Project Report

On

A PRIOR ON USING MATHEMATICAL MODELLING TO UNDERSTAND COVID 19 SCENARIO

Submitted

in partial fulfilment of the requirements for the degree of

MASTER OF SCIENCE

in

MATHEMATICS

by

UTHARA M S

(Register No. SM20MAT016)

(2020-2022)

Under the Supervision of

Smt VEENA V S

DEPARTMENT OF MATHEMATICS

ST. TERESA'S COLLEGE (AUTONOMOUS)

ERNAKULAM, KOCHI - 682011

APRIL 2022

ST. TERESA'S COLLEGE (AUTONOMOUS), ERNAKULAM

CERTIFICATE

This is to certify that the dissertation entitled, **A PRIOR ON USING MATHEMATICAL MODELLING TO UNDERSTAND COVID 19 SCENARIO** is a bonafide record of the work done by Ms. **UTHARA M S** under my guidance as partial fulfillment of the award of the degree of **Master of Science in Mathematics** at St. Teresa's College (Autonomous), Ernakulam affiliated to Mahatma Gandhi University, Kottayam. No part of this work has been submitted for any other degree elsewhere.

Date: 27-05-2022.
Place: Ernakulam

Smt VEENA V S
Assistant Professor,
Department of Mathematics,
St. Teresa's College(Autonomous),
Ernakulam.

Dr.Ursala Paul
Assistant Professor and HoD of the department,
Department of Mathematics,
St. Teresa's College(Autonomous),
Ernakulam.

External Examiners

1: DIVYA MARY DAISE-S 27/5/2022

2: MARY RUNIYA 27/05/2022

DECLARATION

I hereby declare that the work presented in this project is based on the original work done by me under the guidance of **Smt VEENA V S**, Assistant Professor, Department of Mathematics, St. Teresa's College(Autonomous), Ernakulam and has not been included in any other project submitted previously for the award of any degree.

Place: Ernakulam. **UTHARA M S**

Date: 27-05-2022 **SM20MAT016**

ACKNOWLEDGEMENTS

Though I have taken efforts in this project, it would not have been possible without the kind support and help of many individuals. I would like to extend my sincere thanks to all of them. I am highly indebted to **Smt NISHA OOMMEN** and **Smt DHANALAKSHMI O M** for their guidance and constant supervision as well as for providing necessary information regarding the project and also for their support in completing the project. I would like to express my gratitude to my parents for their kind cooperation and encouragement which help me in completion of this project.

I am very grateful to my project guide **Smt VEENA V S** for the immense help during the period of work . Her constant guidance and willingness to share her vast knowledge made us understand this project and its manifestations in great depths ad helped us to complete the assigned tasks on time.

In addition, very energetic and competitive atmosphere of the department had much to do with this work. I acknowledge with thanks to faculty, teaching and non-teaching staff of the department and colleagues.

I am also very thankful to HoD Dr.Ursala Paul for her valuable suggestions, critical examination of work during the progress.

UTHARA M S
SM20MAT016

Place: Ernakulam.
Date: 27/05/2022

Contents

Chapter 1

Introduction

The novel coronavirus (COVID-19) pandemic that emerged from Wuhan city in December 2019 overwhelmed health systems and paralyzed economies around the world. It became the most important public health challenge facing mankind since the 1918 Spanish flu pandemic. The disease started as an outbreak of pneumonia of unknown cause. It rapidly became a devastating pandemic, spreading to every country on earth, and inflicting severe public health and socio-economic burden globally. By the end of August 2020, the pandemic caused over 25.6 million confirmed cases and 854, 000 deaths globally. China was the first epicenter of COVID-19, followed by Europe.

