MATHEMATICAL MODELLING ON COVID-19 EPIDEMIC

A Thesis

Submitted in partial fulfillment of the requirements for the

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in

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By

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DECLARATION BY THE CANDIDATE

I, Kuldeep Singh, declare that the thesis entitled "MATHEMATICAL MODELLING ON COVID-19 EPIDEMIC" submitted for award of degree of Doctor of Philosophy in Mathematics, Lovely Professional University, Phagwara is a pioneering, distinctive, and impartial work accomplished underneath benign supervision of Dr. Rakesh Yadav (Supervisor), Associate Professor in Mathematics Department, School of Chemical Engineering and Physical Sciences, Lovely Professional University, Phagwara, Punjab. I further declare to the best of my knowledge the thesis does not contain any part of any work which has been submitted for the award of any degree in this University or in Other University/Deemed University without proper citation.

Signature of the Supervisor
(Dr. Rakesh Yadav)

Signature of Candidate
(Kuldeep Singh)

CERTIFICATE

This is to certify that the research exemplified in this thesis entitled "MATHEMATICAL MODELLING ON COVID-19 EPIDEMIC" has been done by Kuldeep Singh, under my guidance and supervision for the degree of Doctor of Philosophy of Mathematics, Lovely Professional University, Phagwara (Punjab) India. To the best of my knowledge and belief the thesis:

1. Embodies the work of the candidate himself.
2. Has duly been completed.
3. Fulfills the requirements of the ordinance relating to the Ph.D. degree of the University, and
4. Is up to the standard both in respect of contents and language for being referred to the examiner.

Signature of the Supervisor
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ABSTRACT

The SarsCov2 virus is a potentially lethal infection that is little known and has the potential to pose a considerable risk to public health, given that it is one of the most serious viruses that can impact people. Everyone in this pandemic era is discussing the increase in the disease's infection rate as the epidemic expands. Researchers from a wide variety of backgrounds have applied a wide variety of conceptual frameworks to provide a variety of forecasts for countries like India. The main goal of this research is to utilise a suitable mathematical model to comprehend the dynamics of the Indian population that is afflicted with the Corona virus and the estimated number of people who will become infected in the near future. In this work, many mathematical models were constructed, investigated, and verified for the COVID-19 epidemic to make predictions regarding the various repercussions of the disease. The data that is available in the public domain was utilised to make predictions about the cases that would occur soon, as well as basic reproduction and the case fatality ratio of the COVID-19. Additionally, a transmission model was discussed. The state of the pandemic outbreak in India was examined in this study, and several models were used to provide projections regarding its likely progression into the future. The Indian healthcare system faces a significant challenge when it comes to providing appropriate intensive care units for critically ill patients. It would be extremely beneficial if they had any idea of the cases that might arise in the future.

The main objectives of the research work were:

- To develop and validate the mathematical models on Covid-19 epidemic to forecast the different effects of the disease.
- To anticipate and forecast the various effects of the disease using existing models and data available in public domain.
- To determine the disease's Covid-19 case fatality ratio and basic reproduction number.
- To formulate a mathematical model that will help to make strategies to control Covid-19 epidemic.

In the first chapter, a comprehensive introduction to mathematical biology, epidemic modelling, certain essential mathematical models, and other related topics has been provided. The section on the review of the literature sheds light on a few important studies that have been done by scholars in this field up to this point. In light of the aforementioned, the research gaps have been outlined, and the goals of the study have been suggested. This chapter also provides an explanation of the fundamental mathematical preliminaries as well as the significant ideas, phrases, and concepts that were employed throughout the entire research project. The conclusion of the chapter provides an overview of the other chapters that make up the thesis.

In chapter 2, we have established that the COVID-19 outbreaks in India are a major cause for concern, and although a comprehensive scientific investigation of this pandemic has not yet been completed, it was necessary to calculate the parameters of the pandemic dynamics to design an appropriate quarantine area, determine the number of hospital beds available, and so on. We discussed the Polynomial Approximation Model in this chapter to determine how many people in India have the virus.

In chapter 3, our attention has been directed toward the investigation of the SEIRD model for COVID-19. When trying to make predictions about the amount of cases and deaths, several different factors were taken into consideration. From the collected data on fatalities and confirmed cases of COVID-19, we attempted to determine the basic reproduction number. The basic reproduction number is also dependent on the clinical factors. Next, we have provided an estimation for the spectrum of probable future projections for the total number of fatalities in India.

Since the Covid-19 disease has been deemed a threat on a global level and numerous studies are being published all over the world utilising several mathematical models to estimate the size of this epidemic, a simple econometric time series model was discussed in chapter 4. This was due to the fact that the disease has been declared a threat on a global level. As the weighty increase in the daily COVID-19 infected cases around us was frightening, many researchers are currently working on various mathematics-based estimation models to predict the subsequent trend of this pandemic. Some of India's COVID-19 trajectories were projected based on publicly available data.

This was because the weighty increase in the daily COVID-19 infected cases around us was frightening. A time series model known as the Auto-Regressive Integrated Moving Average Model was used to the Indian Dataset in order to estimate the daily number of COVID-19 infections in the near future. The results of our investigation projected several quite concerning outcomes. In order to avert such a potentially lethal scenario, a number of stringent preventative measures have been advocated. According to our estimates, Indian health officials ought to modify their warmongering interference in order to take into account the accelerated expansion, and rudimentary infection control efforts at hospital levels were immediately required in order to reduce the scale of the COVID-19 pandemic. It was possible that the impacts will become even more severe if the government of India does not adopt stringent prophylactic steps to stop the increase of COVID-19.

In chapter 5, As a reminder that pandemics, as well as other uncommon but catastrophic catastrophes, have occurred in the past and will continue to do so in the future, we discussed the transmission model for COVID-19. Pandemics are rare, yet devastating when they do occur. Transmission models are useful tools for gaining an understanding of the behaviour of contamination when it enters a community and determining the circumstances under which it will be treated or processed. Consequently, there are very few remedies available in India for a severe problem. This is a scenario that is not unique to India; rather, it is shared by countries all over the world. First, a proposal for the model's specifics is made, and then, after that, a discussion of the model's potential benefits follows. Using RPGT, a Transition Diagram of the system as well as equations for Transition Probability and Mean Sojourn Times, Path Probabilities, and the mean time to epidemic impacted (T_0), Average Healthy Time (A_0), and Recovery Period (B_0) were generated, and these were then followed by illustrations. After the creation of tables and graphs, analysis is performed.

In chapter 6, we used a compartmental model with five compartments, i.e., the SEIRD Model, and we did analysis of the dynamics of COVID-19 in India. Through this data-based study, we concluded that inflammation can be controlled by public lockdowns because it will reduce the transmission rates, and due to limited health care

facilities, there will be more chances of recovery and hence the recovery rate will be increased. If we change these two parameters, the curve can be flattened. If we change the values of parameters in the model, we will get different results. As we know, these parameters are not constant over time. So, if we look for disease dynamics at different times, we should change these parameters accordingly. Also, there are a few limitations in our model, and those have been discussed in the earlier sections. These can be improvised in the future. Also, some more parameters can be added to enhance the validation of results, like under reported cases or asymptotic cases.

In the end, the problems under investigation in the study have been justified by the bibliography given in the concluding part of the thesis.

ACKNOWLEDGMENT

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I acknowledge with pleasure the cooperation from the esteemed faculty of the University for their enthusiastic support and encouragement throughout the research work.

Above all, I feel very much obliged to my grandparents, parents, my wife, Ankur Bala, and friends for what I have received from them in the form of motivation, inspiration, love, encouragement, and moral support. Without them, it would have been impossible to carry out this task. They have supported me unconditionally and relentlessly over all these years.

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General Introduction

1.1 Introduction

"Mathematical Biology" is a rapidly growing, unambiguous subject, and the most inspiring application of the new age of applied mathematics. The increasing broad scope of biomathematics is unavoidable as biology becomes highly quantitative as well as qualitative. The complicated nature of the biological sciences makes interdisciplinary collaboration essential. For a person from the background of science, mathematics, or biology, it opens new and exciting branches. Mathematical modelling gives another research tool.

The study of how infectious diseases are transmitted through human populations is the focus of the scientific discipline known as epidemiology. Infectious diseases are among the most common reasons for people to pass away all over the world. Among these deadly diseases, HIV/AIDS, influenza, malaria, and tuberculosis are particularly potent. The health departments of any country are concerned about these diseases, despite their best efforts. Developing countries face a lot of these infectious diseases compared with developed nations. Although the medical facilities have improved in the past years, an epidemic usually disturbs the health care system and declares a health emergency. The cost of these infectious diseases is economically high as well. Due to the spread of these kinds of diseases, every country faces a downfall in the economic and social growth of the nation because of its effects on productivity, business, tourism, and educational institutes.

Although many international organisations like WHO and various NGOs are working hard for the improvement of the system of response and surveillance at the global level, But the desired success is still awaited. The major problem is the poor health care systems of developing countries. Although some factors, such as new medicines, the government's efforts to eliminate poverty, isolation, sanitation, and so on, reduce the likelihood of some diseases occurring, some factors, such as new medicines, the government's efforts to eliminate poverty, isolation, sanitation, and so on.

1.2 History and Modelling of Infectious Diseases


Sir Ronald Ross

"As a matter of fact, all epidemiology, concerned as it is with the variation of disease from time to time or from place to place, must be considered mathematically, however many variables as implicated, if it is to be considered scientifically at all."

Sir Ronald Ross, MD

According to historians, the first major epidemic occurred in Athens between the years 430 and 426 B.C.E. and was known as the plague. In his book "History of the Peloponnesian War," which he wrote between 460 and 400 B.C.E., the scientific historian Thucydides [1] (460–400 B.C.E.) provided the most correct explanation of the pandemic. He recounted everything based on his own first-hand experience, including how the epidemic spread, the symptoms it left behind, and the number of people who died. There is continuing discussion on the causative agent of plague [2-3]. Hippocrates, who lived from 459 to 337 B.C.E., was the first person to identify the variables that contributed to the epidemic of the period. Smallpox was also documented in the Roman Empire and Egypt between the years 165 and 180 CE by historians. Because of this, the deaths of millions of people were caused [4]. Between the years 1348 and 1350, the number of people who died as a direct result of the Black Death is estimated to have ranged anywhere from 50 million to 100 million [4]. The Black Death was a pandemic that swept across Europe and the Mediterranean. Recent data obtained from the DNA of plague victims has led researchers to the conclusion that the infectious

agent Yersinia pestis is responsible for the myriad types of the plague [5]. Since the beginning of the last three centuries, researchers have been using epidemic modelling to study infectious diseases. Daniel Bernoulli constructed a mathematical model in the year 1760 with the intention of analysing the efficacy of variolation in healthy individuals who were infected with the smallpox virus. His goal was to determine whether or not the disease could be prevented through vaccination. His goal was to determine whether or not the virus could be prevented from spreading through variolation. It was the first use of mathematics to be done in order to research any of the infectious diseases. After a considerable amount of time had passed, in the year 1840, In England and Wales, William Farr fitted a normal curve that was based on the number of deaths that were caused by smallpox. In the 19th century, the infectious agent that caused the Black Death reemerged in a few European countries. During the early part of the 20th century, a pandemic that was dubbed influenza was responsible for the deaths of nearly 20 million people. Pandemics such as the Bombay plague in 1905–1906, SARS in 2003, and the H1N1 swine flu pandemic in 2009 have all occurred in the recent past. All of these pandemics began in India. There was an outbreak of the Bombay plague in 1905–1906, as well as the SARS and H1N1 pandemics in 2003 and 2009, respectively. Because viruses evolve so quickly and even though they are capable of crossing species barriers, there is always the possibility of pandemics and epidemics breaking out. These diseases can infect vast numbers of people. John Graunt (1620–1674) was an infectious disease researcher who published his findings in the book "Natural and Political Observations Made upon the Bills of Mortality." Daniel Bernoulli was the first person to use mathematical tools to the study mortality due to smallpox after a century had passed. In 1766, he was the first person to publish a model of epidemiology. Bernoulli believed that, while the inoculation itself was risky, immunising with a live virus obtained from a mild case of smallpox could reduce the amount of people who passed away from the disease. Louis Pasteur made a significant contribution to our understanding of the factors that contribute to disease in the middle of the 19th century. He developed the first vaccines against anthrax and rabies, which contributed to a decrease in deaths caused by puerperal fever. His findings in the field of medical sciences provided direct support for the hypothesis that germs are the cause

of disease. At roughly the same time, Robert Koch, who is credited with being the inventor of modern bacteriology, discovered the specific causal agents of tuberculosis, anthrax, and cholera. This provided empirical support for the theory that infectious diseases are contagious. Additionally, he was well-known for developing Koch's postulates, for which he is named. In the late 1800s, medical research at last provided an explanation for the processes that lead to illness. It was discovered that an infectious bacterial disease might be transmitted from a healthy person to an already diseased person through casual contact between the two parties. The mathematical modelling of infectious diseases received some new guidance as a result of this. William Hamer made an important contribution to the study of mathematical modelling of infectious diseases at the beginning of the 20th century. He was attempting to determine what factors contributed to the continued occurrence of measles. It is possible to deduce from past events that Hamer was the pioneer in the application of the mass action law to the modelling of infectious diseases. However, Sir Ronald Ross is regarded as the father of the contemporary field of mathematical epidemiology. He undertook extensive research on malaria, and one of his findings was that the disease is spread from human to human through mosquitoes. In 1902, Ross was awarded the Nobel Prize for his efforts in malaria treatment. The prevention of the spread of malaria was a top priority for him. Mathematical models of malaria transmission were developed in the second edition of his book, "The Prevention of Malaria," which was released in 1911. The essential reproduction number is now commonly referred to as the threshold quantity. Infectious disease mathematical modelling was not widely accepted at the time. But no matter how many variables epidemiology — which examines how disease spreads over space and time — contains, statistical analysis is required before it can be deemed scientific. He was an outspoken proponent of using mathematical methodologies in epidemiology. It doesn't tell us much about a condition if we just say that it depends on specific components, since we can't develop an estimate of how much each factor influences the overall result unless we know how much each factor influences it. The application of critical reasoning to the challenges at hand is what the mathematical technique of therapy entails, which is actually all that it is.

An epidemic's course is influenced by the rate at which infectious and susceptible populations come into contact, and John Brownlee utilised this data to create and fit a Pearson frequency distribution curve. This research paper was published in 1906 and given the title "Statistical Studies in Immunity, the Theory of Epidemic." It was written by John Brownlee. When it was first introduced in 1927, Kermack and McKendrick's infectious disease transmission model was a significant step forward in mathematical epidemiology. A contribution to the mathematical theory of epidemics [6] was published in which the model was described for the first time. As a result, their model can only replicate disease outbreaks because it doesn't account for natural birth and death rates. Second and third parts of "A Contribution to the Mathematical Theory of Epidemics" were published by Kermack and McKendrick in 1932 and 1933 to add epidemic modelling of illnesses that can become established in a population and continue to spread throughout a population [7, 8, 9]. The mathematical modelling of infectious diseases became increasingly significant in the 1980s, when the HIV epidemic began. Since then, many models have been created, tested, and used in studies on the spread of infectious illnesses. Mathematical epidemiology is already well-established in the scientific literature, and mathematical modelling continues to make essential contributions to both the mathematical and public health fields. According to Sattenspiel [10], Some aspects of the disease's natural history and of the behaviour of its host population can be explained using models. These include the following:

- the impact that an individual's fluctuating levels of infectiousness throughout the course of the disease have on the rate at which the infection is transmitted across the population;
- Long incubation periods have been found to play a significant role in the course of the disease;
- the relationship between a person's degree of sexual activity and the likelihood that they will become unwell;
- risk and transmission rates within a population can be affected by assumptions about the degree to which various groups are intermingled;
- the effects of various shifts in sexual behaviour; and

- pandemic's impact on the world's population, particularly in places where infection rates are very high, such Africa and parts of the Caribbean.

For Kramer and colleagues [11], public health is all about controlling the spread of infectious diseases from one human being to another. Often referred to as the "basic science of public health," epidemiology studies the factors that influence illness risk in human populations and how they are distributed. Infectious disease epidemiology was first developed in the middle of the 19th century and uses the principles of epidemiology to research infectious diseases. It also addresses issues about the factors that lead to the emergence, spread, and persistence of disease. An epidemiological pattern can be identified by comparing the frequency and severity of infectious diseases in different parts of the world. The significance of epidemiological models can be summed up as [11, 12]:

• Epidemic models have the potential to lead to a greater comprehension of the natural history of the disease.

• To better comprehend the dynamics of disease transmission, epidemic models can play a crucial role in calculating and estimating crucial parameters.

• To generate predictions about the success of various approaches to illness prevention and treatment, a model that precisely captures the basic characteristics of disease progression and transmission must first be constructed.

• Epidemic models provide a deeper understanding of the characteristics of thresholds.

• Epidemic models are able to compute an exact number of steady states (states in which the disease is endemic or not present) and can analyse the stability of those states. Additionally, it is capable of determining bifurcation values, which indicate a change in the qualitative nature of population dynamics.

• The simulation of epidemics and the evaluation of the efficacy of various strategies for disease prevention and treatment can be done with the help of epidemiological models.

• It is possible to learn about the current surveillance system for a particular infectious illness and to propose more effective ways of surveillance through the use of epidemic models.

• More evidence-based approaches to disease control can be guided by epidemic models, which can aid in the interpretation of epidemiological data and provide recommendations for specific actions.

• Epidemic models can be used to link global environmental events to the transmission patterns of infectious illnesses.

1.3 General Approach to Modelling

A description of a system that makes use of mathematical concepts, techniques, and terminology is called a mathematical model. Transmissible diseases and the spread of those diseases through populations are what mathematical modelling will focus on, but in principle, mathematical modelling may be used on any system, whether it be biological or not. Mathematical models are built to assist in the explanation of a system, to investigate the consequences of the system's numerous components, and to provide forecasts regarding the behaviour of those components. Biological scenarios need to be transformed into mathematical ones to complete the modelling process. In most cases, scientists begin the process of modelling by providing a thorough description of the system's processes. There should be an objective or biological question in mind while turning this knowledge into mathematical formulae. An equation set is then generated using the system's verbal description. It is important to incorporate just the qualities of the model's components that are relevant to the specific purpose or scientific investigation at hand.

After the model has been formulated, it can be analysed using a variety of mathematical tools, including [1] the following:

• It is possible to analyse it to obtain crucial quantities, which are the factors that regulate how solutions behave as a whole.

• It is possible to either fit it to the data that is already available or use it to encourage studies that can yield data.

• The model's parameters can be estimated.

• To better comprehend the impact of each parameter on the outcome, it is possible to simulate it.

After gaining an understanding of the model, the next step is to interpret the model's outputs in the context of the biological situation that was taken into account and possibly look for a solution to the biological issue that was posed at the outset. Mathematical models typically include both parameters and variables, which are linked to one another through various interactions. There are many different ways that models might be categorised:

Linear/nonlinear: If a model has a reliance on the variables that does not follow a linear pattern, then it is referred to as a nonlinear model. If this is not the case, we must refer to it as linear. Most of the models that we have developed and applied in the process of this research are nonlinear.

Static/dynamic: A dynamic model considers changes in the state of the system that are dependent on the passage of time, whereas a static model calculates the quantities of the system only if the state does not change over the course of time and is therefore time-invariant. Differential and difference equations are the typical mathematical tools used in the construction of dynamic models.

Discrete/continuous: Time or system states are considered as discrete variables in discrete modelling. Time and system states are continuous variables that are included in continuous models.

Deterministic/stochastic: A model is said to be deterministic if each and every possible combination of the states of its variables can be uniquely specified by the model's parameters as well as the values of the variables' starting points. Randomness is a unique characteristic of stochastic models, and probability distributions are used to characterise the states of variable models.

The fields of the natural sciences, such as biology and epidemiology, place a significant emphasis on the use of mathematical models. They assist us in expanding our knowledge regarding a system, arranging biological data in a way that makes sense of it, determining the system's reaction behaviour, determining the most effective performance and intervention tactics, and formulating hypotheses regarding the system.

Mathematical modelling is a process by which we can describe a real - world problem in the Mathematical language.

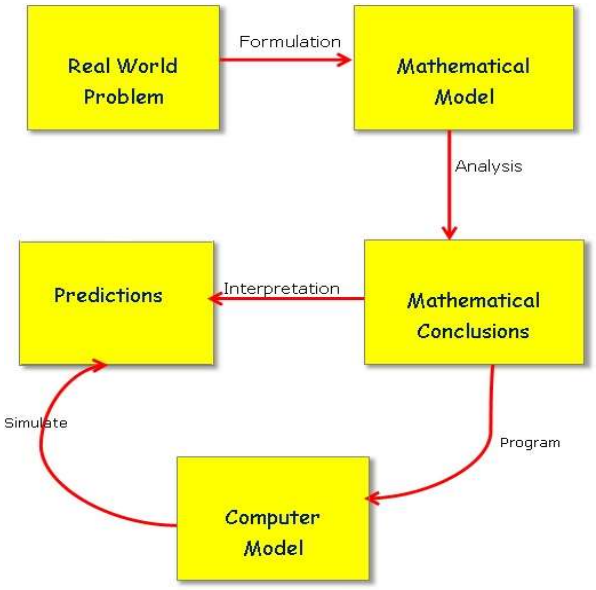


Figure 1.1: Scientific Process to connect real world problem with Mathematics

The concept of mathematical modelling is employed in nearly all disciplines, including physics, chemistry, engineering, etc. Our primary interest is epidemic modelling, or the study of disease patterns in populations. Epidemic modelling [13] helps us to

(i) make prediction the status of disease in near future.

(ii) understand transmission dynamics of the disease

(iii) helps to make the effective control strategies.

Basically, epidemic models are of two types:

(i) Deterministic models

(ii) Stochastic models

Stochastic models usually depend on chance and may be used for a smaller population. These models are very complex and gives us a deeper insight. We can use the term individual-level modelling for such type of models. Such type of models is difficult to analyse, and it is tough to get some analytic results. Also, the diseases dynamics cannot be explained by these models.

On the other side, deterministic models, are used to deal with population of large size. Compartmental models are another name for these models, which may be found [14]. In these kinds of models, the population is partitioned up into a fair amount of different compartments. In deterministic models, chance has no role in the propagation of disease. Depending on the number of compartments, numerous models exist. Before developing these models, it is necessary to understand the following terminology:

Susceptible: A person who is at risk of infection but is not yet infected.

Exposed: A person who does not have visible symptoms but has contracted the infection.

Infectious: A person who can pass infection to others and has the disease with symptoms.

Recovered/Removed: After receiving therapy, etc., the symptoms disappear and the individual is no longer contagious.

Incubation Period: It is the time elapsed between the onset of the first visible symptoms of the disease and exposure to the infection.

Endemic: A disease is endemic when it occurs frequently in a population or region.

Epidemic: In a given population, a disease is described to an epidemic if the number of cases increases dramatically and rapidly.

Pandemic: A pandemic is a sickness that has spread throughout the entire country or the world.

State variables are represented by capital letters such as S, E, I, R, etc. representing various compartments at any point in time t. Below is a summary of the different state variables that underlie these models.

S: Number of people who are susceptible

E: Number of exposed individuals

I: Individuals who have been exposed

R: Individuals who have been recovered

N : Human population as a whole

We begin with the simplest compartmental model with only two classes before moving on to more complex ones.

SI Model: This is the easiest epidemic model containing only two compartments i.e. Susceptible and Infected.

The dynamics of SI model can be understood by

$$\frac{dS(t)}{dt} = -\beta \frac{S(t)}{N} I(t)$$

$$\frac{dI(t)}{dt} = \beta \frac{S(t)}{N} I(t) \ - \gamma I(t)$$

Where $S > 0$, $I > 0$ and $S + I = N$

Since it is an epidemic model, the births and natural deaths are not taken into consideration.

SIS Model: This is the easiest epidemic model. Here, a susceptible catch the infection and again joins the class of susceptible as soon as the infection is over. The population flows as follows:

SIR Model: Here, recovered class is added. The population flows as follows:

SIR model for epidemic scenario is governed by following set of differential equations:

It is assumed that $S + I + R = N$

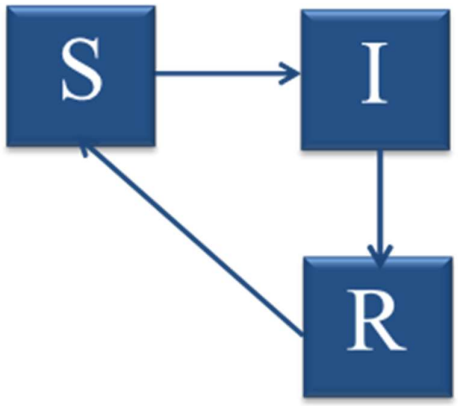
$$\frac{dS(t)}{dt} = -\beta \frac{S(t)}{N} I(t)$$

$$\frac{dI(t)}{dt} = \beta \frac{S(t)}{N} I(t) - (\gamma + \delta) I(t)$$

$$\frac{dR(t)}{dt} = \gamma I(t)$$

SIRS Model: This is an expansion of the SIR model for endemic diseases as mentioned previously. Individuals who have recovered lose their temporary immunity and rejoin

the susceptible group. Observable population flow from one compartment to another is as follows:



SEIR Model: In this case, it is believed that the sickness confers temporary immunity for a limited time. Consequently, the individual remains in the recovered compartment for that duration.

It is also feasible to develop more intricate models by considering additional features, such as passive immunity, deaths, vertical transmission, age structure, etc. "The number of secondary infections caused by a single infected person in a susceptible population is defined as **Basic Reproduction Number** [15]". This number is a dimensionless parameter defined as

$R_0 =$ *(effective transmission rate)* × *(probability that an individual will survive until infectious)* × *(average duration of the infectious period).*

In modelling of epidemics, this number helps us to make forecasting about the spread of the disease. That is, if $R_0 < 1$, we conclude that the disease will wipe out in a short duration of time, if $R_0 \geq 1$, there is an equilibrium, but if $R_0 >> 1$ then the disease is in epidemic state.

Sensitivity Analysis: To tackle the issue of infectious disease and to reduce the fatality, we must observe the factors, which are responsible for the outbreak of the disease. We compute the sensitivity indices of the model's various parameters.

Numerical Simulation: Mathematical models are used to understand the spread of the disease and numerical simulation gives us idea of future scenario and can be done using various computer software like MATLAB, R, Julia, Python etc. Numerical Simulation helps us to forecast the spread of disease in future so that we can prepare ourselves and our health care system to control the damage.

ARIMA Model: ARIMA is an abbreviation for a model in which AR stands for autoregressive model, MA stands for moving average model, and I stand for integrated [16]. ARIMA modelling is controlled by four steps: model evaluation, parameter estimation, diagnostics, and forecasting. Identifying if the time series dataset is seasonal and stationary is the first stage in this time series model. If a time series' statistical characteristics remain constant, it is stationary. The stationarity of the dataset is an important observation to make to obtain accurate forecasts. The unit root test is used to determine the stationarity of a time series. If the series is not stationary, differences are used to make the data stationary. Autocorrelation function (ACF) graphs and partial autocorrelation function (PACF) correlograms can be used to estimate ARIMA model parameters. The graph of the auto correlation function determines the relationship between previous and subsequent values in a time series. The partial auto correlation function graph computes the degree of correlation between lag and variable. We can estimate the best ARIMA model using maximum likelihood estimation (MLE). Once the best model for the time series data set has been chosen, the ARIMA model can be used as a forecasting model to predict future values using those parameters.

Auto Correlation Function (ACF): As far as the lag unit goes, the ACF plot shows the connection between points. An autocorrelation is a measure of how closely a time series' values are linked to those of its predecessors. The x-axis of ACF shows the correlation coefficient, while the y-axis shows the amount of lags. Shows how closely connected the provided time series is with itself by plotting the Autocorrelation function.

