease will invade the population. Therefore, the basic reproduction number is a threshold parameter for a disease and its biological significance is obvious. (Van den Driessche & Watmough, 2002) developed a technique for calculating the basic reproduction number of disease transmission models. This method is called the next generation operator method.

Consider a disease transmission model that has non-negative initial conditions and can be expressed in terms of the following autonomous system:

$$\frac{dx_i}{dt} = \mathcal{F}_i(x) - \mathcal{V}_i(x) \tag{1.1}$$

where $\mathcal{V}_i(x) = \mathcal{V}_i^-(x) - \mathcal{V}_i^+(x)$. (Van den Driessche & Watmough, 2002)

- $\mathcal{F}_i(x)$ the rate of appearance of new infections in compartment i,
- $\mathcal{V}_i^+(x)$ the rate of transfer of individuals into compartment i by all others means,
- $\mathcal{V}_i^-(x)$ be the rate of transfer of individuals out of compartment i,

The functions $\mathcal{F}_i(x)$, $\mathcal{V}_i^+(x)$, $\mathcal{V}_i^-(x)$ are assumed to be at least twice continuous-differentiable in each variable (Van den Driessche & Watmough, 2002).

1.6.4 Determining the Direction of Bifurcation

Bifurcation is a qualitative changes in the behavior of systems, where one or more system parameters are varied. The study of bifurcation is concerned with how the structural and behavioral change occurs when the parameter(s) are changing. The structural change and the transition behavior of a system are the central part of dynamical evolution. The point at which bifurcation occurs is known as the bifurcation point (Layek, 2015).

For the most part, in epidemic models, there are two distinct bifurcations at $R_0 = 1$ forward (supercritical) and backward (subcritical). A forward bifurcation happens when R_0

crosses unity from below; a small positive asymptotically stable equilibrium appears and the disease-free equilibrium losses its stability. On the other hand, a backward bifurcation happens when R_0 is less than unity; a small positive unstable equilibrium appears while the disease-free equilibrium and a larger positive equilibrium are locally asymptotically stable (Huang et al., 1992). Center manifold theory has been used to decide the local stability of a nonhyperbolic equilibrium (linearization matrix has at least one eigenvalue with zero real part) (Carr, 2012).

Theorem 1.6.1. *(Castillo-Chavez & Song, 2004) Consider the following general system of ordinary differential equations with a parameter* β

$$\frac{dx}{dt} = f(x, \beta), f : \mathbb{R}^n \times \mathbb{R} \to \mathbb{R}^n, f \in C^2(\mathbb{R}^n \times \mathbb{R}) \tag{1.2}$$

Without loss of generality, it is assumed that 0 is an equilibrium point for system (1.2) for all values of the parameter β (that is $f(0, \beta) = 0$) for all β and assume that

A1: A = $D_x f(0, 0) = \left(\frac{\partial f_i}{\partial x_j}(0, 0)\right)$ is the linearization of system (1.2) around the equilibrium 0 with β evaluated at 0. Zero is a simple eigenvalue of A and all other eigenvalues of A have negative real parts.

A2: Matrix A has a non-negative a right eigenvector w and a left eigenvector v corresponding to the zero eigenvalue.

Let f_k be the k^{th} component of f and

$$\mathbf{a} = \sum_{k,i,j=1}^{4} v_k w_i w_j \frac{\partial^2 f_k}{\partial x_i \partial x_j}(0, 0), \mathbf{b} = \sum_{k,i,=1}^{4} v_k w_i \frac{\partial^2 f_k}{\partial x_i \partial \beta}(0, 0) \tag{1.3}$$

The local dynamic of (1.2) around 0 are totally governed by parameters **a** and **b**.

1) **a** > 0, **b** > 0, when $\beta < 0$ with $|\beta| << 1$, 0 is locally asymptotically stable, and there exists a positive unstable equilibrium; when $0 < \beta << 1$, 0 is unstable and there exists a negative and locally asymptotically stable equilibrium.

2) **a** < 0, **b** < 0, when $\beta < 0$ with $|\beta| << 1$, 0 is unstable; when $0 < \beta << 1$, 0 is locally asymptotically stable, and there exists a positive unstable equilibrium.

3) **a** > 0, **b** < 0, when $\beta < 0$ with $|\beta| << 1$, 0 is unstable, and there exists a locally asymptotically stable negative equilibrium; when $0 < \beta << 1$, 0 is stable, and a positive unstable equilibrium appears.

4) **a** < 0, **b** > 0, when β changes from negative to positive, 0 changes its stability from stable

to unstable. Correspondingly, a negative unstable equilibrium becomes positive and locally asymptotically stable.

1.6.5 Numerical Methods for System of ODEs

Numerical techniques that listed below are summarized from (Lenhart & Workman, 2007). When a system of ODEs involves equations that can not be solved analytically, numerical methods are used to compute its approximate solution. For example, fourth order Runge Kutta method $(RK4)$ is widely used for solving initial value problems (IVP) for ordinary differential equation (ODE) which is given

$$\dot{x} = \frac{dx}{dt} = f(t, x),\ x(t_0) = x_0$$

on the interval $t_0 \leq t \leq T$, we divide the interval into N small segments of constant length h, which is called the step size given by $h = \dfrac{T - t_0}{N}$. The numerical methods introduced for a single equation can be easily extended to systems of equations. For example, consider the system of Ordinary differential equation with initial condition.

$$\begin{cases} \dfrac{dx}{dt} = f(t, x, y), & x(t_0) = x_0 \\ \dfrac{dy}{dt} = g(t, x, y), & y(t_0) = y_0 \end{cases} \tag{1.4}$$

We want to obtain a numerical solution on the interval $t_0 \leq t \leq T$. The first step is discretizing the interval by defining the time steps given by

$$t_n = t_0 + nh, \quad n = 0, 1, 2, \cdots N$$

where N is the number of steps. Again we use the notation x_n and y_n to denote the approximate values of $x(t_n)$ and $y(t_n)$, respectively. We can summarize the numerical techniques as:

Runge-Kutta Fourth Order

Given a well-posed initial-value problem (IVP) for the above condition (1.4), the Runge-Kutta method of order four $(RK4)$ constructs a sequence of approximation points $(t, x) \approx (t, x(t))$ and $(t, y) \approx (t, y(t))$ to the exact solution of an ODE by $t_{n+1} = t_n + h$ to get the following values of eight slope:

$$\begin{cases} k_{11} = f(t_n, x_n, y_n) \\ k_{21} = f(t_n, x_n, y_n) \\ k_{12} = f(t_n + \frac{h}{2}, x_n + \frac{h}{2}k_{11}, y_n + \frac{h}{2}k_{21}) \\ k_{22} = f(t_n + \frac{h}{2}, x_n + \frac{h}{2}k_{11}, y_n + \frac{h}{2}k_{21}) \\ k_{13} = f(t_n + \frac{h}{2}, x_n + \frac{h}{2}k_{12}, y_n + \frac{h}{2}k_{22}) \\ k_{23} = f(t_n + \frac{h}{2}, x_n + \frac{h}{2}k_{12}, y_n + \frac{h}{2}k_{22}) \\ k_{14} = f(t_n + h, x_n + hk_{13}, y_n + hk_{23}) \\ k_{24} = f(t_n + h, x_n + hk_{13}, y_n + hk_{23}) \end{cases} \tag{1.5}$$

Then we compute the next approximation using weighted averages of the above slopes,

$$\begin{cases} x_{n+1} = x_n + \frac{h}{6}(k_{11} + 2(k_{12} + k_{13}) + k_{14}) \\ y_{n+1} = y_n + \frac{h}{6}(k_{21} + 2(k_{22} + k_{23}) + k_{24}). \end{cases} \tag{1.6}$$

In such process, the continuous time model is reduced to an approximate discrete time model that is amenable to computer simulation.

1.6.6 Autonomous Linear System

Consider a system of ordinary differential equation which are autonomous.

$$\begin{cases} \frac{dx}{dt} = f(x, y), \\ \frac{dy}{dt} = g(x, y). \end{cases} \tag{1.7}$$

The term autonomous refers to the fact that f and g are not trial function of t. Consider a general autonomous vector field

$$\frac{dx}{dt} = f(x), x \in \mathbb{R}^n \tag{1.8}$$

where $f : \mathbb{R}^n \longrightarrow \mathbb{R}^n$

Definition 1.6.1. ***(Layek, 2015)*** *A point $x_e \in \mathbb{R}^n$ is an equilibrium point of the system (1.8) if $f(x_e) = 0$.*

To determine the behavior near a critical point, we will linearize the non-linear system around the critical point and use our knowledge of linear systems. Let (x_0, y_0) be the equilibrium point of (1.7). If f and g are n-times continuously differentiable functions, then using the Taylor series expansion.

$$\begin{aligned} f(x,y) =& f(x_0,y_0) + f_x(x_0,y_0)(x-x_0) + f_y(x_0,y_0)(y-y_0) + \frac{1}{2!}f_{xx}(x_0,y_0)(x-x_0)^2 + \\ & \frac{1}{2!}f_{yy}(x_0,y_0)(y-y_0)^2 + f_{xy}(x_0,y_0)(x-x_0)(y-y_0) + \dots \\ \approx& f(x_0,y_0) + f_x(x_0,y_0)(x-x_0) + f_y(x_0,y_0)(y-y_0) \\ =& f_x(x_0,y_0)(x-x_0) + f_y(x_0,y_0)(y-y_0) \end{aligned}$$

$$\begin{aligned} g(x,y) =& g(x_0,y_0) + g_x(x_0,y_0)(x-x_0) + g_y(x_0,y_0)(y-y_0) + \frac{1}{2!}g_{xx}(x_0,y_0)(x-x_0)^2 + \\ & \frac{1}{2!}g_{yy}(x_0,y_0)(y-y_0)^2 + g_{xy}(x_0,y_0)(x-x_0)(y-y_0) + \dots \\ \approx& g(x_0,y_0) + g_x(x_0,y_0)(x-x_0) + g_y(x_0,y_0)(y-y_0) \\ =& g_x(x_0,y_0)(x-x_0) + g_y(x_0,y_0)(y-y_0) \end{aligned}$$

Then, the linearized form of equation (1.7)can be expressed as:

$$\frac{dx}{dt} = Ax$$

where $A = \begin{bmatrix} f_x & f_y \\ g_x & g_y \end{bmatrix}$, $x = \begin{bmatrix} x \\ y \end{bmatrix}$ and A is called the Jacobian matrix.

Let $x = ue^{\lambda t}$ be solution of the system of differential equation

$$\frac{dx}{dt} = Ax$$

where u is a vector to determined. Then

$$\frac{dx}{dt} = u\lambda e^{\lambda t} = \lambda x \Longrightarrow Ax = \lambda x \Longrightarrow x(A - \lambda I) = 0.$$

The system will have a non-trival solution if $\det(x(A - \lambda I)) = 0$.

Definition 1.6.2. *(Layek, 2015)) A point x_e is said to be stable for a given $\varepsilon > 0$, there exists a $\delta = \delta(\varepsilon) > 0$ such that, for any other solution, $y(t)$ of (1.8) satisfying $|x_e(t_0) - y(t_0)| < \delta$ implies $|x_e(t) - y(t)| < \varepsilon$, for $t > t_0$, $t_0 \in \mathbb{R}$*

Definition 1.6.3. *(Layek, 2015) A point $x_e(t)$ is said to be locally asymptotically stable if it is stable and for any other solution, $y(t)$ of* (1.8)*, there exists a constant $b > 0$ such that if $|x_e(t_0) - y(t_0)| < b$, then $\lim_{t\to\infty}|x_e(t) - y(t)| = 0$.*

Theorem 1.6.2. *(Perko, 2013) Let x_0 be a hyperbolic equilibrium point of the nonlinear system* (1.8) *with $f \in C^1$ (continuously differentiable of order one). Then the stability of the equilibrium point for the nonlinear system is structurally the same as that of the linear system $\dot{x} = Ax$. Where $A = Df(x_0)$.*

A powerful method for analyzing the stability of an equilibrium point is based on the use of Lyapunov functions.

Definition 1.6.4. *(Layek, 2015) A function V: $\mathbb{R}^n \to \mathbb{R}$ is said to be positive define if,*

- $V(x) > 0$, *for all* $x \neq 0$,
- $V(x) = 0$ *if and only if* $x = 0$,
- $V(x) \to \infty$ *as* $x \to \infty$.

Any function V is called a Lyapunov function, if it satisfies the conditions of positive definite and $\frac{dV}{dt} \leq 0$, $\forall x \in D/\{x_0\}$.

Theorem 1.6.3. ***See in (Layek, 2015).*** *Let x_0 be an equilibrium point of the system of (1.8) and consider $V : D \in \mathbb{R}^n \to \mathbb{R}$ be continuously differentiable function such that*

- $V(x_0) = 0$,
- $V(x) > 0\ \forall x \in D \subseteq R^n$,
- $\dfrac{dV}{dt} < 0\ \forall x \in D/\{x_0\}$, $\|x\| \to \infty \Longrightarrow V(x) \to \infty$.

Then the point x_0 is globally asymptotically stable.

Definition 1.6.5. *(Invariant Set) A set E is an invariant set with respect to (1.8) if $x(0) \in E$ implies $x(t) \in E$, $\forall t \in \mathbb{R}_+$ and a set E is positively invariant set with respect to (1.8) if $x(0) \in E$, implies $x(t) \in E$, $\forall t \geq 0$*

CHAPTER 2

LITERATURE REVIEW

In this chapter, we review some related literature on the outbreaks of COVID-19 and its transmission risk that are directly related to the objectives of this study. The analysis based on mathematical models significantly help decision makers to estimate the risk and the potential future growth of the disease in the population. Understanding the transmission dynamics of the infection is also crucial to design appropriate intervention strategies with minimal implementation costs. In general, by approaching infectious diseases from a mathematical perspective, we can identify patterns and common systems in disease function, which would enable us to find some of the underlying structures that govern outbreaks and pandemic with its future trends. In this regards, many research findings were reported on COVID-19, see for example in (Kucharski et al., 2020; Lin et al., 2020; Mizumoto & Chowell, 1920; Tang et al., 2020) and references cited therein.

Semu et al. (2020) proposed and analyzed a mathematical model for the transmission of COVID-19 disease. Their findings shows that the model exhibits a backward bifurcation at $\mathcal{R}_0 = 1$ when recovered individuals do not develop a permanent immunity for the disease. In the absence of reinfection, their model is without backward bifurcation and the disease free equilibrium is globally asymptotically stable for $\mathcal{R}_0 < 1$. They are also investigated various mitigation strategies using the proposed model and it is observed that the asymptomatic infectious group of individuals may play the major role in the reemergence of the disease in the future.

Eshetu Dadi et al. (2020) formulated a dynamical model of COVID-19 to describe the transmission dynamics of the disease. They proved the well possedness of the formulated

model equation. They estabilished both local and global stability of the disease free equilibrium and endemic equilibrium point of the model equation using basic reproduction number (R_0). Their results shows that the disease free equilibrium point is asymptotically stable when $R_0 < 1$ and the endemic states are considered to exist when the basic reproduction number for each disease is greater than one. The sensitivity analysis of the model equation was performed on the key parameters to find out their relative significance and potential impact on the transmission dynamics of COVID-19. The solution of the model equation is numerically supplemented and sensitivity analysis of the model is analyzed to determine which parameter has high impact on the transmission of diseases.

