Mathematical analysis on the dynamics of COVID-19 in India using SIR Epidemic Model

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Abstract

The Coronavirus Disease (COVID-19), the outbreak of which emerged from the Wuhan city of China, is a matter of huge concern for the entire human race. The disease as on August 4, 2020 has invaded around 18.6 million population causing over half a million deaths worldwide and counting. To understand the dynamics of this communicable disease and its transmission among the people in India, a mathematical model governed by ordinary differential equations with appropriate conditions has been established. The model is based on SIR (Susceptible-Infected-Removed) scheme to understand the behavior of susceptible, infective and removed (both recovered and deceased) population in India. The resulting model has been simulated using MATLAB software. The results obtained in this model are interpreted graphically and least squares method is used to predict the transmission rate, recovery rate and mortality rate in the absence of any vaccine/immunization.

Keywords: COVID-19, Coronavirus, Mathematical Modeling, SARS-CoV-2
Mathematics Subject Classification (2020): 92B05, 92C10, 92-08

1. Introduction

SARS-CoV-2 (Severe Acute Respiratory Syndrome Coronavirus 2) is one of the six identified human coronaviruses that causes a respiratory illness in humans known as COVID-19. The virus was initially reported in humans in Wuhan, China in late December 2019 and then began to spread rapidly to other parts of the world. The virus is transmitted by inhalation or exposure to infected droplets or

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fomites, with incubation period usually ranging from 2 to 14 days [1]. On March 11, 2020, World Health Organization (WHO) officially declared COVID-19 as a pandemic. The first case of COVID-19 in India was reported on January 30, 2020 in Kerala's Thrissur district. The infected individual was a medical student who had returned home on vacation from Wuhan University, China. The nationwide cases climbed to 571 till March 24, 2020 and in order to break the chain of the transmission of this deadly virus, a nationwide lockdown was imposed on March 24, 2020 by the Indian Prime Minister for a period of three weeks. Subsequently the lockdown was further extended till May 3, 2020 and then till May 17, 2020. The nationwide restrictions in the lockdown were gradually eased from May 17, 2020 and the lockdown was almost lifted from June 1, 2020 with Standard Operating Procedures (SOPs) [2].

Various studies for the prediction of the growth of COVID-19 in India have already been done using various models such as Exponential Model and Logistic Model while the calculation of basic reproduction number R_0 has also been tried using Susceptible-Infected-Recovered Model [3].

In this paper, we aim to apply the SIR Epidemic Model to the Indian population to predict the future trend, the total number of possible infections in India in absence of any immunization/vaccination and the time of peak infections in India. The data [4] of recovered and deceased individuals is collected weekly starting from January 30, 2020, when the first case of COVID-19 was reported in India and then the solution of the model equations is fitted to the collected data [4] till August 4, 2020 using least squares fitting to estimate the parameters in the model. The model equations with the help of obtained parameters are solved numerically and simulated in MATLAB software to get the model results. In addition, to analyze the trajectory of total tests conducted, total confirmed cases, total active cases and total recoveries in India, the data [4] is plotted into various line graphs.

2. Mathematical Formulation

The study of communicable diseases is one of the primary research areas in the scientific world. Epidemiology is a branch of research that deals with the control, immunization and other remedial aspects of communicable diseases [5, 6]. The mathematical study of infectious diseases has played a vital role for optimal outcome and analytic solution to various complex problems [7].

SIR model is a well known epidemiological model that computes the

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number of people infected with an epidemic in a closed population over time. In this model, the entire population is divided into three compartments; the susceptibles S - who are vulnerable to infection, the infectives I - who have already contracted the infection and are able to transmit it to the susceptible population, and the removed R - who have either died or have recovered from the infection [8].

This model was developed in 1927 by Kermack and McKendrick [9] with the following assumptions:

(*i*) The disease spreads in a closed population, i.e, the total population N is constant.

(*ii*) The number of susceptibles S, who become infected per unit time is proportional to the total number of susceptibles and infectives.

(*ii*) The number of individuals removed R, which include both recovered and deceased individuals, from the infected compartment per unit time is γI, where γ is the removal rate coefficient. The recovered individuals get permanent immunity from the infectious disease.

The progress of individuals within the compartments is schematically represented as:
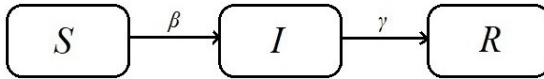
Figure 1: Schematic progress of individuals through various compartments.

