# S-I-R Model and COVID-19 Data-Based Numerical Ro Estimation for Pandemic Modeling

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## Abstract

A contagious disease transmits from human to human or animal to human. At present world is encountered with such a disease, known as COVID-19. More than half a million people have died due to this pandemic. The pandemic started in China and spread within no time to other parts of the world. Italy and USA are the most unfortunate countries as a large number of deaths occurred in these two countries. No doubt this contagious disease has created social as well as economic problems all over the world, especially in underdeveloped countries. The disease easily transmits to a healthy person during social contact. An epidemic model was developed known as the Kermack-McKendrick model described as SIR (Susceptible Infected and Recovered) model, it deals with the rate of transmission of disease and rate of infection. It gives a trend of infectious disease in a large population. The model helps epidemiologists and health policymakers to understand the probable transmission of disease and to take possible and effective measures to control or reduce the spread of the virus. The factor  $R_{o}$ , known as the reproductive number, can be considered as a threshold value for the disease to be an epidemic. In this study, we used the SIR model to study the effect of COVID-19 in Pakistan. Three coupled differential equations of the SIR model have been solved by numerically using COVID-19 data for Pakistan. The R<sub>o</sub> estimated by the current Pakistan COVID-19 data is found to be 2.656 from which control measures will cause a decrease in  $R_o$ . Due to the reduction in  $R_o$ , the apex of the infected population curve predicted to be range from 26 % to 3 %, and the time to reach the apex ranges from 161 to 710 days. Also, the current data is compared with the numerical values by solving the SIR model. However, the model has limitations due to which parameters can be approximately calculated that might match the actual values to some extent. The application of the model is simple and students can easily learn about the computational techniques used to solve the coupled differential equations.

Index Terms: COVID-19, Kermack-McKendrick Model, Pandemic, Runge-Kutta 4th Order, SIR Model.

# I. INTRODUCTION

Pandemic diseases are dangerous for both humans and animals. In past, millions of people have died from many different pandemic diseases like tuberculosis, malaria, HIV/AIDS, etc. Recently COVID-19 that was evolved in China and later spread worldwide has caused almost half a million deaths. The disease had been declared to be a pandemic by WHO [1]. The outbreak of pandemic disease is always a difficult problem for the common man, medical specialists, and the government. Epidemiologists and scientists study such diseases to find a way to control, prevent and reduce the outbreak. Various mathematical models have been proposed to study the effect of different diseases like influenza, HIV/AIDS, malaria, etc. The history of the application of mathematical models to study epidemic diseases is very long. Up till now, many different models have been proposed to study such epidemics. Infectious diseases usually transmit through space from one living organism to another. COVID-19 infection is, however, transmitted through social contact. The lockdown strategy has saved a large population from this virus. Though disease dynamics can be understandable

from biological activities, mathematical models give useful information about the disease. A brief history of the development of mathematical models is given by researcher Brauer [2]. Two researchers Arino and Watmough discussed various mathematical models [3]. Other authors like Hueng Pang and Lee slightly modified the SIR model, they used a population without dispersion by considering the concept of radius. They showed that the propagation of an epidemic depends on population density and the infectious radius [4]. A scientist named Perasso introduced reproduction numbers to study the epidemic model, he used the matrix method to solve the PDE model and to find the reproduction number [5]. Another researcher Sattenspiel discussed mathematical modeling of the epidemic in the human population and reviewed models developed for AIDS, influenza, and malaria [6]. Such a mathematical model is the SIR-Susceptible Infected and Recovered model which is one of the most basic models to address the spread of disease [7]. Other complex models are its variants but the crucial risk factor for the transmittable of an infectious disease is due to the presence of infectious cases in the local population, this tenet is reflected in almost all the mathematical models [11-13].



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 $R_o$  is the basic reproductive number that may be considered the threshold for which the disease can be considered an epidemic. Such models help epidemiologists and health policymakers to understand the probable transmission of disease and to take possible and effective control measures to reduce its spread. In this study, we attempted to estimate the  $R_o$  by using the online available COVID-19 data of Pakistan. The effects on the spread of disease for the population at different values of  $R_o$  are predicted by the numerical solution of the model on similar data.