Partial Auto Correlation Function (PACF): A partial autocorrelation is a description of the relationship between an observation in a time series and previous observations. Deletion of inter-observational relations is a consequence of this procedure. The remaining correlation is known as the partial autocorrelation at lag k after any

correlations generated by words at lower lags have been removed.

Stochastic Processes: It is possible to think of random variables as belonging to a family of stochastic processes [17]. A stochastic process has a state space, which is a collection of all possible outcomes at any given instant in time.. The process can be determined to be in exactly one of its states at any one time. Because of this, stochastic processes have both a time and a state structure. If X represents the state of the system at time t_0 and E is a set that describes a certain collection of states in the system, then the probability that the system, which at time (t_0) is in the state (X), will pass into one of the states of (E) at time t is denoted as $P\{t_0; t, E\}$. This is because X represents the state of the system at time t_0 and E is a set that describes certain collection The process of transitioning from one state to another over the course of time and having the probability distribution $P\{t_0; t, E\}$ is referred to as a stochastic process.

Markov Process: To describe a stochastic process as Markov, it must be possible to predict exactly where it will end up, regardless of how the current state has progressed. Mathematically, if $\{X(t), t \in T\}$ is a stochastic process such that given the value of $X(s)$ the value of $X(t), t > s$, do not depend on the values of $X(u), u < s$ i.e., for $t > s, i \in s$ if $\Pr\left\{X(t) = \frac{i}{X(u)}, 0 \leq u \leq s\right\} = \Pr\{X(t) = \frac{i}{X(s)}\}$, then the process $\{X(t), t \in T\}$ is called a Markov process.

Transition Probabilities: These are the probabilities with which the system changes its state with the passage of time. These are defined as follows:

n-Step Transition Probability: The n-step transition probability from state i to the state j is defined by and is denoted as $\Pr(X_{m+n} = j|X_m = i), n \geq 1$ and is denoted as P_{ij}^n.

One- Step Transition Probability: It is defined by $\Pr(X_n = j|X_{n-1} = i), n \geq 1$ and it is denoted P_{ij}

Regenerative process: Smith (1955) is credited as being the one who initially described the regenerative process, and the analysis of complex systems makes significant use of this concept. During this step of the process, we select those time points for which the conditions of the system are not dependent on the behaviour of the system in the past. Regenerative points are the name given to these specific points. If

$X(t)$ represents the state of system at time point t and t_1, t_2 .... are the time point at which process restarts probabilistically, then these time points are called regenerative points and the process $\{X(t), t_1, t_2 \ldots.\}$ is called a regenerative process. A technique based on regenerative process is called regenerative point technique.

Regenerative Point Graphical Technique (RPGT): In the modern times graph theory is employed in many areas such as computers, engineering, communication, physical sciences etc. Regenerative point graphical technique [18] is a reliability technique which is a combination of graph theory and regenerative point technique. In this technique, the steady state transition probability of a process is calculated using applications of graph theory.

Mean Time to System Failure (MTSF):

Working of components or system depends on the mechanical, physical, or environmental conditions. They cannot be expected to work for an infinite interval of time as aging of components affects the working of the system. Therefore, it is quite important to measure the lifetime of the system, which is known as MTSF. It is the anticipated amount of time that the system will continue to function until it entirely breaks down. Mathematically, If $f(t)$ is the failure time density function of the life time of the system, then

$$\text{MTSF} = \int_0^\infty t\, f(t)dt = -\int_0^\infty t \frac{dR(t)}{dt} dt = -\int_0^\infty t dR(t) = \int_0^\infty R(t)dt = \lim_{s\to 0} R(s)$$

Where $R(s)$ is Laplace transform of the reliability function $R(t)$.

In RPGT, the mean time to system failure is given by

$$\text{MTSF}=\left[\sum_{i,s_r} \left\{\frac{\left\{\Pr\left(0 \xrightarrow{s_r(sff)} i\right)\right\}.\mu_i}{\prod_{k_1\neq 0}\{1-\sum \Pr(k_1-cycle)\}}\right\}\right] \div \left[1-\sum_{s_r} \left\{\frac{\left\{\Pr\left(0 \xrightarrow{s_r(sff)} 0\right)\right\}}{\prod_{k_2\neq 0}\{1-\sum \Pr(k_2-cycl\ )\}}\right\}\right]$$

Where

i: A regenerative un-failed state to which the system can transmit before any failures from the initial state '0' (at time $t = 0$).

$k_i - cycle$: A circuit whose terminals are at the regenerative point k. The circuit may be formed through regenerative /non-regenerative but un-failed states only.

k_i: A regenerative state visited along the path $0 \xrightarrow{s_r(sff)} i$, at which a $k_i - cycle$ is formed through regenerative un-failed states.

$\left(0 \xrightarrow{s_r(sff)} i\right)$: The r^{th} directed simple path from 0 state to i state.

μ_i: The mean sojourn time spent in state i before visiting any other state.

Mean Sojourn Time: It is the expected time taken by the system in each state before transiting to any other state. Sometimes it is also termed as mean survival time. If T_i be the sojourn time in i^{th}state, then mean sojourn time μ_i in i^{th} state is given by

$$\mu_i = \int_0^\infty \Pr(T_i > t)dt$$

$$f(t) = r(t)e^{[-\int_0^t r(u)du]}$$

In the past twenty years, human beings have been suffered with lots of severe infectious diseases, like Ebola and SARS. In fact, if we consider the history perspective, infectious diseases which are our natural enemy, are always invading human beings. Smallpox, cholera, plague, tuberculosis, and syphilis have done great damage to humans in these years. While struggling with these infectious diseases, peoples have very less capabilities. Scientists have gained gradually a few scientific insights about infectious diseases in last hundred years.

For instance, in 1928, a British scientist named Alexander Fleming developed penicillin, which is the first antibiotic ever created in the world.

Infectious diseases caused by viruses are a much greater reason for concern than infectious diseases caused by bacteria. The removal of infectious diseases that are caused by viruses other than smallpox remains a persistent challenge for scientists. When we reach a standstill in the area of biological study, we ought to look for another approach. The study of well-known mathematical models of infectious diseases will unquestionably assist researchers in comprehending the different symptoms of these diseases, which is essential for preventing the spread of viruses. With the help of mathematical models, we can characterize the transmission rate, transmission path and spatial range of infectious disease. We can take guidance from these models to execute effective controls and prevention. We can divide common infectious disease models in

SI, SIR, SEIR, SIRS etc models. In addition, we are able to categorise these models into a great number of different types by modeling them on either partial differential equations, ordinary differential equations, or network dynamics.

Bill Gates warned the world about the Ebola pandemic in Africa in 2015 in a lecture he gave. He said: “If anything kills over 10 million people in the next few decades, it's most likely to be a highly infectious virus rather than a war.” He ended up becoming a soothsayer, which was a shame. SARS-CoV-2, the virus that created the pandemic COVID-19, has been wreaking havoc on people all over the world since the third trimester of 2019.

Epidemiology research focuses mostly on the dynamics of the disease's propagation. Epidemiological modelling is mainly responsible for analysing and tracking the factors that are reason for spread of disease over time and it tries to find the possible methods of control. In addition to Epidemiological modelling, mathematical modelling is also considered as a productive method for the infectious disease research. Mathematical modelling assists us to predict and analyse the behaviour of infectious disease. Scientists and mathematicians are studying mathematical epidemiological models since many decades.

As we see the continuous spread of COVID-19, it is vital to find a significant mathematical model that can simulate this spread. This can be done with the help of many methods like polynomial regression, SEIR model, and ARIMA Neural networks.

1.4 Literature Review

Between January 1950 and December 1978, Kenneth C. Land and David Cantor [19] employed seasonal ARIMA time series analysis to study the monthly birth and death rates in the United States [20]. For the purpose of model selection, the traditional Box-Jenkins diagnostic checks together with certain recommendations made by Nerlove et al. [20] were applied. There are strong second-order autoregressive components for both series, together with seasonal moving averages. There is also some evidence of weekly periodicities in the birth rate series that has been assembled. According to these findings, there must be a method of seasonal adjustment that is superior to the Census

X-II software that is utilised by the organisations that are in charge of providing vital statistics.

Leonid A. Rvachev and Ira M. Longini, JR [21] first proposed a mathematical model in 1985 to anticipate the global blow-out of influenza by gathering data from the first city in the transportation network to contract the disease. From the city that first saw a case of the disease, this information has been collected. On the other hand, the work described in this study represents the first global application of these technologies. In this section, we discussed the model formulation and a method for calculating key parameters. When it came time to anticipate the global spread of "Hong Kong" in 1968-1969, the model was utilised to do so. Expected factors from Hong Kong, where the new influenza was originally reported, were used to make these forecasts. an affliction. It was demonstrated that the forecast accurately reproduced the overall time and geographical distribution of the real epidemic, as verified by sources from the World Health Organization. Finally, the model predicted the general patterns of how the Hong Kong influenza will spread across the geographic region. This provides more evidence that the concepts utilised to construct the model are sound from a theoretical perspective. Almost 425 days of everyday happenings in world society have never been accurately predicted before, hence the forecasting interval from July 27 to September 26 of 1969 may be considered a historical milestone.

In the year 1994, Michael Y. Li and his colleagues [22] talked about the SEIR model in epidemiology with nonlinear incidence rates. This was accomplished by using the theory of competitive systems of differential equations. The following set of differential equations serves as a description of the SEIR model, which is used in epidemiology to analyse the transmission of infectious diseases:

$$\frac{dS}{dt} = -\lambda I^p S^q + \mu - \mu S$$

$$\frac{dE}{dt} = \lambda I^p S^q - (\epsilon + \mu)E$$

$$\frac{dI}{dt} = \epsilon E - (\gamma + \mu)I$$

$$\frac{dR}{dt} = \gamma I - \mu R$$

where $p, q, \gamma, \mu, \lambda$ and ϵ are all positive parameters and S, E, I, and R signify the fractions of the population that are susceptible, exposed, infected, and recovered, respectively. In this model, it was assumed that the birth rate and the death rate were equal (denoted by μ) and as a result, the overall population was in a state of equilibrium. Two Ebola epidemics were simulated in 1996 by Jaime Astacio et al. [23] using SIR and SIR models. It began in 1976 with an epidemic in Yambuku and ended in 1995 in Kikwit, Zaire. Zaire was the site of both outbreaks. The infectiousness of the disease is quantified by a number known as R_0, which is the basic reproductive number. An Ebola infection has an 8.60 relative risk, indicating that the disease is less contagious than previously thought. Scientists will be able to apply the results of these epidemic simulations in future outbreaks to limit the number of possible fatalities.

In 1999, Michael Y. Li and colleagues [24] investigated the SEIR model for the transmission of an infectious disease in a population through direct contact between hosts. The infectious force exhibited characteristics of a proportionate mixing type. In order to better understand the dynamics of population sizes when the disease is eradicated and when it is still prevalent, they devised two criteria. The difference between the two circumstances can be summarised by these thresholds. Assumed that the population's spatial distribution was consistent, and that the mixing of hosts adhered to the notion of "mass action." To be more specific, they presumed that the local population density would remain unchanged over time, despite the fact that the total population size $N(t) = S(t) + E(t) + I(t) + R(t)$ may shift throughout the course of the study. The sizes of the S class, the E class, the I class, and the R class at any given moment are denoted by the variables $S(t)$, $E(t)$, $I(t)$ and $R(t)$, respectively. The per capita contact rate, denoted by λ, is defined as the average number of successful interactions with other individual hosts per unit of time. This rate remains unchanged.

This model relies on a set of ordinary differential equations and was developed by P. van den Driessche [25] in 2002 for use in generic compartmental disease transmission. Both of these contributions were made in the context of disease transmission. It was shown that, if $R_0 < 1$ then the disease-free equilibrium is locally asymptotically stable,

whereas if $R_0 > 1$, then it is unstable. As a result, the value R_0 was designated as the model's threshold parameter. For a wide range of compartmental epidemic models, the approach described here is relevant (Disease Free Equilibrium). The threshold parameter for these models is the basic reproduction number, which is denoted by R_0. In addition to this, the local analysis of the centre manifold will produce a second parameter, the sign of which will indicate whether or not there is a branch of endemic equilibria that is stable close to the threshold $R_0 = 1$. The maintenance of these equilibriums is essential to the prevention and treatment of disease. As a result, bringing R_0 closer to one causes the incidence of the disease to decrease, and this trend continues until the disease is eradicated entirely when R_0 falls below one. Throughout the entirety of the investigation, they have operated under the presumption that there is a DFE that is clearly defined. Although the total population number is not constant, some models can be recast as fractions in order to achieve an equilibrium distribution of individuals across the compartments. That way, the models will be able to take into consideration changes in overall population size. Using the percentages of people in each compartment, a threshold parameter may be determined in this particular case study. However, even though it is a threshold based on fractions rather than on the total number of infected people, the analysis for both the threshold and bifurcation direction is same. Although there are many people infected with Ebola, there are only a small number of people who have been infected at any given time.

In 2003, G. Chowell and coworkers [26] introduced a simple model capable of capturing the influence of average infectiousness in a heterogeneous population. In addition, the effect of separating diagnosed patients was incorporated into the model to study the significance of patient isolation and diagnostic rate in managing a SARS outbreak. They were able to calibrate an SEIJR model with parameters by analysing two cases that had relatively clean exponential growth curves for the number of recognised cases. After that, they utilised the SEIJR model in order to investigate the non-exponential dynamics of the Toronto outbreak. SARS pandemic data was used to create a model of "SEIJR" (susceptible, exposed, infected, diagnosed, and recovered), which was used to derive average attributes and rate constants for those populations. On the basis of data from Ontario (Toronto), Hong Kong (Singapore), Hong Kong

(China), and Singapore, projections were developed based on assumptions and observations, including how isolating persons who have been diagnosed with SARS now affects the spread of the disease. They came to the conclusion that isolating people with diagnosed conditions is something that should be done. Although they do not examine the effect of quarantine by varying the parameter q (Relative measure of infectiousness for the asymptomatic class E), this is likely due to the fact that it is common sense that the total number of cases will decrease if individuals who have had close contact with those who have been positively diagnosed are isolated in a quarantine. In addition, the implementation of relative extreme isolation measures in conjunction with prompt diagnosis has a significant influence on the dynamics of the local environment (the situation in Toronto). On the other hand, the SARS outbreak demonstrated that local disease dynamics that go "undetected" and "unchecked" have the potential to rapidly become a problem on a global scale.

As a result of an auto regression phenomena, Peng Guan and colleagues [27] undertook research in 2004 to examine how artificial neural networks (ANNs) could be used to predict the occurrence of hepatitis A. Using a time series analysis approach called autoregressive integrated moving average (ARIMA), they looked for any signs of an auto regression phenomenon. As a training and verification set, the data from 1981 to 1997 were used, and as a test set, the data from 1998 to 2001 were used. Based on the findings presented in this paper, we are able to deduce that the linear auto regression model exhibited characteristics of a first order auto regression phenomenon. The graph of the regression showed that there was a clear linear tendency, but that did not mean that all of the values were perfectly fitted. There was a significant gap between the values in terms of the amount. Figure 12 291.79 shows that the sum square error of the model is 12 291.79, whereas the sum square error of the training set is 8 944.95 and sum square error of the testing set is 3 346.84. Extrapolation forecasting using ANN produced values that were mostly in line with actual values, but ARIMA model forecasting produced values that were, on average, slightly higher than actual incidence values. Although preliminary learning showed that ANN could recognise some rules, the influence of specific special values over sum square error led to false forecasts of low incidence. Combining traditional methods with artificial neural networks offers the

potential to increase accuracy in prediction by using the characteristics of both approaches. Forecasting the spread of infectious illnesses is critical for their prevention and control, thus they focused their efforts on doing so. You must be able to learn the unknown mapping or function entirely from the examples that are currently accessible in order to complete this issue. The artificial neural networks can predict the mapping even if only a few of its components are known after learning the mapping or one very similar to it. In summing up, ANN has the potential to be a useful instrument for the processing of time series data. Additional research needs to be done on the model's construction as well as its explanation.

In 2004, Abba B. Gumel et al. [28] introduced modelling strategies for controlling SARS epidemics for the first time. There were 774 deaths and 8098 illnesses worldwide as a result of the novel and highly contagious viral disease known as SARS, which initially surfaced in China at the end of 2002 and quickly spread to 32 other countries and areas. SARS could not be quickly recognised or treated because there were no available rapid diagnostic tests, treatments, or vaccines, therefore people who had been exposed to the virus were quarantined. Only in mid-April did China begin reporting more accurate data on SARS-related deaths and cumulative infected cases in the first three regions, when the deterministic model was utilised. During the SARS epidemics in Toronto, Hong Kong, Singapore, and Beijing, they looked studied how isolation and quarantine affected the disease's control. Isolating infected people to reduce the number of people who come into touch with them is a critical part of any SARS epidemic management strategy, whether or not a quarantine is put in place. Effective isolation requires the timely execution of strict sanitary procedures, indicated by a critical threshold level. Values that are lower than this threshold indicate that SARS is under control, whereas values that are higher than this threshold are linked to the occurrence of new community outbreaks or nosocomial infections, both of which are known to contribute to the spread of SARS in each region. Quarantine and sub-optimal isolation should not be implemented at the same time since the available resources can be better used to achieve optimal quarantine. SARS can be eradicated from a population if effective isolation measures are combined with a thorough screening procedure at entry points.

While SARS was spreading in 2005, Arul Earnest et al. employed ARIMA models to anticipate the number of occupied beds at Tan Tock Seng Hospital in real-time. While the pandemic was still going on, these forecasts were made. This information was gathered from Tan Tock Seng Hospital between March 14, 2003 and May 31, 2003, when admissions and occupancy for isolation beds were tracked. A key finding was that ARIMA models can be a helpful tool in the planning of real-time bed capacity during infectious disease outbreaks such as SARS for administrators and clinicians. This model has the potential to be utilised in the process of planning for bed capacity during outbreaks of infectious diseases other than Ebola.

Enteroviruses cause hand, foot, and mouth disease (HFMD), which mainly affects children under the age of 5, according to an explanation from 2005 by L. LIU. Children under the age of five are most commonly affected by HFMD. The situation with HFMD is becoming more severe in China, as evidenced by the rising number of cases reported across the country. As a result, tools for monitoring and forecasting the occurrence of HFMD are urgently required in order to improve management efforts. Autoregressive integrated moving average (ARIMA) models were used to construct forecasts about the prevalence of HFMD in China's Sichuan province, where this study was conducted. The ARIMA model was fit with data on HFMD infections from January 2010 to June 2014 in order to get the best results. To determine whether or not the models that were constructed were accurate representations of the data, we used the coefficient of determination (R^2), the normalised Bayesian Information Criterion (BIC), and the mean absolute percentage of error (MAPE). The ARIMA model that was customised to our data was used to make HMFD incidence projections from April to June of 2014. The goodness-of-fit test resulted in the generation of the best general multiplicative seasonal ARIMA$(1,0,1)$x$(0,1,0)_{12}$ model (R^2 = 0·692, MAPE = 15·982, BIC = 5·265), which also exhibited autocorrelations in the model's residuals that were statistically insignificant (P = 0893). The ARIMA$(1,0,1)$x$(0,1,0)_{12}$ model's forecast incidence values ranged from 4103 to 9987 from July 2014 all the way through December 2014. These values represented proximate forecasts. The ARIMA model can be used to anticipate future trends in HMFD incidence and to provide help for HMFD prevention and control. Due to the HMFD incidence not being fully stationary in the near future,

new observations should be carried out on a regular basis. Additional adjustments may be necessary to the model parameters.

Dengue haemorrhagic fever (DHF) cases in southern Thailand were modelled and projected using a univariate time-series analysis method developed by S. Promprou [31] in a 2006 study. He built autoregressive integrated moving average (ARIMA) models using data acquired between 1994 and 2005. He then used the data collected between January and August 2006 to verify the models. Regressive forecast curves were shown to be consistent with actual value distributions, according to the results of the study. According to the Q-statistic (Q=4.446), the fitting of the ARIMA (1,0,1) model to the data was satisfactory. This suggested that the autocorrelation function did not significantly change when zero was introduced.

A 2008 study fitted an autoregressive integrated moving average (ARIMA) model to dengue incidence in Rio de Janeiro, Brazil, from 1997 to 2004 using the Box-Jenkins technique. Luz, Paula M. et al. [32] conducted the study. They discovered that the number of dengue cases in the preceding one, two, or twelve months can be used to estimate the number of dengue cases in a particular month. They used their calibrated model to make a prediction about the incidence of dengue for the year 2005 using two different approaches: one that looks ahead 12 steps and another that looks ahead 1 step. Because the 1-step ahead technique offers more accurate predictions (P value = 0.002, Wilcoxon signed-ranks test) than the 12-step approach, they conclude that this method is superior. The researchers also looked at different ARIMA models with climate factors as external regressors to see how well they predicted the future. According to their research, ARIMA models are effective tools for tracking the prevalence of dengue in Rio de Janeiro. In addition, these models can be utilised by applying them to surveillance data in order to forecast shifting patterns in the occurrence of dengue.

An SEIR model with variable population size was presented by Chengjun Sun and Ying-Hen Hsieh [33] in 2009. This model was used to investigate vaccination strategy. The total number of infectives as well as their proportion in the population were taken into consideration when developing the three threshold parameters that will govern the eradication of the disease. The global dynamics of the model's impact on the size of the population were investigated. They summarised and compared the correlations between

the two systems with regard to the eradication of diseases, the prevalence of diseases, and the outbreak of diseases. They hypothesised that the substantially low product of vaccination rate combined with the low efficacy of the vaccine might result in complicated dynamics for the system that was under investigation.

For a SIR (susceptible–infected–recovered) epidemic model with time delay, Gul Zaman et al. [34] reported the optimal control tactics in 2009. An SIR epidemic model with a time delay will be used in order to achieve this. A strategy called "optimal control" was employed to increase the total number of susceptibles and recovered patients while reducing the risk of disease spread among those who were already afflicted. After that, they investigated the dynamical behaviour of the controlled SIR epidemic model and derived the basic reproduction number. On top of all this, they demonstrated that an optimal controller exists for the control system and provided numerical simulations based on data from the Ebola epidemic in Congo. For the objective of eradicating Ebola virus, they found that a low contact rate (chance of infection) was ideal, and this is one approach of developing the best treatment techniques for infectious hosts.

The SIS epidemic model was created in 2010 by Julien Arino and a group of other academics [35]. People's journeys between different locations of the world are depicted using this concept. People who travel between *n* cities are at risk of contracting diseases, according to an analytical model they provided. It was used to study the transmission of disease in the model. They used the concepts of disease recovery, transmission, death, birth, and travel between cities in the formulation of their model, which was a system of $2n^2$ ordinary differential equations. This article derived an explicit formula for calculating the fundamental reproduction number, and it was suggested that, to control the disease, actions should be done to reduce R_0 to a value less than 1. Additionally, they talked about that. There will be no disease outbreaks in any cities that can be reached through the disease-free equilibrium city, as long as the system is in a condition of equilibrium. Equilibrium indicates that all cities that may be reached from a city with an endemic illness level are in the same state of equilibrium. These findings are based on the hypothesis that the system is in an unchanging state. Each city's infective population can be calculated numerically by solving system equations

in system form at the beginning of a disease epidemic in a single city (or cities). This can be done at the beginning of the disease outbreak.

Peilin Shi and Lingzhen Dong [36] created and investigated models for the transmission of infectious diseases with fluctuating population sizes and vaccines on susceptible persons as early as 2011.These models were based on the assumption that susceptible individuals are vaccinated against the disease. To begin, they assumed that the susceptible individuals are continuously receiving vaccinations. As well as global stability of both forms of equilibrium, they found results that were similar to thresholds for disease-free and endemic equilibrium existence in these systems. In particular, they demonstrated that the endemic equilibriums are stable on a global scale by transforming the systems in question into integrodifferential equations. Second, they assumed that vaccinations were administered only once during each time period. It was possible for them to demonstrate the existence of systems with impulsive effects that have periodic solutions that are free of disease and are globally stable. They used a valuable bifurcation theorem to discover the presence of periodic solutions. In this scenario, disease-related deaths do not take place. In the end, they compared the results with and without vaccinations, and they illustrated their findings by using numerical simulations.

On a SIR-model that incorporated immunisation and treatment, Urszula Ledzewicz and Heinz Schattler [37] began their research in 2011 on an optimal control problem. It is still required to complete this study by establishing the structure of feasible concatenations using bang-bang controls in order to find an ideal synergy of controlled trajectories, even though they studied the solitary controls' structure. They will be able to find the best mix of controlled trajectories using this information. It is expected that the most effective immunisation method will consist of a single regimen, whereas the most effective treatment schedule is expected to be a bang-bang schedule. Most likely, there will be just one switch from u_{max} to $u = 0$.

Since the early detection and control of tuberculosis epidemics is critical, Shiyi Cao and colleagues [38] developed an appropriate model for predicting TB epidemics in 2013. This was accomplished in order to better prepare for the possibility of a TB outbreak. The Chinese Ministry of Health provided data on the number of tuberculosis cases diagnosed each month between January 2005 and December 2011. The data from

2005 to 2010 was fitted using two models: a SARIMA model and a hybrid model combining a SARIMA model with a generalised regression neural network model. The hybrid model also included a generalised regression neural network model. They came to the conclusion that the hybrid model provided more accurate forecasting of TB incidence than the SARIMA model. In China, there is a discernible seasonal pattern to the occurrence of tuberculosis, which is not observed in other countries.

In 2013, Howard (Howie) Weiss [39] presented and analysed a fundamental transmission model for an infectious disease that can be passed from person to person directly. There is no clear formula for solving the model's three connected non-linear ordinary differential equations. We can, however, get a lot of information about the answers by utilising some simple calculus tools. As he spoke, he highlighted how this simple model provides a theoretical framework for public health activities and how some fundamental aspects of public health require the illumination that this model offers.

Optimal control can be helpful in testing and comparing different vaccination regimens for a particular disease, according to an article by M. H. A. Biswas [40]. SIR (Susceptible, Exposed, Infectious, and Recovered) model was used to an optimal control issue, and the authors of this study proposed to include state variables as constraints on the optimal control problem. They looked into how to deal with this type of problem while imposing upper limits on the number of vaccines that can be utilised at any given time using mixed state control restrictions. Additionally, they looked into the idea of limiting the number of people who could be vaccinated, both with and without constraints on the number of vaccines that might be provided.

Anqi Li [41] presented a model in 2015 with the intention of maximising the effectiveness of Ebola eradication efforts. Since 2014, the disease has become increasingly severe, resulting in the deaths of more than 8966 people. If effective control measures are not taken, the human society will be put in grave danger. This paper primarily addresses the issue by making a forecast regarding the pattern of Ebola transmission by utilising a modified version of the SIR model known as the SEIR model. The parameters of this model are found by obtaining it and basing it on the data from the WHO. This allows for a clear picture of the epidemic situation in the future to

be obtained. In addition, data that is reasonably accurate in the short term can be obtained through the use of this Grey Prediction model, which makes up for the deficiencies of the SEIR model in its ability to predict the short term. As a result, the current state of the Ebola epidemic will almost certainly improve and may even be resolved within a certain amount of time.

Compartmental models of disease transmission were described and analysed by Paritosh Bhattacharya and colleagues [42] in the year 2015. Models of outbreaks were used to demonstrate the fundamental reproduction number and overall epidemic size. In addition to this, they investigated models that contained multiple compartments, including treatment for infectious diseases. They also looked at models that included births and deaths and considered whether or not there was an endemic equilibrium in those models. Additionally, they stated that if we don't have a thorough understanding of how the transmission mechanism works, parameter estimates should be followed with a structural sensitivity analysis. This was in addition to the fact that they stated that the standard statistical uncertainty analysis was inadequate.

