Project Report

On

A BRIEF STUDY ON MATHEMATICAL MODELLING OF INFECTIOUS DISEASE (COVID - 19): A CASE STUDY OF KERALA

Submitted

in partial fulfilment of the requirements for the degree of

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by

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CERTIFICATE

This is to certify that the dissertation entitled, **A BRIEF STUDY ON MATHEMATICAL MODELLING OF INFECTIOUS DISEASE (COVID - 19): A CASE STUDY OF KERALA** is a bonafide record of the work done by Ms. **RINNU BENNY** under my guidance as partial fulfillment of the award of the degree of **Bachelor of Science in Mathematics** at St. Teresa's College (Autonomous), Ernakulam affiliated to Mahatma Gandhi University, Kottayam. No part of this work has been submitted for any other degree elsewhere.

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DECLARATION

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

Ernakulam. **RINNU BENNY**

Date: 20 February 2023 **AB20AMAT030**

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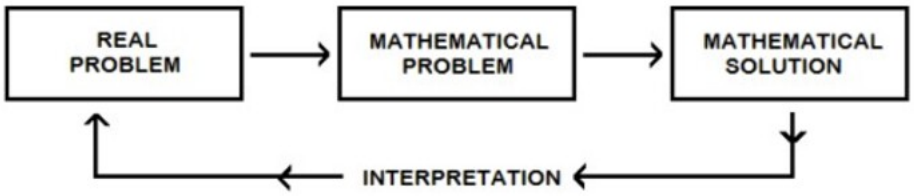
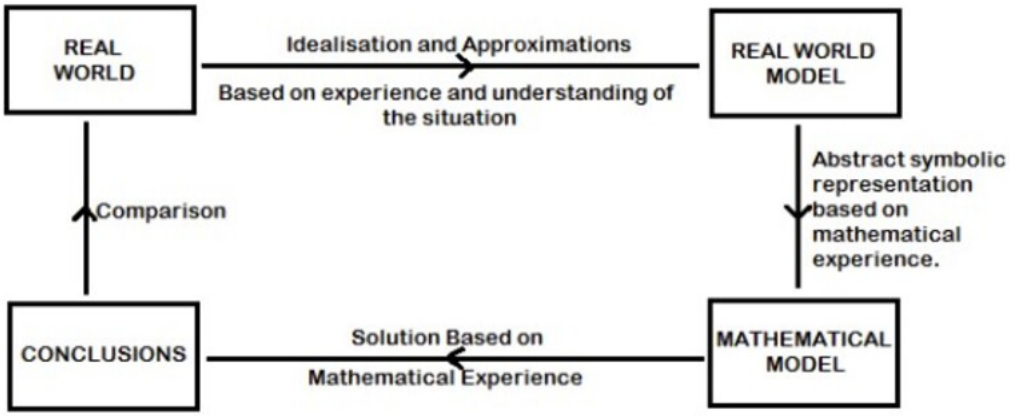
Chapter 1

INTRODUCTION

The technique of characterizing a system using mathematical concepts is known as mathematical modelling. It entails transforming real-world problems into mathematical problems, thereafter solving those mathematical problems by implementing various mathematical concepts and interpreting the solutions in a language understandable in the real world.



It may not be possible to solve a real-world problem when it is transformed into a mathematical problem in all its generalities. As a result, the problem is idealized or approximated into a different problem that is fairly similar to the original problem, which is then translated into a mathematical problem and solved. During this idealization process, the problem under investigation is examined, and the key or essential aspects of the issue are preserved while the non essential aspects are dropped.



The unpredictable nature of infectious diseases is a concern that can jeopardize the ability of health systems and services to satisfy the demands of the population, where mathematical modelling of infectious diseases can aid health services in disease transmission and advise the public in health decision-making. Here, mathematical modelling of infectious disease dynamics acts as an important tool for comprehending disease dynamics, assessing appropriate control measures, forecasting future outbreaks, aiding health services in disease transmission and advising the public in health decision-making.

The mathematical model can forecast the course of infectious diseases, the likely result of an epidemic, and help guide public interventions as a result. To determine parameters for various infectious diseases that are used to calculate the effects of various actions, such as mass vaccination programmes, models use statistics that have been gathered and applied in combination with mathematics. The poor knowledge acquired from huge populations under challenging existing conditions can be made up for in particular with the aid of mathematical modelling.

We cannot just move from an assumption to an equation when the system being described is more complex. We must be significantly more meticulous when stating assumptions as well as defining the system. Flow diagrams are a visual tool for this purpose.

Mathematical models of infectious diseases can be classified as deterministic models and stochastic models. The deterministic model of infectious diseases is an approximation of how an epidemic will behave in a closed system, in which the population is divided into compartments that define disease states, and differential equations appearing as derivatives describe the migrations between these states by determining fluctuations over time. Although deterministic models describe the behaviour of infectious diseases, they do not account for environmental influences or protective behaviours in the susceptible host population.

There are numerous applications for mathematical modelling. In this project, would go over the key elements of mathematical modelling of infectious disease immunization in a closed population. Our aim is to persuade epidemiologists and other public health professionals of the value that mathematical modelling could provide in the field of healthcare.