COVID-19 is transmitted from human-to-human through direct contact with contaminated objects or surfaces and through inhalation of respiratory droplets from both symptomatic and -infectious humans. There is also limited evidence that the virus can be exhaled through normal breathing. The incubation period of COVID-19 ranges from 2 to 14 days, and most infections (over 80%) show mild or no clinical symptoms of the disease The common symptoms of the disease include fever, coughing and shortness of breath for mild cases, and pneumonia for severe cases. Although data clearly shows that most of the COVID-19 related deaths and severe cases typically occur in the elderly and people with comorbidities, such as people with diabetes, hypertension, obesity, kidney disease and other conditions that suppress or compromise the

immune system, younger people and front line healthcare workers are also at high risk of acquiring COVID-19 .

Corona viruses (CoVs) are a major group of RNA viruses that cause diseases in mammals and birds. In humans, these viruses are associated with multiple respiratory diseases of varying severity. For instance, the mild form of coronavirus infections causes diseases such as the common cold, while the severe form can cause diseases such as the severe acute respiratory syndrome (SARS-CoV), middle eastern respiratory syndrome (MERS) and COVID-19 (caused by SARS-CoV-2). "Coronavirus" is derived from the Latin word "Corona", meaning crown or wreath, which is related to the characteristic appearance of the virions of the virus. Zoonotic scientists estimated that there are millions of coronaviruses in the wild, thereby making humans vulnerable to coronavirus pandemics periodically (since, owing to their genetic makeup, human coronaviruses are rated among the most rapidly evolving human viruses). It is believed that human coronaviruses have their origins in bats and rodents, and some human activities, such as urbanization and poultry farming, help in expediting their evolution.

Two pandemics of coronaviruses have occurred in recent years. These include the 2002/2003 pandemic of severe acute respiratory syndrome (SARS-CoV), a highly transmissible disease which started in the Guangdong province of China and spread to 29 countries (causing 8000 cases and 744 fatalities globally). Palm civet and bats were the natural reservoirs of SARS-CoV, which has a mortality rate of 10% . In 2012, a pandemic of the middle eastern respiratory syndrome (MERS-CoV) started out of Saudi Arabia and spread to 27 countries, causing 2519 cases and 866 deaths by January 2020. Over 80% of MERS-CoV occurred in Saudi Arabia. MERS-CoV, which was believed to have originated from bats and then likely spread from infected dromedary (Arabian) camels to humans, has a mortality rate of about 35%. SARS-CoV and MERS-CoV have similar clinical symptoms.

Consequently, control and mitigation efforts against COVID-19 are fo-

cused on the implementation of non-pharmaceutical interventions (NPIs), such as community lockdown, maintaining social (physical)-distancing, using face masks in public, quarantine of suspected cases, isolation and hospitalization of confirmed cases, surveillance and serology testing and contact tracing. This study introduces some of the basic principles and methodologies for using mathematical modeling, backed by rigorous analysis and statistical data analytics, to gain insight into the transmission dynamics and control of infectious diseases, such as COVID-19, in human population.

Mathematical models have the potential to trace and predict the epidemic trajectory under different scenario. Various mathematical, statistical models have been proposed to understand the dissemination trajectory for a pandemic.Among these models, Susceptible(S)-Infected (I) -Recovered(R) model (SIR model) has been frequently used in past to predict the influence of HIV virus.Recently, SIR model has also been applied for prediction of COVID-19 trajectory and its epidemic peak. However, such studies have been carried out at the very earlier stage of pandemic. Moreover, such studies are primarily focused on the COVID-19 spread tracing under normal circumstances i.e. containment strategies (policies) have not been considered in such studies for COVID-19 prediction

In the absence of a ready-to-use vaccine, and besides medical and biological research, mathematical models can play an important role in understanding and predicting disease transmission. Moreover, it helps to implement appropriate measures and efficient strategies to control the pandemic's spread and mitigate its impact.

The objectives of the present study are:
1. To analyze the transmission dynamics of COVID-19 among humans via mathematical modeling.

2. To investigate the impact of control strategies such as lockdown, quarantine and isolation to control the spread of the global pandemic (COVID-19).
3. The impact of lockdown/quarantine of susceptible individuals. What would be the outcomes if there is partial/full lockdown?
4.The impact of vaccine.