According to Wenzhi Chen [43], who published their findings in 2015, the Ebola virus is capable of causing a severe disease, it is an infectious disease that is fatal without treatment, and it is prevalent in western African countries such as Guinea, Sierra Leone, and Liberia. They believed that the Ebola virus spread from person to person after being transmitted from infected animal blood, secretions, or organs first. After that, it was believed that the virus spread from person to person. The mortality rate averages out to be fifty percent. Since there is currently no Ebola vaccine that has been approved for use, active participation in the control of this epidemic disease is extremely vital. In this paper, a mathematical model of the Ebola virus and its spread is developed, along with an analysis of the relevant data.

In 2015, Amenaghawon C. Osemwinyen and colleagues [44] studied and simulated the transmission dynamics of the Ebola Zaire virus using two models: a modified SIR model with the understanding that the recovered can become infected again and the infected die at a certain rate; and a quarantine model, which determined the effects of isolating the infected. Both models were used to explore and mimic the dynamics of Ebola Zaire virus transmission. In addition, a system of Ordinary Differential Equations

(ODE) was developed for the transmission, and a linearized stability methodology was used to solve the equations. This action was taken to simulate the transmission. According to the results of the stability analysis conducted on both models, the Disease-Free Equilibrium (DFE) states are unstable, assuming they exist at all. These equilibrium states indicated that the disease can be quickly reactivated; hence, persistent vigilance and the installation of effective prevention measures are required to limit the disease's capacity to spread. In contrast, numerical experiments were undertaken in which the parameters of the models were assigned hypothetical values, and graphs were generated to determine the impact of these parameters on the spread of the disease. The findings indicated that, due to the features of the Ebola Zaire virus, uncontrolled transmittable interactions between people who are infected and those who are susceptible can result in a highly dangerous outbreak with a high mortality rate, especially since neither immunity nor medications exist to treat the disease at this time. On the other hand, if efficient structures for quarantining are put in place, it will be possible to better manage the situation and bring the outbreak under control.

Figures from 2016 by Xueying Bai et al. [45] show the change in the proportion of each category of people. A total of six populations were studied: those who were susceptible to infection, those who were in the early stages of infection, those who had recovered, and those who died. When compared to the prior model, the new data provide a more detailed description of the proportion of each category of people. Because of this, these numbers show a sharper trend in the pandemic scenario even if humans are not involved in it. Using the model's capacity to represent the epidemic-controlling effects of medications and vaccinations, it is possible to generate predictions about their potential to limit the spread of the disease based on changes to a few parameters. This is conceivable due to the fact that the epidemic situation's variation trend was successfully realised without the involvement of humans. A precise prediction of the therapeutic effects of drugs and vaccines is now achievable because of this.

In 2016, based on the traditional SIR model, Siyuan Zhang [46] improved the differential equation model to take into account the effect of drugs and vaccines on the appearance of Ebola viruses. This was done based on the classical SIR model. In spite of the advancements, the differential equation model continues to be the most important

component of our model. This model, as well as the subsequent discussion, are based on a district that is relatively contained because the spread of Ebola is a concern for the region. They began by defining variables associated with medications and vaccinations, with the goal of increasing the likelihood of rehabilitation using the SIR model in relation to the dose of medicine. In addition to that, they included a new category of people in the crowd: the dead people. Despite this, they continued to count the dead as part of the overall population of the district and consider the overall population to be stable. A computational analysis sheds light on the tendency of the infectious agent under varying initial conditions, which can be interpreted as a reflection of the spread of Ebola. They constructed a relationship between the infective and the susceptible, and used this relationship to find the threshold concerned with medicine. This was all based on the phase trajectory. In addition to this, they examined the sensitivity as well as the robustness of the model, and they came to the conclusion that the values of the parameters will have a significant impact on the outcome.

Ebola is a virus that causes a highly virulent infectious disease, as stated by Harout Boujakjian [47] in the year 2016. This disease has been plaguing Western Africa, having a significant impact on the countries of Liberia, Sierra Leone, and Guinea in 2014. It is critical to the disease's containment and eventual elimination that we have a solid understanding of its transmission and its boundaries. An SEIR model was used to simulate the spread of the disease. The World Health Organization's data has been used to prove the model's validity. The optimum control theory is used to examine the effect of vaccination and quarantine rates on the SEIR model. An investigation into the feasibility of employing these steps in order to effectively limit Ebola was the goal of this study.

T. Berge et al. [48] examined in 2016 if the intake of contaminated bush meat, funeral practises, and environmental contamination can explain the recurrence and durability of Ebola virus disease epidemics in Africa. So that Ebola viruses may be distributed, they created a SIR model that takes into account both direct and indirect Ebola viral transmissions. There is one (endemic) equilibrium in the model that is locally asymptotically stable, but in the absence of Ebola virus shedding in the environment, it is globally asymptotically stable. This was a significant finding. In the case where Ebola

viruses are not supplied, the sub model predicts that the disease will either become extinct or reach an endemic equilibrium on a global scale. More people in the complete model are infected than in the submodel that does not contain Ebola viruses at the endemic level. They came up with a nonstandard finite difference scheme and were able to keep the model's dynamics intact with it. Numerical simulations are provided.

In 2016, Amira Rachah et al. provided a comparison of two independent mathematical models used to describe the transmission of the Ebola virus in West Africa at the time. During the time of the outbreak, the models were used to depict the spread of the virus. In order to improve the accuracy of predictions and the level of control that can be exercised over the progression of the virus, research into numerical simulations and optimal control of the two Ebola models is currently being carried out. In particular, they looked into the circumstances that must exist for the two models to generate results that are consistent with one another when compared side by side.

The use of time series analysis in several research to predict the frequency of dengue hemorrhagic fever patients was explained in 2018 by Fazidah A. Siregar [50]. Due to the lack of a vaccine and a weak public health infrastructure, predicting the occurrence of dengue hemorrhagic fever (DHF) is critical. The goal of this study was to identify a pattern and make predictions about the frequency of DHF in the Asahan region of North Sumatera Province. The district health offices provided information regarding the number of monthly dengue cases reported during the years 2012-2016. In order to make a prediction regarding the occurrence of DHF, an autoregressive integrated moving average (ARIMA) model was utilised to carry out a time series analysis. The findings revealed that there was a seasonal difference in the number of DHF cases that were reported. The SARIMA$(1,0,0)$ $(0,1,1)_{12}$ model turned out to be the most suitable option and best model for the data. Predicting the occurrence of DHF in the Asahan district and developing public health interventions to prevent and manage disease are both made easier with the SARIMA model for DHF.

In 2019, M Siva Durga Prasad Nayak et. al. [51] selected a Seasonal ARIMA $(1,0,0)$ $(0,1,1)_{12}$ as the best suited model to predict the future incidence of dengue fever cases in the forthcoming year. Administrators in the healthcare industry can utilise this information to better plan for an emergency. The model can be dynamically

modified to take into account the most recent data. For more accurate prediction, more complex predictive models that take into account factors such as precipitation, the extrinsic incubation period, and other factors could be developed. It is possible to use the model to predict dengue fever occurrences even in shorter time frames or higher geographic areas, such as districts.

In the research that was published in 2019, Ghazala Nazir and Shaista Gul [52] looked into how the differential transformation method and the variational iteration method could be used to find an approximation of the solution to the Ebola model. In order to construct the correction functional for the problem, the variational iteration method makes use of the general Lagrange multiplier. On the other hand, the differential transformation method makes use of the function that has been transformed from the original nonlinear system. In light of the findings, it became clear that both approaches produce results that are accurate and reliable while also being highly effective for solving ODE systems.

Alok Kumar Sahai [53] stated that their research indicates that India and Brazil will reach the mark of 1.38 million and 2.47 million respectively in the year 2020, while the United States will reach the mark of 4.29 million by the 31st of July. In light of the fact that there is currently no treatment that is proven to be successful, this prognosis will help governments become better prepared to combat the epidemic by increasing the capacity of their healthcare facilities.

Md. Haider Ali Biswas and Sharmin Sultana Shanta created a generic model in 2020 that was based on the SIR type. This model included a control variable function that was referred to as media awareness. According to the findings, more media attention raises awareness among the general public, separating those who are susceptible from those who have been infected in the process. Using the model, researchers have been able to determine how stable each of the equilibrium points is. With this information, numerical simulations have been conducted to examine the impacts of the control that was implemented. Persistent promotion of public health campaigns, the study concludes, has a major impact on reducing the spread of infectious diseases. As a result of the media's coverage of illness outbreaks, the number of people who are exposed to the disease is cut in half. This study also found that the reproduction number, which

reflects a certain threshold in epidemiological terms, is altered by transmission and recovery rates. To assist lessen and limit the disease burden in any circumstance when there is a pandemic or epidemic, their research suggests that in the absence of effective antivirals or vaccinations, raising awareness about the disease through the media may be one of those supporting measures.

In the year 2020, Zeynep Ceylan [55] discussed how the COVID-19 first showed up at the end of December 2019 in Wuhan city, China. As of the 15th of April in the year 2020, there were 1.9 million confirmed cases of COVID-19 all over the world, including 120,000 deaths. While COVID-19 can be controlled through vaccination, there is an urgent need to monitor and forecast its spread, he said. Time series models can be useful in epidemiology, and he discussed how he utilised the Auto-Regressive Integrated Moving Average (ARIMA) model to construct a prediction from the WHO website data between 21 Feb 2020 and 15 Apr. 2020. This prediction was made for the period of time from 21 February 2020 to 15 April 2020. Ceylan predicted the deaths and confirmed cases in Italy, Spain, and France in the near future, based on his research. His research included the development of multiple ARIMA models, each with its own unique set of ARIMA parameters. The ARIMA (0,2,1), ARIMA (1,2,0), and ARIMA (0,2,1) models were chosen as the best ones for Italy, Spain, and France, respectively, because they had the lowest MAPE (Mean Absolute Percentage Error) values. These values were 4.7520, 5.8486, and 5.6335, respectively. His research demonstrates that ARIMA models are appropriate for use when attempting to forecast the incidence of COVID-19 in the years to come. In order to better comprehend the outbreak's current trends and epidemiological stage, the findings of the analysis can be utilised. In addition, the prediction of COVID-19 prevalence trends in Italy, Spain, and France can assist in the formulation of policy and preventative measures for this epidemic in other nations. In addition to this, he went over how time series models contribute significantly to both the analysis and forecasting of disease outbreaks. As a result of this analysis, political leaders and those in charge of public health will be able to better plan and supply resources for the following few days and weeks in order to properly handle the situation in these countries. Real-time updates to the data should be performed so that comparisons and projections into the future are more accurate.

This year's Coronavirus illness (COVID-2019) is a global concern, according to Domenico Benvenuto and colleagues [56]. Currently, a variety of mathematical models are being used to anticipate the likely progression of this epidemic. Because these mathematical models are based on a wide range of inputs and analyses, they are vulnerable to prejudice. Using epidemiological data from Johns Hopkins, he then developed a simple econometric model that might assist anticipate the spread of COVID-19. Finally, he used an Auto Regressive Integrated Moving Average (ARIMA) model to predict the epidemiological trend of the prevalence and incidence of COVID-19. He proclaimed that case definition and data collection needed to be kept up to date in real time so that there could be further comparison or for future perspective.

In the year 2020, Rajesh Ranjan [57] used the SIR model to make a prediction about the outbreak of Covid-19 in India. He found that the Basic Reproduction Number in India ranges from 1.4 to 3.9, and that the pace of infection increase in India is quite similar to that in Washington and California.. COVID-19 data from India was compared to data from various other countries and states in the US that were experiencing a major outbreak. A striking similarity was found between the rates of infection growth in India and Washington and California, as he discovered. Exponential and classic susceptible-infected-recovered (SIR) models, both based on the data that was provided, were used to make daily short- and long-term projections. It was predicted that India would attain equilibrium by the end of May 2020, based on the SIR model, with a final pandemic magnitude of roughly 13,000 people. If India had progressed to the stage of community transmission, this estimate would be worthless. Comparing data from different geographical places also analysed the impact of social distance. Again, this rating was based on the assumption that there was no transmission from the community. The rate of COVID-19 transmission in India was found to be comparable to that in Washington State, the United States, based on the findings of this preliminary investigation. Curves from both places show that the outbreak's early stages were identical in both locations. Using data from the outbreak in Washington, which began 9 days earlier than in India, experts were able anticipate the spread of disease in the latter country more accurately. A poor transmission rate was suggested as the cause for the lower basic reproduction number in several papers that cast doubt on India's testing standards. As a result, the

model's predictions were just as accurate as the data it was built on. According to him, the forecasts will change as a result of the real-time changes in the data. As a result, this paper's conclusions should only be utilised for qualitative comprehension and fair estimates of the outbreak's nature. The conclusions of this research should not be used to make any choices or policy changes.

Ivan Korolev [58] used the SEIRD epidemic model for COVID-19 in 2020 to estimate the Basic Production number and Case fatality ratio of the United States of America and several other countries using the data provided by John Hopkins University in addition to other clinical parameters. The SEIRD model for COVID-19 was used in this study. A good place to start is with his demonstration of the model's inadequacy as highlighted by the number of deaths and confirmed cases thus far. There are many different sets of parameters, each of which can produce short-term observations that are equivalent to one another, but long-term forecasts that are significantly different. Next, he demonstrates that the fundamental reproduction number R_0 can be derived from the data, provided that the clinical parameters are taken into consideration. After that, he estimated it for the United States along with a number of other countries and regions, taking into account the possibility that the number of cases had been underreported. It was also shown that random tests can be used to calibrate the model's starting points and minimise the range of possible estimates for the expected number of deaths in the future. This information was obtained by using a statistical technique known as bootstrapping.

According to Bhalchandra S. Pujari and Snehal Shekatkar [59], writing in the year 2020, the ongoing pandemic of coronavirus has made it an urgent necessity to have reliable epidemiological modelling. Sadly, the majority of the currently available models either have a grain size that is too fine to be effective or a grain size that is too coarse to be reliable. A hybrid strategy that is computationally efficient and utilises the SIR model for specific cities was proposed as a result of this research in order to facilitate the movement of people between these cities, empirical transit networks are established between them. Over 300 Indian cities were taken into account when they applied their methodology to the country's transportation infrastructure. Based on their findings, it was hypothesised that a sizeable portion of the population living in the

United States would be exposed to the epidemic within a period of ninety days after it first appeared. Therefore, even after placing restrictions on international migration, it is necessary to conduct stringent surveillance of domestic transportation networks Because of their hybrid SIR model technique, they are able to anticipate the trajectory of the ongoing pandemic of COVID19 coronavirus in India. This approach includes well-mixed populations within cities as well as intercity coupling based on transportation networks. There only needs to be a relatively small number of people infected with the COVID19 virus in order for the pandemic to be maintained and further spread, as their research has demonstrated. This is due to the fact that the domestic transportation networks play an extremely important role. Therefore, it is of equal importance to monitor the domestic transportation, in addition to putting restrictions on international connections.

Using a mathematical model with five compartments known as the SEIRD model, Vipin Tiwari and his colleagues [60] analysed and predicted the dynamics of COVID-19's dissemination in India in the year 2020. The classic SEIRD model has been updated to account for the impact of India's COVID-19 mitigation policy, commonly known as a statewide lockdown. The modified transmission rate based on intervention techniques such as lockout, the time-dependent reproduction number, and the identification of underreported instances make up the core of their improvised SEIRD model. In addition to that, the data up to July 10, 2020 have been analysed as part of this study. Indian authorities were able to reduce inflammation caused by COVID-19 by as much as 50% via a public shutdown during the early stages of transmission, according to a research based on the data. During the time period covered by the lockdown, the effective reproduction number appeared to have ranged anywhere from two to three times its previous value, according to the findings. On the other hand, in an earlier study referred to as [61], a connection was found to exist between the effectiveness of testing and the transmission of disease. According to the findings of this study, one of the effective defences against the global distribution of COVID-19 is to improve the testing efficiency by conducting a greater number of sample tests. Overall, this study implies that a statewide public shutdown would be an effective means of stopping the spread of COVID-19, not only in India but also around the world. It is without a doubt going

to play a significant part in the epidemic peak suppression of the COVID-19 dissemination. Even though the results that our improved SEIRD model produces are satisfactory, the validity of the mathematical model that is used to predict the spread of an epidemic can be improved by including a few additional parameters. Cases that are either imported or exported, asymptotic, or under-reported are all examples of additional parameters.

An article written in 2020 by Aniruddha Adiga and colleagues [62] discussed several significant computational models for COVID-19 pandemic planning and response that had been developed by researchers in the United States, the United Kingdom, and Sweden. Policymakers and health professionals in each country have employed models to assess the pandemic's evolution, design and analyse control measures, and study a wide range of possible outcomes. As was mentioned, the availability of data, the rapidly developing pandemic, and the unprecedented control measures that were put into place posed challenges for all of the models. In spite of these obstacles, they were of the opinion that mathematical models have the potential to supply policy makers with information that is both helpful and timely. On the other hand, the modellers need to be open and honest about the descriptions of their models, state the limitations in a way that is easily understood, and carry out precise quantifications of sensitivity and uncertainty. It is unquestionably of great assistance to have these models evaluated by an impartial party. On the other hand, those in charge of formulating public policy ought to be aware of the fact that the use of mathematical models for pandemic planning and forecast response relies on a number of assumptions and lacks the data necessary to validate these assumptions.

In 2020, Facal Ndarou et al. [63] proposed a compartmental mathematical model for the spread of COVID-19 disease. The model placed a particular emphasis on the transmissibility of individuals who were considered to be super-spreaders. Based on their findings, they were able to estimate a disease-free equilibrium's minimum basic reproduction number and determine how sensitive their model is to small changes in each of the model's parameters. It was possible for them to determine the fundamental reproduction number threshold in this way. The COVID-19 model that was proposed

has been shown to be appropriate for the outbreak that took place in Wuhan, China, by means of numerical simulations.

Iman Rahimi and colleagues [64] in 2020 described a few primary arguments that are worthy of further discussion and are as follows:

• When it comes to the field of study, the areas of medicine, biochemistry, and mathematics are the ones that receive the most attention from academics.

• According on keyword research, it indicates that interest in COVID-19 will grow over the next few months. In addition, academics are especially interested in coronavirus, epidemic, statistical analysis, human, hospitalisation, quarantine,mortality, and weather occurrences as keywords.

• Several additional factors, such as confirmed cases, risk evaluations, stock markets and ventilation units and beds in intensive care units have been used by researchers in the forecasting process. In addition to China, Pakistan, France, Italy, the United States of America and the United Kingdom, Brazil, Nigeria and Iran were all studied in detail in the case studies.

• Researchers have found that deep learning, SIR, and SEIR are the most effective epidemic models to date. Researchers employed these three models in their work.

• The accuracy of forecasting methods can be improved through the application of hybrid algorithms.

• The vast majority of studies take a deterministic approach, despite the pressing need to develop robust strategies for dealing with unpredictable circumstances.

When Roman Cherniha [65] proposed a nonlinear ordinary differential equations model in 2020, he was hoping to provide a quantitative explanation of the new coronavirus pandemic's spread. One of the model's unique features is its complete integrability, which sets it apart from the rest. Exact model solutions (with the parameters accurately given) lead to findings that are in good agreement with the data from China and Austria, as demonstrated by comparison with publicly available data. Using data from Austria, France, and Poland, we can make some educated guesses about the total number of instances that COVID-19 will cause. respectively. Additionally, the model lends itself to some interesting generalisations.

In the year 2020, Gaetano Perone [66] explained that the novel Coronavirus disease, also known as COVID-19, is a severe respiratory infection that first appeared officially in Wuhan, China, in the month of December 2019. Late in the month of February, the disease started rapidly spreading across the world, which caused serious emergencies on multiple fronts, including the health, social, and economic fronts. Through the use of an autoregressive integrated moving average (ARIMA) model, which is applied to Italy, Russia, and the United States, the purpose of this paper is to make a prediction regarding the short- to medium-term incidence of the COVID19 epidemic. The Worldometer website (https://www.worldometers.info/coronavirus/) provides the data that is used for the analysis, which is based on the number of newly confirmed cases of COVID-19 that occur each day. Italy (4,2,4), Russia (1,2,1), and the United States of America had the best ARIMA models (6,2,3). The results revealed the following: I ARIMA models are sufficiently reliable when new daily cases begin to stabilise; ii) Italy, the United States of America, and Russia reached the peak of COVID-19 infections in the middle of April, the middle of May, and early June, respectively; and iii) Russia and the United States of America will require significantly more time than Italy to reduce COVID-19 cases to near zero.

This may indicate the importance of implementing swift and effective lockdown measures, which have historically been implemented to a larger extent in Italy. Even though the results should be interpreted with caution, it appears that ARIMA models are a useful tool for assisting health officials in monitoring the outbreak's spread. This is despite the fact that the results should be interpreted with caution. The continuous updating of these data, the addition of interventions and other real aspects, and the application of the model to other nations and/or regions all have the potential to produce additional forecasting that is both useful and accurate.

Since the first SARS-CoV-2-infected patient was officially reported in the middle of November 2019, the new coronavirus has infected more than 10 million people, of whom half a million have perished in this short amount of time, according to a study published in 2020 by Ovidiu-Dumitru Ilie et al. The accuracy of COVID-19 monitoring and prediction systems, as well as containment procedures, must be improved as soon as possible. These last three countries are now the most affected by COVID-19, and as

a result, ARIMA models have been built and used to predict the epidemiological trend there. ARIMA models have been constructed and used to predict epidemiological COVID-19 trends in Ukraine. Romanian Government (GOV.RO), World Health Organization (WHO), and European Centre for Disease Prevention and Control (ECDPC) websites were used to acquire daily prevalence data from 10 March 2020 to 10 July 2020 for COVID-19 (ECDC). This was done so that the data would be as accurate as possible. Multiple ARIMA models, each with their own unique set of ARIMA parameters, were developed. the most accurate model for Ukraine, Romania, Moldova, the Republic of Moldova, Serbia, Bulgarian, Hungarian and U.S. models were chosen based on their Mean Absolute Percentage Error (MAPE). These models include ARIMA (1, 1, 0), ARIMA (3, 2, 2), ARIMA (3, 2, 2), ARIMA (3, 1, 1), ARIMA (1, 0, 3), ARIMA (1, 2, 0), ARIMA (1, 1, 0), ARIMA (0, 2, 1), and ARIMA (4.70244, 1.40016, 2.76751, 2.16733, 2.98154, 2.11239, 3.21569, 4.10596, 2.78051). This study provides an idea of the epidemiological stage that each of these regions is currently in and demonstrates that ARIMA models can be used effectively for forecasting during this current crisis.

According to research published in 2020 by Kaustuv Chatterjee et al. [68], India is in the early stage of the COVID-19 epidemic despite having a slower growth rate than the other countries that were studied. Their mathematical model demonstrates that, if nothing is done to stop it, the epidemic will almost certainly reach 3 million cases by the 25th of May in 2020 and will completely overwhelm the healthcare resources that are currently available. The model also suggests that the immediate implementation of NPIs among the general population, including complete lockdowns, has the potential to slow the progression of the epidemic by April 2020, reduce the number of COVID-19 cases, and reduce hospitalisation, ICU, and mortality rates by nearly 90 percent. This will make the disease more manageable, and it will fit within the purview of India's current healthcare resources.

According to a study by Olumuyiwa James Peter and his colleagues [69] published in 2021, the COVID-19 pandemic is one of the strange viruses that has the entire planet in a state of fear and confusion. Because of its elusive nature, the development of an effective vaccine against it has been slowed down. To prevent the virus from spreading

further, various preventative and protective actions, as well as recommendations from medical professionals and governing bodies, have been proposed. Using mathematics as an approach is one of the approaches to better comprehend the virus. In order to better understand the dynamics of the current pandemic, they developed a new mathematical model they dubbed "COVID-19." Several important characteristics of the novel model have been examined, including its invariant region, equilibrium state, fundamental reproduction number, and the global stability of the free disease equilibrium. All of these qualities are regarded valuable in their own right. The nonlinear least squares estimate technique implemented in the MATLAB function lsqcurvefit is used in conjunction with an actual statistical data set covering the period from July 1, 2020, to August 14, 2020, in Pakistan. Analyses of the parameters of the newly proposed model have been conducted in order to find which parameters are most susceptible to modification. These observations were validated by numerical simulations, which also led to the best-fitting curve being obtained for the proposed model. The techniques used by the public health sector and the government to address the circumstances that are causing the pandemic to spread faster will be more effective, according to the conclusions of this study. Efforts will be made to further investigate the recently suggested COVID-19 model to ensure that it complies with the methods used in studies that were recently published.

It was discussed in 2021 that a mathematical analysis on the transmission dynamics of the novel COVID-19 pandemic had been completed [70]. This was done to learn more about how diseases spread and to look at possible preventative and control measures that could help to keep the tide of disease transmission from rising too quickly in the population. First, the human population was divided into those who were susceptible, those who were exposed, those who were infected, those who had recovered, and others under quarantine. If the basic number of fresh transmissions of coronavirus is less than one, the model has a disease-free equilibrium that is globally asymptotically stable, according to the stability analysis. This was discovered through the application of the stability analysis. The findings were analysed using a biological lens, which led to the following conclusions:

• If the management measures that are instated are able to reduce or maintain the basic reproductive number at a value that is less than one, then COVID-19 can be effectively managed or even eradicated. This is an indication that, despite the number of infectious individuals first brought into the community of completely vulnerable individuals, the illness was able to spread.

• It is possible to exercise effective control over the distribution of COVID-19 in the population. It was also necessary to execute three separate simulations in order to compare the effectiveness of various control systems.

• According to the findings of our study, the effects of three interventions with optimal costs of implementation are superior to the reduction in the disease epidemic.

Archana Singh Bhadauria and colleagues [71] conducted research in 2021 to investigate how a lockdown affected the progression of a novel Corona Virus Disease (COVID-19), which first appeared in Wuhan city in China in December 2019. India's government has banned international travel through land checkpoints due to the pandemic scenario, and a nationwide lockdown has been implemented as of March 24, 2020, across the country. In order to investigate the influence that lockdown has on the progression of disease, researchers considered a mathematical model with three dimensions that made use of nonlinear ordinary differential equations. The above-mentioned model was examined by using nonlinear ordinary differential equations and stability theory. Following the computation of the fundamental reproduction ratio, major parameters responsible for the preservation of a fundamental reproduction ratio lower than one are found. Only a complete lockdown, according to the study's conclusions, can wipe disease from the system; without it, disease would always be present in the population. However, if lockdown procedures are only partially applied, techniques such as contact tracing and quarantine can be used to keep the disease under control.

1.5 Proposed Objectives of Study

In view of the above therefore, in the study mathematical modelling on COVID-19 epidemic was carried out. The objectives of the research work include the study:

- To develop and validate the mathematical models on Covid-19 epidemic to forecast the different effects of the disease.
- To predict and forecast the various effects of the disease using existing models and data available in public domain.
- To calculate the basic reproduction number, case fatality ratio of the disease Covid-19.
- To formulate a mathematical model that will help to make strategies to control Covid-19 epidemic.

1.6 Main terms used in Thesis

Susceptible: A person who is at risk of infection but is not yet infected.

Exposed: A person who does not have visible symptoms but has contracted the infection.

Infectious: A person who can pass infection to others and has the disease with symptoms.

Recovered/Removed: After treatment etc., the symptoms are gone, and the person is no more infectious.

Incubation Period: It is the time elapsed between the onset of the first visible symptoms of the disease and exposure to the infection.

Endemic: A disease is referred as endemic if it is regularly found in a population or an area.

Epidemic: A disease is referred as epidemic if the number of cases substantially increases within a short duration in given population.

Pandemic: A disease is called pandemic if it is prevalent in the entire country or the world.

Basic Reproduction Number is defined as the number of secondary infections caused by single infected person in a susceptible population. This quantity is a dimensionless quantity defined as

R_0 = *(probability that an individual will survive until infectious)* × *(effective transmission rate)* × *(average duration of the infectious period).*

This list is in no way comprehensive in any way. In the many wonderful books that are available on the topic, you will find more comprehensive lists of the terms that are used in infectious disease epidemiology. (e.g., [72]).