Ghostine et al. (2021) proposed an extended SEIR model with a vaccination compartment to simulate the novel coronavirus disease (COVID-19) spread in Saudi Arabia. Their model considers seven stages of infection: susceptible (S), exposed (E), infectious (I), quarantined (Q), recovered (R), deaths (D), and vaccinated (V). Initially, they conduct a mathematical analysis to illustrate the non-negativity, boundedness, epidemic equilibrium, existence and uniqueness of the endemic equilibrium, and the basic reproduction number of the model. They used ensemble Kalman filter (EnKF) to constrain the model outputs and its parameters with available data. They apply the proposed assimilation system on real data sets from Saudi Arabia. Finally, they investigate the effect of vaccination on the spread of the pandemic.

Haileyesus and Getachew (2020) developed a deterministic mathematical model of the pandemic COVID-19 transmission in Ethiopia, which allows transmissions by exposed humans. They proposed an SEIR model using system of ordinary differential equations. As their assumption exposed individuals could infect other people with a higher probability than infected compartments. First, they analysed the major qualitative analysis, like the disease free equilibruim point, endemic equilibruim point, basic reproduction number, stability analysis of equilibrium points and sensitivity analysis. Second, they introduced time dependent controls to the basic model and extended to an optimal control model of the disease. They calculated the basic reproduction number R_0 of the system by applying the next generation matrix method. Their findings shows that the model exhibits a forward bifurcation at $\mathcal{R}_0 = 1$ when recovered individuals do not develop a permanent immunity for the disease. Then they analysed using Pontryagin's Maximum Principle to derive necessary conditions for the optimal control of the pandemic.

Djaoue et al. (2020) proposed a COVID-19 model with the mitigation of control strategies

used in Cameroon using biological features of the disease and control strategies based on the isolation of exposed people, confinement (lock-downs) of the human population, testing people living risks area, wearing of masks and respect of hygienic rules. They computed the disease-free equilibrium and derived the basic reproduction number (R_0) that determines the outcome of COVID-19. Their findings shows that the model exhibits a backward bifurcation at $R_0 = 1$ and sensitivity analysis of the system has been performed. They observed that the asymptomatic infectious group of individuals may play a major role in the spreading of transmission by using sensitivity analysis. They are also investigated various mitigation strategies using the proposed model. Generally, they concluded that wearing mask and respecting hygiene rules are fundamental conditions to control the COVID-19.

Liu et al. (2020) develop two differential equations models to account for exposed or latency period, before an infected person is capable of transmitting the infection to other. The first is a model that incorporates infected persons in the exposed class, before transmission is possible. The first model is called SEIRU model. Where $S(t)$ is the number of individuals susceptible to infection at time t, $E(t)$ is the number of asymptomatic noninfectious individuals at time t, $I(t)$ is the number of asymptomatic but infectious individuals at time t, $R(t)$ is the number of reported symptomatic infectious individuals at time t, and $U(t)$ is the number of unreported symptomatic infectious individuals at time t. The second is a model that incorporates a time delay in infected persons, before transmission is possible. It is called SEIRUδ (δ is a time delay). They apply both models to the COVID-19 epidemic in China. They estimate the epidemiological parameters in the models, such as the transmission rate and the basic reproductive number, using data of reported cases. Finally, they evaluate the role of the exposed or latency period in the dynamics of a COVID-19 epidemic.

Çakan (2020) proposed time delayed SEIR epidemic model with compartments consisting of Susceptible (S) against to the disease COVID-19, Exposed (E) to the coronavirus, Infectious (I) and Recovered (R) individuals by taking into account the impact of health care capacity has been examined. They determined the disease-free equilibria and endemic equilibria of the model. Also they analyzed the local and global stabilities of these equilibria by examined corresponding characteristic equation and using LaSalle's Invariance Principle, Lyapunov's direct method respectively. They determined the sensitivity analysis. Finally, from their findings they conclude that the disease induced death rate will increase and the recovery rate will decrease while the level of availability to opportunities provided by health care system

decreases.

Barbarossa et al. (2020) proposed a mathematical model for predicting the evolution in time of detected COVID-19 infections in Germany taking into account the age distribution of cases. They extended SEIR systems of non linear differential equations account for undetected infections, stages of infection, and age groups. They predicted the spread of COVID-19 among the German population by means of mathematical modeling, simulating the implementation or withdrawal of non-pharmaceutical interventions. They simulate different possible strategies for the mitigation of the outbreak, slowing down the spread of the virus and thus reducing the peak in daily diagnosed cases, the demand for hospitalization or intensive care units admissions and eventually the number of fatalities.

Yang and Wang (2020) proposed a mathematical model to investigate the ongoing novel coronavirus epidemic in the Chinese city of Wuhan. The model has two unique features: the incorporation of an environmental reservoir into the disease transmission dynamics and the use of non-constant transmission rates which change with epidemiological status and environmental conditions. Global stability was analyzed using Lyapunov function. They established the global asymptotic stability of the disease-free equilibrium when $R_0 < 1$ and the global asymptotic stability of the endemic equilibrium when $R_0 > 1$. The model was fitted with real data from Wuhan epidemic report.

Chernet et al. (2020) developed a mathematical model for transmission dynamics of COVID-19. They considered SEIAHR model, where the state variables S, E, I, A, H and R represent susceptible, exposed, symptomatically infected, asymptomatically infected, isolated, or hospitalized, and Recovered/immune cases respectively. They have divided the infected cases into two groups: symptomatic and asymptomatic cases. They investigate qualitative analysis including the existence and uniqueness of positive solutions, local and global stability analysis of the diseases-free, and endemic equilibrium points. Result of the sensitivity analysis showed that the most sensitive parameter of the reproductive number is the rate of transmission from asymptotically infected cases to suscepteble individuals.

As mentioned above, all studies were developed mathematical model of COVID-19 transmission dynamic by viewing in different aspects. But many of them did not consider exposed, asymptomatic and symptomatic (infected) individuals in one model. Also many of them did not said about optimal intervention strategies. But from above review (Chernet et al., 2020) used asymptomatic, symptomatic in one model. Eventhough they did not

consider induced death rate on both compartments. To fulfill the entire gap of these studies we introduced asymptomatic (in this compatment there is induced death rate μ_2), infected individuals with optimal control in this study.

CHAPTER 3

RESEARCH METHODOLOGY

In this chapter, we outlined the methods and materials that are used to achieve the general and specific objectives stated in Section 1.3. The study involved the following study area and mathematical procedures.

3.1 Study Area

Ethiopia is in the northeast African region known as the Horn of Africa. Capital Cities of Ethiopia is Addis Ababa. It is the second-most populous nation with 114961850 populations according to UN data (2020 est.) in Africa (after Nigeria) and the 12th in the world. Ethiopia population is equivalent to 1.47% of the total world population. It is bounded by Eritrea to the north, Djibouti to the northeast, Somalia to the east, Kenya to the south, and Sudan and South Sudan to the west. The country occupies total area of 1,104,300 sq km (WHO, 2020c). Ethiopia's economy experienced strong, broad-based growth averaging 9.4% a year from 2010/11 to 2019/20, Ethiopia's real gross domestic product (GDP) growth slowed down to 6.1% in 2019/20 due to COVID-19 (corna virus pandemic). Industry, mainly construction, and services accounted for most of the growth. Agriculture was not affected by the COVID-19 pandemic and its contribution to growth slightly improved in 2019/20 compared to the previous year. Private consumption and public investment explain demand-side growth, the latter assuming an increasingly important role (Worldbank, 2020).

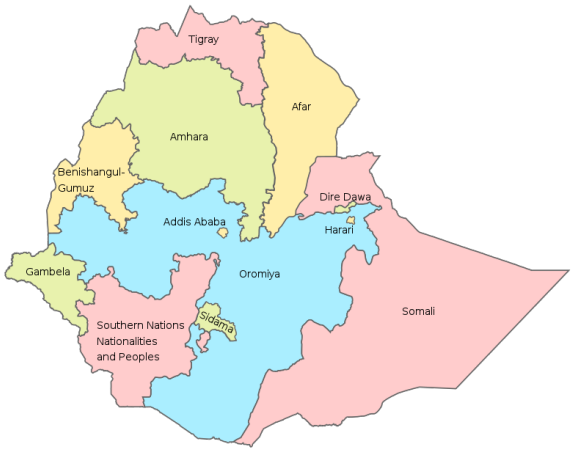

Figure 3.1: Map of Ethiopia:source wikipidia

3.2 Source of Data

The researcher used secondary data and relevant parameters values from literatures in addition to the following:

- reported data on COVID-19 by the Ethiopian Public Health and WHO,
- Other source of information such as book and journals.

3.2.1 Method of Data Analysis

The study involved both qualitative and quantitative analysis. Thus, the data is analyzed using MATLAB Software and the results are displayed in the form of tables and figures.

3.3 Descriptions of Mathematical Procedure

We develop a mathematical model which describes the transmission dynamics of COVID-19 with optimal control using a system of nonlinear ODEs. We performed the qualitative analysis of the model. Both local and global stability analysis of the equilibrium points of the model equations have been done using linearization and Lyapunov functions respectively. Sensitivity analysis of the system have been studied to determine which parameter plays greater role in the transmission dynamics of COVID-19 infection. The optimal control have been derived by using the Pontryagin's minimum principle (PMP). To supplement the analytical solution of the model equation we performed a numerical simulation using $MATLAB\ R2018a$.

CHAPTER 4

MODEL FORMULATION AND ANALYSIS

This chapter presents a deterministic mathematical model for COVID-19 pandemic using a system of nonlinear ordinary differential equations. Model description and analysis are also detailed in order.

4.1 Model Description

In this section, we consider an SEAIR type Mathematical modeling for the dynamics of COVID-19 pandemic. The total population $N(t)$ is divided into five compartments: Susceptible $S(t)$, Exposed $E(t)$, Asymptomatic $A(t)$, Infected $I(t)$ and Recovered $R(t)$ population at time $t \geq 0$. Thus, total population is given by

$$N(t) = S(t) + E(t) + A(t) + I(t) + R(t).$$

The description of all the state variables are given in Table 4.1.

The model assumed that susceptible individuals are recruited (by birth or immigration) into the population at a constant rate b. A proportion of the susceptible individuals become exposed to the COVID-19 infection at a rate $\lambda = \dfrac{\beta(I + qA)}{N}$ which is called force of infection as given in (Eshetu Dadi et al., 2020) when they come into effective contact with an infectious individuals at a rate β, where β is an effective contact rate and q is the transmission coefficient for the asymptomatic individuals. In the model, k is a per capita rate of becoming infectious. A proportion of p of the individuals in the compartment E may develop a symptoms of the

Table 4.1: Notations and description of the model variables

Variable	Description
S(t)	Susceptible populations which are vulnerable to the disease at time t,
E(t)	The number of individuals who are exposed but are not yet infectious at time t,
A(t)	Infectious individuals who are not show symptoms of the disease at time t,
I(t)	Infectious individuals who show symptoms of the disease at time t,
R(t)	Individuals who have been recovered from the infection at time t,
N(t)	Total population at time t,

COVID-19 infection and move to the infected compartment I at a rate pk. The rest of individuals becomes asymptomatic with COVID-19 infection with probability $(1-p)$ and move to the class A at a rate $(1-p)k$. Furthermore, an individual in asymptomatic A compartment is recovered due to natural immunity and move to recovered class R at a rate γ. The infected individuals I recovered after receiving a treatment at a rate α and move to the recovered class R. A recovered individuals may revert to the susceptible class S after losing their immunity at a rate θ. Compared to the model introduced in (Çakan, 2020), the present model differ due to absence of delayed parameter and consideration of asymptomatic compartment. Besides, we assumed that the portion of recovered populations are re-susceptible due to immunity lose. Furthermore, COVID-19 induced death rates μ_2 is also incorporated in the compartment A. All individuals in $N(t)$ suffers natural mortality at a rate d.

In addition to these model description, the formulation of the governed mathematical model is based on the following assumptions: the size of population is constant, natural birth rate and death rate are not equal, all parameters are non-negative, all the individuals in the community are susceptible when there is no disease. The corresponding COVID-19 transmission diagram is depicted in Figure 4.1.

The compartmental epidemic system for COVID-19 is governed by the system of nonlinear

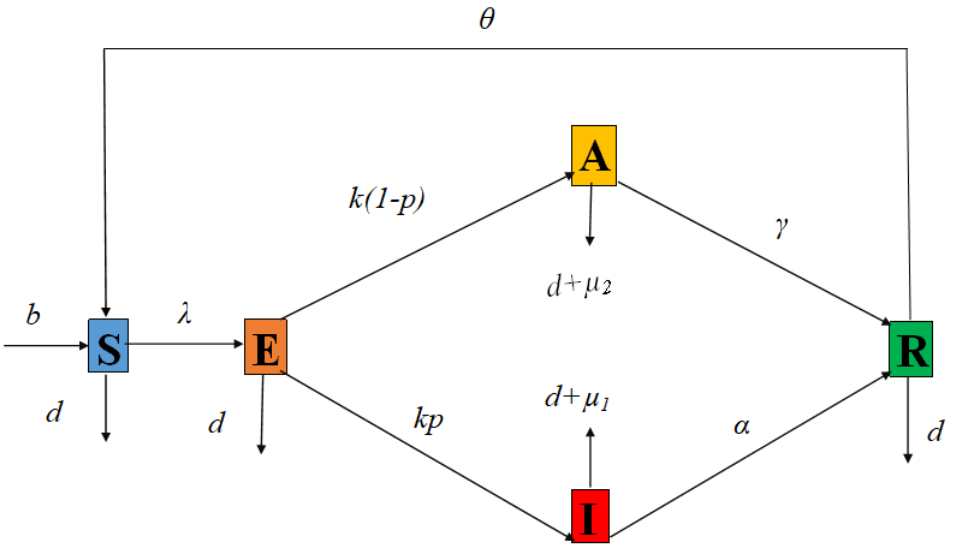

Figure 4.1: Compartmental flow diagram for COVID-19 transmission.

differential equations:

$$\begin{aligned}
\frac{dS}{dt} &= b - \lambda S - dS + \theta R, \\
\frac{dE}{dt} &= \lambda S - (k+d)E, \\
\frac{dA}{dt} &= (1-p)kE - (d+\mu_2+\gamma)A, \\
\frac{dI}{dt} &= pkE - (\mu_1+d+\alpha)I, \\
\frac{dR}{dt} &= \gamma A + \alpha I - (\theta+d)R,
\end{aligned} \tag{4.1}$$

where $\lambda = \dfrac{\beta(I+qA)}{N}$. The non-negative initial conditions are given as $S(0) = S_0 > 0$, $E(0) = E_0 \geq 0$, $A(0) = A_0 \geq 0$, $I(0) = I_0 \geq 0$, $R(0) = R_0 \geq 0$. The parameter descriptions are also given in Table 4.2.