Chapter 2

PRELIMINARIES

2.1 INFECTION

An infection takes place when germs enter a person's body and proliferate, resulting in sickness, organ and tissue damage. The infection causing microorganisms are called pathogens. The major examples of pathogens are bacteria, fungi and viruses. These pathogens vary in several different ways such as shape, function, genetic content, size and to what extreme they can affect a person, an animal or a plant. A person, animal or plant who harbours the pathogenic microorganism without suffering from any disease from them.

These harmful microorganisms enter a human body by physical contact, consuming contaminated food or water or touching the objects used by a person carrying the pathogen. These are the normal ways of transmission of the infection from one person to another. When they are inside the host, they normally take a short or long period of time to reproduce and hence be able to be transmitted to other organisms. The innate immune responses provide the defence in advance against the invading pathogens. The ability of a person's immune responses to conquer the infection shows how strong the person's immunity is. The time period of an infection is the time interval in which an infection enters a host through a pathogen, reproduces and transmits the infection to the next person.

This time period is divided into three subsequent segments such as the pre-infectious period, the incubation period and the last one which is the infectious period. The pre-infectious period also known as the latent period is the beginning of the infectious period. It is the time interval during which the pathogens enter the body, replicate at various parts of the body and become ready to be transmitted. The incubation period is the time interval between the infection and its capability to arise as a disease. The infectious period marks the end of the previous period, therefore the host is not capable of transmitting the infection to others. In our study of the infectious disease which has been prevailing in our planet for a large amount of time, Covid-19 is an infectious disease caused by SARS-CoV-2 virus.

2.2 TRANSMISSION

Microorganisms like bacteria, viruses, fungus, and protozoa, collectively known as germs, are the source of disease. Some germs are helpful which helps us to stay healthy, while others are harmful and cause infection. Infectious diseases spread through direct and indirect transmission of these germs among individuals. Germs can enter the body through the mouth by eating, drinking, or breathing, through the skin by cuts and grazes, eyes, and genitalia.

There are two modes of transmission. Direct transmission is the person to person spread which is the most common way of transmission of an infectious disease. Germs can spread from person to person through air (as droplets), faecal-oral spread, blood (or other body fluids), skin and sexual contact. In an indirect transmission, the transmission of germs occurs from an infected person to an object and then to another person who comes into contact with this object.

This project is a case study of Kerala on mathematical modelling of COVID - 19. The aim of this project is to substantiate whether an epidemic occurred or not between February 2020 and August 2022 for the

given demographic. Mathematical modelling can be used to generate conclusions from problems in many disciplines of science and economics when the models are specified by difference or differential equations. We can use difference equations to solve discrete models and differential equations to solve continuous models.

2.3 DIFFERENTIAL EQUATION

A differential equation is one that involves derivatives of one or more dependent variables with respect to one or more independent variables. There are some classifications for differential equations according to whether there is one or more than one independent variable involved. The various rates of change, expressed by various derivatives and the scientific laws themselves become mathematical equations involving derivatives, that is, differential equations. For example, the rate of change in the number of individuals in a given region over time is given by the difference between the number of individuals entering the region and the number of individuals leaving the region per unit time.

$\frac{dS(t)}{dt}$ denotes the rate of change in the number of susceptible individuals at time t.

$\frac{dE(t)}{dt}$ denotes the rate of change in the number of pre-infectious individuals at time t.

$\frac{dI(t)}{dt}$ denotes the rate of change in the number of infectious individuals at time t.

$\frac{dR(t)}{dt}$ denotes the rate of change in the number of recovered individuals at time t.

$\lambda(t)$ denotes the rate at which susceptible individuals becoming infected per unit time, at time t.

f denotes the rate at which individuals in the pre - infectious category becoming infectious per unit time, at time t.

γ denotes the rate at which infectious individuals recover (become immune) per unit time, at time t.

Chapter 3

MATHEMATICAL MODEL AND SETTING UP OF MODELS

3.1 MATHEMATICAL MODEL

A mathematical model provides a suitable framework in which we can incorporate all of the aforementioned data to estimate changes in the number of susceptible, infectious, and immune individuals, along with the expected number of cases in a population. Consider a simple infectious disease event in which an infection is introduced into a group of individuals. After being in contact with the infection, these individuals will become infectious and subsequently recover.

Let S_t denotes the number of susceptible individuals and I_t denotes the number of infectious individuals at a given time t. The risk of infection among the susceptible at any given time is simply a function of the number of infectious individuals present during that time. Assume that the individuals are infectious only for one time period. Then we can express this statement as $I_{t+1} = kS_{t+1}$, where 'k' is a proportionality coefficient, called a 'contact rate'. The equation $I_{t+1} = kS_{t+1}$ is called the mass action principle in epidemiology.

Contact rate is the proportion of all possible contacts between susceptible and infectious individuals that will lead to the susceptible individuals to be infectious. We can predict the number of susceptible individuals remaining in the next time period as $S_{t+1} = S_t$ - I_{t+1} .