1.7 Summary of Thesis

Owing to the fact that the SarsCov2 virus is one of the most dangerous diseases that can affect humans, the SarsCov2 virus is a potentially fatal pathogen that is poorly understood and has the potential to pose a significant risk to public health. During the pandemic, everyone was talking about the increasing number of people infected with the disease as it spread. Researchers from a wide variety of backgrounds have applied a wide variety of conceptual frameworks in order to generate a variety of forecasts for countries like India. Mathematical models will be used in this study to acquire insight into how many people in India are infected with the Corona virus and how many more will be affected soon. In this work, various mathematical models were developed, investigated, and validated for the COVID-19 epidemic in order to make predictions regarding the various effects of the disease. The data that is available in the public domain was used to make predictions about the cases that will occur in the near future, as well as basic reproduction and the case fatality ratio of the COVID-19. Additionally, a transmission model was talked about. The state of the epidemic outbreak in India was examined in this study, and several models were used to make projections regarding its likely progression into the future. The Indian healthcare system faces a significant challenge when it comes to providing appropriate intensive care units for critically ill patients. It would be very helpful if they had some idea about the cases that are coming up in the future.

In the first chapter, a general introduction to mathematical biology, epidemic modelling, some fundamental mathematical models, and other related topics has been

provided. The section on the review of the literature sheds light on a few important works that have been done by researchers in this field up to this point. In light of the aforementioned, the research gaps have been outlined, and the goals of the study have been suggested. This chapter also provides an explanation of the fundamental mathematical preliminaries as well as the significant ideas, terms, and concepts that were utilised throughout the entire research project. The conclusion of the chapter provides a synopsis of the chapters that are included in the thesis.

In chapter 2, we have established that the COVID-19 outbreaks in India are a major cause for concern, and although a comprehensive scientific investigation of this pandemic has not yet been completed, it was necessary to calculate the parameters of the pandemic dynamics in order to design an appropriate quarantine area, determine the number of hospital beds available, and so on. In this chapter, we covered the Polynomial Approximation Model for estimating the number of people infected across India.

In chapter 3, our attention has been directed toward the investigation of the SEIRD model for COVID-19. When trying to make predictions about the number of deaths and cases, many different parameters were taken into consideration. From the collected data on fatalities and confirmed cases of COVID-19, we attempted to determine the basic reproduction number R_0. The basic reproduction number is also dependent on the clinical parameters. The next step that we took was to make an estimate of the possible range of forecasts regarding the future number of deaths in India.

In chapter 4, in light of the fact that the COVID-19 disease has been identified as a potential threat on a global scale and that numerous studies are being published all over the world making use of a variety of mathematical models to estimate the size of this epidemic, a straightforward econometric time series model was discussed here. Many researchers are currently working on various mathematics-based estimation models to predict the subsequent trend of this pandemic, as the significant increase in daily COVID-19 infected cases around us is frightening. Some trajectories of COVID-19 in India were predicted using data that is available in the public domain. This was because the weighty increase in the daily COVID-19 infected cases around us is frightening. We applied a time series model to the Indian dataset known as the Auto-Regressive

Integrated Moving Average Model in order to make a prediction about the daily number of COVID-19 infections that will occur in the not-too-distant future. The results of our analysis are predicted to be extremely concerning. In order to avoid such a potentially lethal scenario, a number of stringent preventative measures have been proposed. According to our estimates, Indian health officials ought to modify their warmongering interference in order to take into account the accelerated growth, and rudimentary infection control actions at hospital levels were immediately required in order to reduce the scale of the COVID-19 pandemic. If the Indian government does not take stringent precautionary measures to control the spread of COVID-19, then the effects may become even worse.

In chapter 5, there has been much discussion regarding the COVID-19 transmission model as the outbreak serves as a sobering reminder that pandemics, along with other rare but catastrophic events, have occurred in the past and will continue to do so in the future. Transmission models are useful tools for gaining an understanding of the behaviour of contamination as it enters a community and determining the circumstances under which it will be treated or processed. As a consequence, there are very few treatments available in India for a severe problem. This is a situation that is not unique to India; rather, it is shared by countries all over the world. First, a proposal for the model's specifics is made, and then, after that, a discussion of the model's potential benefits follows. Using RPGT, a Transition Diagram of the system as well as expressions for Transition Probability and Mean Sojourn Times, Path Probabilities, and the mean time to epidemic affected (T_0), Average Healthy Time (A_0), and Recovery Period (B_0) were derived, and they were then followed by illustrations. Following the creation of tables and graphs, analysis was performed.

In chapter 6, we have used a compartmental model with five compartments, i.e., the SEIRD Model, and we have done analysis on the dynamics of COVID-19 in India. Through this data-based study, we concluded that inflammation can be controlled by public lockdowns because it will reduce the transmission rates, and due to limited health care facilities, there will be more chances of recovery and hence the recovery rate will be increased. If we change these two parameters, the curve can be flattened. If we change the values of parameters in the model, we will get different results. As we

know, these parameters are not constant over time. So, if we look for disease dynamics at different times, we should change these parameters accordingly. Also, there are a few limitations in our model, and those have been discussed in the earlier sections. These can be improvised in the future. Also, some more parameters can be added to enhance the validation of results, like under reported cases or asymptotic cases.

In the end, the problems under investigation in the study have been justified by the bibliography given in the concluding part of the thesis.

Chapter-2

A Mathematical Model to Predict the Effect of Infection on Population of India by Covid-19 Corona Virus

2.1 Introduction

Currently, the SarsCov2 virus is one of the most venomous pathogens for humans. The SarsCov2 virus is deadly, less understood, and has the capability of causing a large-scale threat to public health. During the pandemic, everyone was talking about the increase in infected people. For a country like India, various predictions have been made by various researchers by using different models. The main aim of this work is to understand the dynamics of the Indian population infected by the coronavirus and how many people will be infected in the near future by using an appropriate mathematical model. We investigated a mathematical model that provides a good approximation of the COVID-19 outbreak in India. Before proceeding, we observed that the size of this outbreak in its starting stage was discussed by [73], [74], and [75], and they used SIR models and logistic models. In past years, at the time of other epidemics, various models were established, a few of them are analytical, stochastic, and phenomenological. Some of the most famous mathematical models used in epidemiology are mentioned below:

2.1.1 The Logistic Model: The logistic growth model was introduced by Haberman in 1998 for population dynamics. The basic assumption of the model is that the rate of change in the number of new cases per capita linearly decreases with the number of

cases. Hence, if I is the number of Infected people, and t is taken as the time, then the model is written as

$$\frac{1}{I}.\frac{dI}{dt} = \omega\left(1 - \frac{I}{P}\right)$$

where ω is infection rate, and P *is* the final epidemic size. This model can be solved easily by differential equations.

2.1.2 SIR Model: If $S(t), I(t)$ and $R(t)$ are the Susceptible, Infected and Recovered peoples at any given time t The equations of this compartmental model are

$$\frac{dS}{dt} = -\frac{\omega}{P}IS$$
$$\frac{dI}{dt} = \frac{\omega}{P}IS - \tau I$$
$$\frac{dR}{dt} = \tau I$$

In the above equations, ω is rate of infection and τ is recovery rate. It can be noticed that P is total population and $S + I + R = P$

2.1.3. Polynomial Regression Model:

We can use polynomial models if there is any curvilinear relationship between the explanatory variables and study. If range of explanatory variables is small, then we can model some nonlinear relationship with polynomials. We say a model is linear if its parameters are linear. So we can consider $y = \beta_0 + \beta_1 x_1 + \beta_2 x_2 + \beta_{11} {x_1}^2 + \beta_{22} {x_2}^2 + \beta_{12} x_1 x_2 + \epsilon$ and the model $y = \beta_0 + \beta_1 x + \beta_2 x^2 + \epsilon$ as linear model. These the polynomials of second order with one and two variables, respectively.

Polynomial Models in One Variable: The polynomial model of order k in one variable may be expressed as $y = \beta_0 + \beta_1 x + \beta_2 x^2 + \cdots + \beta_k x^k + \epsilon$. If we consider $x_j = x^j, j = 1,2, \dots, k$, Then we refer to this model as a multiple linear regression model with k different variables to explain the data, written as $x_1, x_2, \dots, x_k$. Therefore, it is clear to see that the polynomial regression model is incorporated into the linear regression model expressed as $y = X\beta + \epsilon$ Therefore, the techniques that are used for

fitting the linear regression model can also be used for fitting the polynomial regression model.

For example: $E(y) = \beta_0 + \beta_1 x + \beta_2 x^2$ *or* $y = \beta_0 + \beta_1 x + \beta_2 x^2 + \epsilon$ is a polynomial regression model of second order in one variable, and we will call this a quadratic model or a second order model. We will call the coefficients β_1 and β_2 the parameters of linear effect and quadratic effect, respectively. We can use these polynomial models for the approximation of a complex nonlinear relationship. It is possible to make the observation that the polynomial models are nothing more than an expansion of the Taylor series of the unknown nonlinear function.

Hierarchy: If a model includes terms x, x^2, x^3 and so on in a hierarchy, then we refer to that model as being hierarchical. For instance, the hierarchical nature of the model $y = \beta_0 + \beta_1 x + \beta_2 x^2 + \beta_3 x^3 + \beta_4 x^4 + \epsilon$ can be seen from the fact that it contains all of the terms up to order four. The model $y = \beta_0 + \beta_1 x + \beta_2 x^2 + \beta_4 x^4 + \epsilon$ does not constitute a hierarchical structure because it does not include the term x^3. Because only hierarchical models are invariant under linear transformation, we can anticipate that all polynomial models will have this property. When viewed through the lens of mathematics, this requirement appears to be more appealing. It's possible that the requirements for the model will change depending on the context of the situation. The model $y = \beta_0 + \beta_1 x_1 + \beta_{12} x_1 x_2 + \epsilon$, for instance, requires a two-factor interaction, which is provided by the cross-product term. A hierarchical model requires the inclusion of x_2 which is not required from the standpoint of the statistical significance of the data.

Orthogonal Polynomials: When we are trying to fit a linear regression model to a particular data set, we need to start with a straightforward linear regression model. Let us assume that at a later stage, we come to the conclusion that we want to change it to a quadratic, or that we want to increase the order from a quadratic model to a cubic model, etc. In every instance, we will need to start the modelling process from the very beginning-that is, with the basic linear regression model. It would be preferable to have a situation in which adding an additional term merely refined the model in the sense that, by increasing the order, we did not need to do all of the calculations from scratch. This would make the situation more manageable. Prior to the invention of computers,

all of the calculations had to be done by hand, , this aspect was of much greater significance. Trying to accomplish this goal by sequentially applying the powers $x^0 = 1, x, x^2, x^3$ will not be successful. On the other hand, we can accomplish this with the assistance of a set of orthogonal polynomials. A degree of k is assigned to the kth orthogonal polynomial. The Gram-Schmidt orthogonalization technique can be utilised to construct polynomials of this kind. It's possible that we'll run into another problem when we try to fit polynomials into one variable, and that problem is ill-conditioning. One of the assumptions that is made in a standard multiple linear regression analysis is that all of the variables that are considered independent are truly independent. This assumption does not hold true within the framework of the polynomial regression model. Even if poor conditioning is eliminated through centring, there is a possibility that high levels of multicollinearity will still be present. Orthogonal polynomials have the potential to eliminate such a challenge. The Legendre polynomials, Hermite polynomials, and Tehebycheff polynomials are responsible for the classical cases of orthogonal polynomials of special kinds. In this case, we are dealing with discrete orthogonal polynomials, whereas the previous example involved **continuous orthogonal polynomials**, where the integration step was part of the orthogonality relation (where the orthogonality relation involves summation).

Notice that:

- It is unnecessary for us to concern ourselves with the other terms in the model.
- Instead, we should solely focus on the newly included term.
- As a result, fitting polynomials of a higher order can be done easily.
- When a model that fits the requirements appropriately is obtained, the process should come to an end.

Piecewise polynomial (Splines): Sometimes, the data will show that a lower order polynomial does not provide a good fit for the data. Increasing the order of the polynomial is one potential solution to this problem; however, there is no guarantee that this will be successful. It's possible that the higher-order polynomial won't improve the fit all that much. Residuals are a useful tool for analysing situations like these; for instance, the residual sum of squares might not be able to stabilise, or the residual plots

might be unable to explain an unexplained structure. The fact that the response function can behave differently depending on the range of the independent variable is one of the possible explanations for why something like this would occur. To solve issues of this nature, one solution is to use an appropriate function to fit the data in a number of different ranges of the explanatory variable. Therefore, the polynomial will be broken up into its component parts. In order to achieve such a fitting of the polynomial in pieces, the spline function can be utilised. The method of least squares gives us point estimates of linear regression models that are free from deviations, provided that certain preconditions of the model's random error distribution probability are satisfied.

In this chapter, we have tried to estimate the future number of infected people in India using the Polynomial Approximation Model. Generally, in the cases of pandemics, the data is fitted by some exponential functions. But at present, the data is fitted by the polynomial of degree three. The data used for calculation is taken from the websites of the Ministry of Health and Family Welfare from 27-03-2020 to 15-04-2020 and from the websites of John Hopkins University. In the next chapter, we will include other factors in our study. We tried to include the study of the treatment of infected people in the mathematical model.

2.2 Considerations to Keep in Mind While Fitting Polynomial in Single Variable

A few of the considerations, one should keep in mind while fitting polynomial models are as follows:

2.2.1 Order of the Model: It is in our best interest to maintain as low an order for the polynomial model as we can. It may be possible to use only a few transformations in order to maintain the model's first-order status. In the event that this does not meet our expectations, we should move on to the second-order polynomial. It's possible that we'll be abusing regression analysis to a dangerous degree if we try to fit arbitrary higher-order polynomials to the data. There is the possibility of taking into consideration a model that is consistent with the data knowledge and its environment. Because we

already know that a polynomial of order $n-1$ can always pass through n points, we can always find a polynomial of sufficiently high degree such that it provides a "good" data fit. This is possible because we already know that a polynomial of order $n-1$ can always pass through n points. These models are neither accurate predictors nor do they contribute to a deeper comprehension of the unknown function.

2.2.2 Strategy of Model Building: When determining the order of an approximate polynomial, we need to come up with a more effective strategy. It's possible that we could try this by fitting the models one after the other in ascending order and evaluating the significance of the regression coefficients at each step of the model fitting process. It would be best if we kept increasing the order until the t-test became insignificant for the term with the highest order. A forward selection procedure describes this kind of process. We also have the option of utilising a different strategy, which consists of first fitting the appropriate highest order model, and then deleting terms one by one, beginning with the highest order. We are going to keep doing this process until the highest order term that is still remaining has a t statistic that is significant. This kind of process is known as an elimination backward procedure. The model that results from using forward selection and the model that results from using backward elimination are not always the same. In practise, first- and second-order polynomials are used the majority of the time.

2.2.3 Extrapolation: When extrapolating with polynomial models, we need to proceed with extreme caution. There is a possibility that the curvatures of the data region and the extrapolation region will not be identical. It is possible to notice that the predicted response is not based on the actual behaviour of the data. In general, polynomial models have the potential to take unexpected turns in the wrong directions. This may lead to incorrect inferences being drawn when extrapolating or interpolating the data.

2.3 Data Collection

The data was collected from the website of the Ministry of Health and Family Welfare from 27-03-2020 to 15-04-2020 and from the website of John Hopkins University. The collected data is given the table 2.1 below:

Table 2.1: Covid-19 Confirmed Cases (March 27, 2020 to April 04, 2020)

Date	**Infected**	**Recovered**	**Death**
27-03-2020	887	73	20
28-03-2020	987	84	24
29-03-2020	1,024	95	27
30-03-2020	1,071	100	29
31-03-2020	1,251	102	32
01-04-2020	1,590	148	45
02-04-2020	2,032	148	58
03-04-2020	2,567	192	72
04-04-2020	3,082	229	86
05-04-2020	3,588	229	99
06-04-2020	4,314	328	118
07-04-2020	4,858	382	136
08-04-2020	5,360	468	164
09-04-2020	5,916	506	178
10-04-2020	7,600	645	249
11-04-2020	8,446	840	288
12-04-2020	9,205	951	331
13-04-2020	10,453	1,052	358
14-04-2020	10,541	1,205	358
15-04-2020	12,456	1,513	423

The growth of infected people, recovered and deaths between the date 27-03-2020 to 15-04-2020 are being shown with the help of graph plotted below:

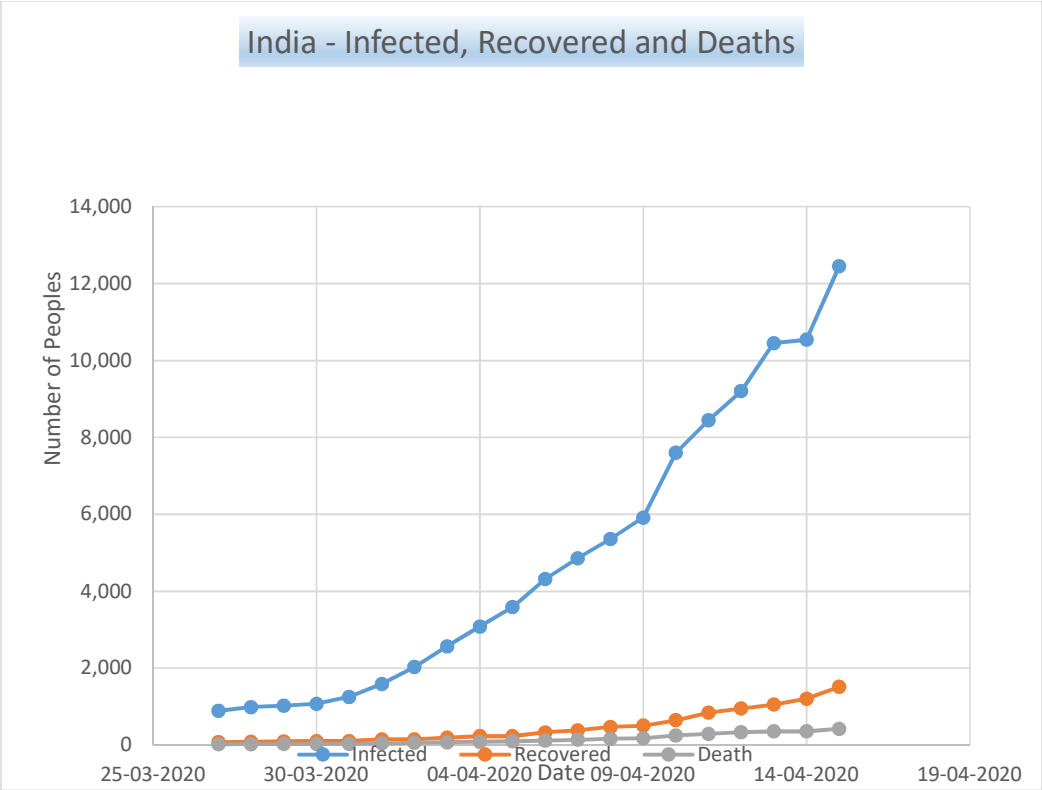


Figure 2.1 Plot of Infected, Recovered and Deaths

2.4 Model Formulation

In this chapter, we have created a Polynomial Approximation Model with the help of statistical tools. We have tried to fit the data with the polynomial of degree two. We have considered that $I(t) = a + bt + ct^2$ .Where t is the time in days and $I(t)$is number of infected people at time t. The constants a, b and c are real in above polynomial.

2.5 Result and Discussion

After analyzing the data, we have found that the curve of Infected Individuals is best fitted with the polynomial $I(t) = a + bt + ct^2$ when the estimated values of coefficients are given by $a = 955.30, b = -88.11, \ c = 33.74$.

The table 2.2 shows the calculation for Approximation of cases and the squared Normalized Error. Where squared normalized error is given by $\left(\frac{\text{Confirmed Case} \quad \text{Estimated Cases}}{\text{Confirmed Cases}}\right)^2$

Table 2.2: Calculation for Approximation of Cases and Squared Normalized Error

Date	**Days**	**Confirmed Cases**	**Approximation of Cases**	**Normalized Error^2**
27-03-2020	1	887	900.9279495	0.000246563
28-03-2020	2	987	914.0352972	0.005465015
29-03-2020	3	1,024	994.6232611	0.000823014
30-03-2020	4	1,071	1142.691841	0.004480851
31-03-2020	5	1,251	1358.241038	0.007348647
01-04-2020	6	1,590	1641.270851	0.001039793
02-04-2020	7	2,032	1991.78128	0.00039175
03-04-2020	8	2,567	2409.772325	0.003751511
04-04-2020	9	3,082	2895.243987	0.003671841
05-04-2020	10	3,588	3448.196265	0.001518213
06-04-2020	11	4,314	4068.629159	0.003235084
07-04-2020	12	4,858	4756.542669	0.000436166
08-04-2020	13	5,360	5511.936796	0.000803519
09-04-2020	14	5,916	6334.811539	0.005011652
10-04-2020	15	7,600	7225.166898	0.002432477

11-04-2020	16	8,446	8183.002874	0.000969616
12-04-2020	17	9,205	9208.319466	1.30044E-07
13-04-2020	18	10,453	10301.11667	0.000211124
14-04-2020	19	10,541	11461.3945	0.007624027
15-04-2020	20	12,456	12689.15294	0.000350368
Sum of Squared Normalized Error				0.049811362

From table 2.2, we have observed that the sum of squared normalized errors is 0.049811362, which is very low. So, with the same coefficients, we have approximated the growth of infected people and tried to explain the same with the graph (Figure 2.2) plotted below:

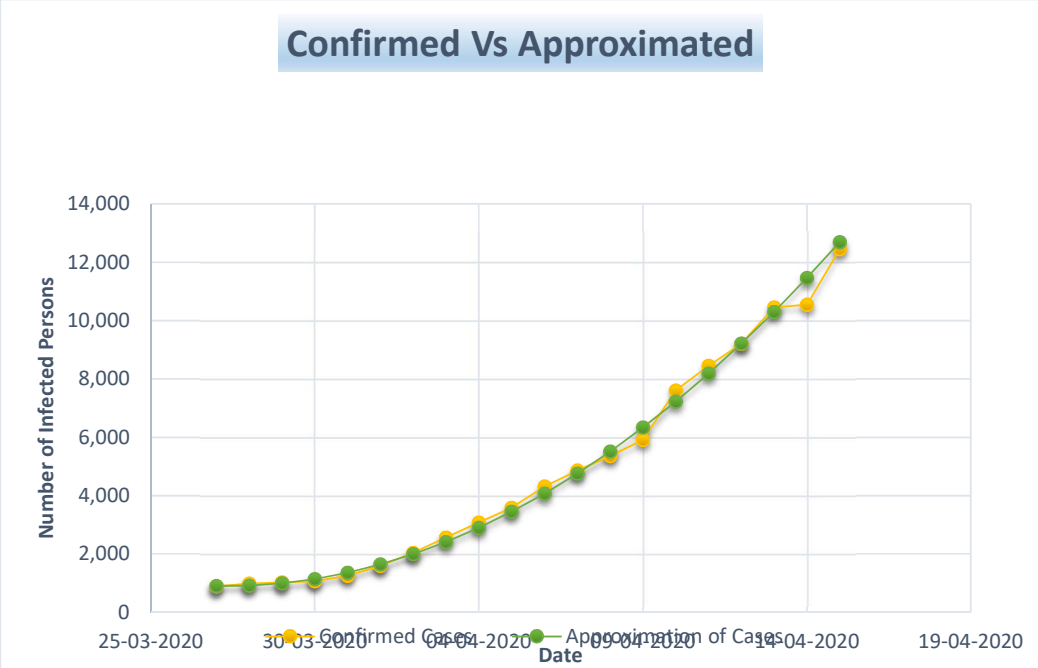


Figure 2.2: Plot of Confirmed Cases and Approximated Cases

The table 2.3 provides the approximated cases of Infected individuals by the dates. This table is prepared by substituting the values of time in polynomial.

Table 2.3: Covid-19 Approximated Cases (Up to July 04, 2020)

Date	**Days**	**Estimated Cases**
31-03-2020	5	1358.241038
05-04-2020	10	3448.196265
10-04-2020	15	7225.166898
15-04-2020	20	12689.15294
20-04-2020	25	19840.15439
25-04-2020	30	28678.17124
30-04-2020	35	39203.20351
05-05-2020	40	51415.25118
10-05-2020	45	65314.31425
15-05-2020	50	80900.39274
20-05-2020	55	98173.48663
25-05-2020	60	117133.5959
30-05-2020	65	137780.7206
04-06-2020	70	160114.8607
09-06-2020	75	184136.0163
14-06-2020	80	209844.1872
19-06-2020	85	237239.3735
24-06-2020	90	266321.5753
29-06-2020	95	297090.7924
04-07-2020	100	329547.025

Figure 2.3 shows the future growth in the infected individuals in India.

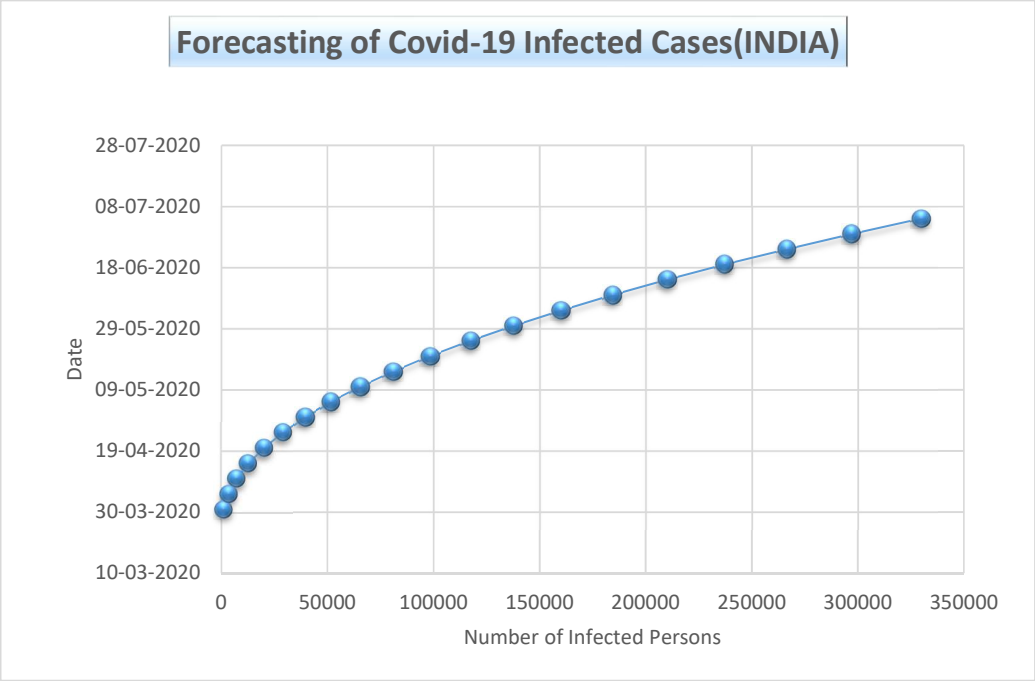


Figure 2.3: Forecast Plot of Covid-19 Infected Cases

2.6 Conclusion

This chapter presents an overview of the mathematical epidemic models of population disease. In this case, the Polynomial Approximation model provides a basic investigation into the spread of the epidemic. Here we defined the Polynomial Approximation Model with the help of polynomials and found the coefficients with the help of data, using the statistical tools. It is also being made clear that the approximation may not be correct because it may be dependent on some other factors as well. In this model, we have approximated the size of epidemic with the data. Usually, such type of approximation is done by usual exponential curve or SIR model and Logistic Models.