In the study I firstly investigate about the model of COVID 19. I introduded a flow chart to observe the flow of the disese. Then next I have studied about the lockdown and its impact. Finaly I have studied about the vaccination model and have made a flow chart chart to know the effect of vaccine . The flow chart is helpfull to understand the models.

Chapter 2

MODEL ON THE DISEASE

In this work, we shall study the transmission mechanism of COVID-19 using a deterministic compartmental model.
Here, the population is divided into four compartments:
S **is the compartment of susceptible individuals;**
E **is the exposed individuals (Infected but not infectious)**
I **is the infected individuals**
R **is the removed individuals**
N **is the total population**
Then we an say that

$$N = S + E + I + R \tag{2.1}$$

Firstly a person will be in S then after getting the virus the person will move to E and after the latency period the person move to sub-population$I$. Then after getting treated or by death the person will move to the R sub-population. This is the step 1 for the modelling of the disease.
The figure 2.1 gives the pictorial representation of the flow of virus.
NOTE: A removed one can become susceptible again.

There are some factors that are responsible for the flow of the virus.

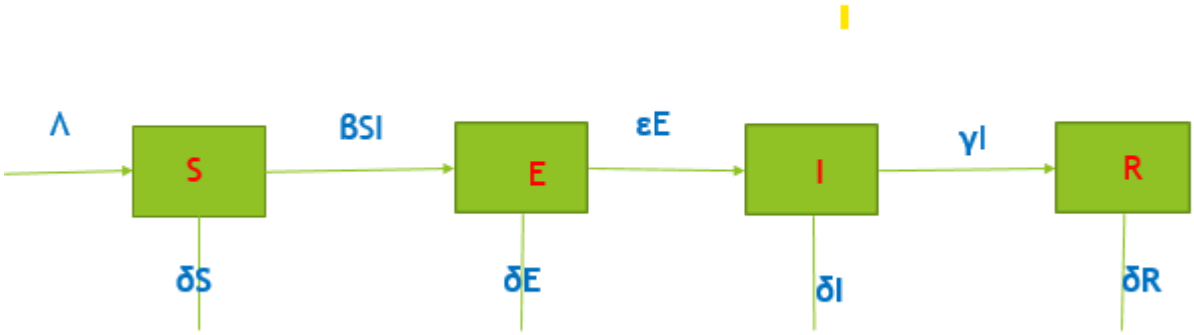

Figure 2.1: flow of the proposed model

1. **The susceptible population S we can have new peoples coming into it (like giving birth).We can call this by birth rate .We represent this factor by the symbol λ .**

2. **In each subpopulation we can see some person removed by death (death caused by natural causes other than this disease).**
   That is the death rate of each subpopulation S,E,I,R are δS,δE,δI,δR
   NOTE:The largest among the death rates is δR

3. **Now a person move from subpopulation $S$to E by a factor called mass effect or bilenear incidence.This happen when a person get interact with a person having the corona virus.We denote this by the symbol βSI**
   Here all the population is mixed together.So a susceptible can get contact with an in infected on this parameter is the reason for the need of quarantine.
   Therefore,
   The relative contact of infected people with susceptible population $= \beta SI$

4. **A person in E have latency period to get into the sub population I.So here the factor responsible is the latency period.We denote it**

by ϵE

.

5. **The parameter that lead a person to move from infectious to removed is the average period of infection. We denote it by γI.**
   The recovery rate = γ

This is how a virus travel in the transport diagram.

2.1 THE MATHEMATICAL MODEL

Now we have to study abut the change that is happening to the population over time due to these factors.In general what we need in a model is S to be large and I to be very small.From the figure 2.1 we arrive at a system of differential equations that tells how each population is changing over time.
The system of differential equation is as follows:

$$\mathbf{dS/dt} = \gamma I\text{-}\beta SI - \delta \mathbf{S} \ldots\ldots (2.2)$$

$$\mathbf{dE/dt} = \beta SI\text{-}\epsilon E - \delta \mathbf{E} \ldots\ldots (2.3)$$

$$\mathbf{dI/dt} = \epsilon E\text{-}\delta \mathbf{I} - \ \gamma I \ldots\ldots (2.4)$$

$$\mathbf{dR/dt} = \gamma I\text{-}\delta \mathbf{R} \ldots\ldots (2.5)$$

Here there is four parameters so we arrive into a system of differential equation with four equations.