4.2 Model Analysis

4.2.1 Invariant Region

Let us determine a region in which the solution of model (4.1) is bounded. For this model the total population time t is given by $N(t) = S(t) + E(t) + A(t) + I(t) + R(t)$. Then, differentiating N with respect to time we obtain:

$$\frac{dN}{dt} = \frac{dS}{dt} + \frac{dE}{dt} + \frac{dA}{dt} + \frac{dI}{dt} + \frac{dR}{dt} = b - \mu_1 I - \mu_2 A - dN.$$

Table 4.2: Description of model parameters

Parameter	Description
b	Recruited rate of susceptible individual
d	Natural death rate
μ_1	Death rate due to disease in the symptomatic compartment.
μ_2	Death rate due to disease in the asymptomatic compartment
β	Effective contact rate of infection
λ	Force of infection rate
p	Probability of exposed individuals joining infectious class
k	Per capita rate of becoming infectious
θ	Rate at which recovered individuals reverts to susceptible class
α	progression from compartment $I(t)$ to $R(t)$ due to effective treatment
γ	Rate at which asymptomatic individuals recovered
q	Transmission rate for asymptomatic individuals

If there is no death due to the disease, we get

$$\frac{dN}{dt} \leq b - dN, \tag{4.2}$$

$$N'(t) + dN(t) \leq b.$$

By integrating factor,

$$\frac{d}{dt}\left(N(t)e^{dt}\right) \leq be^{dt}. \tag{4.3}$$

Integrating both sides of the equation (4.3) and simplifying it, then we have

$$N(t) \leq \frac{b}{d} + ce^{-dt}. \tag{4.4}$$

As $t \to \infty$ in equation (4.4), the population size $N(t) \to \dfrac{b}{d}$, which implies that $0 \leq N(t) \leq \frac{b}{d}$. Thus, the feasible region of the system (4.1)is given by the set

$$\Omega = \left\{(S, E, A, I, R) \in \mathbb{R}^5_+ : 0 \leq N(t) \leq \frac{b}{d}\right\} \tag{4.5}$$

is positively invariant. That is,

$$\left.\frac{dS}{dt}\right|_{S=0} = b + \theta R > 0, \quad \left.\frac{dE}{dt}\right|_{E=0} = \lambda S \geq 0, \quad \left.\frac{dA}{dt}\right|_{A=0} = (1-p)kE \geq 0,$$

$$\left.\frac{dI}{dt}\right|_{I=0} = pkE \geq 0, \quad \left.\frac{dR}{dt}\right|_{R=0} = \gamma A + \alpha I \geq 0.$$

Consequently, this region attracts all solutions of the system and this restricted region will be enough to consider of the dynamics of the model(4.1).

4.2.2 Existence and Uniqueness of the Solution

The validity and authenticity of any mathematical model depends on the existence and uniqueness of the solutions for the governing system of equations.

Theorem 4.2.1. *Let $t_0 > 0$ and the initial conditions satisfies $S(0) > 0$, $E(0) > 0$, $A(0) > 0$, $I(0) > 0$ and $R(0) > 0$ in the prescribed region Ω. Then the solutions of the model system* (4.1) *exists and unique in $\mathbb{R}^5_+$.*

Proof. The right hand side of the model equation (4.1) can be expressed as follows:

$$\begin{aligned}
f_1(S, E, A, I, R) &= b - (\lambda + d)S + \theta R, \\
f_2(S, E, A, I, R) &= \lambda S - (k + d)E, \\
f_3(S, E, A, I, R) &= (k - pk)E - (d + \gamma + \mu)A, \\
f_4(S, E, A, I, R) &= pkE - (\mu + d + \alpha)I, \\
f_5(S, E, A, I, R) &= \gamma A + \alpha I - (\theta + d)R.
\end{aligned}$$

Let Ω denote the region

$$\Omega = \left\{ (S(t), E(t), A(t), I(t), R(t)) \in \mathbb{R}^5_+ : N(t) \leq \frac{b}{d} \right\}.$$

Then equations (4.1) have a unique solution if $\frac{\partial f_i}{\partial x_j}, i,\ j = 1, 2, 3 \ldots 5$, are continuous and bounded in Ω. Here, using notations $x_1 = S, x_2 = E, x_3 = A, x_4 = I, x_5 = R$. When we differentiate the system $\frac{\partial f_i}{\partial x_j}$ it is continuous and bounded in Ω. Here, observe that f has a continuous first partial derivative with respect to each state variables in $\mathbb{R}^5_+$. It follows that f is locally Lipschitz. Thus, the result is the direct outcome of fundamental existence and uniqueness theorem (Perko, 2013) in $\mathbb{R}^5_+$. □

4.2.3 Non-negativity of Solutions

Theorem 4.2.2. *If S(0), E(0), A(0), I(0) and R(0) are all non-negative, then the solutions S(t), E(t), A(t), I(t), and R(t) are all positive for $t \geq 0$.*

Proof. From the system of differential equation (4.1), let us take the first equation:

$$\frac{dS}{dt} = b - \lambda S - dS + \theta R,$$

This equation can be expressed without loss of generality, after eliminating the positive term $(b + \theta R)$, as an inequality

$$\frac{dS}{dt} > -\left(\frac{\beta(I + qA)}{N} + d\right) S,$$

then using separable method of variables and applying integration, the solution of the differentially inequality can be obtained as

$$S(t) \geq S(0)e^{-dt - \frac{\beta}{N}\int (I(t)+qA(t))dt} \geq 0,$$

where $S(0)$ is obtain from initial condition. Since exponential function is always non-negative, the function $e^{-dt - \frac{\beta}{N}\int (I(t)+qA(t))dt}$ is a non-negative quantity. Hence, we can concluded that $S(t) \geq 0$.

Similarly, the second equation for the system (4.1) is given by

$$\frac{dE}{dt} = \lambda S - (k + d)E,$$

after eliminating the positive term λS as an inequality as

$$\frac{dE}{dt} > -(k + d)E.$$

Using separable method of variables and on applying integration, the solution of the foregoing differentially inequality can be obtained as

$$E(t) \geq E(0)e^{-(k+d)t} \geq 0,$$

where $E(0)$ is obtain from initial condition. Recall that an exponential function is always non-negative irrespective of the sign of the exponent, i.e, the exponential function $e^{-(k+d)t}$ is a non-negative quantity. Hence, we can concluded that $E(t) \geq 0$.

Similarly, we obtain

$$A(t) \geq A(0)e^{-(d+\mu+\gamma)t} \geq 0,$$

$$I(t) \geq I(0)e^{-(d+\mu+\alpha)t} \geq 0,$$

$$R(t) \geq R(0)e^{-(d+\theta)t} \geq 0.$$

This proves that the solution of system (4.1) are positive for all $t \geq 0$. □

4.2.4 Disease Free Equilibrium Point

Disease free equilibrium points are steady-state solutions where there is no COVID-19 infection. That is, all the infected classes are zero and the entire population comprise of only susceptible individuals. To find the disease free equilibrium (DFE), we equate the left hand side of the system (4.1) equal to zero at $E(t) = 0, I(t) = 0\ and\ A(t) = 0$. We denote disease-free equilibrium point by E_0. Equating system 4.1 equal to zero, we have that;

$$\begin{cases} b - \lambda S - dS + \theta R = 0, \\ \lambda S - (k + d)E = 0, \\ (1 - p)kE - (d + \mu_2 + \gamma)A = 0, \\ pkE - (\mu_1 + d + \alpha)I = 0, \\ \gamma A + \alpha I - (\theta + d)R = 0, R = 0. \end{cases}$$

Solving for the non-infected state variable, we obtain the disease free equilibrium point

$$E_0 = \left\{S^0, E^0, A^0, I^0, R^0\right\} = \left\{\frac{b}{d}, 0, 0, 0, 0\right\}.$$

4.2.5 The Basic Reproduction Number

In this sectin, we determined the basic reproduction number. We use the next generation method given in (Van den Driessche & Watmough, 2002) to compute R_0. It is obtained by taking the largest (dominant) eigenvalue (spectral radius).

$$R_0 = \rho(FV^{-1}).$$

Next, we derive an expression for the basic reproduction number using the method of the next generation matrix. The first step is rewrite the model equations, starting with newly infective classes:

$$\begin{aligned} \frac{dE}{dt} &= \frac{\beta(I + qA)}{N}S - (k + d)E, \\ \frac{dA}{dt} &= (1 - p)kE - (d + \mu_2 + \gamma)A, \\ \frac{dI}{dt} &= pkE - (\mu_1 + d + \alpha)I, \end{aligned} \tag{4.6}$$

For this model, the associated matrices $\mathcal{F}$ and $\mathcal{V}$ the new infectious terms and the remaining transition terms are respectively given by:

$$\mathcal{F}_i(x) = \begin{bmatrix} \frac{\beta(I+qA)S}{N} \\ 0 \\ 0 \end{bmatrix} \text{ and } \mathcal{V}_i(x) = \begin{bmatrix} (k+d)E \\ (d+\mu_2+\gamma)A - (1-p)kE \\ (d+\mu_1+\alpha)I - pkE \end{bmatrix},$$

The Jacobian matrices at the disease-free equilibrium point of $\mathcal{F}$ and $\mathcal{V}$ are obtained by derivating with respect to $E, A\ and\ I$. As following:

$$F(E_0) = \begin{bmatrix} 0 & \beta q & \beta \\ 0 & 0 & 0 \\ 0 & 0 & 0 \end{bmatrix} \text{ and } V(E_0) = \begin{bmatrix} a & 0 & 0 \\ -(1-p)k & c & 0 \\ -pk & 0 & e \end{bmatrix}$$

where, $a = k + d, c = d + \mu_2 + \gamma, e = \mu_1 + d + \alpha$.

$$|V(E_0| = \begin{vmatrix} a & 0 & 0 \\ -(1-p)k & c & 0 \\ -pk & 0 & e \end{vmatrix} = ace \neq 0.$$

Hence, the matrix $V(E_0)$ is invertible and thus

$$[V(E_0)]^{-1} = \begin{pmatrix} \frac{1}{a} & 0 & 0 \\ \frac{(1-p)k}{bc} & \frac{1}{c} & 0 \\ \frac{pk}{be} & 0 & \frac{1}{e} \end{pmatrix}. \tag{4.7}$$

Moreover,

$$[F(E_0)]\,[V(E_0)]^{-1} = \begin{pmatrix} \frac{\beta qk(1-p)}{ac} + \frac{\beta pk}{ae} & \frac{\beta q}{c} & \frac{\beta}{e} \\ 0 & 0 & 0 \\ 0 & 0 & 0 \end{pmatrix}. \tag{4.8}$$

Since F is non-negative and V is non-singular, then V^{-1} is non-negative and FV^{-1} is non-negative. The matrix FV^{-1} is called next generation matrix for the model, see for example in (Van den Driessche & Watmough, 2002). The eigenvalues of the matrix FV^{-1} can be compute as $\det(FV^{-1} - \lambda I) = \left|FV^{-1} - \lambda I\right| = 0$. Equivalently,

$$|FV^{-1} - \lambda| = \begin{vmatrix} \frac{\beta qk(1-p)}{ac} + \frac{\beta pk}{ae} - \lambda & \frac{\beta q}{c} & \frac{\beta}{e} \\ 0 & 0-\lambda & 0 \\ 0 & 0 & 0-\lambda \end{vmatrix} = 0. \tag{4.9}$$

After simple manipulation, the eigenvalues are:

$$\lambda_1 = \lambda_2 = 0, \lambda_3 = \frac{\beta qk(1-p)}{ac} + \frac{\beta pk}{ae} = \frac{\beta k\left(pc + qe(1-p)\right)}{ace}$$

where, $a = k + d, c = d + \mu_2 + \gamma, e = \mu_1 + d + \alpha$.

Finally, the basic reproductive number is given by $R_0 = \rho(FV^{-1})$ where $\rho(FV^{-1})$ denotes the spectral radius of the matrix FV^{-1} which is the largest non-negative eigenvalue of the next generation matrix. Therefore,

$$R_0 = \lambda_3 = \frac{\beta k\left(p(d+\mu_2+\gamma) + q(\mu_1+d+\alpha)(1-p)\right)}{(k+d)(d+\mu_2+\gamma)(\mu_1+d+\alpha)}.$$

4.2.6 Endemic Equilibrium Point

The Endemic equilibrium point which denoted by E^1 is a steady state solution where the disease persists in the population. The endemic equilibrium $E^1 = (S^*, E^*, A^*, I^*, R^*)$ can be obtained by setting the left hand side in (4.1) equal to zero. That means

$$\begin{cases} b - \lambda S^* - dS^* + \theta R^* = 0, \\ \lambda S^* - aE^* = 0, \\ (1-p)kE^* - cA^* = 0, \\ pkE^* - eI^* = 0, \\ \gamma A^* + \alpha I^* - fR^* = 0. \end{cases}$$

where $a = k + d, c = d + \mu_2 + \gamma, e = \mu_1 + d + \alpha, f = \theta + d$

From the above system we can get the values of endemic equilibrium point.

$$S^* = \frac{a}{\lambda}E^* = \frac{aN^*}{\beta(qA^* + I^*)}E^* \tag{4.10}$$

$$A^* = \frac{(1-p)k}{c}E^* \tag{4.11}$$

$$I^* = \frac{pk}{e}E^* \tag{4.12}$$

$$R^* = \frac{\gamma ke(1-p) + \alpha pck}{cef}E^* \tag{4.13}$$

where $\lambda = \dfrac{\beta(qA^* + I^*)}{N^*}$.

Solving for S^* by inserting 4.11, 4.12 into 4.10.

$$S^* = \frac{aceN^*}{\beta k(qe(1-p) + pc)} \tag{4.14}$$

since $R_0 = \dfrac{\beta k\,(pc + qe(1-p))}{ace}$

$$S^* = \frac{N^*}{R_0}$$

E^* can be obtained by inserting 4.14,4.11,4.13 in to

$$b - \frac{\beta(qA^* + I^*)}{N^*}S^* - dS^* + \theta R^* = 0,$$

$$\implies E^* = \frac{bcef}{acef - [\theta\gamma ke(1-p) + \theta\alpha kpc]}\left(1 - \frac{1}{R_0}\right).$$

From 4.11 we can obtain the value of A^*.

$$A^* = \frac{befk(1-p)}{acef - [\theta\gamma ke(1-p) + \theta\alpha kpc]}\left(1 - \frac{1}{R_0}\right)$$

From 4.12 we can determine the values of I^*.

$$I^* = \frac{pkbcf}{acef - [\theta\gamma ke(1-p) + \theta\alpha kpc]}\left(1 - \frac{1}{R_0}\right).$$

The values of R^* is obtained as follows

$$R^* = \frac{b}{\theta}\left[\frac{acef}{acef - [\theta\gamma ke(1-p) + \alpha\theta kpc]} - 1\right]\left(1 - \frac{1}{R_0}\right).$$

4.3 Stability Analysis of Disease Free Equilibrium Point

The model (4.1) has a unique disease free equilibrium (DFE), E_0, given by $E_0 = (S^0, 0, 0, 0, 0)$, where $S^0 = \dfrac{b}{d}$.

4.3.1 Local Stability of Disease Free Equilibrium Point

Theorem 4.3.1. *The disease-free equilibrium* $E_0 = (\dfrac{b}{d}, 0, 0, 0, 0)$ *of the system* (4.1) *is locally asymptotically stable if* $R_0 < 1$.