Chapter- 3

Estimation through the SEIRD Model for Covid-19

3.1 Introduction

The SIR model and its many variants are the types of epidemiological models that are used most frequently to understand how epidemics spread. Since the outbreak of the novel coronavirus, it has gained popularity among mathematicians who are trying to estimate the size of the outbreak and its consequences to make various policies, such as [76], [77], [78], [79], [80], [81], [82] and others. In this chapter, we have done a study of a modified SIR model, which is known as SEIRD (Susceptible, Exposed, Infectious, Recovered, and Dead), and established various findings. It is well known that the SEIRD model has various degrees of freedom, and it depends on the parameters that are being observed from the clinical diagnosis of the disease and the data of confirmed cases and deaths. The basic reproduction number R_0 can be identified from the data and model. Since it is also well known that the R_0 reveals the spread speed of the virus. In this chapter, we have estimated the case fatality ratio, which is also a key parameter in estimating the number of deaths. During the estimation of R_0 for India, we observed a range from 1.75 to 4.6 depending upon the different values of clinical parameters and initial values. These outcomes reveal that there is no single value of the basic reproduction number that is associated with the data, at least for the short time of observation. Many values of the basic reproduction number that are being observed are right, and the exact value depends on the model and the country.

In order to construct a model, it is necessary to simplify reality through the use of assumptions. The infected individuals are also infectious to others, which is the primary presumption underlying the Kermack–McKendrick model. The total number

of people in the population is assumed to stay the same, which is the second assumption the model makes. Epidemiological models are constructed using ordinary differential equations (ODEs), which are mathematical systems that describe the dynamics that are present in each class. The dynamics of susceptible individuals, infectious individuals, and recovered individuals is one of the earliest forms of epidemiological modelling. In the year 1927, Kermack and McKendrick made the initial suggestion for the model. In order to derive the differential equations, we must first consider the evolution of the classes over time. When an individual who is susceptible comes into contact with an individual who is infectious, the susceptible individual has a certain chance of becoming infected and moves from the class of individuals who are susceptible to the class of individuals who are infected. Every person who contracts the disease during a given period of time counts toward the reduction of the population that is susceptible to it. At the same time, the number of individuals belonging to the class of infectious agents who have recently become infected also rises. When we are developing a model, we need to make sure that the units of the quantities that are being considered are taken into consideration. The process of estimating parameters based on data also benefits from having units. The above equations require that both sides use the same units for their respective answers. Every derivative measures something in terms of units, such as the number of people per unit of time. For differential equation models to be mathematically acceptable and have significance in biology, the differential equations themselves must be well posed. Because the dependent variables in the model denote physical quantities, we also require, for the majority of models in biology and epidemiology, that solutions that begin from positive (nonnegative) initial conditions remain positive (nonnegative) for all. This is necessary because the dependent variables in the model denote physical quantities.

This chapter is organised into four sections. The first is an introduction, and the second is a summary of the SEIRD model. In the next section, we will discuss the data and identify the model. The next section describes the procedure for the estimation and results, along with some figures.

3.2 SEIRD Model

Kermarck and McKendrick proposed the first compartment model for infectious disease. Usually, in epidemiological models, the total population is divided into numerous compartments or categories. To study the dynamics of infectious diseases, we generally use the SEIRD model that divides the total population into five compartments, such as susceptible, exposed, infectious, recovered, and dead. In this basic compartmental model, individuals move from one compartment to another depending upon their personal resilience, resistance, and interaction with the person they are infected with.

Nowadays, we have observed that to analyse infectious diseases, researchers are widely using the SEIRD model. There are a few assumptions for this popular model, and those are as follows:

- We do not consider the natural population dynamics such as nature death, population mobility, and birth.
- It is assumed that contacts between the susceptible and infected are more than sufficient to spread the infection.
- Individuals who were in the recovered compartment will not become infected again.
- Only individuals in an infected compartment have the capability to transmit the disease.

The SEIRD model may be applied to almost all infectious diseases, but there are a few limitations in the case of COVID-19. The study suggests that there is a property of COVID-19 that the individuals in the exposed compartment are also capable of disease transmission. Since we neglect the infectivity of the individuals during the incubation period in the SEIRD model, unreported cases were also ignored in this model. Since we were facing a huge pandemic, there was no certainty that all infected individuals were tested and reported. It was because of a shortage in medical resources and testing policies. Such individuals were probably spreaders, which are hidden in susceptible compartments. So, this model cannot be considered for simulation in the long term

because of its constant parameters. Because of the recovery rate, the transmission rate must be changed if considered for a long time.

The rate of change in the number of infected individuals clearly indicates whether the epidemic is spreading or eradicating.

In this chapter, we have studied a variant of the SIR model (a compartmental model) that includes exposed and dead bodies in its compartments. Various authors like [83], [84], and others have used similar epidemiological models. In fact, many authors have used many advanced variants of the model with more compartments like [85], [86]. We have considered a model containing five compartments for people: susceptible (S), exposed (E), infectious (I), recovered (R), and dead (D). The susceptible compartment has those who are not infected with the virus yet but can be infected. Those exposed are those who are infected but cannot spread it to others. This is called the incubation period. In the infectious compartment, we have those people who are infected with viruses and are capable of transmitting them. Recovered compartments have those who were infected with the virus in the past but recovered. The dead are those who were unable to survive after infection by the virus. The number of people in all five compartments keeps changing over time as follows:

$$\frac{dS(t)}{dt} = -\beta \frac{S(t)}{N} I(t) \tag{3.1}$$

$$\frac{dE(t)}{dt} = \beta \frac{S(t)}{N} I(t) - \sigma E(t) \tag{3.2}$$

$$\frac{dI(t)}{dt} = \sigma E(t) - \gamma I(t) \tag{3.3}$$

$$\frac{dR(t)}{dt} = (1-\alpha)\gamma I(t) \tag{3.4}$$

$$\frac{dD(t)}{dt} = \alpha\gamma I(t) \tag{3.5}$$

$$\frac{dC(t)}{dt} = \lambda\gamma I(t) \tag{3.6}$$

N is total population of India and we will assume that it is fixed and does not change with time i.e., birth and death caused by any other reason are excluded in order to avoid unnecessary complications. In most research papers and literature, the total population is fixed. C(t) is the total number of confirmed cases. It doesn't change how the model works, but it is used to match confirmed case data to the model. During the analysis of the model, it is assumed that the people in the infectious compartment, rather than those exposed are tested for the virus. In the computer programmes, we replaced I(t) in the equation (3.6) with E(t) and the results will remain unchanged. The solution of the SEIRD model has dependency on many parameters. We have used γ and σ as clinical parameters. γ is the parameter which reflects the estimated time of illness. Its value was found varying in the research papers from 1/18 to 1/5 in [84]. σ is the parameter which tells the estimated incubation period of COVID-19. Its value was found varying in the research papers from 1/5 in [87] to 1/3 in [84]. The parameter β tells the infectious rate. Also, we have the relation $\beta = R_0\gamma$, where $R_0$is known as the basic reproduction number, which is used to measures the disease transmission. α is the case fatality ratio and we have referred it as CFR. As discussed in paper [88], the CFR has many limitations and depends on the infectious people. The CFR may not be constant and can increase if the system of health care in India becomes overloaded. But for the simplicity, we have assumed that α is constant and tried to approximate it. Also, λ was estimated. The number of dead and recovered people at time zero are $R(0) = 0$ and $R(0) = 0$. We have chosen the number of infected people at initial stage $I(0)$ and exposed people as $E(0)$. We also made discussion on their choice. At initial stage, Susceptible peoples are $S(0) = N - I(0) - E(0) - R(0) - D(0) = N - I(0) - E(0)$.

3.3 Data of Model

In this estimation, we are dependent on the data of confirmed cases and deaths due to COVID19. The data used by us was collected from the website of Johns Hopkins University. The population of India is taken as 1378159530. The observations were collected from the date January 22, 2020 to May 20, 2020.

3.4 Estimation and Results

In this section, we have described the procedure of estimation used by us. It is same method as used by Ivan Korolev [88]. We have fixed $T_0 = 1,\ I_0 = 0$ and increase E_0 (if needed) starting from $E_0 = 1$. For any vector (α, R_0, λ) of parameters and each value of t, we have calculated the number of deaths $D(t, \alpha, R)$ and the number of reported cases $C(t, R, \lambda)$. Then we have calculated the residual sum of squares for the death's series, given by

$$RSS_D(\alpha, R) = \sum_{t=1} (D(t) - D(t, \alpha, R))^2$$

and the residual sum of squares for the reported cases series, given by

$$RSS_C(R, \lambda) = \sum_{t=1} (C(t) - C(t, R, \lambda))^2$$

Where $D(t)$ and $C(t)$ are the original data reported. Then, we found the values (α_D, R_D) that minimize RSS_D and the values (R_C, λ_C) that minimize RSS_C and then we have estimated jointly (α, R_0, λ) by minimizing

$$RSS_T(\alpha, R, \lambda) = \frac{RSS_D(\alpha, R)}{RSS_D(\alpha_D, R_D)} + \frac{RSS_C(R, \lambda)}{RSS_C(R_C, \lambda_C)}$$

We used the normalization by the preliminary values of the RSS_D and reported cases so that both series contribute roughly equally to the final objective function. If their contribution is not normalized, then RSS_C may dominate. If any of the $\alpha_D, \lambda_C, \alpha$ or λ are at the upper bound of 1, the value of E_0 will be increased until we get rid of the constraint. Then the least value of E_0 was considered for which we do not have any parameter constraint. Others can use the value $E_0 = 1$ always and leave the constraints. Because in this attempt of ours, we used the least value of E_0 so that we can obtain fatality rate close to its upper bound. The number of deaths, which are being forecasted might be considered as highest. But the declaration should also be kept in mind that the model may be incorrect because some of our assumptions, such

as the fatality rate may not be constant over a given time period. This may appear unrealistic.

Next, we discussed the results and calculated parameters with the help of some computer programmes using the languages R and Julia. We have represented the results and estimated parameters with the help of table and graphs. If we consider the COVID-19 confirmed cases and deaths due COVID-19 in India from the date 22-01-2020 to 20-04-2020 with clinical parameters $\sigma = 1/4$ and $\gamma = 1/10$. Here we have fixed $E_0 = 3$ and $I_0 = 0$

Table 3.1 Assumed and Calculated Parameters (January 22, 2020 to April 20, 2020)

Total Population	σ (Assumed)	γ (Assumed)	R_0 (Calculated)	α (Calculated)	$\beta = R_0\gamma$ (Calculated)	λ (Calculated)
1378159530	0.25	0.1	3.005737	0.0326966	0.3005737	0.903463

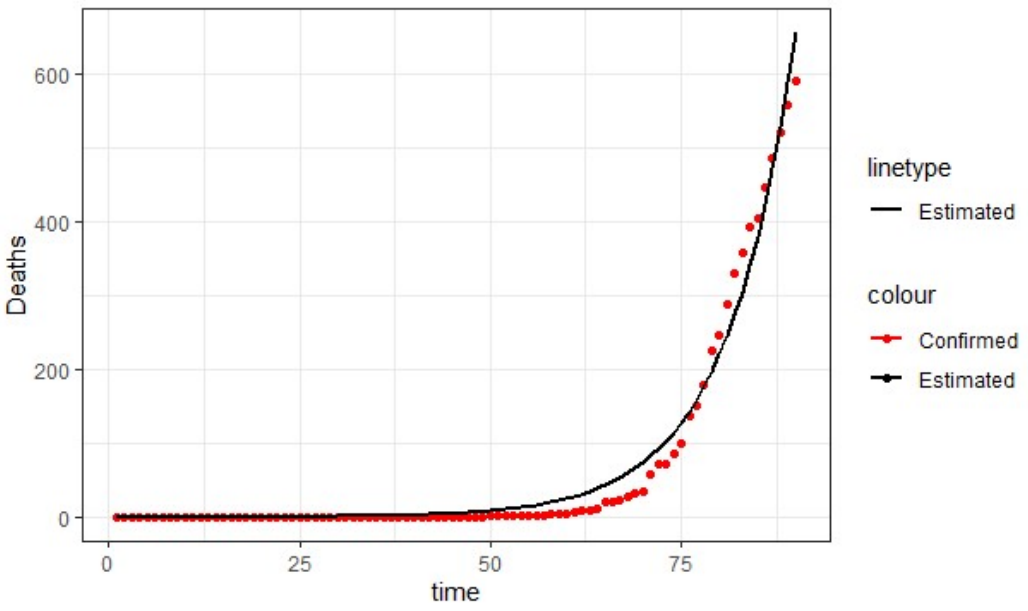


Figure 3.1: Plot of Confirmed and Estimated Deaths (January 22, 2020 to April 20, 2020)

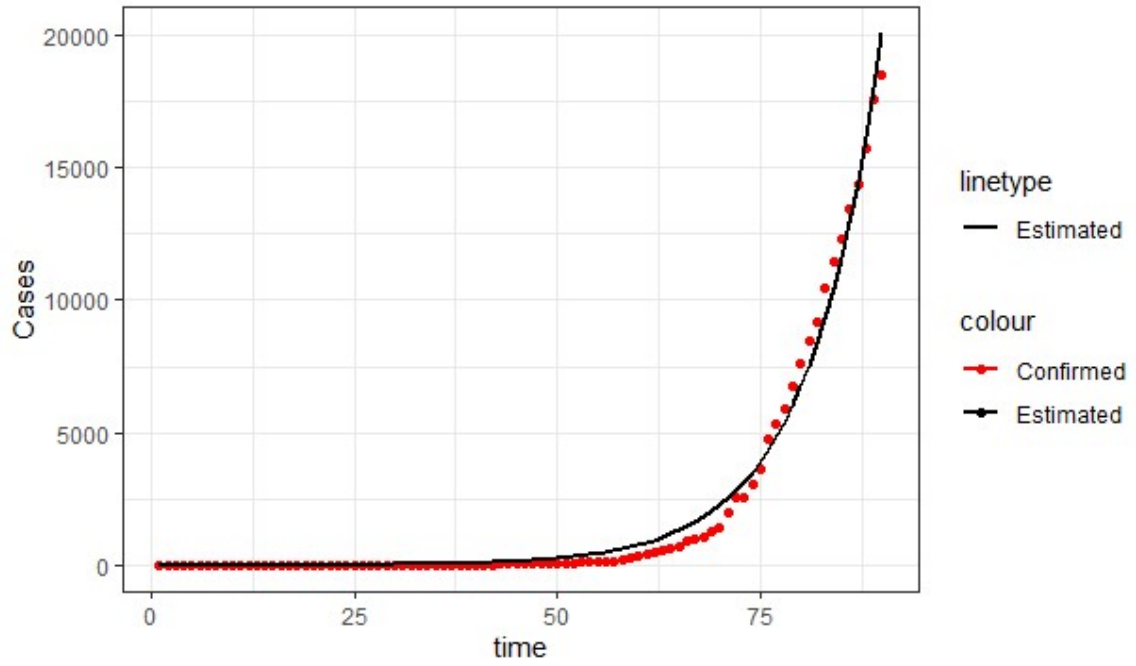


Figure 3.2: Plot of Confirmed and Estimated Cases (January 22, 2020 to April 20, 2020)

If we consider the data from the date 22-01-2020 to 20-05-2020 with clinical parameters $\sigma = \frac{1}{4}$ and $\gamma = \frac{1}{10}$. Here we have fixed $E_0 = 3$ and $I_0 = 0$

Table 3.2: Assumed and Calculated Parameters (January 22, 2020 to May 20, 2020)

Total Population	σ (Assumed)	γ (Assumed)	R_0 (Calculated)	α (Calculated)	$\beta = R_0\gamma$ (Calculated)	λ (Calculated)
1378159530	0.25	0.1	2.6920	0.0373527	0.26920	0.99

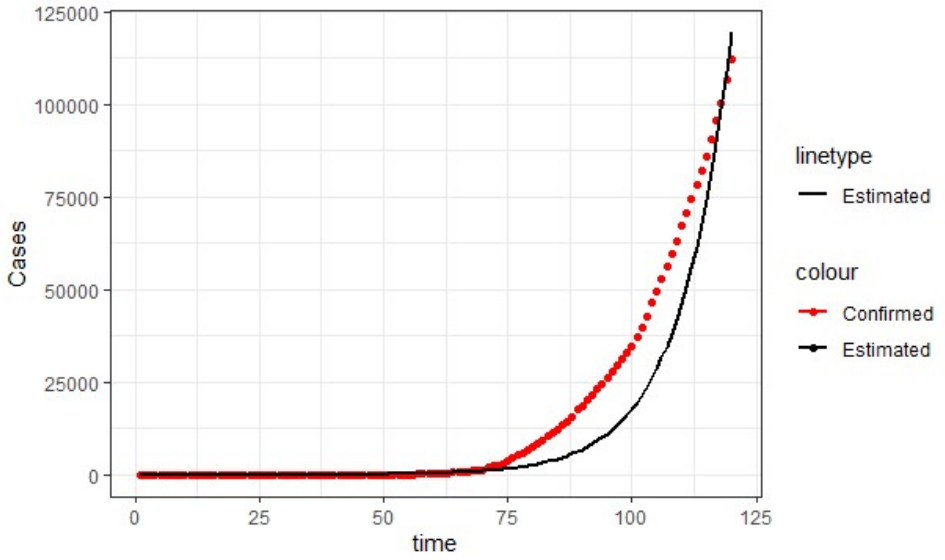


Figure 3.3: Plot of Confirmed and Estimated Cases (January 22, 2020 to May 20, 2020)

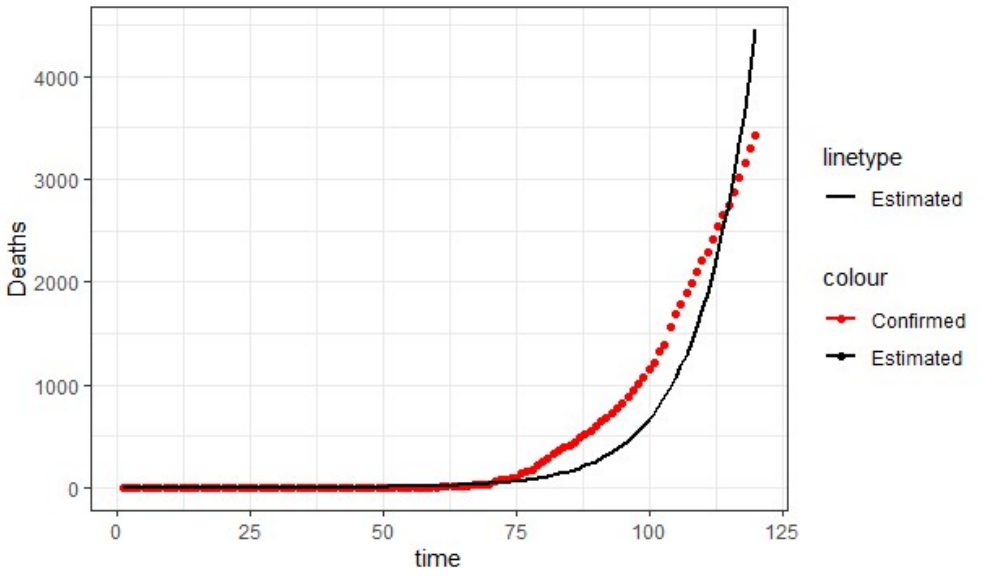


Figure 3.4: Plot of Confirmed and Estimated Deaths (January 22, 2020 to May 20, 2020)

If we keep on changing the value of the clinical parameters and the values of E_0 and I_0. We will get different results.

As we know, the data spread trend of COVID-19 is different for different time periods. We have observed that the SEIR model is considered as the most commonly used method for simulation of COVID-19 data. Individuals in exposed compartments in the SEIRD model are not capable of disease transmission, which is not consistent with COVID-19.

We evaluated the progression of COVID-19 under the assumption of a "one-time enforcement of containment measures" scenario, in which the lockdown and other social distancing norms are maintained for an unspecified amount of time. However, a more realistic reconstruction of the pandemic situation would be to impose an "intermittent lockdown" in specific regions. In this scenario, the containment and other social distancing measures are enforced once the number of active infections reaches a threshold that is determined by the capacity of the regional healthcare system. In this scenario, the containment and other social distancing measures are enforced once the number of active infections reaches a threshold that is determined by the capacity of the regional healthcare system. The measures that were put into place during the lockdown were eventually eased or lifted as the number of active infections dropped below a certain threshold. This was referred to as "unlocking" the lockdown. This cycling between the phases of "lockdown" and "unlock" continues until either the contagion is completely brought under "control" or the possibility of an infection spreading "out of bound" is no longer a concern. The manner in which intermittent intervention is carried out is determined by a variety of controlling factors, including the acquisition of "herd immunity," the availability of appropriate vaccines, the capacity of public health facilities at which all patients can be accommodated and treated, and other such factors. We have found that the number of cases without symptoms is significantly higher than the number of cases with symptoms in the parameter regime that is currently being investigated for this model. In point of fact, individuals who were exhibiting symptoms were given priority when it came to undergoing tests, despite the fact that the number of tests has been significantly increased. This made it impossible to identify a significant portion of the asymptomatic population in a country like India, which has a massive population. For this reason, in order to determine the exact ratio of symptomatic to asymptomatic populations, we require extensive data curation across

the country as well as additional research in this area. The infectiousness of a person who is asymptomatic may be comparable to that of a person who is experiencing symptoms. Because the asymptomatically infectious population freely interacts with the healthy susceptible population, the infection continues to spread throughout the population, resulting in an increase in the number of symptomatic as well as asymptomatic cases. It was essential to identify the origin of the infection and then cut it off from the population of healthy people who were susceptible to it if the infection is to be contained. The only data that was available to validate our prediction of the asymptomatically infected population were those that are scant and sparse. India performs a serology-based (antibody test) survey in selected districts in order to determine the extent of the disease's spread throughout communities and the frequency of asymptomatic cases. The purpose of the test is to determine whether or not the infected individual possesses a particular antibody that was produced by their immune system in response to the viral infection. Regardless of the testing policy, it is essential to keep a social distance between affected areas while also implementing measures of containment, either continuously or intermittently. In addition to this, it was essential for all members of the population to cover their faces with cloth or wear masks. To summarise, a "indefinite lockdown" is not a viable option for putting an end to the spread of the COVID-19 virus. The imposition of a lockdown in India served the larger purpose of providing the opportunity to buy 'time.' In a nutshell, the lockdown slows down the infection, and the time window provided by the lockdown gives us the opportunity to ramp up the healthcare facilities, testing capacity, and other aspects of preparedness so that the COVID-19 does not catch us by surprise when the lockdown is lifted. The effect of lockdown was felt even during the gradual "unlock" phases if social distance, sanitation protocols, and proper mask wearing in public places are adopted by every individual as the "new normal" of lifestyle.

Chapter-4

Prediction of Covid-19 Infected Cases in India Using Time Series Model

4.1 Introduction

Coronavirus was detected as a new type of virus and the disease COVID-19 is spreading quickly in humans from humans. It was declared as a most prevalent epidemic that may raise a horrific tragedy. Research shows that this virus is a member of zoonotic coronaviruses family and type of severe acute respiratory syndrome coronavirus hence it was known by SARS-CoV. The origin of this virus was from a Chinese city named Wuhan, and the first loss of life was reported in late 2019. The coronavirus disease has affected more than 200 countries. There were several adverse effects due to SARS-CoV particularly on old people and persons with chronic illness. COVID-19 had a very red-blooded structure and growing rapidly. Discouragingly, as of May 22, 2021, approximately 26530132 cases were confirmed in India. The virus has expanded its radius all over India as of today. Due to absence of proper method of treatment of this virus, the fruitful planning of the health sector was essential to minimize the damage done by this disease. In such grave circumstances, for the effective planning, the estimation of the cases and deaths were necessary, so that management of our health care system can be done properly. The statistical and mathematical modelling tools was used for making long-term or short-term estimation to plan the resources and supply of material to handle this pandemic. Expected load estimation is necessary for officials in health department to control the damage and resource management. The Automatic Regressive Integrated Moving Average

(ARIMA) model has a simple structure and due to its capacity to explain any time series data set and fast applicability, it has been applied in the different fields, as well as in health sector. In the previous years, Automatic Regressive Integrated Moving Average (ARIMA) model was fruitful in the estimation of various infectious diseases like influenza and malaria. We used this data to observe a prediction model by applying heterogeneous ARIMA models. This model may be helpful to predict the health care system needs that may be helpful for patients in India.

The aim of this chapter is to provide estimation of the covid-19 in India. The data examined in this chapter was firstly taken of the period from 22 January 2020 to 15 June 2020 and after that the period from 22 January 2020 to 22 May 2021. The data was used to examine a case estimation model by applying different ARIMA models. These models may be helpful to estimate the needs of health care system that patients will need in India soon.

4.2 ARIMA Model

The ARIMA is the abbreviation for a model in which AR means *autoregressive model* and MA means *moving average model* and I means *integrated.* The procedure of ARIMA [89-93] modelling is basically controlled by four steps: model assessment, parameter estimation, diagnostics, and forecasting. The first step of this time series model is to check whether the dataset of time series is seasonal and stationary. A time series is called stationary if the properties of statistical nature are constant. The stationarity of dataset is important observation to get accurate forecasts. The unit root test is used to check the stationarity of time series data, If the series is not stationary then differences are used to make the data stationary. The estimation of ARIMA model parameters can done by graph of autocorrelation function (ACF) and partial autocorrelation (PACF) correlogram. The graph of auto correlation function determines the relation of previous and following values in the time series. The graph of partial auto correlation function calculates the correlation degree between lag and variable. Using maximum likelihood estimation (MLE), we can estimate the best ARIMA model. Once the best model is selected for the time series data set, then by using those

parameters, ARIMA model can be taken as a forecasting model for making predictions for future values.

4.2.1 Auto Correlation Function (ACF): The autocorrelation function (ACF) is the plot that is used to see the correlation between the points, up to and including the lag unit. The autocorrelation of a time series is the degree to which it is correlated with its previous values. When displaying an ACF, the correlation coefficient is plotted along the x-axis, and the number of lags is displayed along the y-axis. The plot of the autocorrelation function informs us of the nature of the correlation between the given time series and itself.

4.2.2 Partial Auto Correlation Function (PACF): A summary of the relationship between an observation in a time series and observations at prior time steps is called a partial autocorrelation. This means that the relationships between the observations that occurred in the intervening time steps have been removed. After removing the effect of any correlations that may have been caused by the terms at shorter lags, the correlation that remains is referred to as the partial autocorrelation at lag *k*.

4.3 Prediction of Covid-19 Cases from June 16, 2020, to July 10, 2020

4.3.1 Data Collection (January 22, 2020, to June 15, 2020): In this estimation, we have applied the model to the data of confirmed cases and deaths due to COVID-19. The data, we were using is collected on June 16, 2020, from the website of Johns Hopkins University. The observations are collected from January 22, 2020, to June 15, 2020.