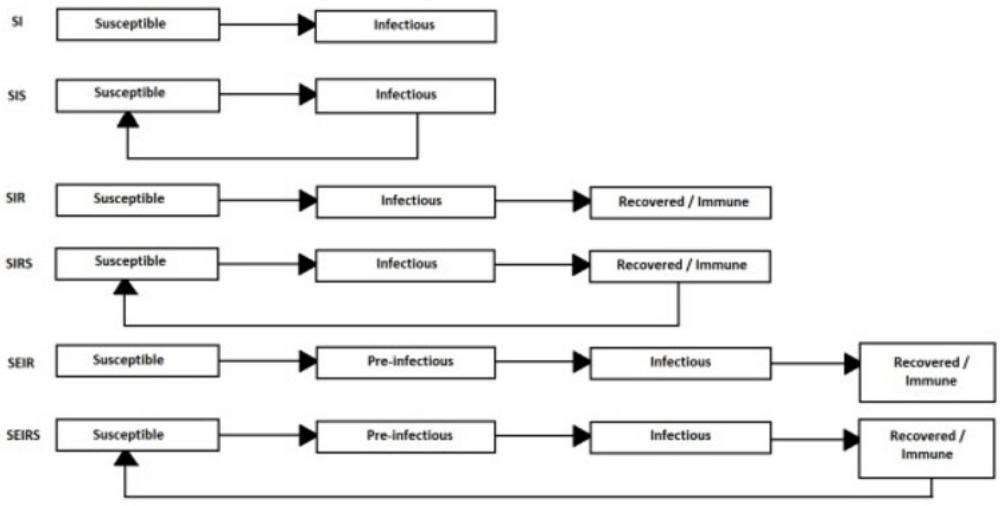
3.2 HOW TO SET UP MODELS?

The following are the steps involved in the development and application of a detailed model:

1. **Identify the question.**
2. **Determine the pertinent facts about the infection in the question.**
3. **Selecting the modelling method.**
4. **Specify model input parameters.**
5. **Set up the model**
6. **Model Validation**
7. **Prediction and optimization**

3.3 THE NATURAL HISTORY OF THE INFECTION

The model structure should showcase the natural history of the infection. As a result, critical sickness categories and transitions, as well as critical population categories, must be described. For the purpose of simplicity, the models presented here do not account for population births and deaths.



3.4 CHOOSE THE TYPE OF MODELLING METHOD

Deterministic models describe what happens 'on average' in a population. Because the input parameters in these models are fixed, the model's predictions, such as the number of cases encountered over time, are predetermined. In contrast, stochastic models allow for random fluctuations in the number of persons who travel between compartments, such as the rate at which infectious people recover from disease. As a result, the model can forecast a wide range of outcomes, such as the number of cases over time or the likelihood of a specific event (such as an epidemic).

3.5 SETTING UP DETERMINISTIC MODEL

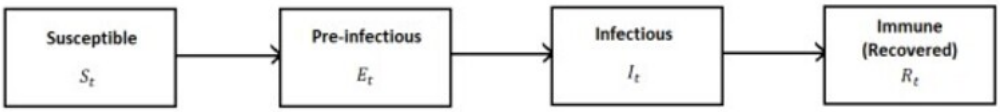
Deterministic model is a mathematical model in which we could always receive the same output for a given input. It is a model in which no randomness is involved. Output of this model always depends upon the initial conditions. Majority of the deterministic model comprises compartmental models where the model population is divided into subgroups such as susceptible, infectious, immune and recovered. This model is set up using the difference equation and differential equation.

The variables of the system are given by the group of susceptible individuals (denoted by S), the group of infected individuals (denoted by I), the group of removed individuals (denoted by R). The model gives us a precise description regarding the various movements in these compartments. These include birth, death and recovery.

Chapter 4

SETTING UP THE MODEL USING DIFFERENTIAL EQUATIONS

In this chapter, we will discuss the formation of differential equations for the susceptible, pre-infectious, infectious, and recovered categories for the given model as illustrated in the figure. Furthermore, the basic reproduction number, growth rate in an epidemic and the average force of infection will be covered in detail.



4.1 DIFFERENTIAL EQUATION FOR THE RATE OF CHANGE IN THE NUMBER OF SUSCEPTIBLE INDIVIDUALS

When considering susceptible individuals in the model exhibiting the transmission of an immunizing infection, we see that as no one enters the susceptible class and newly infected individuals exit this category, the rate of change in the number of susceptible individuals is given by the expression:

$\frac{dS(t)}{dt}$ = - (the number of individuals who are newly infected per unit

time)

$\frac{dS(t)}{dt} = -\lambda(t)S(t)$

$\lambda(t)$**: Force of infection.**

$S(t)$**: Number of susceptible individuals at time t.**

If we assume that individuals randomly encounter one another, then by analogy with the above equation, $\lambda(t)$ **can be substituted by the equation** $\lambda(t) = \beta\ I(t)$ **.**

4.2 DIFFERENTIAL EQUATION FOR THE RATE OF CHANGE IN THE NUMBER OF PRE-INFECTIOUS INDIVIDUALS

By considering the pre-infectious category of the model, we can see that when a newly infected individual enters the category the infectious individual will exist the same. The rate of change in the number of pre-infectious individuals is given by the expression:

$\frac{dE(t)}{dt}$ **= (number of susceptible individuals who are newly infected per unit time) − (number of pre-infectious individuals who become infectious per unit time)**