Proof. The Jacobian matrix at the disease-free equilibrium E_0 of the system (4.1) is

$$J(E_0) = \begin{bmatrix} -d & 0 & -\beta q & -\beta & \theta \\ 0 & -a & \beta q & \beta & 0 \\ 0 & (1-p)k & -c & 0 & 0 \\ 0 & pk & 0 & -e & 0 \\ 0 & 0 & \gamma & \alpha & -f \end{bmatrix} \tag{4.15}$$

where, $a = k + d, c = d + \mu_2 + \gamma, e = \mu_1 + d + \alpha, f = \theta + d$. The eigenvalues of $J(E_0)$ are the solutions of the characteristics equation $\det[J(E_0) - \lambda I_5] = 0$,where I_5 is an identity matrix of order 5. Then we have

$$|J(E_0) - \lambda I_5| = \begin{vmatrix} -d-\lambda & 0 & -\beta q & -\beta & \theta \\ 0 & -a-\lambda & \beta q & \beta & 0 \\ 0 & (1-p)k & -c-\lambda & 0 & 0 \\ 0 & pk & 0 & -e-\lambda & 0 \\ 0 & 0 & \gamma & \alpha & -f-\lambda \end{vmatrix} = 0$$

The corresponding characteristic equation has the following form:

$$(d + \lambda)(f + \lambda)[\lambda^3 + a_1\lambda^2 + a_2\lambda + a_3] = 0 \tag{4.16}$$

where

$a_1 = a + c + e = 3d + k + \gamma + \alpha + \mu_1 + \mu_2$,

$a_2 = (k+d)(d+\mu_2+\gamma)+(k+d)(\mu_1+d+\alpha)+(d+\mu_2+\gamma)(\mu_1+d+\alpha)-\beta k(q(1-p)+p)$,

$a_3 = ace(1 - R_0) = (k + d)(d + \mu_2 + \gamma) + (\mu_1 + d + \alpha)(1 - R_0)$,

$f = \theta + d$,

Then solving equation (4.16) we obtain

$$(d + \lambda)(f + \lambda) = 0, \text{ or } \lambda^3 + a_1\lambda^2 + a_2\lambda + a_3 = 0. \tag{4.17}$$

Clearly, the sign of the first two eigenvalues $\lambda_1 = -d$ and , $\lambda_2 = -e$ are negative. To determine the sign of the remaining eigenvalues we use the Routh-Hurwitz criteria which state that the roots of the characteristic equation:

$$\lambda^3 + a_1\lambda^2 + a_2\lambda + a_3 = 0$$

are real distinct and negative if the coefficients satisfy the conditions $a_1 > 0$, $a_2 > 0$, $a_3 > 0$ and $a_1a_2 - a_3 > 0$. Here, $a_1 > 0 \Longrightarrow a + c + e > 0$ since all parameters are positive. Again, $a_2 > 0 \Longrightarrow ac+ae+ce > \beta k(q(1-p)+p)$, and $a_3 > 0 \Longrightarrow ace(1-R_0) > 0 \Longrightarrow R_0 < 1$. Furthermore,

$a_1a_2 > a_3 \Longrightarrow (a + c + e)(ac + ae + ce - \beta k(q(1 - p) + p)) > ace(1 - R_0)$.

$a_1a_2 > a_3$ if $R_0 < 1$.

Therefore, we can conclude that the disease free equilibrium point of the model equation (4.1) is locally asymptotically stable if $R_0 < 1$. □

4.3.2 Global Stability of the Disease Free Equilibrium Point

Theorem 4.3.2. *The disease free equilibrium of the system* (4.1) *is globally asymptotically stable if* $R_0 < 1$.

Proof. Let $\Omega \subseteq R_+^5$ be an open neighborhood of the disease free equilibrium point E_0. Then define the Lyapunove function L, defined by:

$$L = C_1E + C_2A + C_3I \tag{4.18}$$

where C_i, for i = 1, 2, 3, are some positive constants. The Lyapunov function L is continuously differentiable as the functions of E, A, I and $L(E_0) = 0$ as well as $L > 0, \forall (S, E, A, I, R) \in \mathbb{R}_+^5 - \{E_0\}$

Now differentiating L with respect to time we obtain

$$\frac{dL}{dt} = C_1\frac{dE}{dt} + C_2\frac{dA}{dt} + C_3\frac{dI}{dt}$$

$$= C_1[\frac{\beta(I + qA)S}{N} - aE] + C_2[(1-p)kE - cA] + C_3[pkE - eI]$$

$$\leq C_1[\beta I + \beta qA - aE] + C_2[(1-p)kE - cA] + C_3[pkE - eI], \text{ since } S \leq N$$

$$= [C_3pk + C_2(1-p)k - C_1a]E + [\beta C_1q - C_2c]A + [\beta C_1 - C_3e]I$$

$$= C_1a\left(\frac{C_3pk + C_2(1-p)k}{C_1a} - 1\right)E + [\beta C_1q - C_2c]A + [\beta C_1 - C_3e]I.$$

Now choosing $C_1 = ce$, $C_2 = \beta qe$ and $C_3 = \beta c$; then we have

$$\frac{dL}{dt} = ace\left(\frac{\beta cpk + \beta qe(1-p)k}{cea} - 1\right)E + [\beta ceq - \beta qec]A + [\beta ce - \beta ce]I$$

$\frac{dL}{dt} = ace\left(\frac{\beta cpk + \beta qe(1-p)k}{cea} - 1\right)E + 0$. This implies that
$\frac{dL}{dt} \leq ace(R_0 - 1)E$.

Hence, $\frac{dL}{dt} \leq 0$ for $R_0 < 1$ and $\frac{dL}{dt} = 0$ if and only if $E = 0$. Therefore, the largest compact invariant set in Ω is the singleton set $(\frac{b}{d}, 0, 0, 0, 0)$. Hence, by LaSalle's invariant

principle (La Salle, 1976), every solution to equations of model (4.1) with initial conditions in Ω which approaches the disease-free equilibrium point as time t tends to infinity whenever $R_0 < 1$. This implies that the disease-free equilibrium is globally asymptotically stable in Ω. □

4.4 Stability Analysis of Endemic Equilibrium Point

The endemic equilibrium point denoted by $E^1 = (S^*, E^*, A^*, I^*, R^*)$ is a steady state solution where the disease persists in the population. It is determined above by setting rates of changes of variables with respect to time in the model equation (4.1) to zero.

4.4.1 Local Stability of Endemic Equilibrium Point (EEP)

Theorem 4.4.1. *The Endemic equilibrium Point (EEP) of system (4.1) at E^1 is locally asymptotically stable if $R_0 > 1$.*

Proof. To proof the local stability of endemic equilibrium point of the system (4.1) we use linearizion approach. Thus, the Jacobian $J(E^1)$ matrix at the endemic equilibrium point becomes

$$J(E^1) = \begin{bmatrix} -r-d & 0 & \frac{-\beta S^* q}{N^*} & \frac{-\beta S^*}{N^*} & \theta \\ r & -a & \frac{\beta S^* q}{N^*} & \frac{\beta S^*}{N^*} & 0 \\ 0 & (1-p)k & -c & 0 & 0 \\ 0 & pk & 0 & -e & 0 \\ 0 & 0 & \gamma & \alpha & -f \end{bmatrix} \tag{4.19}$$

where $r = \dfrac{\beta(I^* + qA^*)}{N^*}$. The characteristic equation of the Jacobian matrix (4.19) at the endemic equilibrium point is also given by:

$$P(\lambda) = \lambda^5 + A_1\lambda^4 + A_2\lambda^3 + A_3\lambda^2 + A_4\lambda + A_5 \tag{4.20}$$

where

$A_1 = a + c + e + f + r + d,$

$A_2 = ac + ae + ce + fr + df + (f + r + d)(a + c + e) - \dfrac{\beta k S^*}{N*}[q(1-p) + p],$

$A_3 = (a+c+e)+(f+r+d)(ac+ae+ce+(a+c+e)(fr+df)-\dfrac{S^*}{N*}[R_0ace+\beta k(q(1-p)+p)],$

$A_4 = (fr + df)(ac + ae + ce + \dfrac{\beta k S^*}{N*}(pq - p - q)) - \dfrac{R_0 ace S^*}{N^*}(f + r + d),$

$A_5 = \frac{\beta k S^*}{N^*}(r+d)(pqe - pc - qe).$

Here, $r = \frac{\beta(I^* + qA^*)}{N^*} = \frac{acefbR_0}{N^*(acef - [pck\alpha\theta + (1-p)\gamma\theta ke])}\left(1 - \frac{1}{R_0}\right).$

The eigenvalues of the characteristic polynomial (4.20) will be negative if it fulfill the Routh-Hurwitz conditions that are $A_i > 0$, for $i = 1, 2, 3, 4, 5$. That is,

$A_1 > 0$ since it is the sum of all positives number,

$A_2 > 0 \Longrightarrow ac + ae + ce + fr + df + (f + r + d)(a + c + e) + \frac{\beta kpq}{R_0} > \frac{\beta k}{R_0}[q + p],$

$A_3 > 0 \Longrightarrow (a + c + e) + (f + r + d)(ac + ae + ce + (a + c + e)(fr + df) > \frac{1}{R_0}[R_0 ace +$
$\beta k(q(1-p) + p)],$

$A_4 > 0 \Longrightarrow (fr + df)(ac + ae + ce + \frac{\beta k}{R_0}(pq - p - q)) > \frac{R_0 ace}{R_0}(f + r + d),$

$A_5 > 0 \Longrightarrow \frac{\beta kpqe}{R_0}(r + d) > \frac{\beta k}{R_0}(pc + qe)(r + d),$

and

$A_1A_2 - A_3 > 0, \quad A_1A_2A_3 - A_3^2 - A_1^2A_4 > 0,$

$A_1A_2A_3A_4 + 2A_1A_4A_5 + A_2A_3A_5 - A_1A_2^2A_5 - A_1^2A_4^2 - A_5^2 > 0.$

Hence, the EEP of the model(4.1) will be locally asymptotically stable if $R_0 > 1$. □

4.4.2 Global Stability of Endemic Equilibrium Point (EEP)

Theorem 4.4.2. *The endemic equilibrium point (EEP) at E^1 of model equation (4.1) is globally asymptotically stable if $R_0 > 1$.*

Proof. To analyze the global stability of the endemic equilibrium point, we construct the Lyapunov function defined by

$$L(S^*, E^*, A^*, I^*, R^*) = \left(S(t) - S^* - S^* \ln(\frac{S(t)}{S^*})\right) + \left(E(t) - E^* - E^* \ln(\frac{E(t)}{E^*})\right)$$
$$+ \left(A(t) - A^* - A^* \ln(\frac{A(t)}{A^*})\right) + \left(I(t) - I^* - I^* \ln(\frac{I(t)}{I^*})\right) + \left(R(t) - R^* - R^* \ln(\frac{R(t)}{R^*})\right) \quad (4.21)$$

After differentiating L with respect to time it gives

$$\frac{dL}{dt} = \left(1 - \frac{S^*}{S}\right)\frac{dS}{dt} + \left(1 - \frac{E^*}{E}\right)\frac{dE}{dt} + \left(1 - \frac{A^*}{A}\right)\frac{dA}{dt} + \left(1 - \frac{I^*}{I}\right)\frac{dI}{dt} + \left(1 - \frac{R^*}{R}\right)\frac{dR}{dt}$$

$$= \left(1 - \frac{S^*}{S}\right)(b - \lambda S - dS + \theta R) + \left(1 - \frac{E^*}{E}\right)(\lambda S - (k + d)E) + \left(1 - \frac{A^*}{A}\right)((1-p)kE - (d + \mu_2 + \gamma)A)$$

$$+\left(1-\frac{I^*}{I}\right)(pkE-(\mu_1+d+\alpha)I)+\left(1-\frac{R^*}{R}\right)(\gamma A+\alpha I-(\theta+d)R)$$
$$=[b+(\lambda+d)S^*+aE^*+cA^*+eI^*+fR^*]-\left[b+(b+\theta R)\frac{S^*}{S}+\lambda S\frac{E^*}{E}+(1-p)kE\frac{A^*}{A}+pkE\frac{I^*}{I}\right]$$
$$+\left[(\gamma A+\alpha I)\frac{R^*}{R}+\mu_1 I+\mu_2 A\right]$$

Let $A=[b+(\lambda+d)S^*+aE^*+cA^*+eI^*+fR^*]$ and

$$B=\left[(b+\theta R)\frac{S^*}{S}+\lambda S\frac{E^*}{E}+(1-p)kE\frac{A^*}{A}+pkE\frac{I^*}{I}+(\gamma A+\alpha I)\frac{R^*}{R}+\mu_1 I+\mu_2 A\right]$$

Then we have, $\frac{dL}{dt}=A-B$. Based on this, $\frac{dL}{dt}<0$ if $A<B$ and $\frac{dL}{dt}=0$ if and only if $(S^*=S,E^*=E,A^*=A,I^*=I,R^*=R)$. Therefore, the largest compact invariant set in $\left\{(S^*,E^*,A^*,I^*,R^*)\in\Omega;\frac{dL}{dt}=0\right\}$ is a singleton E^1 which is the endemic equilibrium point of the system (4.1). thus, by LaSalle's invariant principle (La Salle, 1976), E^1 is globally asymptotically stable in Ω if $A<B$ and $R_0>1$. □

4.5 Bifurcation Analysis

We used Theorem 4.1 (Castillo-Chavez & Song, 2004) to determine the direction of bifurcation. In this theorem, there are two important quantities: the coefficients, say **a** and **b**, of the normal form representing the dynamics of the system on the central manifold. These coefficients decide the bifurcation. Let f_k be the k^{th} component of f and

$$\mathbf{a}=\sum_{k,i,j=1}^{5}v_k w_i w_j\frac{\partial^2 f_k}{\partial x_i\partial x_j}(0,0),\mathbf{b}=\sum_{k,i,=1}^{5}v_k w_i\frac{\partial^2 f_k}{\partial x_i\partial\beta}(0,0) \tag{4.22}$$

In particular, if $a<0$ and $b>0$, then the bifurcation is forward; if $a>0$ and $b>0$, then the bifurcation is backward. Using this approach, we can identify the possibility of bifurcation occur for our system 4.1 at $R_0=1$ using Center Manifold theorem (Carr, 2012) . Let $S=x_1$, $E=x_2$, $A=x_3$, $I=x_4$, $R=x_5$ and $N=x_1+x_2+x_3+x_4+x_5$

Moreover, by using vector notation $x=(x_1,x_2,x_3,x_4,x_5)^T$, the system can be written in the form

$\frac{dx}{dt} = (f_1, f_2, f_3, f_4, f_5)^T$ as follow . Then model in (4.1) re-written in the form:

$$\begin{aligned}
\frac{dx_1}{dt} &= b - \lambda x_1 - dx_1 + \theta x_5 = f_1,\\
\frac{dx_2}{dt} &= \lambda x_1 - (k+d)x_2 = f_2,\\
\frac{dx_3}{dt} &= (1-p)kx_2 - (d+\mu_2+\gamma)x_3 = f_3,\\
\frac{dx_4}{dt} &= pkx_2 - (\mu_1+d+\alpha)x_4 = f_4,\\
\frac{dx_5}{dt} &= \gamma x_3 + \alpha x_4 - (\theta+d)x_5 = f_5,
\end{aligned} \tag{4.23}$$

We consider the transmission rate β as a bifurcation parameters so that $R_0 = 1$ iff

$$\beta = \beta^* = \frac{(k+d)(d+\mu_2+\gamma)(\mu_1+d+\alpha)}{k\left(p(d+\mu_2+\gamma) + q(\mu_1+d+\alpha)(1-p)\right)}$$

The disease free equilibrium is given by $(x_1 = \dfrac{b}{d},\ \ x_2 = 0,\ \ x_3 = 0,\ \ x_4 = 0,\ \ x_5 = 0)$. Then the linearizion matrix of (4.23) at a disease free Equilibrium is given by:

$$J(E_0) = \begin{bmatrix}
-d & 0 & -\beta^* q & -\beta^* & \theta\\
0 & -a & \beta^* q & \beta^* & 0\\
0 & (1-p)k & -c & 0 & 0\\
0 & pk & 0 & -e & 0\\
0 & 0 & \gamma & \alpha & -f
\end{bmatrix} \tag{4.24}$$

Where, $a = k + d,\ \ c = d + \mu_2 + \gamma,\ \ e = \mu_1 + d + \alpha,\ \ f = \theta + d.$

It is clear that 0 is a simple eigenvalue of J calculated at β^*. The right eigenvector $w = (w_1, w_2, w_3, w_4, w_5)^T$, associated with this simple zero eigenvalue can be obtained from $J.w = 0$.

$$\begin{aligned}
-dw_1 - \beta^* q w_3 - \beta^* w_4 + \theta w_5 &= 0,\\
-aw_2 + \beta^* q w_3 + \beta^* w_4 &= 0,\\
(1-p)kw_2 - cw_3 &= 0,\\
pkw_2 - ew_4 &= 0,\\
\gamma w_3 + \alpha w_4 - f w_5 &= 0.
\end{aligned} \tag{4.25}$$

From equation (4.25) we consider

$$w_1 = \left(\frac{\beta^* q(1-p)k}{c} + \frac{\beta^* pk}{e} - \frac{\theta\alpha(1-p)k}{ec} + \frac{\theta pk}{e^2}\right) w_2,$$

$$w_2 > 0, \quad w_3 = \frac{(1-p)k}{c} w_2,$$

$$w_4 = \frac{pk}{e} w_2, \quad w_5 = \left(\frac{\alpha(1-p)k}{ec} + \frac{pk}{e^2}\right) w_2.$$

Next we compute the left eigenvector $v.J = 0$, $v = (v_1, v_2, v_3, v_4, v_5)^T$.
$v_1 = 0$, $v_5 = 0$, $v_2 > 0$, $v_3 = \frac{\beta^* q}{c} v_2$ and $v_4 = \frac{\beta^*}{e} v_2$.