Table 4.1: Data of Confirmed Cases

Date	Cases	Date	Cases	Date	Cases
22-01-2020	0	11-03-2020	62	29-04-2020	33062
23-01-2020	0	12-03-2020	73	30-04-2020	34863
24-01-2020	0	13-03-2020	82	01-05-2020	37257
25-01-2020	0	14-03-2020	102	02-05-2020	39699
26-01-2020	0	15-03-2020	113	03-05-2020	42505

27-01-2020	0	16-03-2020	119	04-05-2020	46437
28-01-2020	0	17-03-2020	142	05-05-2020	49400
29-01-2020	0	18-03-2020	156	06-05-2020	52987
30-01-2020	1	19-03-2020	194	07-05-2020	56351
31-01-2020	1	20-03-2020	244	08-05-2020	59695
01-02-2020	1	21-03-2020	330	09-05-2020	62808
02-02-2020	2	22-03-2020	396	10-05-2020	67161
03-02-2020	3	23-03-2020	499	11-05-2020	70768
04-02-2020	3	24-03-2020	536	12-05-2020	74292
05-02-2020	3	25-03-2020	657	13-05-2020	78055
06-02-2020	3	26-03-2020	727	14-05-2020	81997
07-02-2020	3	27-03-2020	887	15-05-2020	85784
08-02-2020	3	28-03-2020	987	16-05-2020	90648
09-02-2020	3	29-03-2020	1024	17-05-2020	95698
10-02-2020	3	30-03-2020	1251	18-05-2020	100328
11-02-2020	3	31-03-2020	1397	19-05-2020	106475
12-02-2020	3	01-04-2020	1998	20-05-2020	112028
13-02-2020	3	02-04-2020	2543	21-05-2020	118226
14-02-2020	3	03-04-2020	2567	22-05-2020	124794
15-02-2020	3	04-04-2020	3082	23-05-2020	131423
16-02-2020	3	05-04-2020	3588	24-05-2020	138536
17-02-2020	3	06-04-2020	4778	25-05-2020	144950
18-02-2020	3	07-04-2020	5311	26-05-2020	150793
19-02-2020	3	08-04-2020	5916	27-05-2020	158086
20-02-2020	3	09-04-2020	6725	28-05-2020	165386
21-02-2020	3	10-04-2020	7598	29-05-2020	173491
22-02-2020	3	11-04-2020	8446	30-05-2020	181827
23-02-2020	3	12-04-2020	9205	31-05-2020	190609

24-02-2020	3	13-04-2020	10453	01-06-2020	198370
25-02-2020	3	14-04-2020	11487	02-06-2020	207191
26-02-2020	3	15-04-2020	12322	03-06-2020	216824
27-02-2020	3	16-04-2020	13430	04-06-2020	226713
28-02-2020	3	17-04-2020	14352	05-06-2020	236184
29-02-2020	3	18-04-2020	15722	06-06-2020	246622
01-03-2020	3	19-04-2020	17615	07-06-2020	257486
02-03-2020	5	20-04-2020	18539	08-06-2020	265928
03-03-2020	5	21-04-2020	20080	09-06-2020	276146
04-03-2020	28	22-04-2020	21370	10-06-2020	286605
05-03-2020	30	23-04-2020	23077	11-06-2020	297535
06-03-2020	31	24-04-2020	24530	12-06-2020	308993
07-03-2020	34	25-04-2020	26283	13-06-2020	320922
08-03-2020	39	26-04-2020	27890	14-06-2020	332424
09-03-2020	43	27-04-2020	29451	15-06-2020	343091
10-03-2020	56	28-04-2020	31324		

4.3.2 Discussion and Results: Fruitful strategies were required to control and prevent the spread of the outbreak. Forecasting the epidemiological trend was needed for the deployment of the medical staff and resources as well as for the economic growth of the country. Thus, it was a necessity of the hour to create a well-grounded model for forecasting, which may be helpful for the government in deciding strategies for the country. Time series analysis is significant in making hypotheses for understanding the trend of disease and forecasting the phenomena. The ARIMA model was one of the most popular forecasting methods for time series data due to its structure, simplicity, and acceptable performance in forecasting. The first step was to convert the collected univariate data set into time series data by running R code and observing the graph of the cumulative data of COVID-19 confirmed cases.

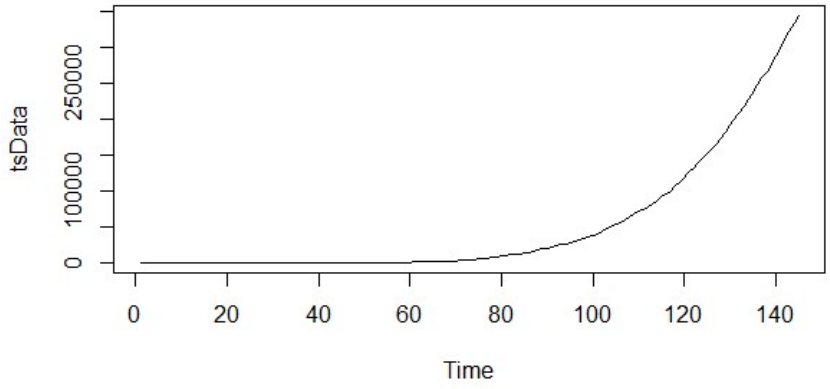


Figure 4.1: Cumulative Confirmed Cases of Covid-19 in India

Now we did some data analysis to find the seasonality and non-stationary in our data set. We used autocorrelation analysis to check the dependence, i.e., we examined the correlation between past and current value to get the value of *p, d,* and *q*. We used unit root test with the help of R code to examine what should be used to make data stationary.

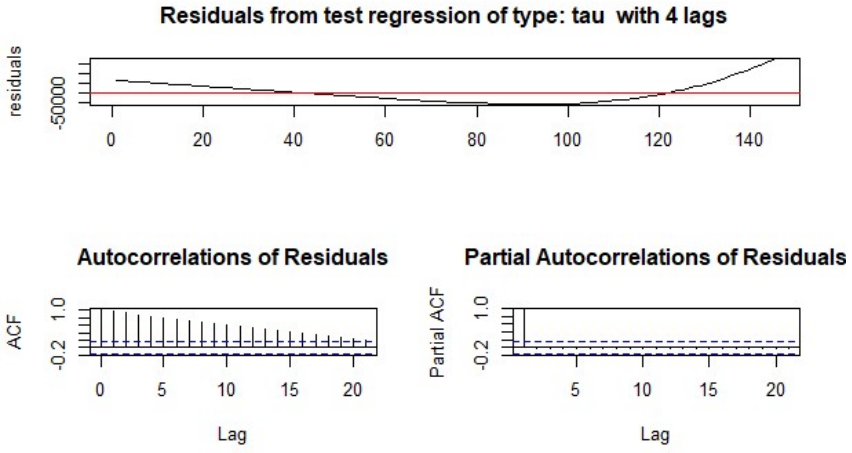


Figure 4.2: Residual from Test Regression

Since the time series data was not stationary at initial level, after applying differencing, we have obtained the plot of stationary data:

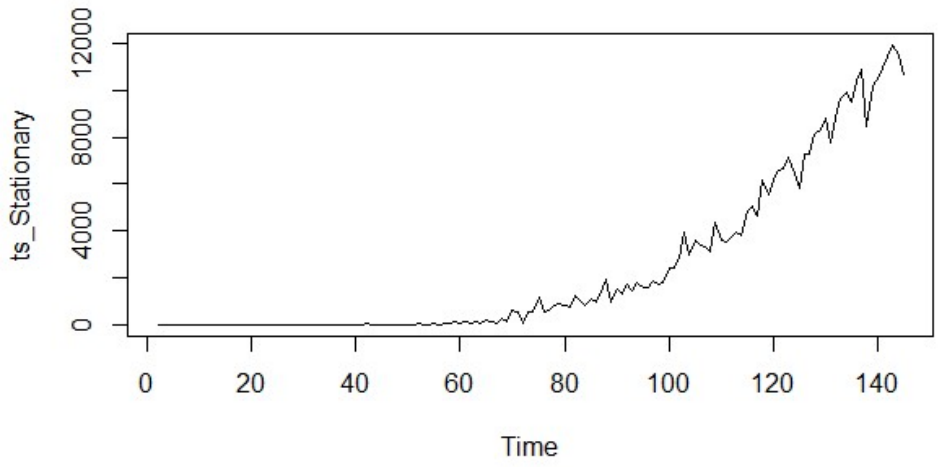


Figure 4.3: Stationary Data Plot

Now, since the data is ready, and all assumptions are satisfied for the modelling. For the values of p and q in ARIMA(*p,d,q*), we run the functions *acf()* and *pacf()* in R. These three variables are all positive integers that describe the model's autoregressive order, integrated order, and moving average order. The maximum likelihood (ML) method was used to estimate the model. A Box-Ljung test was performed to test the overall randomness based on the number of lags. It was applied to the residuals of the fitted model instead of the original series.

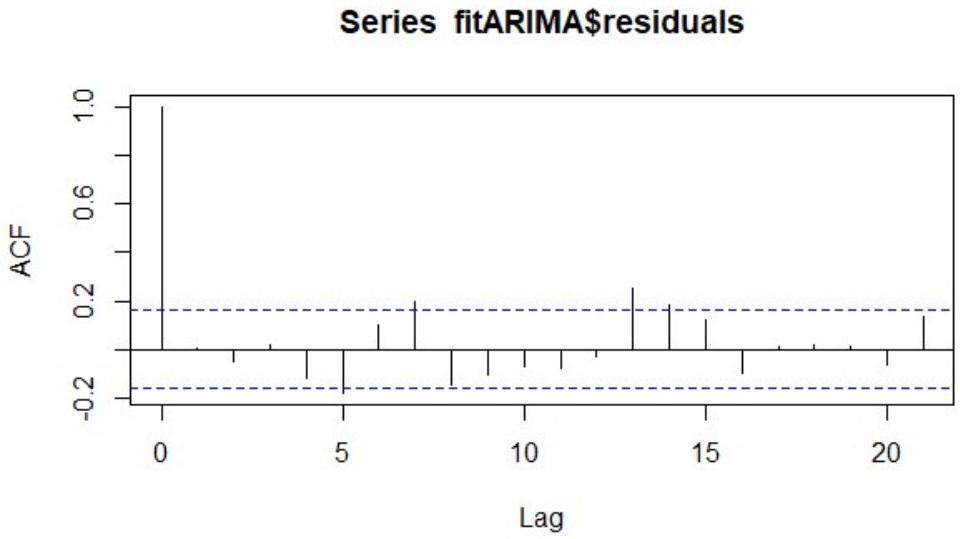


Figure 4.4: Series Residual

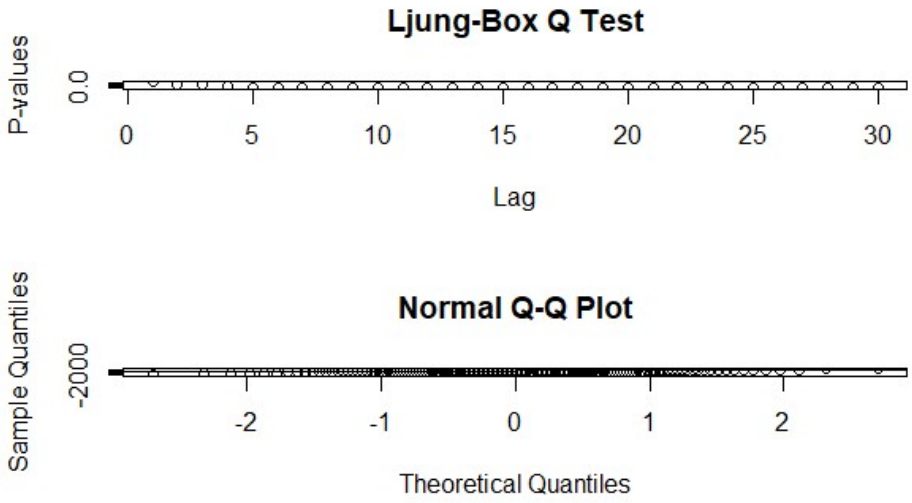


Figure 4.5: Ljung-Box Q Test and Normal Q-Q Plot

Several ARIMA models like ARIMA (2,2,2), ARIMA (0,2,0), ARIMA (1,2,0), ARIMA (0,2,1), ARIMA (1,2,1), ARIMA (0,2,2), ARIMA (1,2,2), ARIMA (0,2,3), ARIMA (1,2,3) were selected for test and ARIMA (0,2,2) was selected as the best ARIMA model. R code was used to perform to the analysis. Level of statistical

significance was set to 5%. Then using the parameters of the best model, prediction values and graph of confirmed cases of COVID-19 in India was obtained as in table below:

Table 4.2: Prediction Values of Covid-19 Cases

Date	Lower	Mean	Upper
16-06-2020	353657	354795.9	355935
17-06-2020	364783	366692.7	368603
18-06-2020	376043	378780.5	381518
19-06-2020	387404	391058.5	394714
20-06-2020	398850	403525.9	408202
21-06-2020	410375	416181.9	421989
22-06-2020	421973	429025.6	436078
23-06-2020	433639	442056.3	450474
24-06-2020	445369	455273	465178
25-06-2020	457158	468675.2	480192
26-06-2020	469005	482261.8	495519
27-06-2020	480904	496032.1	511160
28-06-2020	492853	509985.4	527118
29-06-2020	504849	524120.9	543393
30-06-2020	516888	538437.7	559987
01-07-2020	528968	552935.1	576902
02-07-2020	541085	567612.2	594140
03-07-2020	553236	582468.4	611701
04-07-2020	565419	597502.8	629587
05-07-2020	577631	612714.8	647799
06-07-2020	589869	628103.4	666338
07-07-2020	602130	643667.9	685206
08-07-2020	614412	659407.7	704404
09-07-2020	626711	675321.8	723932
10-07-2020	639027	691409.7	743793

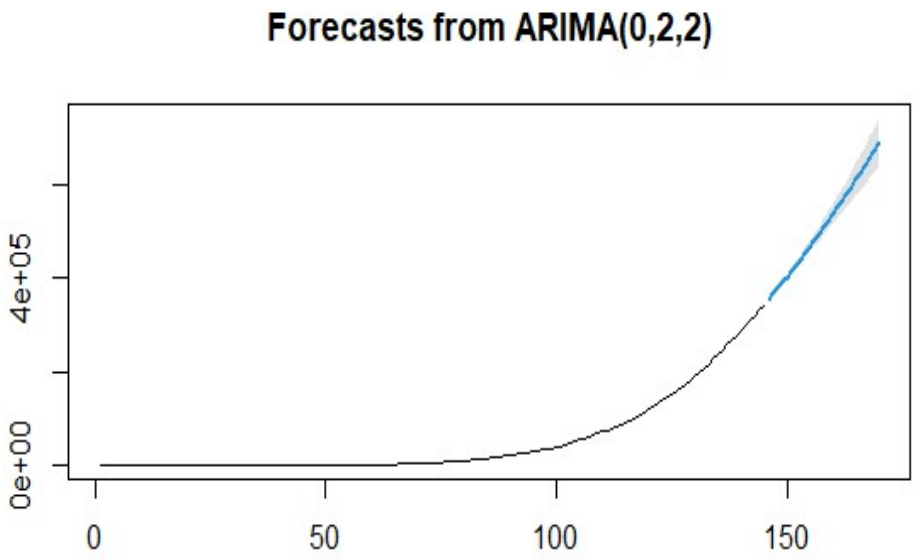


Figure 4.6: Forecast from ARIMA (0,2,2)

In the above study, the situation of the epidemic outbreak on June 16, 2020 in India was discussed, and future trends are estimated by the Automatic Regressive Integrated Moving Average model. This was a great problem for the Indian health care system to arrange intensive care units for the neediest patients. If they had any idea about the future cases, it could be a great help. The number of confirmed cases in India was growing by the day. The country needed an improved health care system to avoid unmanageable damage.

4.4 Prediction of Covid-19 Cases from May 23, 2021, to June 16, 2021

4.4.1 Data Collection (January 22, 2020, to May 22, 2021): In this part, we employed the model on the data set of COVID-19 confirmed cases. The data, we used, was collected from the Johns Hopkins University's website. The observations were collected from January 22, 2020, to May 22, 2021.

Table 4.3: Data of Confirmed Cases

Date	**Confirmed Cases**	**Date**	**Confirmed Cases**	**Date**	**Confirmed Cases**
22-01-2020	0	03-07-2020	648315	12-12-2020	9857029
23-01-2020	0	04-07-2020	673165	13-12-2020	9884100
24-01-2020	0	05-07-2020	697413	14-12-2020	9906165
25-01-2020	0	06-07-2020	719664	15-12-2020	9932547
26-01-2020	0	07-07-2020	742417	16-12-2020	9956557
27-01-2020	0	08-07-2020	767296	17-12-2020	9979447
28-01-2020	0	09-07-2020	793802	18-12-2020	10004599
29-01-2020	0	10-07-2020	820916	19-12-2020	10031223
30-01-2020	1	11-07-2020	849522	20-12-2020	10055560
31-01-2020	1	12-07-2020	878254	21-12-2020	10075116
01-02-2020	1	13-07-2020	906752	22-12-2020	10099066
02-02-2020	2	14-07-2020	936181	23-12-2020	10123778
03-02-2020	3	15-07-2020	968857	24-12-2020	10146845

04-02-2020	3	16-07-2020	1003832	25-12-2020	10169118
05-02-2020	3	17-07-2020	1039084	26-12-2020	10187850
06-02-2020	3	18-07-2020	1077781	27-12-2020	10207871
07-02-2020	3	19-07-2020	1118206	28-12-2020	10224303
08-02-2020	3	20-07-2020	1155338	29-12-2020	10244852
09-02-2020	3	21-07-2020	1193078	30-12-2020	10266674
10-02-2020	3	22-07-2020	1238798	31-12-2020	10266674
11-02-2020	3	23-07-2020	1288108	01-01-2021	10286709
12-02-2020	3	24-07-2020	1337024	02-01-2021	10323965
13-02-2020	3	25-07-2020	1385635	03-01-2021	10340469
14-02-2020	3	26-07-2020	1435616	04-01-2021	10356844
15-02-2020	3	27-07-2020	1480073	05-01-2021	10374932
16-02-2020	3	28-07-2020	1531669	06-01-2021	10395278
17-02-2020	3	29-07-2020	1581963	07-01-2021	10413417
18-02-2020	3	30-07-2020	1634746	08-01-2021	10413417

19-02-2020	3	31-07-2020	1695988	09-01-2021	10450284
20-02-2020	3	01-08-2020	1750723	10-01-2021	10466595
21-02-2020	3	02-08-2020	1803695	11-01-2021	10479179
22-02-2020	3	03-08-2020	1855745	12-01-2021	10495147
23-02-2020	3	04-08-2020	1908254	13-01-2021	10512093
24-02-2020	3	05-08-2020	1964536	14-01-2021	10527683
25-02-2020	3	06-08-2020	2027074	15-01-2021	10542841
26-02-2020	3	07-08-2020	2088611	16-01-2021	10557985
27-02-2020	3	08-08-2020	2153010	17-01-2021	10571773
28-02-2020	3	09-08-2020	2215074	18-01-2021	10581823
29-02-2020	3	10-08-2020	2268675	19-01-2021	10595639
01-03-2020	3	11-08-2020	2329638	20-01-2021	10610883
02-03-2020	5	12-08-2020	2396637	21-01-2021	10625428
03-03-2020	5	13-08-2020	2461190	22-01-2021	10639684
04-03-2020	28	14-08-2020	2525922	23-01-2021	10654533

05-03-2020	30	15-08-2020	2589952	24-01-2021	10667736
06-03-2020	31	16-08-2020	2647663	25-01-2021	10676838
07-03-2020	34	17-08-2020	2702681	26-01-2021	10689527
08-03-2020	39	18-08-2020	2767253	27-01-2021	10701193
09-03-2020	43	19-08-2020	2836925	28-01-2021	10720048
10-03-2020	56	20-08-2020	2905825	29-01-2021	10733130
11-03-2020	62	21-08-2020	2975701	30-01-2021	10746174
12-03-2020	73	22-08-2020	3044940	31-01-2021	10757610
13-03-2020	82	23-08-2020	3106348	01-02-2021	10766245
14-03-2020	102	24-08-2020	3167323	02-02-2021	10777284
15-03-2020	113	25-08-2020	3224547	03-02-2021	10790183
16-03-2020	119	26-08-2020	3310234	04-02-2021	10802591
17-03-2020	142	27-08-2020	3387500	05-02-2021	10814304
18-03-2020	156	28-08-2020	3463972	06-02-2021	10826363
19-03-2020	194	29-08-2020	3542733	07-02-2021	10838194

20-03-2020	244	30-08-2020	3621245	08-02-2021	10847304
21-03-2020	330	31-08-2020	3691166	09-02-2021	10858371
22-03-2020	396	01-09-2020	3769523	10-02-2021	10871294
23-03-2020	499	02-09-2020	3853406	11-02-2021	10880603
24-03-2020	536	03-09-2020	3936747	12-02-2021	10892746
25-03-2020	657	04-09-2020	4023179	13-02-2021	10904940
26-03-2020	727	05-09-2020	4113811	14-02-2021	10916589
27-03-2020	887	06-09-2020	4204613	15-02-2021	10925710
28-03-2020	987	07-09-2020	4280422	16-02-2021	10937320
29-03-2020	1024	08-09-2020	4370128	17-02-2021	10950201
30-03-2020	1251	09-09-2020	4465863	18-02-2021	10963394
31-03-2020	1397	10-09-2020	4562414	19-02-2021	10977387
01-04-2020	1998	11-09-2020	4659984	20-02-2021	10991651
02-04-2020	2543	12-09-2020	4754356	21-02-2021	11005850
03-04-2020	2567	13-09-2020	4846427	22-02-2021	11016434

04-04-2020	3082	14-09-2020	4930236	23-02-2021	11030176
05-04-2020	3588	15-09-2020	5020359	24-02-2021	11046914
06-04-2020	4778	16-09-2020	5118253	25-02-2021	11063491
07-04-2020	5311	17-09-2020	5214677	26-02-2021	11079979
08-04-2020	5916	18-09-2020	5308014	27-02-2021	11096731
09-04-2020	6725	19-09-2020	5400619	28-02-2021	11112241
10-04-2020	7598	20-09-2020	5487580	01-03-2021	11124527
11-04-2020	8446	21-09-2020	5562663	02-03-2021	11139516
12-04-2020	9205	22-09-2020	5646010	03-03-2021	11156923
13-04-2020	10453	23-09-2020	5732518	04-03-2021	11173761
14-04-2020	11487	24-09-2020	5818570	05-03-2021	11192045
15-04-2020	12322	25-09-2020	5903932	06-03-2021	11210799
16-04-2020	13430	26-09-2020	5992532	07-03-2021	11229398
17-04-2020	14352	27-09-2020	6074702	08-03-2021	11244786
18-04-2020	15722	28-09-2020	6145291	09-03-2021	11262707

19-04-2020	17615	29-09-2020	6225763	10-03-2021	11285561
20-04-2020	18539	30-09-2020	6312584	11-03-2021	11308846
21-04-2020	20080	01-10-2020	6394068	12-03-2021	11333728
22-04-2020	21370	02-10-2020	6473544	13-03-2021	11359048
23-04-2020	23077	03-10-2020	6549373	14-03-2021	11385339
24-04-2020	24530	04-10-2020	6623815	15-03-2021	11409831
25-04-2020	26283	05-10-2020	6685082	16-03-2021	11438734
26-04-2020	27890	06-10-2020	6757131	17-03-2021	11474605
27-04-2020	29451	07-10-2020	6835655	18-03-2021	11514331
28-04-2020	31324	08-10-2020	6906151	19-03-2021	11555284
29-04-2020	33062	09-10-2020	6979423	20-03-2021	11599130
30-04-2020	34863	10-10-2020	7053806	21-03-2021	11646081
01-05-2020	37257	11-10-2020	7120538	22-03-2021	11686796
02-05-2020	39699	12-10-2020	7175880	23-03-2021	11734058
03-05-2020	42505	13-10-2020	7239389	24-03-2021	11787534

04-05-2020	46437	14-10-2020	7307097	25-03-2021	11846652
05-05-2020	49400	15-10-2020	7370468	26-03-2021	11908910
06-05-2020	52987	16-10-2020	7432680	27-03-2021	11971624
07-05-2020	56351	17-10-2020	7494551	28-03-2021	12039644
08-05-2020	59695	18-10-2020	7550273	29-03-2021	12095855
09-05-2020	62808	19-10-2020	7597063	30-03-2021	12149335
10-05-2020	67161	20-10-2020	7651107	31-03-2021	12221665
11-05-2020	70768	21-10-2020	7706946	01-04-2021	12303131
12-05-2020	74292	22-10-2020	7761312	02-04-2021	12392260
13-05-2020	78055	23-10-2020	7814682	03-04-2021	12485509
14-05-2020	81997	24-10-2020	7864811	04-04-2021	12589067
15-05-2020	85784	25-10-2020	7909959	05-04-2021	12686049
16-05-2020	90648	26-10-2020	7946429	06-04-2021	12801785
17-05-2020	95698	27-10-2020	7990322	07-04-2021	12928574
18-05-2020	100328	28-10-2020	8040203	08-04-2021	13060542

19-05-2020	106475	29-10-2020	8088851	09-04-2021	13205926
20-05-2020	112028	30-10-2020	8137119	10-04-2021	13358805
21-05-2020	118226	31-10-2020	8184082	11-04-2021	13527717
22-05-2020	124794	01-11-2020	8229313	12-04-2021	13689453
23-05-2020	131423	02-11-2020	8267623	13-04-2021	13873825
24-05-2020	138536	03-11-2020	8313876	14-04-2021	14074564
25-05-2020	144950	04-11-2020	8364086	15-04-2021	14291917
26-05-2020	150793	05-11-2020	8411724	16-04-2021	14526609
27-05-2020	158086	06-11-2020	8462080	17-04-2021	14788003
28-05-2020	165386	07-11-2020	8507754	18-04-2021	15061805
29-05-2020	173491	08-11-2020	8553657	19-04-2021	15320972
30-05-2020	181827	09-11-2020	8591730	20-04-2021	15616130
31-05-2020	190609	10-11-2020	8636011	21-04-2021	15930774
01-06-2020	198370	11-11-2020	8683916	22-04-2021	16263695
02-06-2020	207191	12-11-2020	8728795	23-04-2021	16610481

03-06-2020	216824	13-11-2020	8773479	24-04-2021	16960172
04-06-2020	226713	14-11-2020	8814579	25-04-2021	17313163
05-06-2020	236184	15-11-2020	8845127	26-04-2021	17636186
06-06-2020	246622	16-11-2020	8874290	27-04-2021	17997113
07-06-2020	257486	17-11-2020	8912907	28-04-2021	18376421
08-06-2020	265928	18-11-2020	8958483	29-04-2021	18762976
09-06-2020	276146	19-11-2020	9004365	30-04-2021	19164969
10-06-2020	286605	20-11-2020	9050597	01-05-2021	19557457
11-06-2020	297535	21-11-2020	9095806	02-05-2021	19925517
12-06-2020	308993	22-11-2020	9139865	03-05-2021	20282833
13-06-2020	320922	23-11-2020	9177840	04-05-2021	20664979
14-06-2020	332424	24-11-2020	9222216	05-05-2021	21077410
15-06-2020	343091	25-11-2020	9266705	06-05-2021	21491598
16-06-2020	354065	26-11-2020	9309787	07-05-2021	21892676
17-06-2020	366946	27-11-2020	9351109	08-05-2021	22296081

18-06-2020	380532	28-11-2020	9392919	09-05-2021	22662575
19-06-2020	395048	29-11-2020	9431691	10-05-2021	22992517
20-06-2020	410451	30-11-2020	9462809	11-05-2021	23340938
21-06-2020	425282	01-12-2020	9499413	12-05-2021	23703665
22-06-2020	440215	02-12-2020	9534964	13-05-2021	24046809
23-06-2020	456183	03-12-2020	9571559	14-05-2021	24372907
24-06-2020	473105	04-12-2020	9608211	15-05-2021	24684077
25-06-2020	490401	05-12-2020	9644222	16-05-2021	24965463
26-06-2020	508953	06-12-2020	9677203	17-05-2021	25228996
27-06-2020	528859	07-12-2020	9703770	18-05-2021	25496330
28-06-2020	548318	08-12-2020	9735850	19-05-2021	25772440
29-06-2020	566840	09-12-2020	9767371	20-05-2021	26031991
30-06-2020	585481	10-12-2020	9796744	21-05-2021	26289290
01-07-2020	604641	11-12-2020	9826775	22-05-2021	26530132
02-07-2020	625544				

4.4.2 Discussion and Results: High-yielding strategies were the requirement of time to control and prevent the spread of COVID-19. Estimating the trend of the epidemic was required to deploy the medical staff and available resources in view of the growth of the country in every aspect. Thus, it was the demand of the time to make a well-designed model for estimation, which would be productive for the government to make strategies for the country. Analysis using time series is significant to make hypotheses for awareness of the trend of COVID-19 and estimation of phenomena. The Automatic Regressive Integrated Moving Average model was one of the most prevalent estimating methods for data in time series because of its simplicity, structure, and sustainable performance in estimation. The initial step is to convert the data collected in the univariate time series dataset by running R code and noticing the cumulative data graph of confirmed cases.