$\frac{dE(t)}{dt} = \lambda(t)\ S(t)$ **-** $f\ E(t)$

$\lambda(t)\ S(t)$**: The number of susceptible individuals who are newly infected per unit time.**

$fE(t)$**: The number of pre-infectious individuals who become infectious per unit time.**

f**: The rate at which individuals become infectious.**

4.3 DIFFERENTIAL EQUATION FOR THE RATE OF CHANGE IN THE NUMBER OF INFECTIOUS AND IMMUNE INDIVIDUALS

The rate of change in the number of infected and immune individuals can be expressed as follows:

$\frac{dI(t)}{dt} = fE(t)$ - $\gamma I(t)$

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

$I(t)$**: The number of infected individuals.**
$E(t)$**: The number of pre − infectious individuals.**
γ**: The rate at which infected individuals recover and become immune.**

4.4 METHODS FOR CHECKING DIFFERENTIAL EQUATIONS

4.4.1 DRAWING MODEL DIAGRAMS

A model diagram is created based on the provided differential equations. We may be able to understand that the differential equations are correctly formulated by producing this model diagram. To use this method, we must first comprehend it thoroughly.
The number of equations in the model must be equal to the number of compartments in the model diagram. If a minus or plus sign is introduced in front of a term in an equation, then the quantity reflected by that term either exits or enters that compartment.

4.4.2 CHECK FOR POPULATION SIZE

Summing up the differential equations in the model describing the transmission of an immunizing infectious disease in a closed population provides a helpful check. It is useful to determine whether the demographic assumptions have been correctly incorporated into the model.

For example, when we combine the equations for one model of infectious disease spread in a population, we obtain the following conclusions:

$\frac{dS(t)}{dt} + \frac{dE(t)}{dt} + \frac{dI(t)}{dt} + \frac{dR(t)}{dt} = [\text{-}\lambda(t)S(t)] + [\lambda(t)S(t) \text{ - } fE(t)] + [fE(t) \text{ - } \gamma I(t)] + [\gamma I(t)]$

$\frac{dS(t)}{dt} + \frac{dE(t)}{dt} + \frac{dI(t)}{dt} + \frac{dR(t)}{dt} = \mathbf{0}$

$\frac{dS(t)}{dt} + \frac{dE(t)}{dt} + \frac{dI(t)}{dt} + \frac{dR(t)}{dt}$ represents the rate of change of total population size. The fact that the equation equals zero suggests that the population in the model remains constant over time. This is consistent with our assumption of a closed population.

4.4.3 CHECK THE NUMBER AND DIRECTIONS OF THE ARROW

If the differential equation for a given compartment is correctly formulated, the number of arrows in or out of the compartment in the modem diagram must be equal to the number of terms in the differential equation for that compartment. Additionally, the direction of the arrow determines whether there should be a plus or minus sign in front of the term that corresponds to it. If an arrow exits the compartment, the term for that arrow is preceded by a minus sign; if the arrow enters the compartment, the term is preceded by a plus sign.

4.5 THE BASIC REPRODUCTION NUMBER

The basic reproduction number, R_o, is defined as the average number of infectious persons that result from the introduction of a typical infectious person into a completely susceptible population. When an infection is introduced into a completely susceptible population, the condition $R_o > 1$ is believed to be an important 'threshold' requirement that must be achieved for the number of infectious persons to increase. The expression for R_o is given by:

$R_o = \beta N D$

where,

β**: Rate at which two specific individuals come into effective contact per unit time.**

D**: Duration of infectiousness.**

N**: Size of the population.**

Assuming that the rate at which individuals recover from being infectious (γ) and the average duration of infectiousness are related through the equation D = $\frac{1}{\gamma}$, we can rewrite the above equation as:

$R_o = \frac{\beta N}{\gamma}$

βN**: Number of individuals effectively contacted by a given infectious person per unit time.**

$\beta N D$**: Number of individuals effectively contacted by a given infectious person during the entire infectious period.**

For the purpose of simplicity, we will look at the equations of the Susceptible-Infectious-Recovered (SIR) model. The consequences of population births and deaths are not taken into account. $S(t)$, $I(t)$ and $R(t)$ are the number of the individuals who move from one compartment to the other per unit time. The number of infectious individuals will increase at any given time if the number of individuals infectious per unit time $\beta S(t) I(t)$ exceeds the number of infectious individuals who stop being infected per unit time ($\gamma I(t)$) can be expressed as $\beta S(t) I(t) > \gamma I(t)$.

If an infectious individual is placed into a completely susceptible population, the number of individuals who are initially susceptible to infection equals the population size. Substituting $S(t) =$ N into the previous expression indicates that the following conditions must be satisfied for the number of infected people to increase after one infectious person enters the population:

$\beta N I(t) > \gamma I(t)$

By cancelling the number of infectious persons at time t (I(t)), we get $\beta N > \gamma$.
Now divide both the sides of the above expression by the rate at which individuals recover i.e., γ.