Computation of a : To evaluate **a**, we use the following partial derivatives. Since the first and fifth component of v are zero, we don't need the derivatives of f_1 *and* f_5. From the derivatives of f_2, f_3 *and* f_4 , the only ones that are nonzero are the following:

$$\frac{\partial^2 f_2}{\partial x_1 \partial x_3} = \frac{\partial^2 f_2}{\partial x_3 \partial x_1} = \frac{b\beta^* q}{d}, \quad \frac{\partial^2 f_2}{\partial x_1 \partial x_4} = \frac{\partial^2 f_2}{\partial x_4 \partial x_1} = \frac{b\beta^*}{d}.$$

then we get

$$\mathbf{a} = 2v_2 \left[w_1 w_3 \frac{b\beta^* q}{d} + w_1 w_4 \frac{b\beta^*}{d}\right]$$

$$= 2v_2 w_1 \frac{b\beta^*}{d} [w_3 q + w_4] = \frac{b\beta^*}{d} v_2 \left(\frac{\beta^* q(1-p)k}{c} + \frac{\beta^* pk}{e} - \frac{\theta\alpha(1-p)k}{ec} + \frac{\theta pk}{e^2}\right) w_2$$
$$\left[\frac{(1-p)k}{c} w_2 q + \frac{pk}{e} w_2\right]$$

$$= 2v_2 \frac{b\beta^*}{d} \left(\frac{\beta^* q(1-p)k}{c} + \frac{\beta^* pk}{e} - \frac{\theta\alpha(1-p)k}{ec} + \frac{\theta pk}{e^2}\right) w_2^2 \left[\frac{(1-p)k}{c} q + \frac{pk}{e}\right].$$

Computation of b: We find the following partial derivatives to evaluate **b**.
$\frac{\partial^2 f_2}{\partial x_3 \partial \beta} = q$, $\frac{\partial^2 f_2}{\partial x_4 \partial \beta} = 1$, then we obtain $\mathbf{b} = qv_2 w_3 + v_2 w_4 > 0$
Since all the terms in the expressions of **b** are positive ($\mathbf{b} > 0$), the presence of the bifurcation at $\beta = \beta^*$ depends only on the sign of **a**.

Forward bofurcation occurs if and only if

$$\frac{\beta^* q(1-p)k}{c} + \frac{\beta^* pk}{e} < \frac{\theta\alpha(1-p)k}{ec} + \frac{\theta pk}{e^2}.$$

4.6 Sensitivity Analysis

Sensitivity analysis of the basic reproductive number can be used to design a mitigation strategy to slow the spread of the pandemic by reducing R_0. Sensitivity analysis (Sanchez & Blower, 1997) for the basic reproductive number mainly helps to discover parameters that have a high impact on the values of R_0 and hence should be targeted for designing intervention strategy. The following definition is used to find the sensitivity index of each of the parameters involved in R_0.

Definition 4.6.1. *Normalized forward sensitivity index of R_0 which is differentiable with respect to a given parameter P is defined as (Chitnis et al., 2008).*

$$\phi_P^{R_0} = \frac{P}{R_0}\frac{\partial R_0}{\partial P} \tag{4.26}$$

The explicit expression of R_0 is given by

$$R_0 = \frac{\beta k\left(p(d+\mu_2+\gamma)+q(\mu_1+d+\alpha)(1-p)\right)}{(k+d)(d+\mu_2+\gamma)(\mu_1+d+\alpha)}.$$

$$\phi_\beta^{R_0} = \frac{\beta}{R_0}\frac{\partial R_0}{\partial \beta} = 1,$$

$$\phi_k^{R_0} = \frac{k}{R_0}\frac{\partial R_0}{\partial k} = \frac{d}{k+d},$$

$$\phi_q^{R_0} = \frac{q}{R_0}\frac{\partial R_0}{\partial q} = \frac{q(1-p)(\mu_1+d+\alpha)}{p(d+\mu_2+\gamma)+q(\mu_1+d+\alpha)(1-p)},$$

$$\phi_p^{R_0} = \frac{p}{R_0}\frac{\partial R_0}{\partial p} = \frac{p(d+\mu_2+\gamma)-q(\mu_1+\alpha+d)}{p(d+\mu_2+\gamma)+q(\mu_1+d+\alpha)(1-p)}.$$

We can get the values of other parameters by similar form with above parameters. Their values are listed in table 4.3.

The sensitivity indices of the basic reproductive number with respect to the main parameters are arranged in table 4.3. Those parameters that have positive indices, β, k, q and p show that they have great impact on expanding the disease in the population if their values are increasing. The basic reproduction number increases as their values increase, it means that the average number of secondary cases of infection increases in the population. Furthermore, those parameters in which their sensitivity indices are negative, d, μ_1, μ_2, γ and α have an

Table 4.3: Sensitivity Indices of the Basic Model Parameters in R_0.

Parameter	**Sensitivity indices**
β	1
k	0.0099
q	0.0187
p	0.3752
d	-0.0091
μ_1	-9.8133$\times 10^{-5}$
μ_2	-1.0642$\times 10^{-4}$
γ	-0.0175
α	-0.9779

influence of minimizing the burden of the disease in the community as their values increase. And also as their values increase, the basic reproduction number decreases, which leads to minimizing the endemic nature of the disease in the community. Parameter values are taken from Table 6.2.

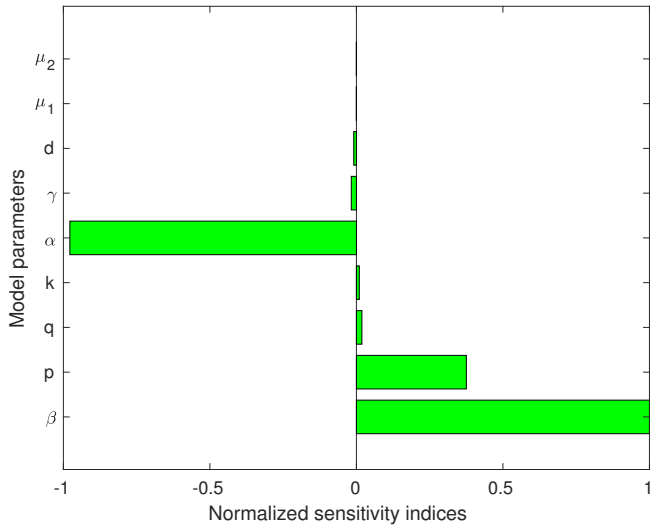

Figure 4.2: Normalized sensitivity indices of R_0 with respect to parameters of the model (4.1)

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CHAPTER 5

OPTIMAL CONTROL ANALYSIS

In chapter 4, we presented a mathematical model for the transmission dynamics of COVID-19 and studied its well-possedness mathematically and epidemiologically without giving intervention mechanism. In this chapter, the intervention mechanism is addressed using the theory of optimal control.

5.1 Extension into Optimal Control Model

In this section, we extend the basic model (4.1) in to optimal control model. In the model, we introduce two control function $u_1(\cdot)$ and $u_2(\cdot)$. The first control u_1 represents personal protective measures (wearing face mask, keeping personal sanitation (hand washing, using sanitizer) and social distancing) that help to reduce contact rate. The control u_2 denotes the effort made to increase the treatment efficiency in order to raise the size of recover population. We assume that the controls are bounded between 0 and 1. In the context of this assumption, when the controls take the minimum value 0, it means no extra measures are implemented for the reduction of the COVID-19 disease. While the maximum value 1 corresponds to 100 $\%$ successfully implementation of the prevention program which is unrealistic. Thus, we assumed $0 \leq u_i < 1, i = 1, 2$. After incorporating the two controls in (4.1) we obtain the

following optimal control model:

$$\begin{aligned}
\frac{dS}{dt} &= b - \lambda(1-u_1)S - dS + \theta R,\\
\frac{dE}{dt} &= \lambda(1-u_1)S - (k+d)E,\\
\frac{dA}{dt} &= (1-p)kE - (d+\mu_2+\gamma)A,\\
\frac{dI}{dt} &= pkE - (\mu_1+d)I - (\alpha+u_2)I,\\
\frac{dR}{dt} &= \gamma A + (\alpha+u_2)I - (\theta+d)R.
\end{aligned} \tag{5.1}$$

where $\lambda = \dfrac{\beta(I+qA)}{N}$ and the non-negative initial conditions are $S(0) = S_0 > 0, \quad E(0) = E_0 \geq 0, \quad A(0) = A_0 \geq 0, \quad I(0) = I_0 \geq 0, \quad R(0) = R_0 \geq 0$. Our main goal here is to minimize the total number of newly exposed and infections in the intervention period, while also minimizing the total cost of controlling the disease dynamics. For this, we define the cost functional for the minimization problem as

$$J[u_1, u_2] = \int_0^T \left(C_1 E(t) + C_2 I(t) + \frac{1}{2}\sum_{i=1}^{2} B_i u_i^2 \right) dt \to min \tag{5.2}$$

subject to (5.1) with associated initial conditions. The positive constants C_1 and C_2 measures the relative importance of reducing the associated classes on the spread of the disease while the relative weight constants B_i is a measure of the relative cost of interventions associated with the control u_i for $i = 1, 2$ and balances the units of integrand to reduce the dominance of any of the term in the integral.

Here, the total cost on a finite time horizon $[0, T]$ consists of the cost induced by the COVID-19 disease itself and the cost incurred due to intervention and treatment efforts. Thus, we divided the total cost induced into costs due to proportion of exposed individuals $\int_0^T C_1 E(t)dt$, infected population $\int_0^T C_2 I(t)dt$ and cost of prevention and treatment $\int_0^T \frac{1}{2}\sum_{i=1}^{2} B_i u_i^2 dt$. We also assumed that cost of protective measure and treatment efficacy are nonlinear and takes a quadratic nature, which is found to be consistent with previous works in the literature, see for example in (Legesse & Shiferaw, 2020; Ullah & Khan, 2020; Zamir et al., 2020) and references cited therein.

The associated admissible control set is defined by

$$\mathrm{U} = \{(u_1, u_2) : [0, T] \to [0, 1] \text{ where } u_1 \text{ and } u_2 \text{ are Lebesgue measurable function.}\} \tag{5.3}$$

Hence, we are looking for the optimal control pair (u_1^*, u_2^*) such that

$$J(u_1^*, u_2^*) = min\{J(u_1, u_2) : u_1, u_2 \in \mathrm{U}\} \tag{5.4}$$

subject to the control induced state (5.1) with prescribed initial data. The solution of the optimal control problem is the vector function $(S^*, E^*, A^*, I^*\ R^*) \in \mathbb{R}_+^5$ associated with an optimal control pair $(u_1^*, u_2^*) \in \mathrm{U}$ on the time interval $[0, T]$ that minimize the cost functional (5.2).

5.2 Existence of the Optimal Control Problem

In this section, we prove the existence of such optimal control functions which minimize the cost function in the finite intervention period.

Theorem 5.2.1. *There exists an optimal control pair* (u_1^*, u_2^*) *and corresponding solution vector* $(S^*, E^*, A^*, I^*, R^*)$ *to the control induced state initial value problem (5.1) that minimizes the cost functional* $J(u_1, u_2)$ (5.2) *over the set of admissible control* U (5.3).

Proof. All the state variable involved in the model are continuously differentiable. Therefore, we need to verify the following four conditions given in (Fleming & Rishel, 2012).

i. The set of all solutions to system (5.1) with corresponding control functions in U is non empty.

ii. The control set is convex and closed.

iii. The integral of the objective functional is convex.

iv. The integrand $F(t, S, E, A, I, R, u)$ in equation(5.2) is convex with respect to control variables and additionally fulfills that $F(t, S, E, A, I, R, u) \geq g(u)$, where g is continuous and $||u||^{-1}g(u) \to +\infty$ as $||u|| \to \infty$.

In order to established condition (i), we refer to Picard-Lindelo̊f existence theorem (Levinson & Coddington, 1955). If the solutions of the state equations are a prior bounded and if the state equations are continuous and Lipschitz continuous in the state variables, then there is a unique solution corresponding to every admissible control in the given domain. With the result that, if $g(t, x, u)$ is bounded, continuous, and Lipschitz in the state variable, then there

exists a unique solution corresponding to every admissible control U. Hence, for any $u \in \mathrm{U}$ and the state variables, we have

$$0 \leq N(t) \leq \frac{b}{d} \tag{5.5}$$

and non empty by model assumption. Furthermore, with the bounded established in (5.5), clearly, the state system is continuous and bounded. It is possible to show the boundedness of the partial derivative with respect to the state variable, i.e $\frac{\partial g}{\partial x}$, exist and finite, which established the system is Lipschitz with respect to the state variables (Levinson & Coddington, 1955). This show that the proof of condition (i) is complete.

To prove (ii), consider

$$\mathrm{U} = \{u \in \mathbb{R}^2 : ||u|| \leq 1, \ || \cdot || \text{ is an Euclidean norm.}\}$$

Now assume that $v_1, v_2 \in \mathrm{U}$ such that $||v_1|| \leq 1$ and $||v_2|| \leq 1$. Then for any $\lambda \in [0, 1]$, $||\lambda v_1 + (1-\lambda)v_2|| \leq \lambda||v_1|| + (1-\lambda)||v_2|| \leq 1$. This implies that the control set U is convex and closed.

Next we verify condition (iii), the integral of the cost function is given by

$$F(t, S, E, A, I, R, u) = C_1 E(t) + C_2 I(t) + \frac{1}{2}\sum_{i=1}^{2} B_i u_i^2$$

Recall that any affine function is convex and the sum of convex function is also convex (Perelson et al., 1997). Therefore, F is convex on U.