2.2 METHODOLOGY

An aim of a model is to create a positive solution. To find this we need to find a feasible solution where we would have a solution or non-negative solution.

2.2.1 FEASIBLE SOLUTION

For a feasible solution the susceptible population to be positive and the others need to be zero.The total population will always be positive So that there is no disease. We denote the feasible region as Σ.
Since,
the total population N is always positive its rate of change will also be positive.

$$\mathbf{dN/dt \geq 0}$$

We know that

$$\mathbf{dN/dt = d(S+E+I+R)/dt}$$

For each terms we have expressions from the system of linear equations
That is,

$$\frac{dN/dt}{} = \gamma I\text{-}\beta SI - \delta \mathbf{S} + \beta SI\text{-}\epsilon E - \delta \mathbf{E} + \epsilon E\text{-}\delta \mathbf{I} - \ \gamma I + \gamma I\text{-}\delta \mathbf{R}$$

$$= \lambda - \delta \mathbf{S} - \delta \mathbf{E} - \delta \mathbf{I} - \delta \mathbf{R}$$

$$= \lambda - \delta(\mathbf{S+E+I+R})$$

$$= \lambda - \delta \mathbf{N}$$

$$\Rightarrow \lambda - \delta \mathbf{N} \geq \mathbf{0}$$

$$\Rightarrow \lambda \geq \delta \mathbf{N}$$

$$\Rightarrow \frac{\lambda}{\delta} \geq \mathbf{N} \ldots\ldots (2.6)$$

$$\Rightarrow \frac{\lambda}{\delta} \geq \mathbf{S+E+I+R}$$

This gives the feasible region.Thus the feasible region and the subset of R^4 and is the ratio of birth rate and death rate.

2.3 EQUILIBRIA

This model give rise to two equilibrium's:

1. **Disease free equilibrium**
2. **Endemic equilibrium**

1.Disease free equilibrium
It is the case where thee is no disease .That is, the E,I,R sub populations eventually becomes zero.

2.Endemic equilibrium
It is the case when the disease comes and the corona virus is going to stay in the population where none of the rates changes anymore .

$\star$To find the disease free equilibrium

Disease free equilibrium happens when $E = 0$. Now we know that if E is zero then eventually I and R becomes zero.
We know that

$$\mathbf{dI/dt} = \epsilon E - \delta \mathbf{I} - \gamma I$$
$$\Rightarrow \epsilon E = (\delta + \gamma) I$$

$$\mathbf{I} = \epsilon/(\delta + \gamma) E$$

Also,

$$\mathbf{dR/dt} = \gamma I\text{-}\delta\mathbf{R}$$
$$\gamma I\text{-}\delta\mathbf{R}=\mathbf{0}$$
$$\mathbf{R}= (\gamma/\delta)\mathbf{I}$$
$$\Rightarrow \mathbf{R}=(\gamma/\delta)\epsilon/(\delta+\gamma)E$$

Also,

$$\mathbf{dS/dt} = \gamma I\text{-}\beta SI - \delta\mathbf{S}$$
$$0\gamma - \delta\mathbf{S}$$
$$\Rightarrow \tfrac{\lambda}{\delta} = \mathbf{S}$$

Therefore the disease free equilibrium $\boldsymbol{P}_0$ is $(\boldsymbol{S}, 0, 0, 0) \ldots\ldots (2.7)$

That is, $\boldsymbol{P}_0 = (\lambda/\delta, 0, 0, 0)$

$\star$***To find the endemic equilibrium***

Endemic equilibrium happens when $\boldsymbol{E \neq 0}$

This is the second phase of modelling. When $\boldsymbol{E^* \neq 0}$ $\boldsymbol{I^* \neq 0}$ $\boldsymbol{R^* \neq 0}$