$\frac{\beta N}{\gamma} > 1$
Substituting $\frac{1}{\gamma} = D$ into the above expression, we get the result that the number of infectious persons increases following the introduction of an infectious person into a susceptible population as: $\beta N D > 1$

4.6 PREDICTIONS FOR EARLY STAGES IN AN EPIDEMIC

One of the key takeaways from the simple theory of epidemics is that we should be able to estimate the basic reproduction number of the infection using data on the prevalence of infectious individuals during the early stages of an epidemic of a new or reemerging disease. There are various formulas for estimating R_o from the early-stage of epidemic. Each of them necessitates estimations which is known as the epidemic growth rate, which is denoted by Λ. This prediction or estimation could aid in directing the public health response to a new disease.

4.7 GROWTH RATE IN AN EPIDEMIC

The number of infectious individuals increases at a roughly constant rate during the early stage of an epidemic. This rate is termed as the epidemic growth rate.
During the initial stage of an epidemic, the following expression is obtained for the number of infectious individuals at time t $(I(t))$.
$I(t) \approx I(0)e^{\Lambda t}$
where,
$I(0)$ **= Number of infected individuals at the early stage.**

Taking natural logarithm on both sides, we get a relation between $I(t)$

and Λ.

$\ln(I(t)) = \ln(I(0)) + \Lambda t$

Plotting the natural logarithm of the number of infected individuals against time, we get the result as a straight line and the gradient of that line being Λ.

Hence, we can estimate the growth rate of an epidemic using empirical data which is achieved by plotting the natural logarithm of the observed number of individuals and calculating the gradient of the resulting line.

4.8 EQUATIONS FOR BASIC REPRODUCTION NUMBER

The equations that connect the basic reproduction number and the epidemic growth rate is obtained as a result from different assumptions about the average duration and distribution of both pre-infectious and infectious periods.

The infections for which the pre-infectious duration is short when compared to the infectious duration. The expression for the basic reproductive number is given as:

$R_o = 1 + \Lambda D$

If neither the pre-infectious time period nor infectious time period is short, then the equation for R_o is expressed as:

$R_o = (1 + \Lambda D)\ (1 + \Lambda D')$

where,

D **= Average infectious time period**

D' **= Average pre-infectious time period**

4.9 ESTIMATING THE AVERAGE FORCE OF INFECTION

As aforementioned, the relationship between the force of infection and the total number of infectious individual at time t, provided these individuals contact each other randomly is represented by the equation given below.

$\lambda(t) = \beta I(t)$

β: Rate of effective contact between two specific individuals per unit of time

Since the population of infectious people changes over time, the force of infection must likewise change over time if infections are to be minimized. Furthermore, in the absence of vaccination or other treatments, the average infection force remains roughly constant. We will omit the t and use the symbol λ to symbolize this average value.

Chapter 5

A CASE STUDY OF KERALA USING BASIC REPRODUCTION NUMBER

5.1 INTRODUCTION

The largest worldwide health catastrophe of the twenty-first century has been the severe acute respiratory syndrome coronavirus (COVID-19). Patients infected with COVID-19 often exhibit common symptoms such as coughing, fever, and respiratory problems. In the worst scenarios, it may result in life-threatening medical issues like pneumonia and kidney failure, which could result in patient death.

In order to save lives and lessen the social and economic effects of the disease, it is crucial from a strategic and health care management perspective to understand how a disease spreads and how to predict when it will do so. The outbreak began in Wuhan, a Chinese city, in December 2019. As a result of the connections between cities, nations, and even continents, the virus has since multiplied exponentially in many nations around the world. On March 11, 2020, the World Health Organization declared it a global epidemic. According to research on COVID-19, it spreads by respiratory droplets and direct human contact.

India, the second most populous nation in the world, is a developing nation. Controlling COVID-19's spread in India was therefore very dif-

ficult. The first case of COVID-19 in India was reported from Kerala on 30 January 2020. Social distancing and awareness campaigns were conducted as primary measures to prevent human-to-human transmission of the virus. The Indian government declared the first official 14-day nationwide lockdown on March 25, 2020. As a result, the public lockdown has been imposed in India in five stages.
Under certain conditions, mathematical models have the ability to track and predict the epidemic trajectory. Various mathematical and statistical models have been proposed to comprehend the dissemination trajectory for a pandemic. Among these models, Susceptible (S) - Infected (I) - Recovered (R) - Model (SIR model) has been frequently used in the past to predict the dynamics of various contagious diseases.

5.2 SIR MODEL FOR COVID – 19 - SETTING UP OF MODEL

The SIR Model for COVID - 19 consists of three compartments - susceptible, infected and recovered.

5.3 SETTING UP OF EQUATIONS

In order to predict the epidemic of a disease, we are required to find the value of R_o using the SIR model. Let us consider SIR model of first form and second form.

In the SIR model of first form,

$N(t) = S(t) + I(t) + R(t)$ ..... (i)

where,

N(t) = Total population size at time t

S(t) = Total number of individuals who are susceptible at time t

I(t) = Total number of individuals who are infectious at time t

R(t) = Total number of individuals who are immune or recovered at time t

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

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

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

For the SIR model of second form, divide equation (i) throughout by N(t), we get

$s(t) + i(t) + r(t) = 1$

$\frac{ds(t)}{dt}$ = - $\beta s(t)i(t)$

$\frac{di(t)}{dt}$ = $\beta s(t)i(t)$ - $\gamma i(t)$

$\frac{dr(t)}{dt} = \gamma i(t)$

β is the average number of contacts of an infected person per unit time. It is also known as infection rate of the disease.