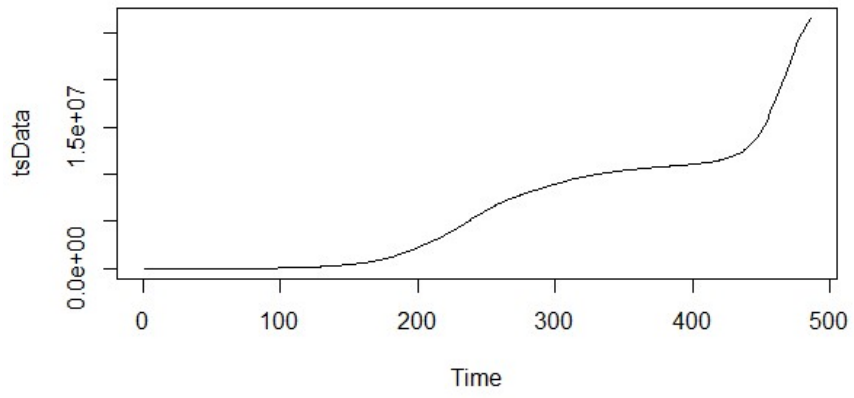


Figure 4.7: Cumulative Confirmed Cases of Covid-19 in India

Now we should perform some data analysis to figure out the seasonality and non-stationarity in time series data. Autocorrelation analysis was used to determine the dependence, i.e., the correlation between current and past values was examined to obtain the value of p, d, and q. Also, unit root test was used with the help of R code to conclude what to do to make data stationary.

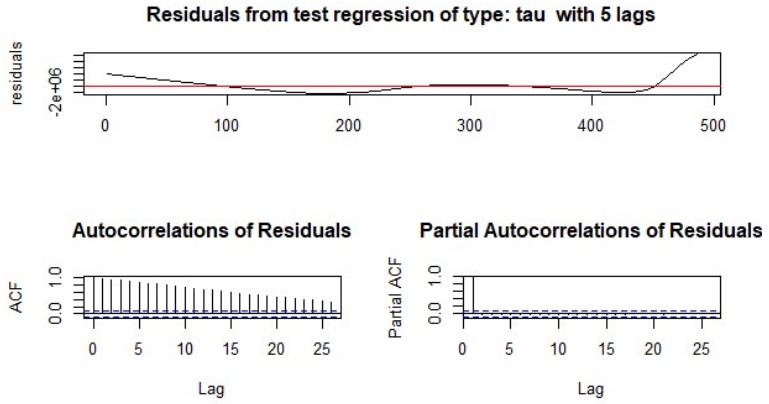


Figure 4.8: Residuals from regression

We applied differencing to data to make it stationary because at Initial level, time series data was not stationary. The plot obtained was of stationary data:

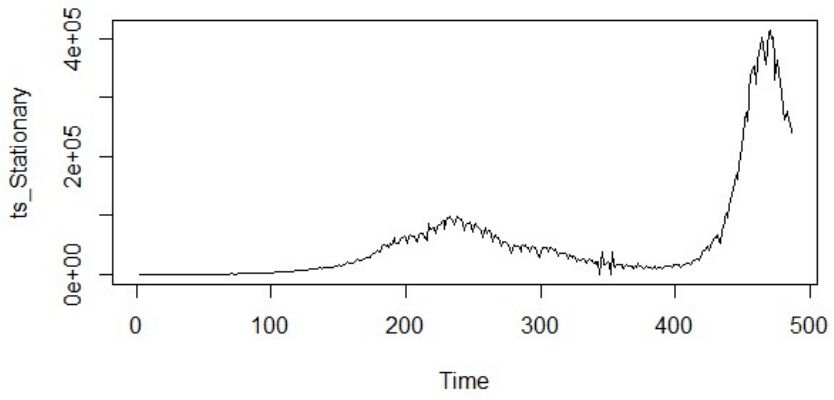


Figure 4.9: Stationary Data Plot

Now, since the data was well prepared and all presumptions were well satisfied for the modelling, We will run the predefined functions *acf()* and *pacf()* in R for the values of p and q in ARIMA(*p, d,q*). These three variables are referred to as the autoregressive order, integrated and moving average order of this model,

respectively, and are whole numbers. We have used the maximum likelihood (ML) method for the prediction of the model. We also used the Box-Ljung test for testing of overall randomness based on the number of lags. This test was not applied to the original series but to the residuals of the fitted model.

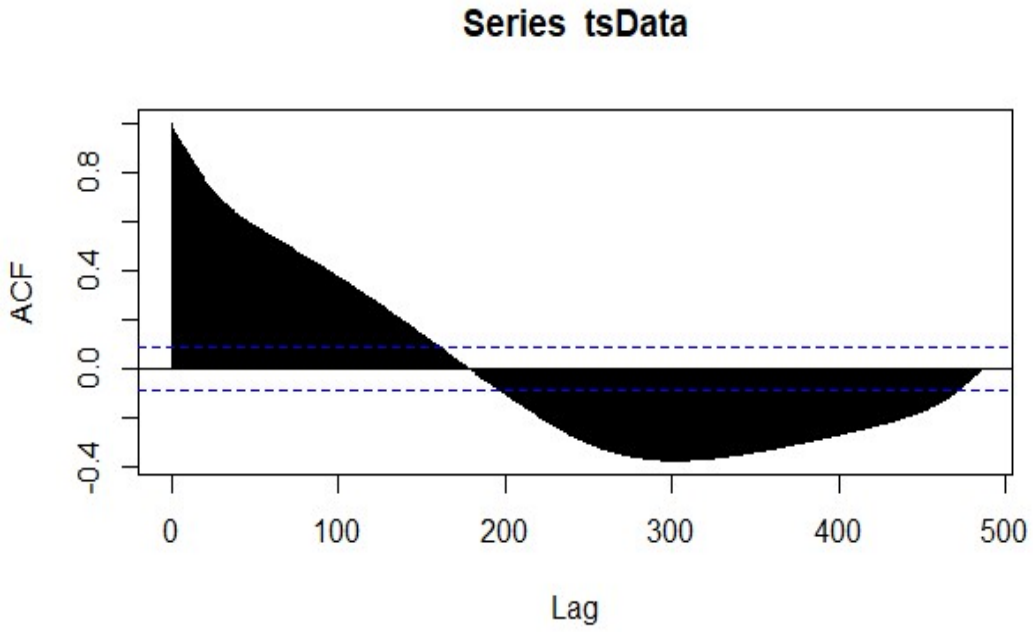


Figure 4.10: Time Series Data

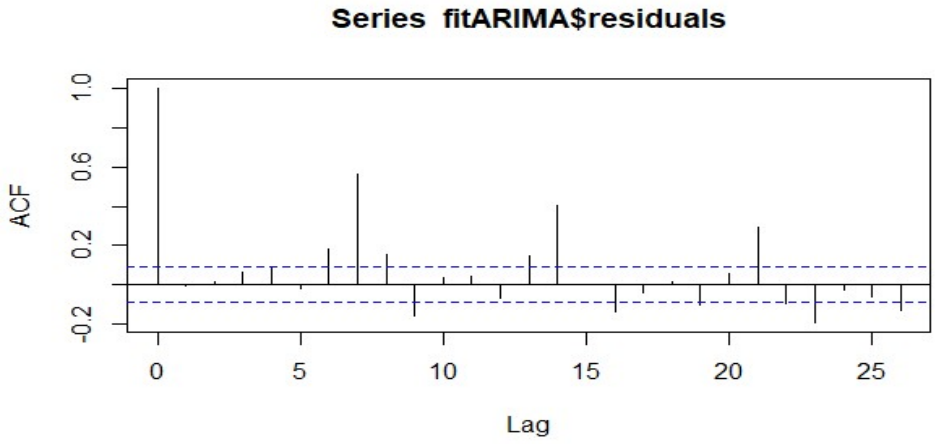


Figure 4.11: Time Series Residuals

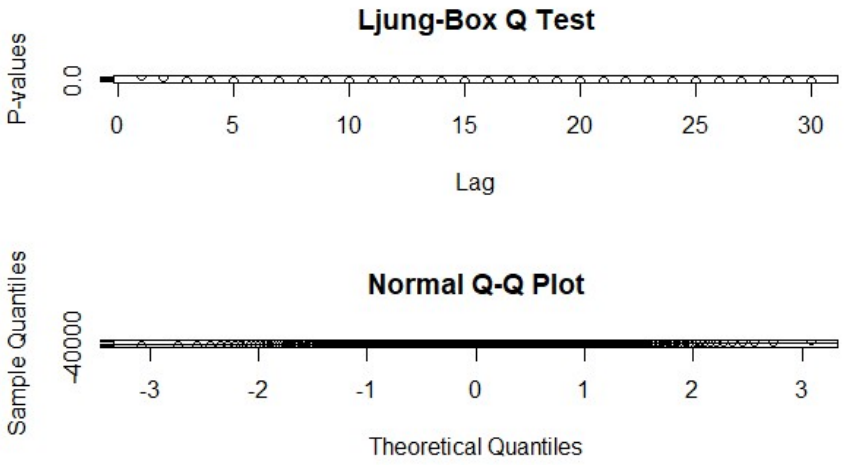


Figure 4.12: Ljung-Box Test and Normal Q-Q Plot

Several ARIMA models like ARIMA (2,2,2), ARIMA (0,2,0), ARIMA (1,2,0), ARIMA (0,2,1), ARIMA (1,2,2), ARIMA (2,2,1), ARIMA (3,2,2), ARIMA (2,2,3), ARIMA (1,2,3), ARIMA (3,2,3), ARIMA (2,2,4), ARIMA (1,2,4), ARIMA (3,2,4) were selected for test and ARIMA (0,2,2) was selected as the best model. We used R code to perform the above analysis. Level of statistical significance was set to 5%. By using the best model's parameter, estimation values and graphs for the COVID-19 cases was obtained for India as in the table below:

Table 4.4: Forecast Table for COVID-19 Cases

Date	Lower	Mean	Upper
23-05-2021	26746058	26766883	26787707
24-05-2021	26957364	27006525	27055686
25-05-2021	27161399	27243945	27326491
26-05-2021	27361266	27483073	27604879
27-05-2021	27555625	27720888	27886151
28-05-2021	27746514	27959712	28172909
29-05-2021	27932985	28197761	28462536
30-05-2021	28116321	28436405	28756489

31-05-2021	28295939	28674592	29053245
01-06-2021	28472648	28913130	29353612
02-06-2021	28646115	29151398	29656681
03-06-2021	28816856	29389874	29962892
04-06-2021	28984693	29628190	30271688
05-06-2021	29149962	29866629	30583297
06-06-2021	29312576	30104974	30897372
07-06-2021	29472760	30343391	31214022
08-06-2021	29630483	30581753	31533022
09-06-2021	29785898	30820157	31854415
10-06-2021	29939006	31058528	32178050
11-06-2021	30089915	31296925	32503935
12-06-2021	30238642	31535302	32831962
13-06-2021	30385267	31773694	33162121
14-06-2021	30529816	32012075	33494333
15-06-2021	30672350	32250464	33828578
16-06-2021	30812898	32488847	34164795

In this investigation, the current situation of the COVID-19 outbreak on May 22, 2021 in India was investigated, and future trends were predicted by the ARIMA model. The main problem for the healthcare system in India was to make arrangements for the intensive care units, ventilators, etc. for the needy patients. As the number of COVID-19 cases is increasing day by day, if the officials in the healthcare system have information about the approximation of future cases, it might be helpful for them. The Indian health care system must be improved to avoid a chaotic blow:

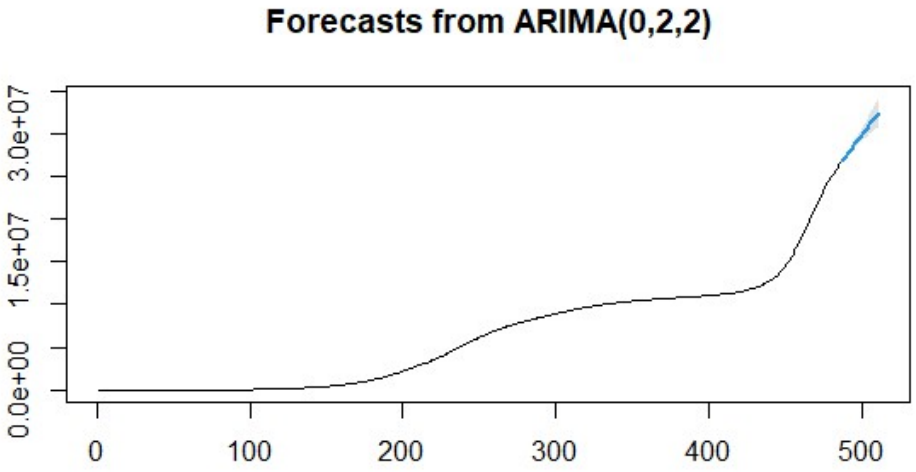


Figure 4.13: Ljung-Box Test and Normal Q-Q Plot

4.5 Conclusion

The estimation of epidemiological data was essential for health care departments in order to improve the distribution and monitoring of available resources. When it comes to the analysis of epidemics and the estimation of confirmed cases, models of time series play a significant role. In this chapter, we took the Indian data set and applied the ARIMA model to it. The authorities of health departments in India may benefit from these findings to formulate their policies regarding resource supply, management of staff, hospital beds, and extra care facilities in order to better handle the situation in India over the next few weeks. In order to ensure accurate results for the specific calculations in the future, one must regularly update the data in the R code.

Chapter-5

RPGT-Transmission Model to Control Covid-19 Epidemic

5.1 Introduction

COVID-19 first showed up in Wuhan, and because of its high transmission rate, the infection has been quickly spreading everywhere in the world. Coronaviruses are a huge group of zoonotic viruses, i.e., they are communicated from animals to people, and cause side effects ranging from the basic virus to more serious illnesses like Middle East Respiratory Syndrome, which is sent from dromedaries to people, and serious intense respiratory syndrome, which is sent from civets to people. A few known COVID-19 variants that have not yet contaminated people are flowing into certain creatures. The current episode has had seriously adverse health and financial outcomes across the globe, and it does not appear as though any nation will be unaffected. This affects not only the health and economy, but the entire society, causing emotional changes in how organisations and buyers act. Researchers from all fields have been keeping an eye on the spread of the virus. They have stepped up their efforts to speed up new diagnostics and are working on different antibodies to protect against COVID-19. Zeb et al. [94] investigated the mathematical model of COVID-19 with confinement class. Cao et al. [95] determined the clinical highlights of COVID-19 and contemplated the momentary aftereffects of 18 patients and 102 patients with COVID-19 in escalated care units. Zhu et al. [96] inspected that few local health facilities reported a group of patients with pneumonia for obscure reasons connected to the seafood and wholesale wet animal market in Wuhan, Hubei Province, China. The Place for Disease Control and Prevention dispatched a fast reaction group to help wellbeing experts in Hubei

Province and Wuhan City and lead an epidemiological investigation to find the wellspring of pneumonia groups. This prompted a portrayal of another Coronavirus found in examples of pneumonia patients toward the start of the pestilence. Ghostine et al. [97] examined the Extended SEIR Model with Vaccination for Forecasting the covid-19 Pandemic in Saudi Arabia using an Ensemble Kalman Filter. Sarkar et al. [98] talked about the numerical models which have been created to examine the transmission elements of covid-19. Nonetheless, these models experience the ill effects of different wellsprings of vulnerabilities, because of the fragmented depiction of the natural cycles overseeing the illness spread, and furthermore because of some elaborate boundaries being ineffectively known. One approach to relieve these vulnerabilities is to oblige plague estimating models with accessible information. Singh and Yadav [99] discussed Forecasting the size of covid-19 in India utilizing the ARIMA Model. Gumel et al. [100] examined the introduction on utilizing math to comprehend covid-19 dynamics: Modelling, examination, and recreations. Kumar et al. [101] dissected the washing unit in a paper factory utilizing RPGT. Kumar et al. [102] examined the bread-making system and considered the behaviour analysis. Singh and Yadav [103] studied the SEIRD model for covid-19. In this chapter, parameters were observed to make forecasts about deaths and the number of cases. Kumar et al. [104] contemplated the benefit of an edible oil refinery plant. Singh and Yadav [105] discussed the Polynomials Approximation Model for the estimation of the number of infected peoples in India

Using Regenerative Point Graphical technique (RPGT) Transition Diagram of the system, expressions for Transition Probability and Mean Sojourn Times, Path Probabilities, Mean time to Epidemic affected (T_0), Average Healthy Time (A_0), and Recovery Period (B_0) were derived followed by illustrations. Tables and graphs are drawn followed by analysis.

5.2 Notations

- E: F: G: H :: Sanitization: Wearing Mask: Social Distancing: Quarantine State.
- e, f, g, h :: denotes corresponding failure in observing precautions respectively.
- H_1, H_2 :: Signify home isolation, Lockdown including micro lockdown which are standby to Quarantine State (H)

- n_i /m_i (i=1, 2, 3, 4):: recovery/causing pandemic mean rates due to non-wearing mask, not keeping social distance, non-observing sanitization, non-observing Quarantine properly.

f_j: Fuzziness measure of the j-state.

5.3 Assumptions

- Affected and recovery rates are exponentially distributed and are independent.
- On recovery, an affected person is as healthy as not affected due to COVID-19.
- The rates of recovery and being affected are independently distributed.
- When a person is tested for COVID-19 positivity, no further covid-19 affection is possible.
- A study is carried out for a steady state.

5.4 State Transitions Diagrams

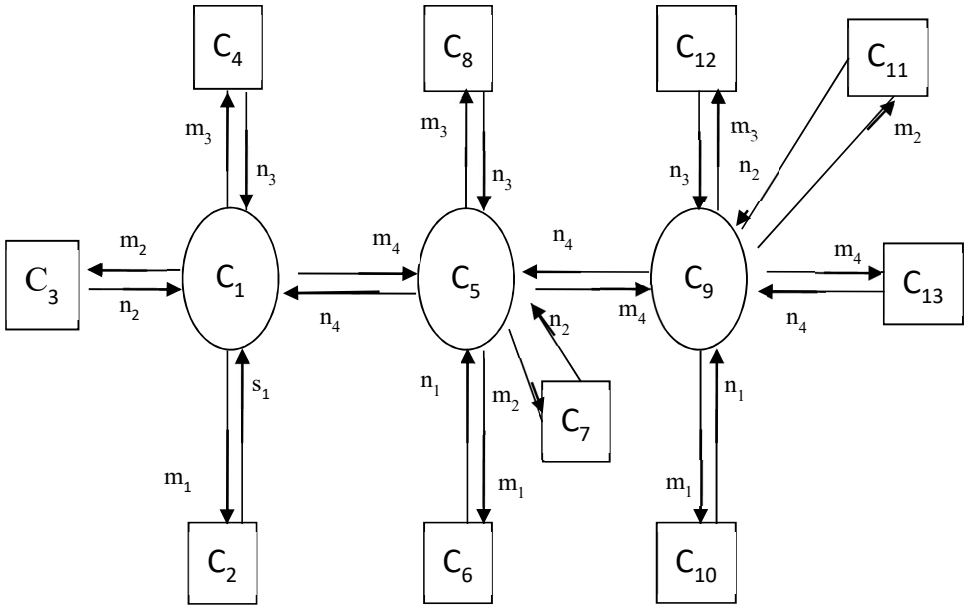


Figure 5.1: Transition Diagram of the system

The states C_1, C_5, C_9 are the healthy states, C_2, C_3, C_4, C_6, C_7, C_8, C_{10}, C_{11}, C_{12}, C_{13} are virus affected states in which a human is said to be COVID-19 affected. Whereas C_1 is taken as the initial (base) state of system.

C_1 = EFGH, C_2 =eFGH, C_3 =EfGH, C_4 =EFgH,
C_5 =EFGH_1, C_6 =eFGH_1, C_7 =EfGH_1, C_8 =EFgH_1,
C_9 = EFGH_2, C_{10} =eFGH_2, C_{11} = EfGH_2, C_{12} = EFgH_2,
C_{13} = EFGh

5.5 Transition Probability and Mean Sojourn Times

$p_{i,j}(t)$: Probability distribution function from i to j. q_{ij}: Transition probability from i to j. $q_{i,j} = p_{i,j}^*(0)$; where * designate Laplace transform.
where η_i^1 is waiting period for detection/testing.

Table 5.1: Transition Probabilities

$p_{i,j}(t)$	$q_{ij} = p^*_{i,j}(0)$
$p_{1,i}(t) = m_j e^{-(m_1+m_2+m_3+m_4)t}$; i =2,3,4,5 & j = 1,2,3,4	$q_{1,i}$= $m_j/(m_1+m_2+m_3+m_4)$ i =2,3,4,5 & j = 1,2,3,4
$p_{2,1}= n_1 e^{-n_1 t}$	$q_{2,1}$= 1
$p_{3,1}= n_2 e^{-n_2 t}$	$q_{3,1}$= 1
$p_{4,1}= n_3 e^{-n_3 t}$	$q_{4,1}$= 1
$p_{5,1}(t) = n_4 e^{-(m_1+m_2+m_3+m_4+n_4)t}$ $p_{5,i}(t) = m_j e^{-(m_1+m_2+m_3+m_4+n_4)t}$ i =6,7,8,9 & j = 1,2,3,4	$q_{5,1}$= $n_4/(m_1+m_2+m_3+m_4+n_4)$ $q_{5,i}$= $m_j/(m_1+m_2+m_3+m_4+n_4)$ i =6,7,8,9 & j = 1,2,3,4
$p_{6,5}= n_1 e^{-n_1 t}$	$q_{6,5}$= 1
$p_{7,5}= n_2 e^{-n_2 t}$	$q_{7,5}$= 1
$p_{8,5}= n_3 e^{-n_3 t}$	$q_{8,5}$= 1
$p_{9,5}(t) = n_4 e^{-(m_1+m_2+m_3+m_4+n)t}$ $p_{9,i}(t) = m_j e^{-(m_1+m_2+m+m_4+n_4)t}$ i =10,11,12,13 & j = 1,2,3,4	$q_{9,5}$= $n_4/(r_1+r_2+r_3+r_4+n_4)$ $q_{9,i}$= $m_j/(m_1+m_2+m_3+m_4+n_4)$ i =10,11,12,13 & j = 1,2,3,4
$p_{10,9}= s_1 e^{-s_1 t}$	$q_{10,9}$= 1
$p_{11,9}= s_2 e^{-s_2 t}$	$q_{11,9}$= 1
$p_{12,9}= s_3 e^{-s_3 t}$	$q_{12,9}$= 1
$p_{13,9}= s_4 e^{-s_4 t}$	$q_{13,9}$= 1

Table 5.2: Mean Sojourn Time

$S_i(t)$	**$\eta_i = S_i^*(0)$**
$S_1(t) = e^{-(m_1+m_2+m_3+m_4)t}$	$\eta_1 = 1/(m_1+m_2+m_3+m_4)$
$S_{1+i}(t) = e^{-n_i t}, i = 1,2,3$	$\eta_{1+i} = 1/n_i, i = 1,2,3$
$S_i(t) = e^{-(m_1+m_2+m_3+m_4+n_4)t}, i = 5,9$	$\eta_i = 1/(m_1+m_2+m_3+m_4+n_4), i = 5,9$
$S_{5+i}(t) = e^{-it}, i = 1,2,3$	$\eta_{5+i} = 1/n_i, i = 1,2,3$
$S_{9+i}(t) = e^{-it}, i = 1,2,3,4$	$\eta_{9+i} = 1/n_i, i = 1,2,3,4$

From Table 5.2 the expressions for η_1, η_5, η_9, it was observed that if rates for being COVID-19 effective were higher, then the mean sojourn time for a person to remain healthy was very small, hence such an atmosphere should be created so that causes which lead to covid-19 affected should be the bare minimum and from the expressions for states when a person is covid-19 affected i.e., η_{1+i}, where i= 2, 3, 4, 6, 7, 8, 10, 11, 12, 13 if the values of recovery rates are higher, then the mean sojourn time for a human to remain covid-19 affected will be small, hence recovery rates should be maintained higher.

5.6 Evaluation of Path Probabilities ($E_{i,,j}$)

Applying RPGT and using '1' as the initial state of the framework: Transition probability factors of all reachable states from the initial (base) state 'ξ' = '1' are: Probabilities from state '1' to various vertices are given as

$E_{1,1} = 1$

$E_{1,i} = q_{1,i}$ where i = 2, 3, 4

$E_{1,5} = q_{1,5}/(1-q_{5,6}q_{6,5})(1-q_{5,7}q_{7,5})(1-q_{5,8}q_{8,5})\{(1-q_{5,9}q_{9,5})/(1-q_{9,10}q_{10,9})(1-q_{9,11}q_{11,9})$

$(1-q_{9,12}q_{12,9})(1-q_{9,13}q_{13,9})\}$

$E_{1,i} = q_{1,5}q_{5,i}/(1-q_{5,6}q_{5,6})(1-q_{5,7}q_{7,5})(1-q_{5,8}q_{8,5})\{(1-q_{5,9}q_{9,5})/(1-q_{9,10}q_{10,9})(1-q_{9,11}q_{11,9})$

$(1-q_{9,12}q_{12,9})(1-q_{9,13}q_{13,9})\}$; i = 6,7, 8.

$E_{1,9} = q_{1,5}q_{5,9}/(1-q_{5,6}q_{6,5})(1-q_{5,7}q_{7,5})(1-q_{5,8}q_{8,5})(1-q_{9,10}q_{10,9})(1-q_{9,11}q_{11,9})(1-q_{9,12}q_{12,9})$

$(1-q_{9,13}q_{13,9})\{(1-q_{5,9}q_{9,5})/(1-q_{9,10}q_{10,9})(1-q_{9,11}q_{11,9})(1-q_{9,12}q_{12,9})(1-q_{9,13}q_{13,9})\}$

$E_{1,i} = q_{1,5}q_{5,9}q_{9,i}/(1-q_{5,6}q_{6,5})(1-q_{5,7}q_{7,5})(1-q_{5,8}q_{8,5})(1-q_{9,10}q_{10,9})(1-q_{9,11}q_{11,9})(1-q_{9,12}q_{12,9})$

$(1-q_{9,13}q_{13,9})\{(1-q_{5,9}q_{9,5})/(1-q_{9,10}q_{10,9})(1-q_{9,11}q_{11,9})(1-q_{9,12}q_{12,9})(1-q_{9,13}q_{13,9})\}$;

where i = 10, 11, 12, 13.

Probabilities from state '9' to different vertices are given as

$E_{9,1} = q_{9,5}q_{5,1}/(1-q_{5,6}q_{6,5})(1-q_{5,7}q_{7,5})(1-q_{5,8}q_{8,5})(1-q_{1,2}q_{2,1})(1-q_{1,3}q_{3,1})(1-q_{1,4}q_{4,1})$

$\{(1-q_{5,1}q_{1,5})/(1-q_{1,2}q_{2,1})(1-q_{1,3}q_{3,1})(1-q_{1,4}q_{4,1})\}$

$E_{9,i} = q_{9,5}q_{5,1}q_{1,i}/(1-q_{5,6}q_{6,5})(1-q_{5,7}q_{7,5})(1-q_{5,8}q_{8,5})(1-q_{1,2}q_{2,1})(1-q_{1,3}q_{3,1})(1-q_{1,4}q_{4,1})$

$\{(1-q_{5,1}q_{1,5})/(1-q_{1,2}q_{2,1})(1-q_{1,3}q_{3,1})(1-q_{1,4}q_{4,1})\}$; where i = 2, 3, 4.

$E_{9,5} = q_{9,5}/(1-q_{5,6}q_{6,5})(1-q_{5,7}q_{7,5})(1-q_{5,8}q_{8,5})\{(1-q_{5,1}q_{1,5})/(1-q_{1,2}q_{2,1})(1-q_{1,3}q_{3,1})(1-q_{1,4}q_{4,1})\}$

$E_{9,i} = q_{9,5}q_{5,i}/(1-q_{5,6}q_{6,5})(1-q_{5,7}q_{7,5})(1-q_{5,8}q_{8,5})\{(1-q_{5,1}q_{1,5})/(1-q_{1,2}q_{2,1})(1-q_{1,3}q_{3,1})(1-q_{1,4}q_{4,1})\}$;

Where i = 6,7, 8.