The rate equations describing the model are:

$$\frac{ds}{dt} = -\beta si \tag{1}$$

$$\frac{di}{dt} = \beta si - \gamma i \tag{2}$$

$$\frac{dr}{dt} = \gamma i \tag{3}$$

where $s = \frac{S}{N}$, $i = \frac{I}{N}$, $r = \frac{R}{N}$, β is the contact rate, γ is the removal rate and N is the total population of India. We take $N = 138 \times 10^7$ [10]. Obviously $s + i + r = 1$.

3. Solution and Analysis

Assuming that the whole population is initially susceptible. Therefore, $s = \frac{S}{N} \approx 1$. Hence equation (2) reduces to;

$$\frac{di}{dt} = \beta i - \gamma i = (\beta - \gamma)i \tag{4}$$

In order to estimate the proportion of infected population at any time t, we integrate equation (4) from 0 to t. We therefore have;

$$i(t) = i_0 \exp[(\beta - \gamma)t] \tag{5}$$

Equation (5) gives the total proportion of infectives present at time t.

To find the proportion of removed individuals in the population at any time t, we use equation (5) in equation (3). We have;

$$\frac{dr}{dt} = \gamma i_0 \exp[(\beta - \gamma)t] \tag{6}$$

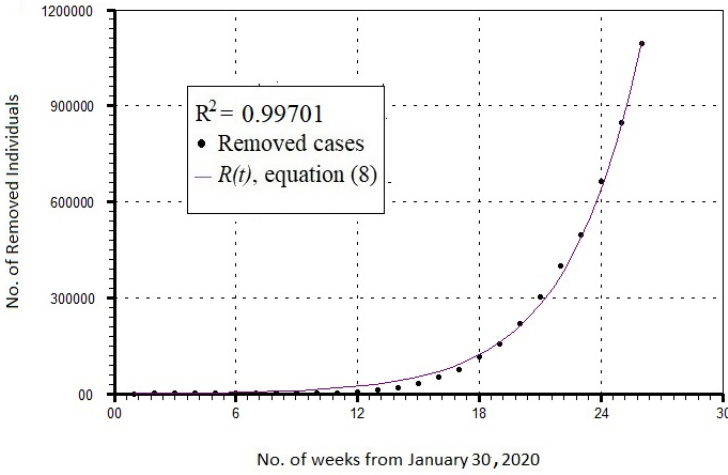Integrating from 0 to t and noting that there are no removed individuals initially, i.e, $r_0 = 0$, we have;

$$r(t) = \frac{\gamma}{\beta - \gamma} i_0 [\exp\{(\beta - \gamma)t\} - 1] \tag{7}$$

Using $r = \frac{R}{N}$ and $i_0 = \frac{I_0}{N}$, we have;

$$R(t) = \frac{\gamma}{\beta - \gamma} I_0 [\exp\{(\beta - \gamma)t\} - 1] \tag{8}$$

which is of the form $y(t) = \frac{w}{k}[\exp(kt) - 1]$, where $y(t) = R(t), w = \gamma I_0$ and $k = \beta - \gamma$.

Using least squares fitting to fit the this equation to the weekly total removed cases in India from January 30, 2020 [4], we get $w = \gamma I_0 = 54.384$ and $k = \beta - \gamma = 0.401$.

Figure 2: Least Squares fitting of equation (8) to the total removed cases.

Taking $I_0 =$ number of initial positive cases in India after which the infection spread locally $= 22$, [2], we computed $\gamma = 2.472$ and $\beta = 2.873$.

We now define and deduce two important quantities - the basic reproduction number $\mathbf{R_0}$ and epidemic doubling time τ.

The basic reproduction number $\mathbf{R_0}$ is the most important quantity for analyzing the behavior of any communicable disease using a mathematical model. It is defined as the number of secondary infections arising due to a single primary infection in a susceptible population. If $\mathbf{R_0} > 1$, the epidemic spreads. If $\mathbf{R_0} < 1$, the epidemic doesn't spread and dies out [11]. It is given by;

$$\mathbf{R_0} = \frac{\beta}{\gamma} \qquad (9)$$

For India as on August 4, 2020, with $\beta = 2.873$ and $\gamma = 2.472$, the basic reproduction number $\mathbf{R_0} = \frac{\beta}{\gamma} = 1.162$.

The epidemic doubling time τ is defined as the time required for the infectives in a population to get doubled. It is given by;

$$\tau = \frac{\ln 2}{\gamma(\mathbf{R_0} - 1)} \qquad (10)$$

For India as on August 4, 2020, with $\gamma = 2.472$ and $\mathbf{R_0} = 1.162$, we get the epidemic doubling time, $\tau = 1.730$ weeks.