# II. METHODOLOGY

The differential equations can be numerically solved by computational methods such as the Runge-Kutta 4<sup>th</sup> order (RK4) method. In this study, the RK4 method is simulated on MS Excel® and applied to Pakistan's COVID-19 data. MS Excel® is user-friendly and users can modify parameters to observe changes.

A preview of the model is shown in figures i.e., figure I, and figure II.



Figure I: Pandemic Modeling using SIR Model and Numerical Estimation of  $R_0$  by COVID-19 Data

|    |             |   |   |          |          | RK4 r    | nethod   |          |          |          |          |          |          |          |          |
|----|-------------|---|---|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|
|    |             |   | S | d Iĝ     | I I      | R        | S        | I I      | R        | S        | I        | R        | S        | i - 1    | R        |
| t  | S           | 1 | R | K1       | K1       | K1       | K2       | K2       | К2       | К3       | K3       | КЗ       | K4       | К4       | K4       |
| 0  | 220,037,333 | 2 | 0 | -0.37942 | 0.236568 | 0.142857 | -0.40186 | 0.250559 | 0.151306 | -0.40319 | 0.251386 | 0.151806 | -0.42712 | 0.266303 | 0.160813 |
| 1  | 220,037,333 | 2 | 0 | -0.42707 | 0.266272 | 0.160795 | -0.45232 | 0.28202  | 0.170304 | -0.45382 | 0.282951 | 0.170867 | -0.48075 | 0.299741 | 0.181006 |
| 2  | 220,037,332 | 3 | 0 | -0.48069 | 0.299706 | 0.180985 | -0.50912 | 0.317431 | 0.191689 | -0.5108  | 0.31848  | 0.192322 | -0.54111 | 0.337377 | 0.203733 |
| 3  | 220,037,332 | 3 | 1 | -0.54105 | 0.337338 | 0.20371  | -0.57305 | 0.357289 | 0.215758 | -0.57494 | 0.358469 | 0.21647  | -0.60905 | 0.379739 | 0.229315 |
| 4  | 220,037,331 | 3 | 1 | -0.60898 | 0.379696 | 0.229288 | -0.645   | 0.402152 | 0.242849 | -0.64713 | 0.40348  | 0.243651 | -0.68553 | 0.427421 | 0.258108 |
| 5  | 220,037,330 | 4 | 1 | -0.68545 | 0.427372 | 0.258079 | -0.72599 | 0.452647 | 0.273342 | -0.72839 | 0.454142 | 0.274244 | -0.77161 | 0.481089 | 0.290517 |
| 6  | 220,037,330 | 4 | 1 | -0.77152 | 0.481034 | 0.290484 | -0.81715 | 0.509483 | 0.307664 | -0.81985 | 0.511166 | 0.30868  | -0.86849 | 0.541496 | 0.326996 |
| 7  | 220,037,329 | 5 | 2 | -0.86839 | 0.541434 | 0.326958 | -0.91975 | 0.573456 | 0.346295 | -0.92279 | 0.575349 | 0.347438 | -0.97754 | 0.609489 | 0.368054 |
| 8  | 220,037,328 | 5 | 2 | -0.97743 | 0.609418 | 0.368012 | -1.03524 | 0.645461 | 0.389777 | -1.03866 | 0.647592 | 0.391064 | -1.10029 | 0.686018 | 0.414268 |
| 9  | 220,037,327 | 6 | 2 | -1.10016 | 0.685939 | 0.414221 | -1.16523 | 0.726507 | 0.438718 | -1.16907 | 0.728906 | 0.440167 | -1.23844 | 0.772157 | 0.466285 |
| 10 | 220,037,326 | 7 | 3 | -1.2383  | 0.772068 | 0.466232 | -1.31153 | 0.817729 | 0.493805 | -1.31587 | 0.82043  | 0.495436 | -1.39395 | 0.869112 | 0.524834 |
| 11 | 220,037,324 | 7 | 3 | -1.39378 | 0.869011 | 0.524773 | -1.47622 | 0.920406 | 0.555809 | -1.48109 | 0.923446 | 0.557645 | -1.56897 | 0.97824  | 0.590734 |
| 12 | 220,037,323 | 8 | 4 | -1.56879 | 0.978127 | 0.590666 | -1.66157 | 1.035976 | 0.625599 | -1.66706 | 1.039397 | 0.627665 | -1.76598 | 1.101071 | 0.664908 |
| 13 | 220,037,321 | 9 | 4 | -1.76578 | 1.100944 | 0.664832 | -1.87021 | 1.166056 | 0.704151 | -1.87638 | 1.169907 | 0.706476 | -1.98772 | 1.239326 | 0.748396 |

Figure II: Excel Simulation of SIR Model

The details of the model are provided in the following articles:

# A. Sir Model

For modeling an epidemic, a population-based model was developed (1927) [14], and [15]. It is an epidemiological compartmental model in which the entire population is thought to be divided into compartments.