$E_{9,9} = 1$

$E_{9,i} = q_{9,i;}$ where 'i' = 10, 11, 12, 13

5.7 Measures of Covid-19 Virus effectiveness

The MTEE, $\mathbf{A_0}$, and $\mathbf{B_0}$ measures due to the virus are evaluated under steady state condition and utilizing C_1 is the initial (base) state.

5.8 Mean time to Epidemic affected (T_0)

Regenerative healthy states to which a human can transit (initial state '1'), before entering any virus affected state are: 'i' = 1, 5, 9, Mean time to Epidemic affected (T_0), using RPGT is given as $T_0 = (E_{1,1}\boldsymbol{\eta}_1+E_{1,5}\boldsymbol{\eta}_5+E_{1,9}\boldsymbol{\eta}_9)/(1-q_{1,5}q_{5,1})$

5.9 Average Healthy Time (A_0)

Regenerative states at which the system is available are 'j' = 1, 5, 9, & regenerative states are 'i' = 1 to 13. Average Healthy Time (A_0) using RPGT is as under

$A_0 = \left[\sum_j \boldsymbol{E_{\xi,j}}\, \boldsymbol{f_j}\boldsymbol{\eta_j}\right] \div \left[\sum_i \boldsymbol{E_{\xi,i}}\, \boldsymbol{f_j}\, \boldsymbol{\eta_i^1}\right]$

$A_0 = (E_{9,1}\boldsymbol{\eta}_1+E_{9,5}\boldsymbol{\eta}_5+E_{9,9}\boldsymbol{\eta}_9)/D$

Where $D = E_{1,i}\boldsymbol{\eta}_i$; $1 \le i \le 13$

5.10 Recovery Period (B_0)

Regenerative states where in which virus affected person is busy in recovery are j = 2 to13, & regenerative states are 'i' = 1 to 13. Recovery Period (B_0) using RPGT is given as under

$B_0 = \left[\sum_j \boldsymbol{E_{\xi,j}}\, \boldsymbol{\eta_j}\right] \div \left[\sum_i \boldsymbol{E_{\xi,i}}\, \boldsymbol{\eta_i^1}\right]$

$B_0 = (E_{1,j}\boldsymbol{\eta}_j)/D$; $2 \le j \le 13$.

5.11 Illustrations

Assuming $n_i = n$ $(1 \le i \le 4)$ and $m_i = m$ $(1 \le i \le 4)$ for ease of calculations and taking m= 0.10, 0.20, 0.30 and n= 0.50, 0.60. 0.70, we get

5.11.1 Mean time to Epidemic affected (T_0)

Table 5.3: Mean time to Epidemic affected (T_0)

m \ n	0.50	0.60		0.70
0.10	3.77	3.63		3.56
0.20	2.42	1.39		1.29
0.30	1.45	1.30		1.23

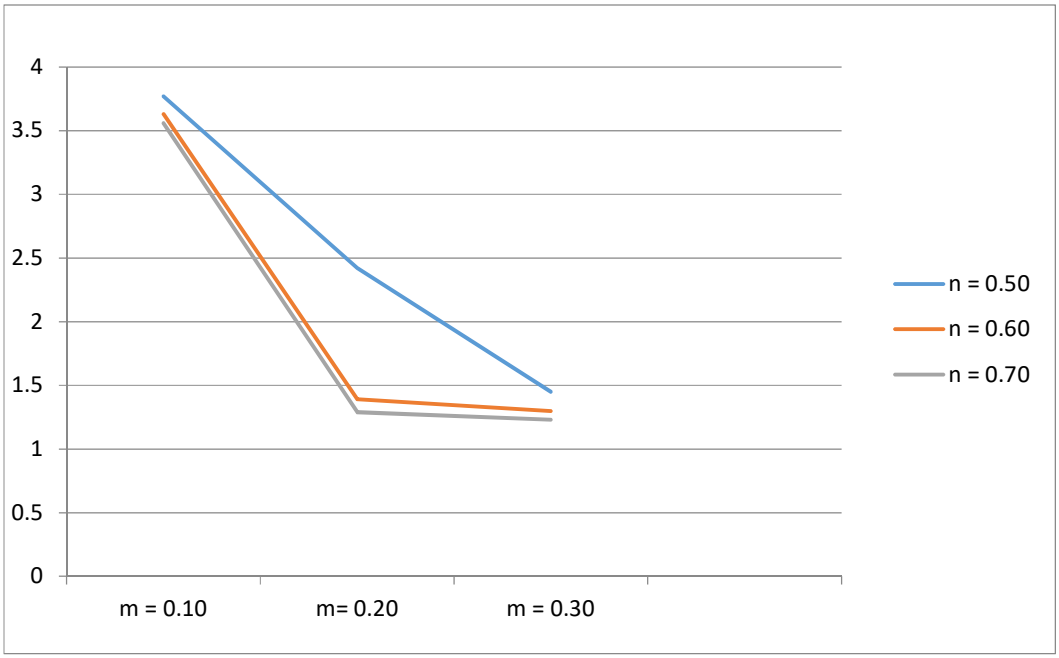


Figure 5.2: Mean time to Epidemic affected (T_0)

From Table 5.3 and Graph 5.2, as we see in columns, it is concluded that the value of T_0 decreases rapidly, i.e., with the increase in virus causing rates, while observing along rows, it is concluded that the value of T_0 is not significantly increased with the increasing recovery rates, which is practically observed too.

5.11.2 Average Healthy Time (A_0)

Table 5.4: Average Healthy Time (A_0)

m \ n	0.50	0.60	0.70
0.10	0.71	0.78	0.82
0.20	0.68	0.75	0.82
0.30	0.40	0.47	0.55

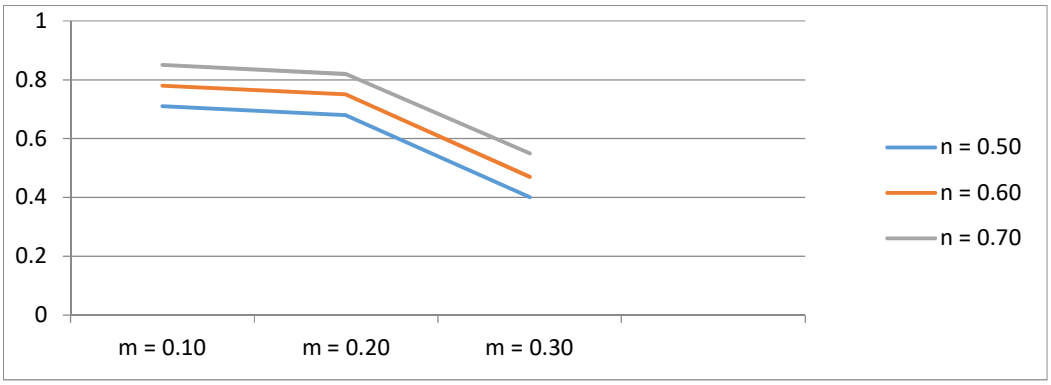


Figure 5.3: Average Healthy Time (A_0)

From Table 5.4 and Graph 5.3, as we see in columns, it is concluded that the value of A_0 decreases rapidly, i.e., with the increase in virus causing rates while observing along the rows, it is concluded that the value of A_0 is not significantly increased with the increasing recovery rates, which is practically observed too.

5.11.3 Recovery Period (B_0)

Table 5.5: Recovery Period (B_0)

m \ n	0.50	0.60	0.70
0.10	0.31	0.25	0.21
0.20	0.49	0.44	0.40
0.30	0.69	0.62	0.59

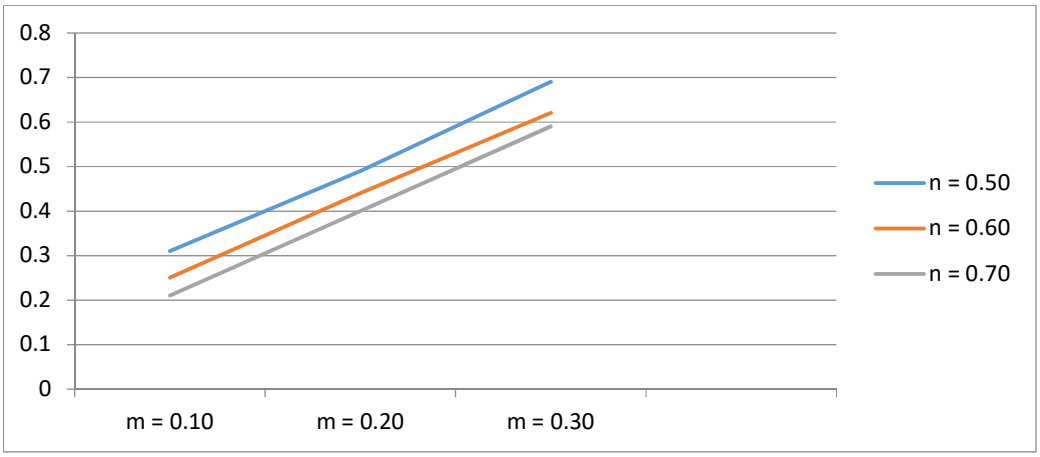


Figure 5.4: Recovery Period (B_0)

From Table 5.5 and Graph 5.4, as we see in columns, it is concluded that the value of B_0 increases rapidly, i.e., with the increase in virus causing rates, while observing along the rows, it is concluded that the value of B_0 decreases with the increasing recovery rates, which is practically observed too.

5.12 Conclusion

The application of RPGT has been used to discuss the transmission analysis of COVID-19. In this chapter, three main reasons which cause positivity for COVID-19 affected have been discussed, considering isolation and lockdown situations also. If rates of recovery and causes of a pandemic are known before hand, then exact calculations can be determined by applying the derived formulae in this chapter. In the future, there may be more factors that cause the effects of COVID-19 that may also be included in the study.

Chapter-6

A Compartmental Model on Covid-19 Transmission

6.1 Introduction

The coronavirus disease (Covid-19) is an infectious disease at the present time. Recently, almost every country is facing serious problems due to this virus. Many people were being confirmed as patients with COVID-19. The asymptotic and exposed were more harmful to society. Because this asymptotic class was more dangerous than any other class, because they were not showing any symptoms, as a result, more people were interacting with them without taking any care. Because of this, the disease was spreading rapidly. Also, since we had limited medical capacity in most countries and the cases were increasing faster, but due to this limited medical capacity, most countries were doing fewer tests to diagnose the disease. This fact also increased the number of infected cases. The spread of any epidemic depends on the infectivity of the pathogen and the availability of a susceptible population. Since the way things work is still not clear, math is used to estimate the number of worst-case and best-case scenarios. Our main objective of this work was to study the dynamics of the disease COVID-19 by considering a deterministic compartmental model based upon the data set of India, so that we could take some of the preventive measures to control its effects on the nation. We estimated the basic reproduction number and tried to figure out how the disease spreads by using the number of reported cases and the estimated parameters of the model.

The SIR model and its advanced variants are epidemiological models, which are used mostly, so that one can understand the spread of epidemics. Since the outbreak of SarsCov-2, it has gained popularity among researchers who are trying to make some

estimations about the size of this epidemic outbreak and its consequences to formulate some policies.

In this chapter, we considered a modified SIR model, which was known as SEIRD (Susceptible, Exposed, Infectious, Recovered, and Dead), and concluded with various findings. It is well known in the field of mathematical modelling that the SEIRD model has many degrees of freedom and depends upon the clinical parameters that can be taken from the clinical diagnosis of COVID-19 and the data of confirmed cases and deaths. We have identified $\boldsymbol{R_0}$ (basic reproduction number) from the available data and this model. As we know from the previous research on epidemics that the $\boldsymbol{R_0}$ reveals the speed of spread of the virus. In this study, we also predicted the case fatality ratio, which is again an important parameter to predict the number of deaths. When we tried to estimate $\boldsymbol{R_0}$ for India, we noticed a range from 1.75 to 4.6 depending upon the initial values and distinct values of clinical parameters. The outcome from this study show that a single value of basic reproduction number cannot be calculated by the available dataset, at least for the short time of observation. There were many values of the $\boldsymbol{R_0}$ that were being observed were correct and the exact value depends on the model and the country.

The chapter is structured into five partitions. The first portion is introductory, next part contains an introduction to the SEIRD model. The data and identification of models have been discussed in the third section. The last portion describes the procedure for the prediction and results along with some graphs, and then we have discussed the limitations and future scope. We have concluded.

6.2 Mathematical Model

Here we have studied a variant of the SIR model (a compartmental model), in which two more compartments were exposed, and two dead were included. Many authors have discussed such epidemiological models in their research papers. In fact, a few of them have used many similar variants of this model, which were more advanced and had more compartments. We have considered a model containing five compartments of the population: susceptible (S), exposed (E), infectious (I), recovered (R), and dead (D).

People in susceptible compartments were those who were not infected with the virus yet but had the possibility of being infected. People who got infection and could not spread infection further were in the exposed compartment. This period is known as the incubation period. In the third compartment, we put those people who got infected with viruses and were proficient at transmitting the diseases. We called this compartment "infectious." We put those people who were infected by the virus in the trial period and recovered successfully in a separate compartment and named the compartment "Recovered compartment." We placed those who became infected with the virus but were unable to survive in the dead compartment.

The population in all the five compartments keeps changing over time as follows:

$$\frac{dS(t)}{dt} = -\beta \frac{S(t)}{N} I(t) \tag{6.1}$$

$$\frac{dE(t)}{dt} = \beta \frac{S(t)}{N} I(t) - \sigma E(t) \tag{6.2}$$

$$\frac{dI(t)}{dt} = \sigma E(t) - \gamma I(t) \tag{6.3}$$

$$\frac{dR(t)}{dt} = (1-\alpha)\gamma I(t) \tag{6.4}$$

$$\frac{dD(t)}{dt} = \alpha\gamma I(t) \tag{6.5}$$

The total population of India was considered as and it was assumed that it is fixed and will not change as the time changes, i.e., birth and death caused by any possibility are not included, so that unnecessary complications may not arise. The majority of research articles available in the literature have considered a fixed total population. Total number of confirmed cases with time was taken as $\mathrm{C(t)}$ and does not make any impression on the model dynamics but we can use it to match the data of confirmed cases with the model. When we do the analyses of the model, we assumed that people in the Infectious compartment are tested positive with the virus. Many parameters had impact on the solution of this SEIRD model like the clinical parameters as γ and σ and the parameter of estimated time of illness, which is taken as γ. The value of γ may be found distinct in the research articles from 1/18 to 1/5 in [84]. The estimation of incubation period for the disease was given by the parameter σ. Its value was observed

between the range 1/5 in [87] and 1/3 in [84]. The parameter β gave us the rate of infectious. Also, we know the relation $\beta = R_0\gamma$, where R_0 was considered as the basic reproduction number, we used it to measures the transmission of disease. Case fatality ratio was denoted by α and we used the term CFR for case fatality ratio. As observed in paper [88], there were many limitations on CFR and had dependency on the infectious people. The CFR was not constant and might increase if the health care system of India becomes overloaded. But to avoid complications, we considered that α is constant and tried to make estimation of it. Also, we estimated λ. The number of dead and recovered people at initial time were taken as zero. At the initial stage, we assumed that the number of infected people was $I(0)$ and exposed people were as $E(0)$. At initial time, Susceptible peoples were taken as the expression below: $S(0) = N - I(0) - E(0) - R(0) - D(0) = N - I(0) - E(0)$.

6.3 Data of the Model

In this study of approximation, we were strongly dependent on the data of confirmed cases and death due to this disease, COVID-19 caused by the infection from the deadly virus Sars-Cov2. We used the data that we have collected from the website of Johns Hopkins University. We have taken the Indian population as 1380004385.

6.4 Methods and Results

In this part of chapter, we have tried to elaborate the process of estimation used by us. This method has been used by various authors. The values of $T_0 = 1, I_0 = 0$ is taken as fixed and we started from $E_0 = 1$ and then E_0 may be increased (if needed). Let (α, R_0, λ) be a vector of parameters then for this vector and every value of t, $D(t, \alpha, R)$ (number of deaths) and $C(t, R, \lambda)$ (number of reported cases) was calculated. Then the residual sum of squares for the series of deaths was calculated, which is given by

$$RSS_D(\alpha, R) = \sum_{t=1} (D(t) - D(t, \alpha, R))^2$$

and for the series of reported cases, we calculated the residual sum of squares by

$$RSS_C(R,\lambda) = \sum_{t=1} (C(t) - C(t,R,\lambda))^2$$

Where $C(t)$ and $D(t)$ are the original values as reported. Then, next step was to find the values (α_D, R_D) so that RSS_D can be minimized and to find the values (R_C, λ_C) so that RSS_C can be minimized and after that we predicted (α, R_0, λ) by minimizing

$$RSS_T(\alpha,R,\lambda) = \frac{RSS_D(\alpha,R)}{RSS_D(\alpha_D,R_D)} + \frac{RSS_C(R,\lambda)}{RSS_C(R_C,\lambda_C)}$$

The preliminary values of the RSS_D and reported cases have been used for normalization for almost equal contribution in final objective function. If we do not normalize their contribution, then RSS_C will dominate. We increased the value of E_0 to get shot of the constraint if some of the values of α_D, λ_C, α or λ have reached at upper bound of 1. We considered the least value of E_0, so that we had no parameter constraint. We have chosen the least value of E_0 to obtain the rate of fatality near the upper bound. Any other person may use the value $E_0 = 1$ and ignore the constraints. We should consider the number of deaths the highest in this forecast. This may seem unrealistic, but we should declare that one should keep in mind that the model may not be correct as a few of our assumptions, like the fatality rate, may not remain constant over any specific period. Now let us discuss the results and the parameters that were calculated with the help of some computer programmes using the language R. Next, we represented the estimated parameters and obtained results in the form of graphs and tables. We have taken the following values:

Table 6.1: The values of Parameters used in Model

Parameters	**Value Assigned**	**Sources**
β	0.4809	Adapted from 16.
σ	0.1923	Adapted from 17.
α	0.0215	Adapted from 16.
γ	0.1	Assumed
R_0	4.809	$\frac{\beta}{\gamma} = R_0$

Then we got summary of the model as follows:

Table 6.2: Summary of the Model

	S	**E**	**I**	**R**	**D**
Min.	11259477	8.189788e-01	0.000000e+00	0.000000e+00	0.000000e+00
1st Qu.	38204543	1.669369e+03	1.227928e+03	7.440355e+02	1.634825e+01
Median	1365789511	6.058544e+05	3.752063e+06	2.907367e+06	6.388185e+04
Mean	878725877	3.454894e+07	6.627867e+07	3.918412e+08	8.609694e+06
3rd Qu.	1380000728	2.046555e+07	7.038617e+07	9.993779e+08	2.195874e+07

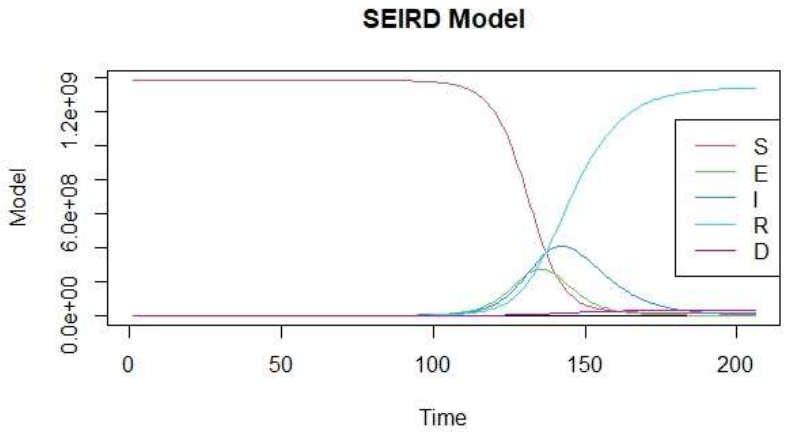


Figure 6.1: SEIRD Model

6.5 Limitations and Future Scope

As we all know, an epidemic model can only be useful if the data and assumptions are as close to original as possible. We have also made some unrealistic assumptions. A few of them are described below:

- Since the population of India is large and we have non-uniform mixing. People are more likely to get in touch with individuals in their locality. This can be tackled in some other advanced models.
- We have an assumed isolated population in the mode. But population mixing allows this virus to spread multiple times.
- If we consider the model for a longer times, we must make the model more sophisticated by considering the factor of birth rate. Because people are generally not born with immunity.
- As we know, the virus spreads faster among young populations, or densely populated areas. But it may be more deadly for the older generation. So, we must consider some more complex models that take care of age structure.
- This model ignores the variations of its parameters and considers their average. But as we have observed, a few individuals stay infectious for many days. Also, some people might make contact with a very large population. If we are

considering a high-level epidemic, then it is suitable, but if we are looking for a smaller scale, we must change the model.

Regardless of its limitations, the SEIRD model is a great start to understanding the epidemic dynamics. Also, the approach of differential equations for the inter-compartment flow in the model is very powerful.

6.6 Conclusion

In this study we have used compartmental model with five compartments i.e., SEIRD Model and we have done analysis about the dynamics of COVID-19 in India. Through this data-based study, we can conclude that Inflammation can be controlled by public lockdowns because it will reduce the transmission rates and due to limited health care facilities, there will be more chances of recovery and hence recovery rate will be increased. If we change these both parameters, the curve can be flattened. If we change the values of parameters in the model, we will get different results. As we know that these parameters are not constant over the time. So, if we look for disease dynamics in different time, we should change these parameters accordingly. Also, there are few limitations in our Model and those have been discussed in earlier section. These can be improvised in future. Also, some more parameters can be added to enhance the validation of results like under reported cases, asymptotic cases.

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List of Papers Published and Communicated from the Thesis

[1] Yadav, R., & Singh, K. (2020). An epidemic model to predict the effect of infection on population of India by COVID-19 corona virus. *Plant Archives*, *20*(2), 1561-1564.

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[5] Yadav, R., & Singh, K. (2021) Prediction of Covid-19 Infected Cases in India Using Time Series Model. *AIP conference proceedings*- ***Accepted***

[6] Yadav, R., & Singh, K. (2021) A Compartmental Model on Covid-19 Transmission. *AIP conference proceedings*- ***Accepted***

List of Conferences

1. Presented paper entitled “Prediction of Covid-19 Infected Cases in India Using Time Series Model” in the International Conference on “Recent Advances in Fundamental and Applied Sciences” (RAFAS-2021) held on June 25-26, 2021, organized by School of Chemical Engineering and Physical Sciences, Lovely Professional University, Punjab.
2. Presented paper entitled “A Compartmental Model on Covid-19 Transmission” in the International Conference on “International Conference on Materials for Emerging Technology” (ICMET-2021) held on February 18-19, 2022, organized by Department of Research Impact and Outcome, Division of Research and Development, Lovely Professional University, Punjab.
3. Presented paper entitled “Strategic Transmission Model for Covid-19 Using RPGT” in the International Conference ICMMAAC-2021 held on February 5-7, 2021, organized by JECRC University, Jaipur.

Certificates of Conferences

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This is to certify that Prof./Dr./Mr./Ms. **Mr. Kuldeep Singh**

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has given poster presentation on **Prediction of Covid-19 Infected Cases in India Using Time Series Model**

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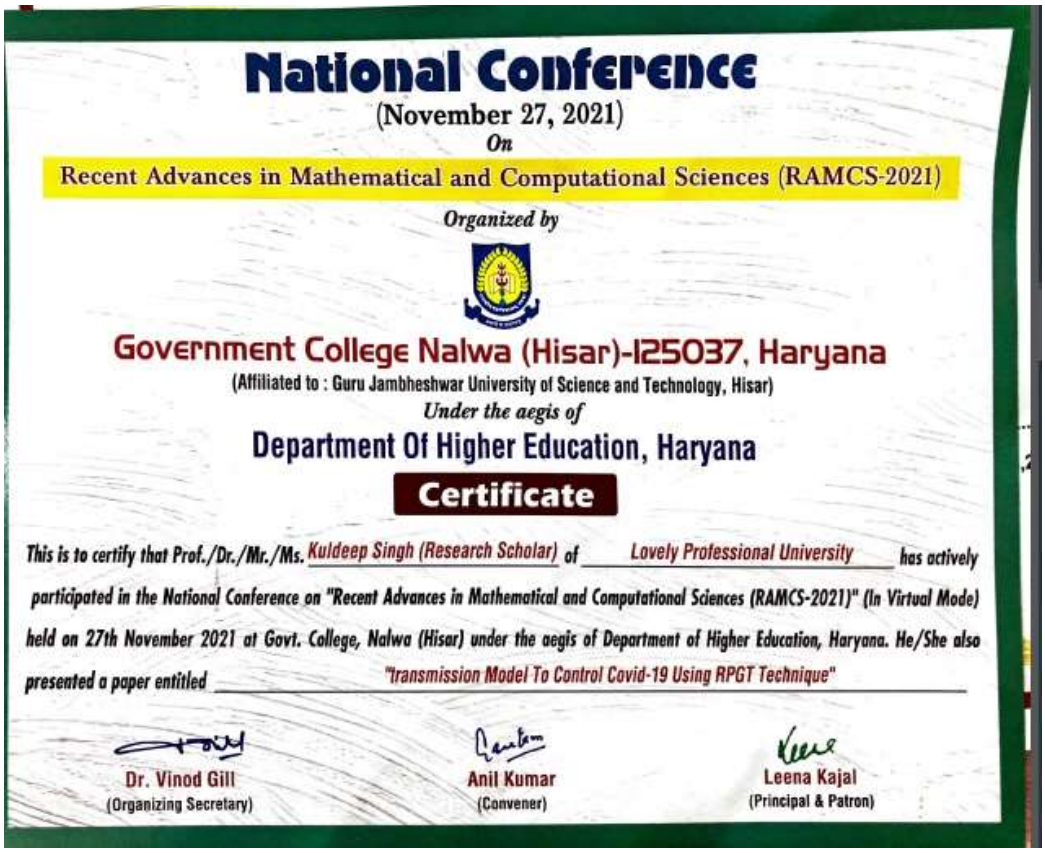

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Department Of Higher Education, Haryana

Certificate

This is to certify that Prof./Dr./Mr./Ms. Kuldeep Singh (Research Scholar) *of* Lovely Professional University *has actively participated in the National Conference on "Recent Advances in Mathematical and Computational Sciences (RAMCS-2021)" (In Virtual Mode) held on 27th November 2021 at Govt. College, Nalwa (Hisar) under the aegis of Department of Higher Education, Haryana. He/She also presented a paper entitled* "transmission Model To Control Covid-19 Using RPGT Technique"

Dr. Vinod Gill	Anil Kumar	Leena Kajal
(Organizing Secretary)	(Convener)	(Principal & Patron)

तारीख / Date 27.8.2021
ज्ञापन संख्या / Memo no: MGNCRE/SAP/HARYANA/40

सत्यमेव जयते

भारत सरकार / Government of India
महात्मा गांधी राष्ट्रीय ग्रामीण शिक्षा परिषद / Mahatma Gandhi National Council of Rural Education
उच्च शिक्षा विभाग/Department of Higher Education
शिक्षा मंत्रालय / Ministry of Education

Certificate of Appreciation

This is to certify that **Mr. Kuldeep Singh** from **Government College for Women, Ratia** coordinated in formation of five student volunteer team in the area of Hospital Management, Non-Hospital Management, Support to Covid affected families, Medical Supplies, Psychosocial support to Covid patients and their family members as a part of **Beat Covid Campaign** initiative of MGNCRE, Ministry of Education Government of India. His extraordinary efforts are highly appreciated.

Mr. Samarth Sharma
Programme Coordinator
MGNCRE, Ministry of Education
Government of India

Dr. Shatrughan Bhardwaj
Regional Coordinator
MGNCRE, Ministry of Education
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Dr W G Prasanna Kumar
Chairman
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