Then

(2.3)+(2.4)

$$\Rightarrow \beta SI\text{-}\epsilon E - \delta\boldsymbol{E} + \epsilon E\text{-}\delta\boldsymbol{I} - \ \gamma I$$
$$\Rightarrow \beta SI\text{-}(\delta+\gamma)I - \delta\boldsymbol{E} = \ \boldsymbol{0}$$

Since we know the value of I , we get

$$\beta S\epsilon/(\delta+\gamma)EI\text{-}(\epsilon+\delta)E = \mathbf{0}$$
$$\Rightarrow [\beta S(\epsilon/(\delta+\gamma))\text{-}(\epsilon+\delta)]E = \mathbf{0}$$

There fore the endemic equilibrium is $\mathbf{S^*} = (\epsilon+\delta)(\delta+\gamma)/\beta\epsilon \ldots\ldots (2.8)$

2.4 GENERAL REPRODUCTION NUMBER

This is last phase of disease modelling.
GENERAL REPRODUCTION NUMBER is the number of new case any single individual is going to create. We denote this by $\mathbf{R}^0$.

We know that ,

$$\mathbf{S} \geq \lambda/\delta$$
$$\Rightarrow (\epsilon+\delta)(\delta+\gamma)/\beta\epsilon \geq \lambda/\delta$$
$$\textbf{iff } \mathbf{1} \geq \lambda\beta\epsilon/\delta(\epsilon+\delta)(\delta+\gamma)$$

That is,

- $R^0 \leq 1$ *is the disease free equilibrium*

- $R^0 \geq 1$ *is the endemic equilibrium*

  By the help of this study we can control the disease by using proper parameters such as quarantine , lockdown to make R^0 **less than 1 and this we will have a disease free equilibrium.This ishow we model the corona virus disease**

Chapter 3

MODEL ON LOCK DOWN

Due to the pandemic, where the worldwide infection and decease rate are really very alarming, the world needs quick recovery and for that, a proper prediction regarding the transmission range, transmission trend and decision making of lockdown measures are needed. From the existing literature, it is clear that there have been many attempts to predict the diseasespreading all over the world.However , the isolation and social distancing guidelines is required to analyse the decisions .The analysis for the effect of a lockdown was performed without the influence of the other control measures, like social distancing and mask wearing, to quantify its absolute effect. Hypothetical lockdown timing was shown to be the critical parameter in ameliorating pandemic peak incidence. More importantly, we found that well-timed lock downs can split the peak of hospitalizations into two smaller distant peaks while extending the overall pandemic duration. The timing of lock downs reveals that a "tunneling" effect on incidence can be achieved to bypass the peak and prevent pandemic caseloads from exceeding hospital capacity.
The resolved factor R depends on S and I,so here we have restricted our implementation to SI. With the progress of disease spreading over a longer time, the new births have been considered. In this scenario, the system can be represented by

$$\mathbf{dS/dt} = \lambda - (1-\alpha)r(1-\mu)SI - \alpha S \ldots\ldots (3.1$$
$$\mathbf{dI/dt} = (1-\alpha)r(1-\mu)SI - aI - \mu I \ldots\ldots (3.2)$$

This is the lockdown model .

Here,

a = recovery rate

α= lockdown rate of susceptible

μ=isolation rate of infectious

To detect the effectiveness of social distancing approach we have divided the infected population into two categories by extending the conventional SEIR model. The first one is called Type I who are generally the detectable infected persons and the second one is called Type II who are undetectable infected person. If the probability of an infected people becoming detectable is denoted by p^1 and becoming undetectable is p^2, then

$$p^1 + p^2 = 1 \ldots\ldots (3.3)$$

If the transmission rates among Type I and Type II people are denoted by r_1 and r_2 respectively and the recovery rates for the same area 1 $(a_1)$and area 2 (a_2), then

$$L^0 = p^1(r_1/a_1) + p^2(r_2/a_2) \ldots\ldots \textbf{(3.4)}$$

In practical scenario, Type II population has a higher transmission rate than that of a Type I population. The controllable measure of the disease is indicated by spectral radius which in turn shows that if the basic reproduction number $L^0 \geq 1$ then there is some outbreak , and $L^0 \leq 1$ then no outbreaks there.