The basic structure of the model is illustrated in figure III.



The movement between the compartments is a function of rates. The transmission of the disease is due to the mixing of an infected individual with a susceptible population. Therefore, at any given point in time, some of the population from the susceptible compartment becomes infected and thus becomes part of the infected compartment. Similarly, some of the individual either gains immunity or decrease are moved from the infected compartment to the recovered group. These changes in the population among the compartments are assumed to be continuous and governed by the following differential equations:

$$\frac{dS}{dt} = -\beta SI \tag{1}$$

$$\frac{dI}{dt} = \beta SI - \gamma I \tag{2}$$

$$\frac{dR}{dt} = \gamma I \tag{3}$$

Where;

S(t) = Susceptible Population,

I(t) = Infected People among the Population, and R(t) = Recovered People among the Population (this includes both populations are which are recovered and deceased due to disease).

S + I + R = N = Total Population (which will remain constant)

Also;

t = Time in Days, and

 $\beta$  and  $\gamma$  = Transmission Coefficients between the Susceptible to Infected and Infected to Recovered Population.

$$\beta = \frac{\kappa \tau}{N}$$
 = Transmission Coefficient

It is a measure of the prospect that contact between a susceptible and an infective may result in a new infection.

Here;

 $\kappa$  = Contact per Unit Time, and  $\tau$  = Transmissibility of the Disease.

 $\gamma = \frac{1}{D}$  = Removal Rate or Removal Coefficient.

It is a measure of the fraction of the infective population that ceases to be infective.

The model has some limitations such as it is considered the population to be closed for the initial conditions at t = 0: S(0) = N if I(0) = R(0) = 0 and this value will continue to project the future cases but in actuality, the population is a compartment or due to disease only but there are other factors dynamic. Moreover, the model considers deaths within the due to which the number of death in the population will vary as compared to the model. And the value of the coefficient will also vary as effective measures will be followed to control the disease.

#### B. R<sub>o</sub> (Basic Reproductive Number)

The basic reproduction number,  $R_o$  is defined as the expected number of secondary cases produced by an infected individual in a completely susceptible population. The  $R_o$  can also be defined by the following proportionality:

$$R_o \alpha \left(\frac{infection}{contact}\right) \left(\frac{contact}{time}\right) \left(\frac{time}{infection}\right)$$

As by the SIR model, it is defined that the following sum:

$$\frac{dS}{dt} + \frac{dI}{dt} + \frac{dR}{dt} = \frac{dN}{dt} = 0$$

Considering finite differences of time:

$$\frac{\Delta S}{\Delta t} + \frac{\Delta I}{\Delta t} + \frac{\Delta R}{\Delta t} = \frac{\Delta N}{\Delta t} = 0$$

$$\frac{\Delta I}{\Delta t} = \beta S(t)I(t) - \gamma I(t)$$
$$\frac{\Delta I}{\Delta t} = \gamma \left(\frac{\beta}{\gamma}S(t) - 1\right)I(t)$$

The above equation gives:

$$R_o = \frac{\beta}{\gamma} S(0) \tag{4}$$

If  $R_o > 1$  then  $\frac{\Delta I}{\Delta t} > 1$  thus from a biological standpoint epidemic will occur as the disease shows contagious comportment [16]. The value of  $R_o$  is contingent on both the host and disease population [1].

#### C. Numerical Estimation of Sir Variables and Ro

The equations [i.e., eq. (1) - eq. (3)] are coupled differential equations that can be solved by numerical methods. In this study, we have used the Runge-Kutta 4<sup>th</sup> order (RK4) method [17].

$$y_{n+1} = y(t + \Delta t) = y_n + \frac{1}{6}(K_1 + 2K_2 + 2K_3 + K_4)$$

Here;

 $y_n = y_0 =$  Initial condition.