$\frac{S}{N}$ is the fraction which is susceptible to contracting the disease.

β $\frac{S}{N}$ is the average number of new infected individuals generated by one infected individual per unit time.

$\beta \frac{S}{N} I$ is the average of new infected individuals generated by all infected individuals per unit time.

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

Here, negative sign indicates decrease in S(t) as $\frac{dS(t)}{dt} < 0$

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

where,

$\gamma = \frac{1}{D}$

D = **the number of days in the infectious period.**

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

R_o **denotes the relationship between the proportions of the population that is susceptible.**

$R_o = \frac{\beta S}{\gamma}$ ..... **(ii)**

$R_o = \frac{\beta}{\gamma}$ [**N** $\cong$ **S**]..... **(iii)**

where,

β = **Rate of Infection**

γ = **Rate of Recovery**

In general, an epidemic will occur if the number of infected people increases, i.e., $i(t)$ **is an increasing function.**

We know that,

$\frac{di(t)}{dt}$ = $\beta s(t) i(t)$ - $\gamma i(t)$

$i(t) > 0$ .....[$i(t)$ **is an increasing function**]

$\beta s(t) i(t) - \gamma i(t) > 0$

$(\beta s - \gamma) i > 0$

$\beta s > \gamma$

$\frac{\beta s}{\gamma} > 1$

$R_o > 1$ .....[from (ii)]

Similarly, an epidemic will not occur if the number of infected people decreases, i.e., $i(t)$ is a decreasing function.

$i(t) < 0$ .....[$i(t)$ **is a decreasing function**]

$\beta s(t)i(t) - \gamma i(t) < 0$

$(\beta s - \gamma)i < 0$

$\beta s < \gamma$

$\frac{\beta s}{\gamma} < 1$

$R_o < 1$ .....[from (ii)]

From the above two conditions, we can conclude that:

- **If $R_o > 1$, an epidemic will occur as the number of infected individual increases.**
- **If $R_o < 1$, an epidemic will not occur as the number of infected individual decreases.**

5.4 FINDING R_o FOR SIR MODEL OF COVID -19 FOR KERALA

Using the above conditions for R_o, we will verify the results whether an epidemic occurs or does not occur in a given population.

5.4.1 SETTING UP OF THE QUESTION

Consider the data for the confirmed, death and recovery cases in a given demographics. Here, we have chosen the population statistics for Kerala between February 2020 and August 2022. The population data for each case and year is presented in tabular format.

MONTH (2020)	CONFIRMED	RECOVERED	DEATH
FEBRUARY	2	3	0
MARCH	238	21	2
APRIL	256	359	1
MAY	772	207	6
JUNE	3173	1714	15
JULY	19171	10719	49
AUGUST	51772	38519	221
SEPTEMBER	120721	76682	448
OCTOBER	236999	212100	742
NOVEMBER	169877	198389	760
DECEMBER	157951	153767	828

Data for the year 2020

MONTH (2021)	CONFIRMED	RECOVERED	DEATH
JANUARY	168245	161726	671
FEBRUARY	130225	151291	454
MARCH	65181	88907	424
APRIL	446599	167397	687
MAY	955396	1048584	3507
JUNE	397586	499202	4420
JULY	466596	399382	3546
AUGUST	666472	608035	4007
SEPTEMBER	623625	695658	4299
OCTOBER	287799	344519	6594
NOVEMBER	173157	200187	8451
DECEMBER	105363	121909	7662

Data for the year 2021

MONTH (2022)	CONFIRMED	RECOVERED	DEATH
JANUARY	778491	433716	6601
FEBRUARY	473545	793526	10938
MARCH	32766	54248	2580
APRIL	9045	9063	1155
MAY	16525	12420	679
JUNE	84456	60767	276
JULY	79702	95027	461
AUGUST	33532	37820	358

Data for the year 2022

We will be considering the above data for each cases of each month for the calculation of R_o.

5.5 CALCULATION OF R_o

Using the aforementioned conditions for the basic reproduction number, we are required to calculate the value of R_o in order substantiate the occurrence of epidemic in each month of 2020, 2021 and 2022 for the given population of Kerala.

Consider the data of February 2020.
Here, $\beta = 2$ and $\gamma = 3$
We know that,
$R_o = \frac{\beta}{\gamma} = \frac{2}{3} = 0.667$

Consider the data of March 2020.
Here, $\beta = 238$ and $\gamma = 21$
We know that,
$R_o = \frac{\beta}{\gamma} = \frac{238}{21} = 11.333$

Consider the data of April 2020.
Here, $\beta = 256$ and $\gamma = 359$
We know that,

$R_o = \frac{\beta}{\gamma} = \frac{256}{359} = \mathbf{0.713}$

Consider the data of May 2020.

Here, $\beta = 772$ and $\gamma = 207$

We know that,

$R_o = \frac{\beta}{\gamma} = \frac{772}{207} = \mathbf{3.729}$

Consider the data of June 2020.