Allowing all to keep their interpersonal contacts up-to a fraction of normal contacts and cancelling mass gatherings, these two approaches of maintaining social distance have been considered here.

The lockdown in the whole country announced by government has definitely acted as infection controller and helped to face the challenge of COVID-19 in the desired form.

Chapter 4

MODEL ON COVID VACCINATION

Vaccines can prevent infectious diseases. Vaccines do prevent measles, polio, hepatitis B, influenza and many others.When most people in a community are protected by vaccination, the ability of the pathogen to spread is limited. This is called 'herd' or 'indirect' or 'population' immunity.When many people have immunity, this also indirectly protects people who cannot be vaccinated, such as those who have compromised immune systems.

To bring this pandemic to an end, a large share of the world needs to be immune to the virus. The safest way to achieve this is with a vaccine. Vaccines are a technology that humanity has often relied on in the past to bring down the death toll of infectious diseases.Within less than 12 months after the beginning of the pandemic, several research teams rose to the challenge and developed vaccines that protect from SARS-CoV-2.

Vaccines greatly reduce the risk of infection by training the immune system to recognize and fight pathogens such as viruses or bacteria. Most research on COVID-19 vaccines involves generating responses to all or part of the spike protein that is unique to the virus that causes COVID-19. When a person receives the vaccine, it will trigger an immune response. If the person is infected by the virus later on, the immune system recognizes the virus and, because it is already pre-

pared to attack the virus, protects the person from COVID-19.

⋆How safe are the COVID-19 vaccines?

The safety requirements for COVID-19 vaccines are the same as for any other vaccine and will not be lowered in the context of the pandemic.Safety trials begin in the lab, with tests and research on cells and animals first, before moving onto human studies.The principle is to start small and only move to the next stage of testing if there are no safety concerns.Clinical trials are evaluating COVID-19 vaccines in tens of thousands of study participants to generate the scientific data and other information needed to determine safety and effectiveness.These clinical trials are being conducted by manufacturers according to rigorous standards. The COVID-19 vaccines are tested in a broad population of people – not only young, physically fit. volunteers, but also older people and people with underlying health conditions After deployment, the vaccines will continue to be carefully monitored for safety and effectiveness.

⋆What is done to fast-track vaccine development in a public health emergency?

Continuous dialogue between developers and regulatory experts and early scientific advice helps speed up vaccine development. Advising companies on regulatory requirements helps ensure that standards of safety and efficacy are embedded early in the process and are not compromised by fast-track development.Resource mobilization for COVID-19 vaccines is done simultaneously which allows for accelerated development and manufacturing of vaccines.Companies are expanding manufacturing capacity and large-scale production, to facilitate vaccine deployment without delay once approved.