To get the total proportion of Infectives, we divide equation (1) by equation (3), and get;

$$\frac{ds}{dr} = -\frac{\beta}{\gamma}s = -\mathbf{R_0}s \tag{11}$$

Integrating, we get;

$$s(t) = s_0 \exp\{-r(t)\mathbf{R_0}\} \tag{12}$$

Since the disease ultimately dies out [11], we have $i(t \to \infty) = i(\infty) = 0$. Also, the total population is constant, therefore $r(t \to \infty) = 1 - s(t \to \infty)$, or $r(\infty) = 1 - s(\infty)$. Then from equation (12) with $t \to \infty$ we have;

$$s(\infty) = s_0 \exp[-r(\infty)\mathbf{R_0}] \tag{13}$$
$$\tag{14}$$

which gives;

$$s(\infty) = s_0 \exp[\{s(\infty) - 1\}\mathbf{R_0}] \tag{15}$$

Taking $s_0 \approx 1$, $\mathbf{R_0} = 1.162$ and solving for $s(\infty)$, we get $s(\infty) = 0.735$ or $s(\infty) = 1$. We reject $s(\infty) = 1$, because the infection has spread and ultimately the proportion of removed population $r(\infty) > 0$, so $s(\infty) < 1$.

To get the proportion of total number of infectives in the population, we have the following equation;

$$i_{total} = 1 - s(\infty) = 1 - 0.735 = 0.265. \tag{16}$$

Thereafter, we solve equations (1) - (3) numerically and simulate the results in MATLAB software.
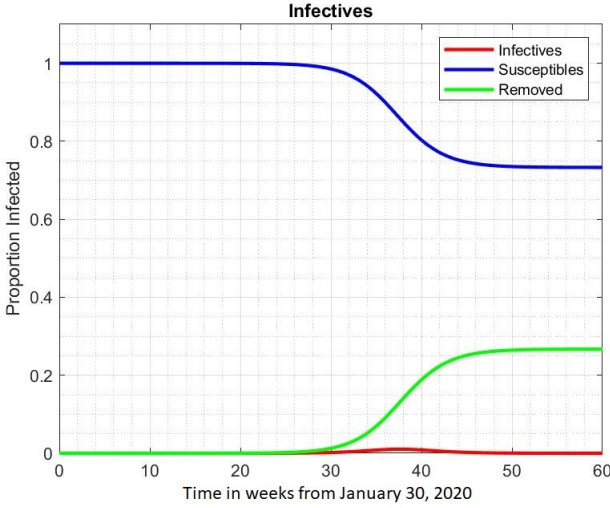
Figure 3: Simulation of the proportion of Susceptibles (s), Infectives (i), and Removed (r) individuals over weeks (t) with $\beta = 2.873$, $\gamma = 2.472$, showing peak infections in week 37 and the pandemic almost getting over in India by week 44 after January 30, 2020.

To analyze the trajectory of the total tests done and total confirmed cases, we plot the data [4] collected till August 4, 2020 from India in the line graph below;
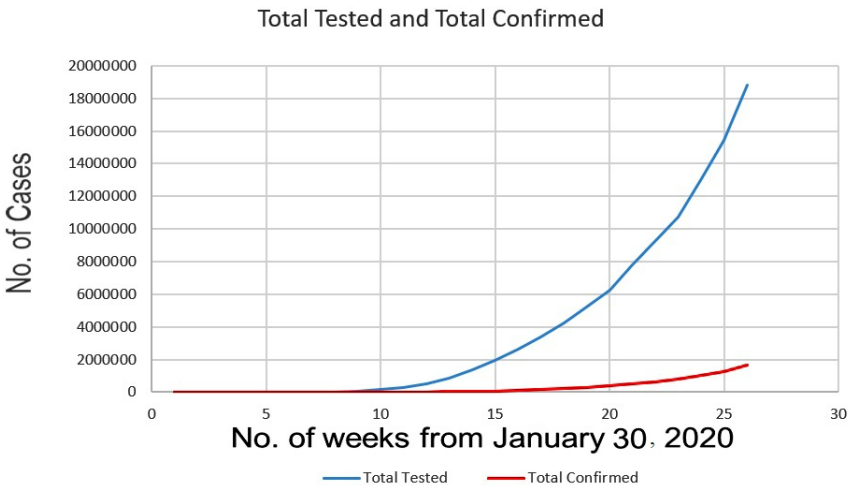
Figure 4: Line graph showing the trajectory of total tests done and total confirmed cases in India for 26 weeks since January 30, 2020.