Finally, to verify condition (iv), we note that the integrand $F(t, S, E, A, I, R, u)$ of the objective functional is clearly convex in control. To prove the bound on the $F(t, S, E, A, I, R, u)$ we note that the state system (5.1) is linear in control variable u with coefficients depending on state variables. The integrand of the cost functional $F(t, S, E, A, I, R, u) = C_1 E(t) + C_2 I(t) + \frac{1}{2}\sum\limits_{i=1}^{2} B_i u_i^2$ is the sum of convex function and hence convex with respect to control variables. Furthermore,

$$F(t, S, E, A, I, R, u) = C_1 E(t) + C_2 I(t) + \frac{1}{2}\sum_{i=1}^{2} B_i u_i^2 \geq \frac{1}{2}\sum_{i=1}^{2} B_i u_i^2. \tag{5.6}$$

Let $\eta = min\left(\frac{B_1}{2}, \frac{B_2}{2},\right) > 0$ and define a continuous function $g(u) = \eta||u||^2$. Then from equation (5.6) we have $F(t, S, E, A, I, R, u) \geq g(u)$. Clearly $||u||^{-1}g(u) \to +\infty$ as $||u|| \to \infty$. Thus, condition (iv) is achieved. With this we conclude that the existence of an optimal control $F(S^*, E^*, A^*, I^*, R^*, u^*)$ that minimizes the cost functional of (5.2) over the set of admissible control U. The proof is completed. □

5.3 Characterization of Optimal Control Solutions

Pontryagin's Minimum Principle (Pontryagin et al., 1962) provides the necessary conditions that an optimal pair must satisfy. This principle states that for the optimal control pair (u_1^*, u_2^*) and corresponding optimal states $(S^*, E^*, A^*, I^*, R^*)$ to minimizes the objective functional (5.2) subjected to the control induced state (5.1) over a fixed time interval $[0, T]$, there exists a non-trivial absolutely continuous mapping $\lambda : [0, T] \to \mathbb{R}^5, \lambda = (\lambda_1(t), \lambda_2(t), \lambda_3(t), \lambda_4(t), \lambda_5(t))$ called the adjoint vector, such that

1. The Hamiltonian function is defined as

$$\mathcal{H} = C_1 E(t) + C_2 I(t) + \frac{1}{2}\sum_{i=1}^{2} B_i u_i^2 + \sum_{i=1}^{5} \lambda_i(t) g_i(t, S, E, A, I, R, u_1, u_2), \tag{5.7}$$

   where g_i stands for the right hands of the constraints (5.1) for $i = 1, 2, 3, 4, 5$.

2. The optimality condition of the system

$$\frac{\partial \mathcal{H}}{u_1} = 0, \quad \frac{\partial \mathcal{H}}{u_2} = 0 \tag{5.8}$$

3. Hamiltonian system

$$S' = \frac{\partial \mathcal{H}}{\partial \lambda_1}, \quad E' = \frac{\partial \mathcal{H}}{\partial \lambda_2}, \quad A' = \frac{\partial \mathcal{H}}{\partial \lambda_3}, \quad I' = \frac{\partial \mathcal{H}}{\partial \lambda_4}, \quad R' = \frac{\partial \mathcal{H}}{\partial \lambda_5}; \tag{5.9}$$

$$\lambda_1' = -\frac{\partial \mathcal{H}}{\partial S}, \quad \lambda_2' = -\frac{\partial \mathcal{H}}{\partial E}, \quad \lambda_3' = -\frac{\partial \mathcal{H}}{\partial A}, \quad \lambda_4' = -\frac{\partial \mathcal{H}}{\partial I}, \quad \lambda_5' = -\frac{\partial \mathcal{H}}{\partial R}; \tag{5.10}$$

4. Minimality condition

$$\mathcal{H}(S^*(t), E^*(t), A^*(t), I^*(t), R^*(t), u^*(t), \lambda^*(t)) = \min_{u \in U} \mathcal{H}(S(t), E(t), A(t), I(t), R(t), u(t), \lambda(t)) \tag{5.11}$$

   holds for almost all $t \in [0, T]$.

5. Moreover, the transversality condition

$$\lambda_i(T) = 0, \qquad i = 1, \ldots, 5 \tag{5.12}$$

   also holds true.

In the following result, we give the characterization of optimal control.

Theorem 5.3.1 (Necessary optimality conditions)**.** *Let* (u_1^*, u_2^*) *be solution to the optimal control problem* (5.1)–(5.4) *and* $(S^*, E^*, A^*, I^*, R^*)$ *be the corresponding optimal state. Then there exists an adjoint function* $\lambda_i^*(t)$*,* $i = 1, 2, 3, 4, 5$ *that satisfy the adjoint system*

$$\begin{cases} \lambda_1' = \frac{(\lambda_2-\lambda_1)(u_1-1)(qA+I)\beta}{N} + d\lambda_1, \\ \lambda_2' = (\lambda_3 - \lambda_4)\, pk + \lambda_2\,(d+k) - \lambda_3\, k - C_1, \\ \lambda_3' = (\lambda_1 - \lambda_2)\,(1-u_1)\,\dfrac{\beta q S}{N} + \lambda_3\,(d + \mu_2 + \gamma) - \lambda_5\gamma, \\ \lambda_4' = -C_2 + (\lambda_1 - \lambda_2)\,(1-u_1)\,\dfrac{\beta S}{N} + \lambda_4\,(\mu_1 + d + (\alpha + u_2)) - \lambda_5(\alpha + u_2), \\ \lambda_5' = (\lambda_5 - \lambda_1)\,\theta + d\lambda_5. \end{cases} \tag{5.13}$$

subject to the transversality conditions $\lambda_i^*(T) = 0$ for $i = 1, 2, 3, 4, 5$.

Moreover, the optimal control (u_1^*, u_2^*) is given by

$$\begin{aligned} u_1^* &= \min\left\{\max\left\{0, \frac{\lambda^* S^*(\lambda_2 - \lambda_1)}{B_1}\right\}, 1\right\} \\ u_2^* &= \min\left\{\max\left\{0, \frac{I^*(\lambda_4 - \lambda_5)}{B_2}\right\}, 1\right\}. \end{aligned} \tag{5.14}$$

Proof. To prove this theorem, we follow the approach given in (Legesse & Shiferaw, 2020; Ullah & Khan, 2020; Zamir et al., 2020). In particular, by Corollary 4.1 in Fleming and Rishel (Fleming & Rishel, 2012), the convexity of the integrand in (5.2) with respect to u_i guarantees the existence of an optimal control as proved above. The adjoint equations and transversality conditions can be obtained via the Pontryagin's Minimum Principle such that:

$$\begin{aligned} \frac{d\lambda_1}{dt} &= -\frac{\partial \mathcal{H}}{\partial S}(t, S, E, A, I, R, u_1, u_2, \lambda) = 0, \\ \frac{d\lambda_2}{dt} &= -\frac{\partial \mathcal{H}}{\partial E}(t, S, E, A, I, R, u_1, u_2, \lambda) = 0, \end{aligned}$$

,

$$\frac{d\lambda_3}{dt} = -\frac{\partial \mathcal{H}}{\partial A}(t, S, E, A, I, R, u_1, u_2, \lambda) = 0,$$

$$\begin{aligned} \frac{d\lambda_4}{dt} &= -\frac{\partial \mathcal{H}}{\partial I}(t, S, E, A, I, R, u_1, u_2, \lambda) = 0, \\ \frac{d\lambda_5}{dt} &= -\frac{\partial \mathcal{H}}{\partial R}(t, S, E, A, I, R, u_1, u_2, \lambda) = 0, \end{aligned}$$

subjected to transiversality conditions $\lambda_i(T) = 0,\ i = 1, 2, \ldots 5$.

Considering the optimality conditions given by $\frac{\partial \mathcal{H}}{\partial u_i} = 0$, the optimal control u_i^* can be explicitly obtained in terms of state and adjoint variables. That means for the optimality condition, we differentiate the Hamiltonian function with respect to u_i and equate it to zero by taking into account the boundedness on u_i. For this reason, we have the following optimality condition:

$$\frac{\partial \mathcal{H}}{\partial u_i} = 0 \ \ i = 1, 2$$

which implies that

$$\frac{\partial \mathcal{H}}{u_1} = B_1 u_1 + \frac{\lambda_1 \beta \left(Aq + I\right) S}{N^*} - \frac{\lambda_2 \beta \left(Aq + I\right) S}{N^*} = 0 \Rightarrow u_1^* = \frac{\beta \left(A^* q + I^*\right) S^* \left(\lambda_2 - \lambda_1\right)}{N^* B_1}$$

$$\frac{\partial H}{u_2} = -I\,\lambda_4 + I\,\lambda_5 + B_2\,u_2 = 0 \Rightarrow u_2^* = \frac{I^*\left(\lambda_4 - \lambda_5\right)}{B_2}$$

From boundedness on $u_i^*(t)$ and minimality condition, we have:

$$u_1^*(t) = \begin{cases} 0, & \text{if } \ \frac{\partial \mathcal{H}}{\partial u_1} > 0 \\ \frac{\beta\,(A^*q + I^*) S^* (\lambda_2 - \lambda_1)}{N^* B_1}, & \text{if } \ \frac{\partial \mathcal{H}}{\partial u_1} = 0 \\ 1, & \text{if } \ \frac{\partial \mathcal{H}}{\partial u_1} < 0 \end{cases}$$

$$u_2^*(t) = \begin{cases} 0, & \text{if } \ \frac{\partial \mathcal{H}}{\partial u_2} > 0 \\ \frac{I^*(\lambda_4 - \lambda_5)}{B_2}, & \text{if } \ \frac{\partial \mathcal{H}}{\partial u_2} = 0 \\ 1, & \text{if } \ \frac{\partial \mathcal{H}}{\partial u_2} < 0 \end{cases}$$

Concluding that, the optimal control $u_i^*(t)$ can be summarized as

$$u_1^* = \min\left\{\max\left\{0, \frac{\beta\ \left(A^*q + I^*\right) S^* \left(\lambda_2 - \lambda_1\right)}{N^* B_1}\right\}, 1\right\},$$

$$u_2^* = \min\left\{\max\left\{0, \frac{I^*\left(\lambda_4 - \lambda_5\right)}{B_2}\right\}, 1\right\}.$$

This completes the proof of the theorem. □

CHAPTER 6

NUMERICAL SIMULATIONS

6.1 Numerical Simulation of the System

In this section, we present numerically the behaviour of the solutions of the system (4.1) and (5.1) for different values of parameters given in the model and explain the impact of control strategies on the spread of coronavirus outbreak. We conducted numerical simulation in order to investigate the effects of the control strategies on the transmission dynamics of COVID-19.

6.2 Parameter Estimations

In this section, we fit the proposed model using real data of COVID-19 infection cases in Ethiopia and we estimate the unknown model parameters. The simulation process are performed using software $MATLAB\ R2018b$. Table 6.1 depicts the monthly real data of total confirmed cases of COVID-19 infection in Ethiopia from March 2020 to April 2021 extracted from WHO situation reports (WHO, 2020b).

To solve the dynamic parameter estimation problem, we formulate system 4.1 in the following form

$$y' = f(t, y, \theta), y(t_0) = y_0 \tag{6.1}$$

where y is the vector of dependent variables and θ is the vector of unknown parameters. The error is sum of squares error and is represented by

$$E(\theta) = \sum_{i=1}(y_i - \bar{y}_i)^2 \tag{6.2}$$

The expression $\bar{y}_i(t)$ represents the actual total confirmed cases of COVID-19 and $y_i(t)$ are

Table 6.1: Cumulative confirmed cases of COVID-19 infection from March 2020 to April 2021.

No	Month	Total confirmed cases	No	Month	Total confirmed cases
1	March	26	8	October	96169
2	April	131	9	November	110074
3	May	1172	10	December	124264
4	June	5846	11	January	137650
5	July	17530	12	February	159072
6	August	22253	13	March	206589
7	September	74584	14	April	257442

the corresponding model solutions at time t_i. The aim is minimizing objective function

$$\min E(\theta) \quad subject \quad to \quad Equation \quad 6.1 \tag{6.3}$$

to obtain our parameter estimates. In the process of least-squares fitting, we are looking for a value $\bar{\theta}$ of model parameter θ such that the squared sum of errors is the minimum. Clearly, such a problem is nonlinear least squares problem, since the dependence of a solution $y(t, \theta)$ on the parameter θ is through a highly nonlinear system of differential equations.

The parameter estimation algorithm is written below:

The model parameters of the model system (4.1) are estimated using least-square fitting

Algorithm 1 Parameter estimation

1: Guess initial parameter values θ_0. Set $\theta = \theta_0$.
2: Using MATLAB ode23s solver, solve equation 6.1 using θ to solve the solution of the system.
3: Evaluate error using equation 6.2.
4: Check convergence criteria. If not converged go to 2.
5: On convergence, set θ=$\bar{\theta}$ to current parameter values.

methods which provides a better fit for the model solution to the real data as shown in figure 6.1 and the corresponding parameters value are depicted in Table 6.2 below for the numerical simulation.

In the next section, we study the dynamics of COVID-19 through numerical simulations by

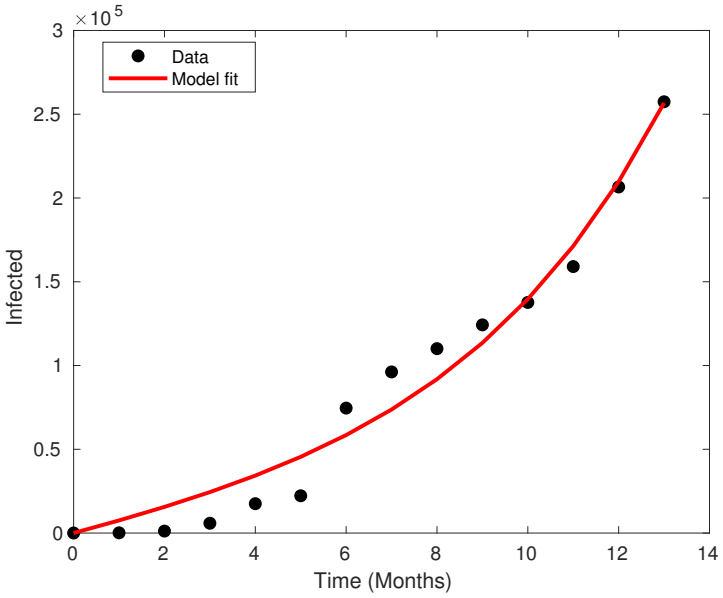


Figure 6.1: SEAIR model fit with real data on the number of COVID-19 cases in Ethiopia

using the fitted values of parameters in the proposed model with appropriate initial conditions with the help of least square method.

6.3 Simulation Results and Discussion

In this section, we illustrate numerically the solution of the optimal control problem proposed in system (5.1) and explain the impact of control strategy on the spread of corona virus diseases. For this purpose, we use the forward-backward sweep method presented in the book of Lenhart and Workman (Lenhart & Workman, 2007).

To briefly summarize the numerical simulation procedure, first we perform forward fourth order Runge-Kutta scheme to solve system (5.1) over the interval $[0, T]$ with its initial condition and the transversality conditions $\lambda_i(T) = 0$; $i = 1, 2, 3, 4, 5$, where $T = 20$ is simulation time. In contrary we use backward fourth order Runge-Kutta scheme to solve system (5.13) using the current iteration solution of (5.1). The control is updated by using a convex combination of the previous control and the values computed in the characterizations process. The iteration continuous until the values of the unknowns at the previous iteration are very close to the values of present iteration.