The transformation of SIR model equations into the RK4 formalism is given by:

$$S_{n+1} = S(t + \Delta t) = S_n + \frac{1}{6} \left( K_1^{\ S} + 2K_2^{\ S} + 2K_3^{\ S} + K_4^{\ S} \right) (5)$$

$$K_1^{\ S} = -\beta \ S_n \ I_n$$

$$K_2^{\ S} = -\beta \ \left( S_n + \frac{K_1^{\ S} \ \Delta t}{2} \right) \left( I_n + \frac{K_1^{\ I} \ \Delta t}{2} \right)$$

$$K_3^{\ S} = -\beta \ \left( S_n + \frac{K_2^{\ S} \ \Delta t}{2} \right) \left( I_n + \frac{K_2^{\ I} \ \Delta t}{2} \right)$$

$$K_4^{\ S} = -\beta \ \left( S_n + K_3^{\ S} \ \Delta t \right) \left( I_n + K_3^{\ I} \ \Delta t \right)$$

Similarly,

$$I_{n+1} = I(t + \Delta t) = I_n + \frac{1}{6} \left( K_1^{\ I} + 2K_2^{\ I} + 2K_3^{\ I} + K_4^{\ I} \right) (6)$$
$$R_{n+1} = R(t + \Delta t) = R_n + \frac{1}{6} \left( K_1^{\ R} + 2K_2^{\ R} + 2K_3^{\ R} + K_4^{\ R} \right)$$
(7)

The *K* coefficients for equations [i.e., eq. (6) and eq. (7)] can be transformed similarly as given in eq. 5. The RK4 method is used in this study to find the population and other parameters by estimated  $R_o$  values. This numerical technique along with Euler forward method was also applied for the spread of Ebola (Hossain et al., 2017) [21].

For the estimation of  $R_o$ , the following relation is derived by Eq. (2) as finite differences in time:

$$\Delta I = (\beta SI - \gamma I) \Delta t$$

$$\frac{\Delta I}{\gamma} = \left(\frac{\beta SI - \gamma I}{\gamma}\right) \Delta t$$

$$\frac{\Delta I}{\gamma} = (R_o I - I) \Delta t$$

$$R_o - 1 = \frac{\Delta I}{I\gamma \Delta t}$$

$$R_o = \frac{\Delta I}{\frac{\Delta R}{\Delta t} \Delta t} + 1$$

$$R_o = \left(\frac{\Delta I}{\Delta R}\right) + 1$$

Here;  $\Delta I = I_n - I_{n-1}$ , and  $\Delta R = R_n - R_{n-1}$ 

The  $R_o$  approximated at different points of Pakistan COVID-19 data is averaged and then calculated the parameters of the SIR model by eq. (5) –eq. (7). The effect of disease control measures will reduce the value of  $R_o$  so parameters at that particular value are also estimated.

## III. RESULT

The estimation of  $R_o$  along with the COVID-19 available data is presented in table I. The value of  $R_o$  is estimated by eq. (8).

We have an arbitrarily selected interval of five days for which the R<sub>o</sub> is calculated from the officially online available data of Pakistan starting from February 26<sup>th</sup>, 2020 (t = 0) to April 21<sup>st</sup>, 2020 (t = 54) [19].

| Table I: Pakistan COVID-19 Data and Es | timation of R <sub>o</sub> |
|--|----------------------------|
|--|----------------------------|

(8)