To analyze the trajectory of total active cases and total recoveries, we plot the data [4] collected till August 4, 2020 from India in the line graph below;
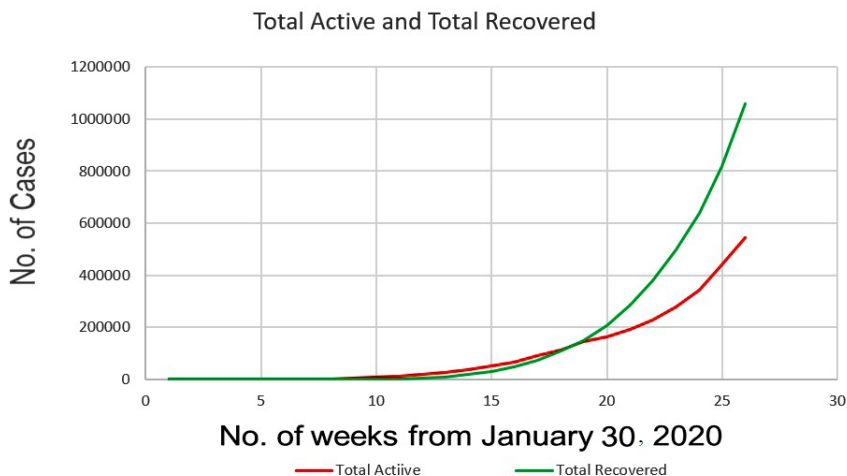
Figure 5: Line graph showing the trajectory of total active cases and total recoveries in India for 26 weeks since January 30, 2020.

4. Discussion and Conclusion

A mathematical model based on SIR scheme has been established to understand the dynamics of COVID-19 in India. The infected population, the susceptibles and the removals (both recovered and deceased individuals) are estimated using a system of ordinary differential equations with suitable initial conditions. The data [4] reflecting the weekly information regarding tests conducted, new cases, recoveries and other information has been interpreted to understand the future implications of the contagion.

The graph in **Figure 4** shows that a very less percentage of the total tested individuals come out to be positive. It also shows that the testing rate in India has considerably increased over the last few weeks.

From the graph in **Figure 5**, we are able to conclude that the recovery rate in India is improving as the time goes by and in around 18th week, the number of recoveries in India overtook the number of active cases for the first time.

The key findings of our study are summarized as under:

i) As $\mathbf{R_0}$ = 1.162, this means that a single infected individual transmits the infection to 1.162 susceptible individuals on an average.

ii) Presently, it takes 1.730 weeks in India to double the infected cases. It should be noted that confirmed cases is a subset of infected cases and a significant portion of the infected cases can go unreported.

iii) According to our study, India is likely to witness the peak of infected cases in mid October 2020 and the pandemic will almost be over in India by early December 2020 if the current trend continues.

iv) Our study finds that around 26.5% of the Indian population may get infected by COVID-19 ultimately, if no vaccine is developed.

References

[1] T. Singhal. *A review of coronavirus disease-2019 (COVID-19)*. The Indian Journal of Pediatrics, 1-6, 2020.

[2] Ministry of Health and Family Welfare. *www.mohfw.gov.in*. Retrieved 04/08/2020.

[3] R. Rajan. *Predictions for Covid-19 Outbreak in India Using Epidemological Models*. medRxiv 1-11, 2020.

[4] *https:www.covid19india.org*. Retrieved 04/08/2020.

[5] F. Brauer, P. Driessche, J. Wu. *Mathematical Epidemiology*. Springer, 2015.

[6] W. Arhens, I. Pigeot. *Handbook of Epidemiology*. Springer, 2005.

[7] F. Brauer, C. Castillo-Chavez. *Mathematical Models in Population Biology and Epidemiology*. Second Edition, Springer, 2012.

[8] M. A. Khanday. *Introduction to Modeling and Biomathematics*. Dilpreet Publishing House, New Delhi, 2016.

[9] W. O. Kermack, A. G. McKendrick, *A Contribution to the Mathematical Theory of Epidemics*. Proc. R. Soc. A 1927, 117, 700-721.

[10] Ministry of Statistics and Programme Implementation. *www.mospi.nic.in*. Retrieved 04/08/2020

[11] H. Weiss. *The SIR model and the Foundations of Public Health*. MATerials MAThematics, 2013 (3), 17.