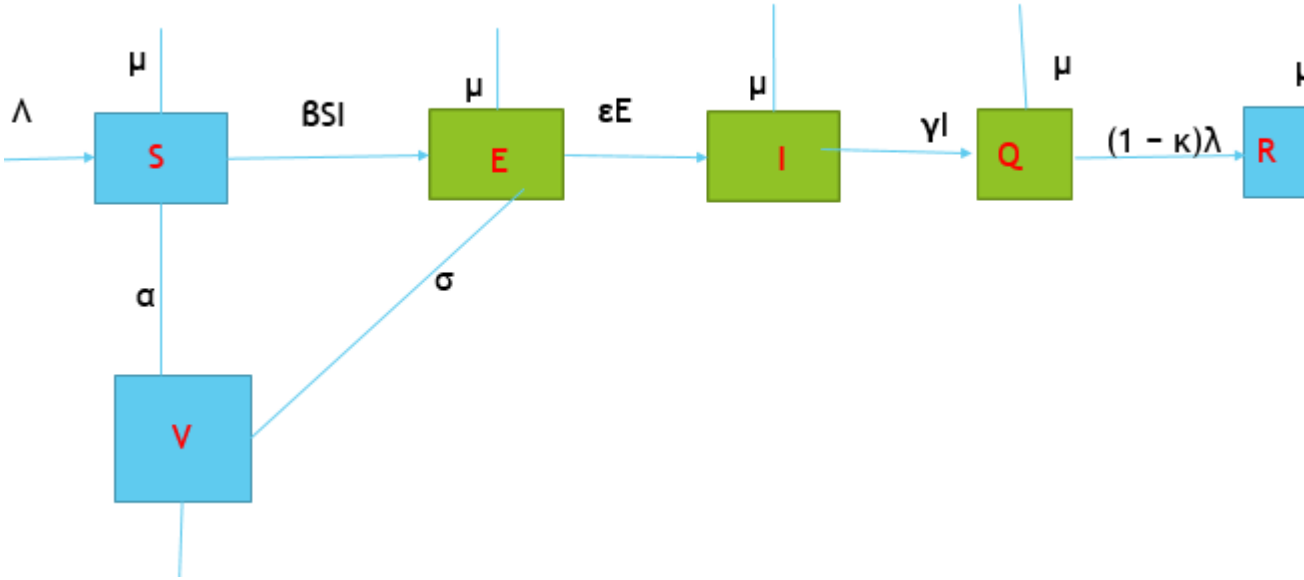

Figure 4.1: flow of vaccination model

4.1 VACCINATION MODEL

This work therefore aims to study the impact of vaccination on the COVID-19 spread. An extended SEIR model comprising of seven compartments—susceptible, exposed, infectious, quarantined, recovered, deaths, and vaccinated—is then proposed. First, we 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 mode .

We extend the SEIR model to seven compartments to simulate the epidemic of COVID19. Seven state variables are considered within a population, that is, S(t), E(t), I(t), Q(t), R(t), D(t), and V(t), denoting the number of susceptible, exposed (infected, but not yet infectious), infectious (not yet quarantined), quarantined (confirmed and infected), recovered, dead, and vaccinated cases, respectively. The disease transmission flow of the proposed model is sketched in Figure 4.1

The model is then governed by the following set of nonlinear ordinary differential equations:
Here,

$$\begin{aligned}
\frac{dS(t)}{dt} &= \Lambda - \beta S(t)I(t) - \alpha S(t) - \mu S(t), \\
\frac{dE(t)}{dt} &= \beta S(t)I(t) - \gamma E(t) + \sigma\beta V(t)I(t) - \mu E(t), \\
\frac{dI(t)}{dt} &= \gamma E(t) - \delta I(t) - \mu I(t), \\
\frac{dQ(t)}{dt} &= \delta I(t) - (1-\kappa)\lambda Q(t) - \kappa\rho Q(t) - \mu Q(t), \\
\frac{dR(t)}{dt} &= (1-\kappa)\lambda Q(t) - \mu R(t), \\
\frac{dD(t)}{dt} &= \kappa\rho Q(t), \\
\frac{dV(t)}{dt} &= \alpha S(t) - \sigma\beta V(t)I(t) - \mu V(t),
\end{aligned}$$

Q(t) = the number of quarantined cases

V(t) = the number of vaccinated cases

κ **= average quarantine time**

In this vaccination modelling the original population N is again subdivided into 2.That is to Q **and** V**.**

Thus,

$$N = S + E + I + R + Q + V \tag{4.1}$$

In the transport diagram of vaccination model one person travel from I **to** Q **from the and from** Q **to** R **by the recovery time.**

The coefficients $\lambda, \beta, \alpha, \mu, \gamma, \sigma, \delta, \kappa$**, and** ρ **represent the new births and new residents transmission rate divided by** N**, vaccination rate (rate of people who are vaccinated), average latent time, average quarantine time, mortality rate, average days until recovery days until death, respectively.**

σ **is the vaccine inefficiency and (1-**σ**)is the vaccine efficiency.**

If $\sigma = 0$ **the vaccine offers 100% protection against the disease.**

Chapter 5

Conclusion

We have developed a mathematical model that is able to simulate the impact of SARS-CoV-2 variants and vaccines on the spread of COVID-19. It is based on the models proposed of disease.We were able to simulate other main mechanisms influencing the disease spread In chapter 2 I discussed about the model. It is to be noted from this analysis that one of the very key parameters is the disease transmission coefficient γ which plays a significant role in determining the basic reproduction number R^0.