Here, $\beta = 3173$ and $\gamma = 1714$

We know that,

$R_o = \frac{\beta}{\gamma} = \frac{3173}{1714} = \mathbf{1.851}$

Consider the data of July 2020.

Here, $\beta = 19171$ and $\gamma = 10719$

We know that,

$R_o = \frac{\beta}{\gamma} = \frac{19171}{10719} = \mathbf{1.788}$

Consider the data of August 2020.

Here, $\beta = 51772$ and $\gamma = 38519$

We know that,

$R_o = \frac{\beta}{\gamma} = \frac{51772}{38519} = \mathbf{1.344}$

Consider the data of September 2020.

Here, $\beta = 120721$ and $\gamma = 76682$

We know that,

$R_o = \frac{\beta}{\gamma} = \frac{120721}{76682} = \mathbf{1.574}$

Consider the data of October 2020.

Here, $\beta = 236999$ and $\gamma = 212100$

We know that,

$R_o = \frac{\beta}{\gamma} = \frac{236999}{212100} = \mathbf{1.117}$

Consider the data of November 2020.

Here, β = 169877 and γ = 198389

We know that,

$R_o = \frac{\beta}{\gamma} = \frac{169877}{198389} = \mathbf{0.856}$

Consider the data of December 2020.

Here, β = 157951 and γ = 153767

We know that,

$R_o = \frac{\beta}{\gamma} = \frac{157951}{153767} = \mathbf{1.027}$

Consider the data of January 2021.

Here, β = 168245 and γ = 161726

We know that,

$R_o = \frac{\beta}{\gamma} = \frac{168245}{161726} = \mathbf{1.040}$

Consider the data of February 2021.

Here, β = 130225 and γ = 151291

We know that,

$R_o = \frac{\beta}{\gamma} = \frac{130225}{151291} = \mathbf{0.860}$

Consider the data of March 2021.

Here, β = 65181 and γ = 88907

We know that,

$R_o = \frac{\beta}{\gamma} = \frac{65181}{88907} = \mathbf{0.733}$

Consider the data of April 2021.

Here, β = 446599 and γ = 167397

We know that,

$R_o = \frac{\beta}{\gamma} = \frac{446599}{167397} = \mathbf{2.667}$

Consider the data of May 2021.

Here, β = 955396 and γ = 1048584

We know that,

$R_o = \frac{\beta}{\gamma} = \frac{955396}{1048584} = \mathbf{0.911}$

Consider the data of June 2021.

Here, β = 397586 and γ = 499202

We know that,

$R_o = \frac{\beta}{\gamma} = \frac{397586}{499202} =$ **0.796**

Consider the data of July 2021.

Here, β = 466596 and γ = 399382

We know that,

$R_o = \frac{\beta}{\gamma} = \frac{466596}{399382} =$ **1.168**

Consider the data of August 2021.

Here, β = 666472 and γ = 608035

We know that,

$R_o = \frac{\beta}{\gamma} = \frac{666472}{608035} =$ **1.096**

Consider the data of September 2021.

Here, β = 623625 and γ = 695658

We know that,

$R_o = \frac{\beta}{\gamma} = \frac{623625}{695658} =$ **0.896**

Consider the data of October 2021.

Here, β = 287799 and γ = 344519

We know that,

$R_o = \frac{\beta}{\gamma} = \frac{287799}{344519} =$ **0.835**

Consider the data of November 2021.

Here, β = 173157 and γ = 200187

We know that,

$R_o = \frac{\beta}{\gamma} = \frac{173157}{200187} =$ **0.864**

Consider the data of December 2021.

Here, β = 105363 and γ = 121909

We know that,

$R_o = \frac{\beta}{\gamma} = \frac{105363}{121909} = \mathbf{0.864}$

Consider the data of January 2022.

Here, β = 778491 and γ = 433716

We know that,

$R_o = \frac{\beta}{\gamma} = \frac{778491}{433716} = \mathbf{1.795}$

Consider the data of February 2022.

Here, β = 473545 and γ = 793526

We know that,

$R_o = \frac{\beta}{\gamma} = \frac{473545}{793526} = \mathbf{0.596}$

Consider the data of March 2022.

Here, β = 32766 and γ = 54248

We know that,

$R_o = \frac{\beta}{\gamma} = \frac{32766}{54248} = \mathbf{0.604}$

Consider the data of April 2022.

Here, β = 9045 and γ= 9063

We know that,

$R_o = \frac{\beta}{\gamma} = \frac{9045}{9063} = \mathbf{0.998}$

Consider the data of May 2022.

Here, β = 16525 and γ = 12420

We know that,

$R_o = \frac{\beta}{\gamma} = \frac{16525}{12420} = \mathbf{1.330}$

Consider the data of June 2022.

Here, β = 84456 and γ = 60767

We know that,

$R_o = \frac{\beta}{\gamma} = \frac{84456}{60767} = \mathbf{1.389}$

Consider the data of July 2022.

Here, β = 79702 and γ = 95027

We know that,

$R_o = \frac{\beta}{\gamma} = \frac{79702}{95027} = 0.838$

Consider the data of August 2022.