| Dava | Susceptible<br>Population<br>S | ceptible Infected Cases |            | Death |            | Recovered from<br>Infection |            | Recovered<br>Population<br>R     |      | AD      | n              |
|------|--------------------------------|-------------------------|------------|-------|------------|-----------------------------|------------|----------------------------------|------|---------|----------------|
| Days |                                | New                     | Cumulative | New   | Cumulative | New                         | Cumulative | Sum of<br>Recovered<br>and Death | ΔΙ   |         | K <sub>0</sub> |
| 4    | 220037333                      | 0                       | 4          | 0     | 0          | 0                           | 0          | 0                                | 0    | 0.286   | 1.000          |
| 9    | 220037333                      | 0                       | 6          | 0     | 0          | 1                           | 1          | 0                                | 0    | 0.429   | 1.000          |
| 14   | 220037333                      | 1                       | 20         | 0     | 0          | 1                           | 2          | 0                                | 1    | 1.429   | 1.700          |
| 19   | 220037333                      | 134                     | 187        | 0     | 0          | 1                           | 4          | 0                                | 54   | 13.357  | 5.043          |
| 24   | 220037325                      | 151                     | 646        | 0     | 3          | 0                           | 5          | 8                                | 138  | 46.143  | 3.991          |
| 29   | 220037216                      | 140                     | 1197       | 1     | 9          | 2                           | 23         | 32                               | 211  | 85.500  | 3.468          |
| 34   | 220036897                      | 174                     | 2039       | 1     | 26         | 24                          | 82         | 108                              | 252  | 145.643 | 2.730          |
| 39   | 220036049                      | 244                     | 3062       | 4     | 45         | 39                          | 170        | 215                              | 494  | 218.714 | 3.259          |
| 44   | 220033299                      | 206                     | 4695       | 3     | 66         | 155                         | 727        | 793                              | 316  | 335.357 | 1.942          |
| 49   | 220027111                      | 546                     | 6383       | 15    | 111        | 68                          | 1446       | 1557                             | 536  | 455.929 | 2.176          |
| 54   | 220017280                      | 70                      | 8418       | 8     | 176        | 102                         | 1970       | 2146                             | 1147 | 601.286 | 2.908          |
|      | Average $R_o = 2.656$          |                         |            |       |            |                             |            |                                  |      |         |                |

S=N=220,037,337 Population of Pakistan [18]

The average  $R_o$  value found is used to find the approximate no. of infected cases and recovered population by using the RK4 method as described in equations [ i.e., eq. (5) –eq. (7)]. The data obtained from the model is compared with the available data represented in table II but the coefficients *K* of the RK4 model are not given here for simplicity. The graphical comparison of the model with actual data is presented in figure IV and figure V.

For the removal rate coefficient  $\gamma$  the D is taken to be 14 days and transmission coefficient  $\beta$  is found by Eq. (4) [20].

| Days | Susceptible Population | Infected    | l Cases | Recovered Population<br>R |       |  |  |
|------|------------------------|-------------|---------|---------------------------|-------|--|--|
|      | S                      | Actual Data | Model   | Actual Data               | Model |  |  |
| 0    | 220,037,333            | 2           | 2       | 0                         | 0     |  |  |
| 1    | 220,037,333            | 0           | 2       | 0                         | 0     |  |  |
| 2    | 220,037,332            | 0           | 3       | 0                         | 0     |  |  |
| 3    | 220,037,332            | 2           | 3       | 0                         | 1     |  |  |
| 4    | 220,037,331            | 0           | 3       | 0                         | 1     |  |  |
| 5    | 220,037,330            | 0           | 4       | 0                         | 1     |  |  |
| 6    | 220,037,330            | 1           | 4       | 0                         | 1     |  |  |
| 7    | 220,037,329            | 0           | 5       | 0                         | 2     |  |  |
| 8    | 220,037,328            | 1           | 5       | 0                         | 2     |  |  |
| 9    | 220,037,327            | 0           | 6       | 0                         | 2     |  |  |

Table I1: Model Vs Actual Data of Pakistan COVID-19

| Pandemic Modeling   | y using SIR  | Model and | Numerical     | Estimation  | of Ro by     | COVID-19 Data |
|---------------------|--------------|-----------|---------------|-------------|--------------|---------------|
| i anacinic mouching | , moning one | mouce and | i winner wear | Dominiation | $o_j no o_j$ | COTID 17 Duta |