To perform the numerical simulation, we assumed the initial population of

$$(E(0), A(0), R(0)) = (50000, 45000, 30000)$$

and the remaining $I(0) = 26$ from the collected real data. Also the initial susceptible population is obtained from $S(0) = N(0) - (E(0) + A(0) + I(0) + R(0)) = 114836824$ and the total population of Ethiopia is $N(0) = 114961850$ populations (2020 est.) (WHO, 2020c). The natural death rate is computed as $d = \dfrac{1}{66.71 \times 12}$ per month, where 66.71 years is the average life expectancy in Ethiopia (WHO, 2020a). The recruitment rate, is then calculated as $b = d \times N(0) = 143608$ per month. The estimation of basic reproduction number for the

Table 6.2: The values of parameters used in the simulations

Parameter	**Value**	**Reference**
b	143608 per month	Estimated
d	$\frac{1}{66.71\times12}$ per month	(WHO, 2020a)
μ_1	0.0001 per month	Estimated
μ_2	0.0057 per month	Estimated
β	0.5946	Estimated
p	0.9692	Estimated
k	0.1249	Estimated
θ	0.0024 per month	Estimated
α	0.5001 per month	Estimated
γ	0.2970 per month	Estimated
q	0.4722	Estimated

model is given by

$$R_0 = \frac{\beta k\left(p(d+\mu_2+\gamma)+q(\mu_1+d+\alpha)(1-p)\right)}{(k+d)(d+\mu_2+\gamma)(\mu_1+d+\alpha)} = 2.0525 > 1.$$

Since $R_0 > 1$, the prevalence of COVID-19 will result in an epidemic.

The cost coefficients corresponding to control variables are estimated to be $B_1 = 25$, $B_2 = 75$ and the relative importance of reducing the associated classes on the spread of the disease are $C_1 = 3$ and $C_2 = 5$. Using all necessary information above , we analysis and compare the numerical results of the effect of controls on the spread of COVID-19 in populations.

We analyse and compare numerical results from simulations with the following conditions.

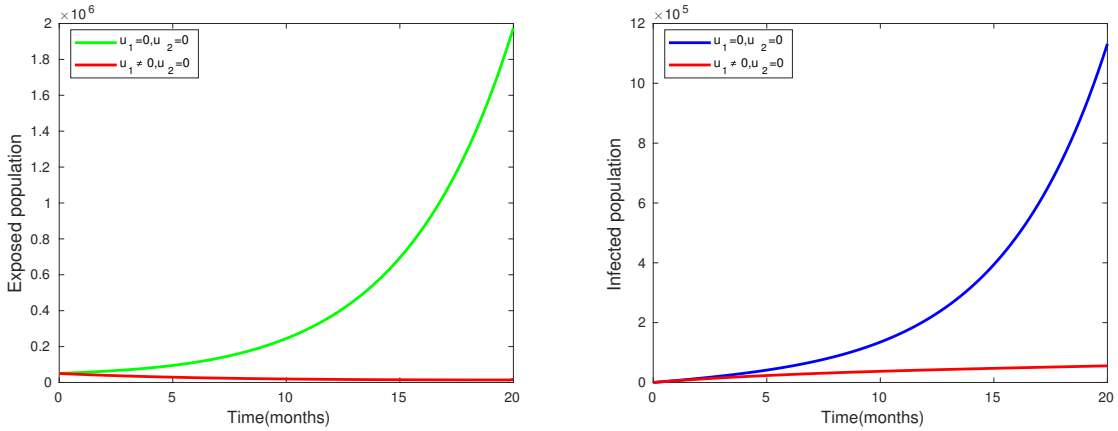
- **Strategy A**: Using personal protective (u_1) of susceptible population without treatment ($u_2 = 0$) of infectious population.

- **Strategy B**: Using treatment (u_2) of infectious population without personal protective ($u_1 = 0$) of susceptible population.

- **Strategy C**: Using both controls, personal protective (u_1) of susceptible population and treatment (u_2) of infectious population.

A. Control with personal protective only

Personal protective minimizes the rate of contacting of susceptible individuals with exposed as well as infectious compartments. From figure 6.2 we see that the decreasing of exposed population and slowly increasing of infectious population due to the implementation of personal protective. This implies that optimized personal protective reduces the burden of COVID-19 disease. Moreover, we can see that after implementing this strategy the number of exposed population goes to zero after 20 months. It is possible to minimize infected-COVID-19 humans but unable to eliminate by this strategy in the stated time. Also control function u_1 is shown in figure 6.3.



(a) Exposed population with and without control.

(b) Infected population with and without control.

Figure 6.2: Exposed and Infected population when $u_1 \neq 0$ and $u_2 = 0$.

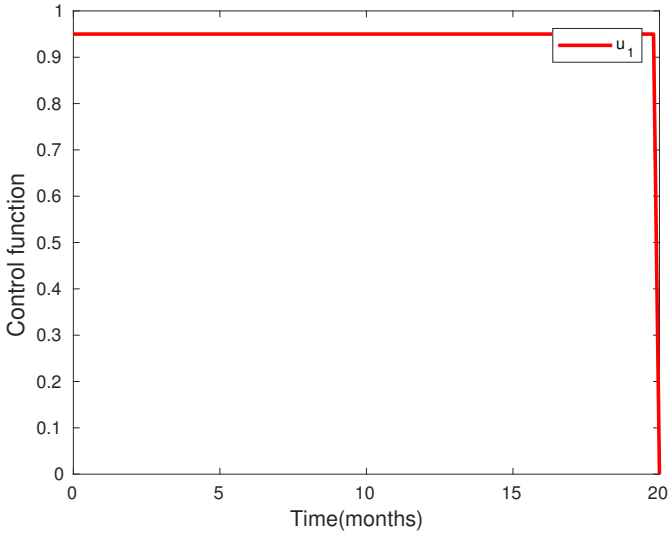
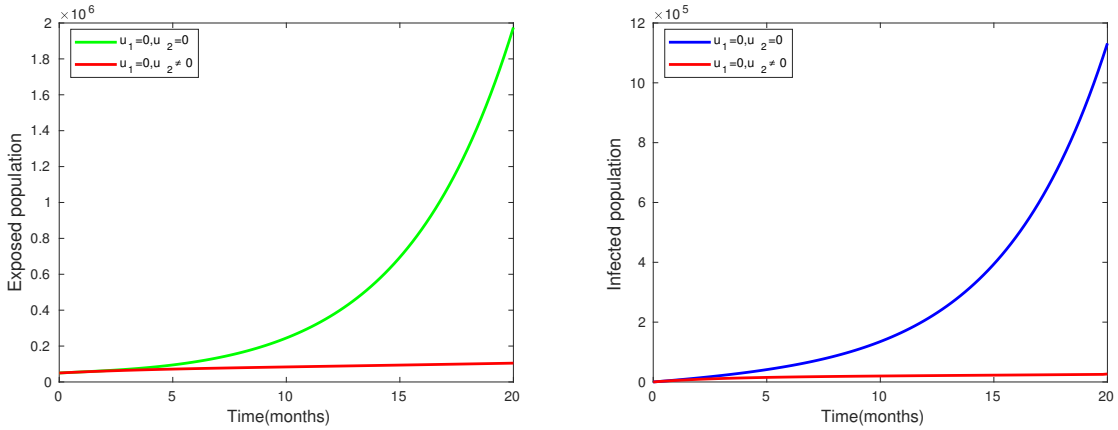


Figure 6.3: Profile of control function u_1 when $u_2 = 0$.

B. Control with treatment only

Under this strategy we used control u_2 and we set u_1 zero. From the figure 6.4 we can conclude that the applied strategy seems effective in reducing the disease burden within the intervention period and thus can be consider as optimal candidate to manage the burden of COVID-19 infection. Control function u_2 is plotted in figure 6.5.



(a) Exposed population with and without control.

(b) Infected population with and without control.

Figure 6.4: Exposed and Infected population when $u_1 = 0$ and $u_2 \neq 0$.

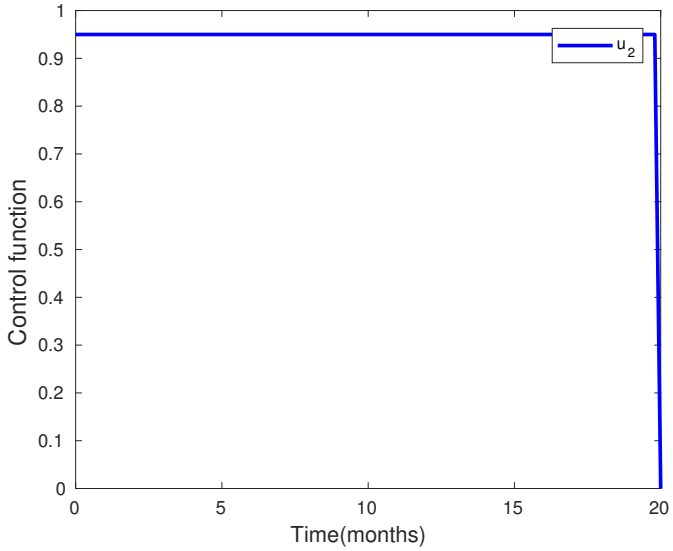
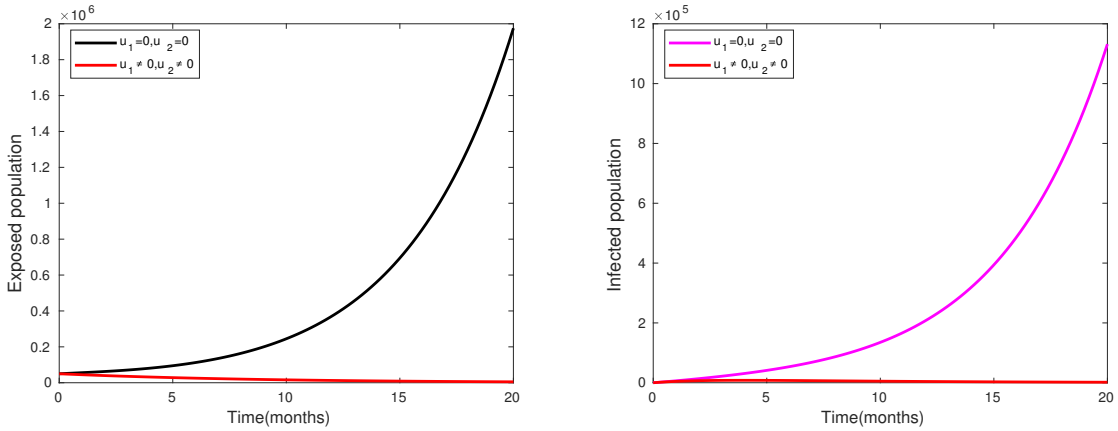


Figure 6.5: Profile of control function u_2 when $u_1 = 0$.

C. Control with personal protective and treatment

Here, we simulated the model using both strategies namely, personal protective control u_1 and treatment control u_2 was to minimize the objective function. Clearly figure 6.6 shows as both exposed and infected population is dramatically decreasing. Thus, the best choice is applying both controls to eradicate the COVID-19 pandemic.



(a) Exposed population with and without control.

(b) Infected population with and without control.

Figure 6.6: Exposed and Infected population when $u_1 \neq 0 \ \ and \ \ u_2 \neq 0$.

From figure 6.8 we can conclude that exposed, asymptomatic and infected populations are decreasing when control is applied and they are increasing without control.

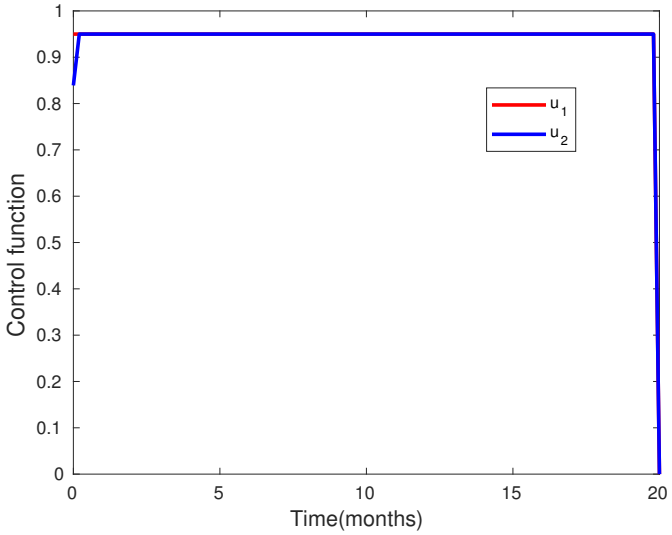
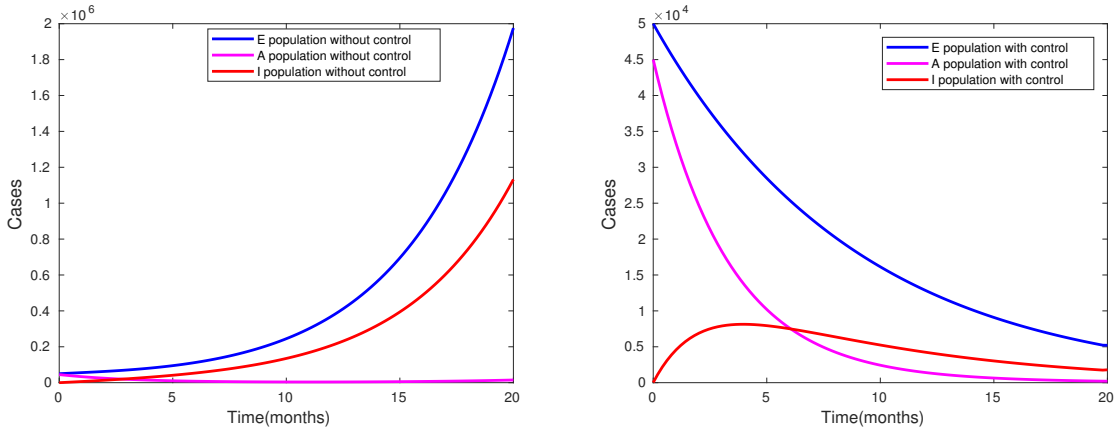


Figure 6.7: Profile of control function u_1 and u_2 .



(a) COVID-19 cases without control.

(b) COVID-19 cases with control.

Figure 6.8: Comparing COVID-19 cases with and without optimal control.

CHAPTER 7

RESULT AND DISCUSSION

7.1 Result and Discussion

In this thesis, we have considered COVID-19 disease. We have developed a five-compartmental epidemic model, namely susceptible, exposed, asymptomatic, infective and recovered populations. The well-posedness of the model was established both in the mathematical and epidemiological sense by showing that all solutions of the model are positive and bounded with initial conditions.

We have discussed about the invariant region. Using the next generation matrix method, we have found

$$R_0 = \frac{\beta k\left(p(d+\mu_2+\gamma)+q(\mu_1+d+\alpha)(1-p)\right)}{(k+d)(d+\mu_2+\gamma)(\mu_1+d+\alpha)} = 2.0525$$

as basic reproduction number of the system, which helps us to determine the dynamical behavior of the system.

We have established two distinct equilibriums for the model with both local and global stability on the disease-free and endemic equilibrium points. The system (4.1) is locally asymptotically stable at the disease free equilibrium point E_0 when $R_0 < 1$. When $R_0 > 1$, the endemic equilibrium E^1 exists and the system becomes unstable at E_0 and locally asymptotically stable at E^1.