COVID-19 has been declared as pandemic by WHO and is currently become a major global threat. Prediction of a disease may help us to understand the factors affecting it and the steps that we can take to control it. The Government of India has taken preventive measures such as complete lockdown in the very early stage of disease, physical distancing and case isolation. The most important issue is that many healthcare professionals are visiting each and every household in the hot spot area across the country to trace and isolate infected persons to curtail the spread of disease.

In this work on chapter 3, we presented that isolation of the infected human overall can reduce the risk of future COVID-19 spread. Our model shows that the coronavirus spreads through contact and describes how fast something changes by counting the number of people who are infected and the likelihood of new infections. Those new infections are what induce the epidemic. For this reason, we think that this research

may lead to better guessing of the spread of this pandemic in the future. This paper is devoted to implement the coronavirus mathematical model containing isolation class. The reproductive number-related stability is discussed.
In future, these shortcomings will be attempted to overcome for getting improved result of the scenario and experimental results show that our proposed approach is well suited in its concerned domain. However, the prediction will change based on some external factors like government decisions and human actions, so we can't train the data as of today to be true for a different situation in future. Our modified SEIR model is not only productive than the traditional one, but also more capable of handling and adopting the current situation.
In the fourth chapter the vaccination models help us to know the effect of covid vaccine in the society. The flowchart proposed in the vaccination model and the disease modelling can help to figure out the flow of the virus due to the pandemic.

Thus, its forecasts are as reliable and can capture the dynamics of the pandemic. Due to real time change in data daily, the predictions will accordingly change.

"if we control this contact rate, the control of the current disease is possible, otherwise it will be the worse"

REFERENCES

[1] **Abba B. Gumel, , Calistus N, Enahoro A. Iboi b. - Infectious Disease Modelling**

[2] **Ahona Ghosh · Sandip Roy · Suparna Biswas - Mathematical Modelling For Decision Making of Lockdown during COVID-19**

[3] **Anwar Zeb , Ebraheem Alzahrani and d Gul Zaman - Mathematical modeling of COVID-19 transmission: the roles of intervention strategies and lockdown**

[4] **Brijesh P. Singh1 Gunjan Singh2 1 Department of Statistics, Institute of Science, Banaras Hindu University, Varanasi-221005 2 School of Applied Sciences, Amity University, Lucknow-226028 - Modeling Tempo of COVID-19 Pandemic in India and Significance of Lockdown**

[5] **Central university of Rajasthan - Mathematical Modelling of COVID-19 transmission : the roles of intervention strategies and lock down**

[6] **Li, Q., Guan, X., Wu, P., Wang, X., Zhou, L., Tong, Y., ... Xing, X. (2020). Early transmission dynamics in Wuhan, China, of novel coronavirus–infected pneumonia. New England Journal of Medicine.**

[7] **Rabih Ghostine, Mohamad Gharamti - Mathematical modelling of Covid-19 with the effect of vaccine**

[8] **Sarita Bugalia , Vijay Pal Bajiya - Mathematical modeling of COVID-19 transmission: the roles of intervention strategies and lockdown**

[9] **Vipin Tiwari, Namrata Deyal , Nandan S. Bisht1 1Department of Physics, KU, SSJ campus Almora (263601), Uttarakhand, India - Mathematical modelling based study and prediction of COVID-19 epidemic dissemination under the impact of lockdown in India**

[10] **World Health Organization: Updated WHO advice for international traffic in relation to the outbreak of the COVID-19. WHO, Geneva. https://www.who.int/ith/ COVID-19adviceforinternationaltraffic/en/. Accessed 11 Dec 2021**