| 10 | 220.037.326 | 0    | 7    | 0    | 3   |
|----|-------------|------|------|------|-----|
| 10 | 220,037,320 | 1    | 7    | 0    | 3   |
| 12 | 220,037,324 | 0    | 8    | 0    | 3   |
| 12 | 220,037,323 | 3    | 9    | 0    | 4   |
| 13 | 220,037,321 | 1    | 10   | 0    | 5   |
| 15 | 220,037,317 | 1    | 10   | 0    | 6   |
| 16 | 220,037,317 | 7    | 12   | 0    | 7   |
| 10 | 220,037,313 | 3    | 15   | 0    | 8   |
| 18 | 220,037,312 | 22   | 17   | 0    | 9   |
| 10 | 220,037,307 | 13/  | 10   | 0    | 10  |
| 20 | 220,037,300 | 54   | 21   | 0    | 12  |
| 20 | 220,037,302 | 61   | 21   | 0    | 13  |
| 22 | 220,037,290 | 159  | 24   | 0    | 15  |
| 23 | 220,037,233 | 34   | 30   | 0    | 17  |
| 23 | 220,037,287 | 151  | 34   | 8    | 19  |
| 25 | 220,037,201 | 131  | 38   | 11   | 22  |
| 26 | 220,037,271 | 103  | 43   | 12   | 25  |
| 20 | 220,037,257 | 104  | 49   | 25   | 28  |
| 28 | 220,037,230 | 66   | 55   | 29   | 32  |
| 29 | 220,037,240 | 140  | 62   | 32   | 36  |
| 30 | 220,037,237 | 211  | 70   | 37   | 41  |
| 31 | 220,037,223 | 118  | 78   | 41   | 46  |
| 32 | 220,037,195 | 99   | 88   | 50   | 52  |
| 33 | 220,037,177 | 240  | 99   | 83   | 59  |
| 34 | 220.037.157 | 174  | 112  | 108  | 66  |
| 35 | 220.037.135 | 252  | 126  | 138  | 75  |
| 36 | 220.037.109 | 159  | 141  | 161  | 84  |
| 37 | 220.037.081 | 190  | 159  | 162  | 95  |
| 38 | 220,037,049 | 178  | 179  | 172  | 107 |
| 39 | 220,037,013 | 244  | 202  | 215  | 121 |
| 40 | 220,036,972 | 494  | 227  | 310  | 136 |
| 41 | 220,036,927 | 449  | 255  | 484  | 153 |
| 42 | 220,036,875 | 202  | 287  | 528  | 172 |
| 43 | 220,036,817 | 282  | 324  | 635  | 194 |
| 44 | 220,036,752 | 206  | 364  | 793  | 219 |
| 45 | 220,036,679 | 316  | 410  | 848  | 246 |
| 46 | 220,036,596 | 219  | 461  | 1119 | 277 |
| 47 | 220,036,503 | 266  | 519  | 1190 | 312 |
| 48 | 220,036,399 | 341  | 585  | 1474 | 352 |
| 49 | 220,036,281 | 546  | 658  | 1557 | 396 |
| 50 | 220,036,149 | 536  | 741  | 1773 | 446 |
| 51 | 220,035,999 | 106  | 833  | 1900 | 502 |
| 52 | 220,035,832 | 613  | 938  | 1976 | 565 |
| 53 | 220,035,643 | 710  | 1056 | 2036 | 636 |
| 54 | 220,035,430 | 70   | 1189 | 2146 | 717 |
| 55 | 220,035,191 | 1147 | 1338 | 2274 | 807 |
|    |             |      |      |      |     |

S(0) = N = 220,037,337 Population of Pakistan [18]  $I(0) = 2, R(0) = 0, \gamma = 0.071, R_o = 2.656, \beta = 8.622 \times 10^{-10}$ 

When the disease spread control measures are taken the effect will cause the epidemic disease to stop infecting the susceptible population. Quantitatively, these can be reflected by the minimization in the value of  $R_0$  which will cause the change in the number of infected populations and also the duration to which the peak of the epidemic may

occur for a closed population. These effects are provided in table III as  $R_o$  is reduced in steps of 10 percent from the estimated average  $R_o$ . The infected population and time are plotted in figure VI for different reduced values of  $R_o$ . Also, figure VII shows the effect of  $R_o$  on the population which may be infected.