Here, β = 33532 and γ = 37820

We know that,

$R_o = \frac{\beta}{\gamma} = \frac{33532}{37820} = 0.886$

5.6 OBSERVATION

The value of R_o for each month of 2020, 2021 and 2022 is presented in tabular format.

MONTH (2020)	VALUE OF R_o
FEBRUARY	0.667
MARCH	11.333
APRIL	0.713
MAY	3.729
JUNE	1.851
JULY	1.788
AUGUST	1.334
SEPTEMBER	1.795
OCTOBER	1.117
NOVEMBER	0.856
DECEMBER	1.027

R_o value for the year 2020

MONTH (2021)	VALUE OF R_o
JANUARY	1.040
FEBRUARY	0.860
MARCH	0.733
APRIL	2.667
MAY	0.911
JUNE	0.796
JULY	1.168
AUGUST	1.096
SEPTEMBER	0.896
OCTOBER	0.835
NOVEMBER	0.864
DECEMBER	0.864

R_o value for the year 2021

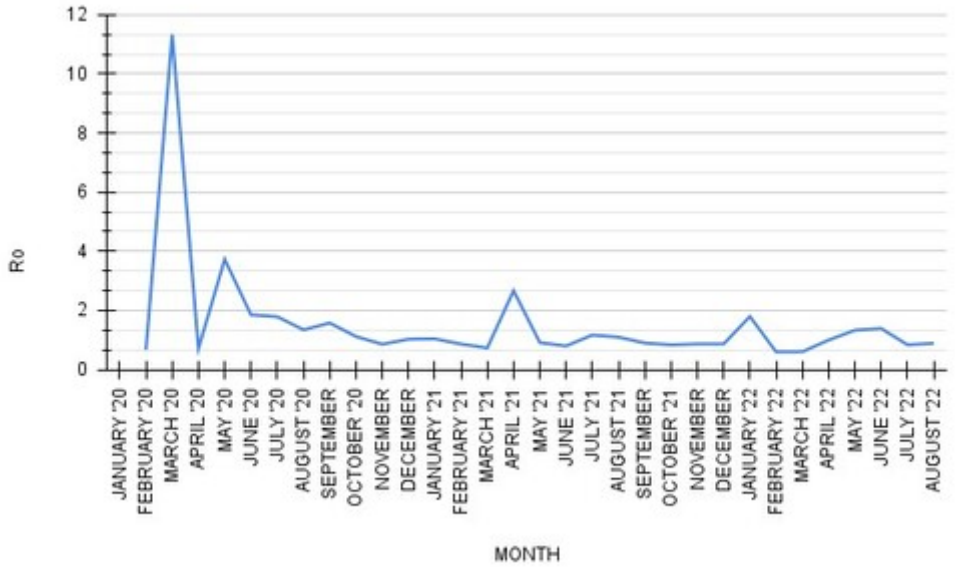
MONTH (2022)	VALUE OF R_o
JANUARY	1.795
FEBRUARY	0.596
MARCH	0.604
APRIL	0.998
MAY	1.330
JUNE	1.389
JULY	0.838
AUGUST	0.886

R_o value for the year 2022

From the above observation, we can scrutinize that for the months with $R_o > 1$, the number of infected individuals were high which led to the occurrence of epidemic, whereas, for the months with $R_o < 1$, the number of infected individuals were comparatively low which did not led to the occurrence of the epidemic in the given population.

5.7 VERIFICATION OF RESULTS

The following graph depicts the peaks and troughs of the epidemic during three consecutive years, from February 2020 to August 2022.



We were able to validate whether an epidemic actually occurred or not for the given population between February 2020 and August 2022 using basic reproduction number, R_o. The number of infectious individuals were high when $R_o > 1$ which led to the occurrence of epidemic and the number of infectious individuals were low when $R_o < 1$ which did not led to the occurrence of epidemic.

In order to strengthen our result, we can verify the fact that the first official nationwide lockdown was in the month of March 2020. Here, we can observe that the R_o value for March 2020 was greater than 1, i.e., $R_o = 11.333$.

Hence, we have substantiated whether an epidemic occurred or not for each month during 2020, 2021 and 2022 using basic reproduction number and the obtained results are accurate.

Chapter 6

CONCLUSION

We recognised the applications of mathematical modelling in our life after reading the content offered in this project. We understand that this is only an attempt to introduce the reader to a few novel techniques. In this project, we were able to substantiate whether an epidemic occurred or not between February 2020 and August 2022 for the given demographic.

Mathematical modelling is a wide, diverse area that implores engineers, scientists, and mathematicians to engage their interest and commitment in order to tackle the issues faced by humanity. A mathematical model is an abstract depiction of a phenomenon created through the use of equations that generate perspectives of the general behaviour of an epidemic event, as well as serving as a means of examining the influence of specific factors on the spread of disease. It is crucial to keep in mind that these models are created for specific situations utilising the information that is currently available and making assumptions in the absence of such knowledge while evaluating their forecasts. These assumptions may have a significant impact on how these models forecast the future and how those predictions are interpreted.

Mathematical modelling is a highly versatile method used in the epidemiology of infectious diseases that enables extrapolations of epidemic behaviours as well as the detection of patterns in epidemics.

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