The main aim of this thesis is to setup an optimal control problem relative to the epidemic model so as to minimize the exposed and infective populations as well as to minimize the cost of control. We have considered two kinds of controls as they reduce the transmission dynamic of COVID-19 disease. The control functions are u_1 (personal protective control) and u_2 (treatment control). They minimize the objective functional (cost function) as given in

(5.2). The numerical simulation of the model system (4.1) and (5.1) have been performed and the simulation process is carried out using software MATLAB R2018b. Also we found the value of the parameters using least-square fitting methods with software MATLAB R2018b.

CONCLUSSION AND RECOMMENDATION

Conclussion

In this thesis work, we develop mathematical model which describes the transmission dynamic of COVID-19 with optimal control using a system of nonlinear ordinary differential equations. The well-posedness of the model was established both in the mathematical and epidemiological sense by showing that all solution of the model is positive and bounded with initial conditions in a certain meaning full set.

We performed the qualitative analysis of the model. Both local and global stability analysis of the equilibrium points of the model equations have been done using Jacobian matrix and Lyapunov functions respectively. Sensitivity analysis of the model have been studied and determine a parameter which plays greater role in the transmission dynamics of COVID-19 disease.

The proposed mathematical model is extended to the optimal control problem. Here we have used two controls, personal protective (u_1) for susceptible population and treatment (u_2) for infected population. Then, the hamiltonian, adjoint variables, the characterization of controls and the optimality of our model were derived and analyzed using pontryagin's minimum principle (PMP).

Finally, different simulation cases were comparatively performed to obtain the best control strategies. The numerical simulation results demonstrate good agreement with our analytical results. The simulation results also clearly shown that the COVID-19 can be minimized by applying preventive measure such as social distancing, hand washing using soap and sanitizer and treatment.

Recommendation

The mathematical models on epidemic diseases are rather simple, but they give insight into some of the consequences of public health policies. Controlling the spread of COVID-19 disease is now a challenging and important issue to study. So, to predict and identify the cost-effective strategies to control the spread of COVID-19 disease and minimize the cost of the control programme are the primary goals of health administrators, policy-makers and researchers. From the findings of this study we recommend all person as they keep their

distance, washing their hands with soap, using sanitizer and face mask. Also we recommend that, the government should give a treatment for those who are already infected and infectious.

Future Work

In this thesis, we have developed a deterministic model of SEAIR compartments. But, the stochastic model of these compartments is not addressed in this thesis. This will be addressed in the future.

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Appendix A

The Matlab code for non linear ODE system of (4.1 and 5.1).

Listing A.1: Matlab Program for SEAIR model with and without control.

```
function y = Covid_19con2
test = -1;
tf=20;
delta1 = 0.001;
M = 99;
t = linspace(0,tf,M+1);
h = tf/M;
h2 = h/2;
b=143608; % recruitment rate of the susceptible population
N =114961850;                % Total population of Ethiopia
d=1/(66.71*12);                % Natural death rate
beta = 0.5946    ;             % contact rate
theta = 0.0024 ;             %
p = 0.9692   ;           %
mu1 =0.0001;             %
mu2= 0.0057;     %
q = 0.4722 ; %
alpha= 0.5001;
k =0.1249;    %
gamma=  0.2970;     %
C1 =3;
```

```
C2=5;
B1 =25;
B2 =75;
x1=zeros(1,M+1);
x2=zeros(1,M+1);
x3=zeros(1,M+1);
x4=zeros(1,M+1);
x5=zeros(1,M+1);
u1 = zeros(1,M+1);
u2 = zeros(1,M+1);
lambda1 = zeros(1,M+1);
lambda2 = zeros(1,M+1);
lambda3 = zeros(1,M+1);
lambda4 = zeros(1,M+1);
lambda5 = zeros(1,M+1);
x1(1) = 114836824;
x2(1) = 50000;
x3(1) = 45000;
x4(1) = 26;
x5(1) = 30000;

while(test < 0)
    oldx1 = x1;
    oldx2 = x2;
    oldx3 = x3;
    oldx4 = x4;
    oldx5 = x5;
    oldu1 = u1;
    oldu2 = u2;
    oldlambda1 = lambda1;
    oldlambda2 = lambda2;
    oldlambda3 = lambda3;
```

```
oldlambda4 = lambda4;
oldlambda5 = lambda5;
for i = 1:M % forward in state
    auxu1 = 1-u1(i);
    auxu2 = u2(i);
    m11 = b -(beta*(x4(i)+q*x3(i))/N)*x1(i)*auxu1-d* x1(
        i)+theta*x5(i);
    m12 = (beta*(x4(i)+q*x3(i))/N)*x1(i)*auxu1-(k +d)*x2
        (i);
    m13 = (1-p)*k*x2(i)-(d+gamma +mu2)*x3(i);
    m14 = p*k*x2(i)-(mu1+d+alpha*auxu2)*x4(i);
    m15 = gamma*x3(i)+alpha*auxu2*x4(i)- (theta+d)*x5(i);
    aux1 =x1(i)+h2*m11; aux2 = x2(i)+h2*m12; aux3 = x3(i)
        +h2*m13; aux4 = x4(i)+h2*m14; aux5 = x5(i)+h2*m15;
    auxu1 = 1-0.5 * (u1(i) + u1(i+1));
    auxu2 = 0.5 * (u2(i) + u2(i+1));
    m21 = b - (beta*(aux4+q*aux3)/N)*aux1*auxu1-d * aux1
        +theta*aux5;
    m22 = (beta*(aux4+q*aux3)/N)*aux1*auxu1-(k +d)*aux2;
    m23 = (1-p)*k*aux2-(d+gamma +mu2)*aux3;
    m24 = p*k*aux2-(mu1+d+alpha*auxu2)*aux4;
    m25 = gamma*aux3+alpha*auxu2*aux4- (theta+d)*aux5;
    aux1 =x1(i)+h2*m21; aux2 = x2(i)+h2*m22; aux3 = x3(i)
        +h2*m23; aux4 = x4(i)+h2*m24; aux5 = x5(i)+h2*m25;
    auxu1 = 1-0.5 * (u1(i) + u1(i+1));
    auxu2 = 0.5 * (u2(i) + u2(i+1));
    m31 = b - (beta*(aux4+q*aux3)/N)*aux1*auxu1-d * aux1
        +theta*aux5;
    m32 = (beta*(aux4+q*aux3)/N)*aux1*auxu1-(k +d)*aux2;
    m33 = (1-p)*k*aux2-(d+gamma +mu2)*aux3;
    m34 = p*k*aux2-(mu1+d+alpha*auxu2)*aux4;
    m35 = gamma*aux3+alpha*auxu2*aux4- (theta+d)*aux5;
```

```
        aux1 =x1(i)+h*m31; aux2 = x2(i)+h*m32; aux3 = x3(i)+
            h*m33; aux4 = x4(i)+h*m34; aux5 = x5(i)+h*m35;
        auxu1 = 1-u1(i+1);
        auxu2 = u2(i+1);
       m41 =  b - (beta*(aux4+q*aux3)/N)*aux1*auxu1-d * aux1
          +theta*aux5;
       m42 =  (beta*(aux4+q*aux3)/N)*aux1*auxu1-(k +d)*aux2;
       m43 = (1-p)*k*aux2-(d+gamma +mu2)*aux3;
       m44 =  p*k*aux2-(mu1+d+alpha*auxu2)*aux4;
       m45 = gamma*aux3+alpha*auxu2*aux4- (theta+d)*aux5;
       x1(i+1) = x1(i) + (h/6)*(m11 + 2*m21 + 2*m31 + m41);
       x2(i+1) = x2(i) + (h/6)*(m12 + 2*m22 + 2*m32 + m42);
       x3(i+1) = x3(i) + (h/6)*(m13 + 2*m23 + 2*m33 + m43);
       x4(i+1) = x4(i) + (h/6)*(m14 + 2*m24 + 2*m34 + m44);
       x5(i+1) = x5(i) + (h/6)*(m15 + 2*m25 + 2*m35 + m45);

end
for i = 1:M
    j = M + 2 - i;
     auxu1 = 1-u1(j);
     auxu2 = u2(j);
     k2 = d + gamma + mu2;
     k3 = mu1 + d;
     k4 = lambda1(j) - lambda2(j);
     k5 = lambda2(j) - lambda3(j);
     k6 = lambda3(j) - lambda4(j);
     k7 = lambda5(j) - lambda1(j);
     n11 = lambda1(j)*d + (k4*auxu1*(q*x3(j)+x4(j))*beta)
         ./N;
     n12 = lambda2(j)*d*k6*p*k+k5*k-C1;
     n13 = (beta*q*x1(j)./N)*auxu1*k4+lambda3(j)*k2-
         lambda5(j)*gamma;
```

```
n14 = -C2+(beta*x1(j)./N)*auxu1*k4+lambda4(j)*(k3+
    alpha*auxu2)-alpha*auxu2*lambda5(j);
n15 = k7*theta+d*lambda5(j);
aux1 = 0.5*(x1(j)+x1(j-1)); aux3 = 0.5*(x3(j)+x3(j
  -1));
auxL1 = lambda1(j)-h2*n11; auxL2 = lambda2(j)-h2*n12
  ; auxL3 = lambda3(j)-h2*n13;
auxL4 = lambda4(j)-h2*n14; auxL5 = lambda5(j)-h2*n15
  ;
auxu1 = 1-u1(j);
auxu2 = u2(j);
k2 = d + gamma + mu2;
k3 = mu1 + d;
k4 = lambda1(j) - lambda2(j);
k5 = lambda2(j) - lambda3(j);
k6 = lambda3(j) - lambda4(j);
k7 = lambda5(j) - lambda1(j);
n21 = auxL1*d + (k4*auxu1*(q*aux3+aux4)*beta)./N;
n22 = auxL2*d*k6*p*k+k5*k-C1;
n23 = (beta*q*aux1./N)*auxu1*k4+auxL3*k2-lambda5(j)*
    gamma;
n24 = -C2+(beta*aux1./N)*auxu1*k4+auxL4*(k3+alpha*
    auxu2)-alpha*auxu2*auxL5;
n25 = k7*theta+d*auxL5;
aux1 = 0.5*(x1(j)+x1(j-1)); aux3 = 0.5*(x3(j)+x3(j
  -1));
auxL1 = lambda1(j)-h2*n21; auxL2 = lambda2(j)-h2*n22
  ;
auxL3 = lambda3(j)-h2*n23; auxL4 = lambda4(j)-h2*n24
  ; auxL5 = lambda5(j)-h2*n25;
auxu1 = 1-u1(j);
auxu2 = u2(j);
```

```
k2 = d + gamma + mu2;
k3 = mu1 + d;
k4 = lambda1(j) - lambda2(j);
k5 = lambda2(j) - lambda3(j);
k6 = lambda3(j) - lambda4(j);
k7 = lambda5(j) - lambda1(j);
n31 = auxL1*d + (k4*auxu1*(q*aux3+aux4)*beta)./N;
n32 = auxL2*d*k6*p*k+k5*k-C1;
n33 = (beta*q*aux1./N)*auxu1*k4+auxL3*k2-lambda5(j)*
    gamma;
n34 = -C2+(beta*aux1./N)*auxu1*k4+auxL4*(k3+alpha*
    auxu2)-alpha*auxu2*auxL5;
n35 = k7*theta+d*auxL5;
aux1 = x1(j-1); aux3 = x3(j-1);
auxL1 = lambda1(j)-h.*n31; auxL2 = lambda2(j)-h.*n32
   ; auxL3 = lambda3(j)-h.*n33;
auxL4 = lambda4(j)-h.*n34; auxL5 = lambda5(j)-h.*n35
   ;
auxu1 = 1-u1(j);
auxu2 = u2(j);
k2 = d + gamma + mu2;
k3 = mu1 + d;
k4 = lambda1(j) - lambda2(j);
k5 = lambda2(j) - lambda3(j);
k6 = lambda3(j) - lambda4(j);
k7 = lambda5(j) - lambda1(j);
n41 = auxL1*d + (k4*auxu1*(q*aux3+aux4)*beta)./N;
n42 = auxL2*d*k6*p*k+k5*k-C1;
n43 = (beta*q*aux1./N)*auxu1*k4+auxL3*k2-lambda5(j)*
    gamma;
n44 = -C2+(beta*aux1./N)*auxu1*k4+auxL4*(k3+alpha*
    auxu2)-alpha*auxu2*auxL5;
```

```
        n45 = k7*theta+d*auxL5;
        lambda1(j-1) = lambda1(j) - h/6*(n11 + 2*n21 + 2*n31
            + n41);
        lambda2(j-1) = lambda2(j) - h/6*(n12 + 2*n22 + 2*n32
            + n42);
        lambda3(j-1) = lambda3(j) - h/6*(n13 + 2*n23 + 2*n33
            + n43);
        lambda4(j-1) = lambda4(j) - h/6*(n14 + 2*n24 + 2*n34
            + n44);
        lambda5(j-1) = lambda5(j) - h/6*(n15 + 2*n25 + 2*n35
            + n45);
    end

    D = (beta.*(q.*x3+x4).*(lambda2-lambda1)).*x1;
    E= x4.*(lambda4-lambda5);
     u1 =  min(0.95,max(0,D./N.*B1));
     u2 = min(0.95,max(0,E./B2));
     u1 = 0.5*(u1 + oldu1);
     u2 = 0.5*(u2 + oldu2);
     dt = t(i+1)-t(i);
     J = sum(( C1*x2+C2*x4+ +1/2*B1*u1.^2+1/2*B2*u2.^2 )*dt);
     temp1 = delta1*sum(abs(x1)) - sum(abs(oldx1 - x1));
     temp2 = delta1*sum(abs(x2)) - sum(abs(oldx2 - x2));
     temp3 = delta1*sum(abs(x3)) - sum(abs(oldx3 - x3));
     temp4 = delta1*sum(abs(x4)) - sum(abs(oldx4 - x4));
     temp5 = delta1*sum(abs(x5)) - sum(abs(oldx5 - x5));
     temp6 = delta1*sum(abs(u1)) - sum(abs(oldu1 - u1));
     temp7 = delta1*sum(abs(u2)) - sum(abs(oldu2 - u2));
     temp8 = delta1*sum(abs(lambda1)) - sum(abs(oldlambda1 -
        lambda1));
     temp9 = delta1*sum(abs(lambda2)) - sum(abs(oldlambda2 -
        lambda2));
```

```
    temp10 = delta1*sum(abs(lambda3)) - sum(abs(oldlambda3 -
        lambda3));
    temp11 = delta1*sum(abs(lambda4)) - sum(abs(oldlambda4 -
        lambda4));
    temp12 = delta1*sum(abs(lambda5)) - sum(abs(oldlambda5 -
        lambda5));
    test = min(temp1, min(temp2, min(temp3, min(temp4, min(
        temp5,min(temp6,min(temp7, min(temp8, min(temp9, min(
        temp10,min(temp11,temp12)))))))))));
end


y(1,:) = t;
y(2,:) = x1;
y(3,:) = x2;
y(4,:) = x3;
y(5,:) = x4;
y(6,:) = x5;
y(7,:) = lambda1;
y(8,:) = lambda2;
y(9,:) = lambda3;
y(10,:) = lambda4;
y(11,:) = lambda5;
y(12,:) = u1;
y(13,:) = u2;
y(14,:) = J;
box on
hold on
plot(y(1,:),y(5,:),'r','LineWidth',2)
xlabel('Time(months)','fontsize',12)
ylabel('Infected Population','fontsize',13)
legend('Infected population without control','Infected
   population with control')
```

```
end
```