**Table III:** Effect on Different Parameters due to Minimization of  $R_o$ 

| Reduced R <sub>o</sub> | Ro  | Time for the Peak<br>of the Epidemic<br>T, Days | Transmission<br>Coefficient<br>β | Max Infected<br>Population<br>I <sub>max</sub> | Percentage of the<br>Infected Population |  |  |  |  |
|------------------------|---|---|----------------------------------|--|--|--|--|--|--|
| Ro                     | 2.656                                     | 161   | 8.622x10 <sup>-10</sup>          | 56265566                                       | 26%                                      |  |  |  |  |
| 10% R <sub>o</sub>     | 2.390                                     | 190   | 7.760 x10 <sup>-10</sup>         | 47756383                                       | 22%                                      |  |  |  |  |
| 20% R <sub>o</sub>     | 2.125                                     | 231   | 6.897 x10 <sup>-10</sup>         | 38430006                                       | 17%                                      |  |  |  |  |
| 30% R <sub>o</sub>     | 1.859                                     | 296   | 6.035 x10 <sup>-10</sup>         | 28291410                                       | 13%                                      |  |  |  |  |
| 40% R <sub>o</sub>     | 1.594                                     | 415   | 5.173 x10 <sup>-10</sup>         | 17618033                                       | 8%                                       |  |  |  |  |
| 50% R <sub>o</sub>     | 1.328                                     | 710   | 4.311 x10 <sup>-10</sup>         | 7343918  | 3%                                       |  |  |  |  |
| N=220,037,337 P        | N=220,037,337 Population of Pakistan [18] |   |                                  |  |  |  |  |  |  |



Figure IV: Infected Population Comparison





Figure VI: Reduced Ro and Peak of Epidemic



Figure VII: Infected Population and Ro

#### IV. DISCUSSION

In this study, we have discussed the methodology to approximate the basic reproduction number Ro and the RK4 method for the numerical solution of the SIR model. The R<sub>o</sub> estimated by the current Pakistan COVID-19 data is found to be 2.656 while some other studies estimated values of 2.28 (Zhang, Sheng, et al., 2020) [22], 3.58, and 2.2 (Li, Qun, et al., 2020) [23]. From such different studies. it is much more difficult to find an accurate measure of  $R_0$ . As the spread of a disease depends upon many factors such as demography, environmental conditions and social norms of that particular society, etc., which also makes uncertainty in Ro value. Even the methodology and modeling technique affects its value. Also in our study, the value of R<sub>o</sub> depends upon the reliability of COVID-19 data. The effective reduction in basic reproductive numbers shows the control of the epidemic.

These control measures include social distancing, lockdowns, the ceasing of large public gatherings, and hygiene measures such as hand washing, fomite disinfection, etc., which may be helpful in reducing the spread.

Figure IV shows the comparison of the infected population as it can be seen the model-generated data is increasing with respect to time but the actual data fluctuation. As the infection spreads due to contact the lockdown and other effective procedures to control the spread of infection. The actual data also represents that control measures are not effectively followed by the population although the infected population number is less than the values predicted by the model.

Figure V shows a comparison of the recovered population. As the SIR model does not consider control measures and only takes into account the recovery duration. This reflects in the data as well. The recovered population rate is greater as compared to the rate predicted by the model.

The SIR model and its numerical solution techniques provide an approximate way to predict the future of the epidemic disease. The model provides some very valuable information about the infected population such as when will the apex of the disease occur and how much of the total population of that country or region will be infected and the time it would take for the peak of the infected population to occur as shown in figure VI and figure VII. However, after the peak the infected population reduces. But this model does have limitations such as the population being fixed and does not account for an increase in the population such as births. Similarly, the recovered population compartment considers that the population which had recovered cannot be infected again. The transmission factor from infected to recovered population might not be constant as the recovery period may vary and also be contagious after vaccination [20-23].

#### V. CONCLUSION

The mathematical modeling provides an effective approximation for epidemic disease. Our methodology provides a much simpler approach to numerically estimating  $R_o$ . The methodology does not require complicated calculations and may be used for a quick estimation. These models aid the health policymakers and

concerned authorities to take effective control measures for minimizing the contagiousness of disease and groundwork for the health care system for such COVID-19 disease. Though the model estimations are not accurate to the actual statistics, however, it is useful from a basic understanding point of view and teaching. Students of the relevant field might find this model and techniques as a starter and apply it to more complex and realistic infectious disease models.

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# **Authors Contributions**

Fayzan Ahmed's contribution to this study was the concept, technical implementation, paper writing, and correspondence. The methodology to conduct this research work was proposed by Majid Iqbal along with the project administration. Data collection and supervision were performed by Arshad Iqbal. Zaheer Uddin facilitated the data compilation and validation.

## **Conflict of Interest**

The authors declare no conflict of interest.

#### **Data Availability Statement**

The testing data is available in this paper.

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# References

- World Health Organization. (2020, April 22). Archived: WHO Timeline - COVID-19. Retrieved From: https://www.who.int/newsroom/detail/27-04-2020-who-timeline---covid-19
- [2] Brauer, F. (2017). Mathematical epidemiology: Past, present, and future. *Infectious Disease Modelling*, 2(2), 113-127.
- [3] Arino, J., & Watmough, J. (2019). Current trends in mathematical epidemiology. *Bulletin of Mathematical Biology*, 81(11), 4311-4312.
- [4] Paeng, S. H., & Lee, J. (2017). Continuous and discrete SIR-models with spatial distributions. *Journal of mathematical biology*, 74(7), 1709-1727.
- [5] Perasso, A. (2018). An introduction to the basic reproduction number in mathematical epidemiology. *ESAIM: Proceedings and Surveys*, 62, 123-138.
- [6] Sattenspiel, L. (1990). Modeling the spread of infectious disease in human populations. *American Journal of Physical Anthropology*, 33(S11), 245-276.
- [7] Keeling, M. J., & Rohani, P. (2011). Stochastic dynamics. In *Modeling infectious diseases in humans and animals* (pp. 190-231). Princeton University Press.
- [8] World Health Organization. (2020). Naming the coronavirus disease (COVID-19) and the virus that causes it. *Brazilian Journal Of Implantology And Health Sciences*, 2(3).
- [9] Worldometers. (2020, April, 21). COVID-19 Coronavirus Pandemic: Coronavirus Cases. Retrieved From: https://www.worldometers.info/coronavirus/

- [10] Virological.org. (2020, May 23). Epidemiological Data from the nCoV-2019 Outbreak: *Early Descriptions from Publicly Available Data*. Retrieved From: http://virological.org/t/epidemiologicaldata-from-the-ncov-2019-outbreak-early-descriptions-frompublicly-available-data/337
- [11] Bauch, C. T. (2003). Interepidemic intervals in forced and unforced SEIR models. *Fields Inst Commun*, *36*, 33-44.
- [12] Allman, E. S., Allman, E. S., & Rhodes, J. A. (2004). Mathematical models in biology: an introduction. Cambridge University Press.
- [13] Diekmann, O., & Heesterbeek, J. A. P. (2000). Mathematical epidemiology of infectious diseases: model building, analysis and interpretation (Vol. 5). John Wiley & Sons.
- [14] Chen, D. (2014). Modeling the spread of infectious diseases: A review, analyzing and modeling spatial and temporal dynamics of infectious diseases. 19-42
- [15] Weiss, H. H. (2013). The SIR model and the foundations of public health. *Materials matematics*, 0001-17.
- [16] Jones, J. H. (2007). Notes on R0. California: Department of Anthropological Sciences, 323, 1-19.
- [17] Boudreau, J. F., & Swanson, E. S. (2017). Applied computational physics. Oxford University Press.
- [18] Worldometers. (2020, April 19). Pakistan Population. Retrieve From https://www.worldometers.info/world-population/pakistanpopulation/.
- [19] covid.gov.pk. (2020, April 22). Pakistan Cases Details, COVID-19: Health Advisory Platform by Ministry of National Health Services Regulations and Coordination. Retrieved From: http://covid.gov.pk/stats/pakistan
- [20] World Health Organization. (2020). Report of the WHO-China joint mission on coronavirus disease 2019 (COVID-19). Brazilian Journal of Implantology and Health Sciences, 2(3).
- [21] Hossain, M. T., Miah, M. M., & Hossain, M. B. (2017). Numerical study of kermack-mckendrik SIR model to predict the outbreak of ebola virus diseases using euler and fourth order runge-kutta methods. *American Academic Scientific Research Journal for Engineering, Technology, and Sciences, 37*(1), 1-21.
- [22] Zhang, S., Diao, M., Yu, W., Pei, L., Lin, Z., & Chen, D. (2020). Estimation of the reproductive number of novel coronavirus (COVID-19) and the probable outbreak size on the Diamond Princess cruise ship: A data-driven analysis. *International journal* of infectious diseases, 93, 201-204.
- [23] Li, Q., Guan, X., Wu, P., Wang, X., Zhou, L., Tong, Y., ... & Feng, Z. (2020). Early transmission dynamics in Wuhan, China, of novel coronavirus–infected pneumonia. *New England journal of medicine*.