



Mathematical Modelling on Delta Variant Using Fractional SIR Model

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Abstract:

The present mutation situation is complex in the study of the COVID-19 variant from the Covid family. The fractional epidemiological model is used to study the transmission rate dictating the propagation of infection between infected and susceptible populations using the susceptible-infected-recovered (SIR) model. Initially, data were taken as not prominent for the COVID-19 variants, and the rate of transmission was sufficiently concealed. Based on the numerical data, the outcome of the exponent system depends on the production of fractional power. Then, we make important predictions using the fractional SIR Model.

Index Terms - SIR Model, Jacobian, Basic Reproduction Number, Epidemic Disease.

Introduction

Human Beings have been combating against the outburst of contagious diseases throughout the olden times. COVID-19, an infectious disease primarily appeared in December 2019 in the food market of Wuhan city of China (Khan et al. 2020). While the disease was bizarre and highly infectious, people were thwarted to prevent its transmission throughout the globe. It swiftly turned into the biggest corona virus epidemic. The mortality rate of this outbreak grows day by day and in 2021 the mortality rate of this outbreak was the highest. A survey using population models says that at the primary stage of the COVID-19 epidemic, the basic reproduction number, which is the average number of secondary infections caused by one infected individual during the incubation period fell between 1.5 and 3.5 globally (Boldog et al. 2019). Until now, the disease rapidly spread in almost all countries, and the global number of COVID-19 cases is rising at an accelerated rate. As of 22 April 2021, 144,213,316 cases were confirmed worldwide causing 3,065,499 deaths. After the USA, India has borne the brunt of the outbreak, reporting 15,924,732 cases. Effective measures are needed to counter the epidemic conditions like complete lockdown, sanitizing infected areas, and developing the extent of medical amenities. The transmission of COVID-19 has been investigated by experts from various disciplines to overcome the epidemic situation. On 24 March 2020, the Government of India (GOI) commanded a nationwide complete lockdown in the country for 21 days as a preventive measure against the COVID-19 pandemic (Danchin et al. 2020). This lockdown was further extended for few more months by local and state governments based on the severity of the infection. This lockdown slowed the growth rate of the pandemic to a rate of doubling of infected cases every eight days (R_0 close to 2) (Demirci & Ozalp). After a complete and partial lockdown, the Government of India has executed unlocking strategies followed by the enforcement of a series of rules and regulations along with precautionary measures in the infected areas.

Indian states have much social, economic, and geographical diversity; hence the transmission rate of COVID-19 was different in each region. It is observed that the transmission of COVID-19 is extremely affected by the contact rate and density of the infected individuals in the region. It is also seen in a previous study that the contact rate is directly proportional to the population density of the region. Thus, the transmission ability of infection was even higher in regions with high populations like West Bengal, Delhi, Maharashtra, Bihar, and Ahmadabad. In view of these interpretations, we have built a basic compartmental model that analyzes the transmission rate using population density and contact rate parameters. To understand the spread of COVID-19 in a large area, the disease's spread should be investigated in each possibly smallest distinctive region. Therefore, we were stimulated to calculate the numerical value of the transmission rate of the disease at the district level in India. In the battle against the COVID-19 outburst, the use of mathematical modeling improves our knowledge of disease dispersion and preventive measures. The formation of an efficient epidemiological model is a challenging task. The vagueness of the transmission dynamics can be divided and allocated to various sources of uncertainty in the concerned parameters. Gupta et al. 2020 used long-term climatic records of various geographical parameters, air temperature, rainfall, evapotranspiration, solar radiation, humidity, wind speed, and population density at the regional level to investigate the density of COVID-19 infections. Moreover, their study suggests that the relatively hot and dry regions in lower altitudes of the Indian Territory are more prone to COVID-19 infection. Rafiq et al. 2020 developed a prognostic yet deterministic model by identification techniques to forecast the spread of COVID-19 for 30 days in the ten most affected states of India. Using linear mixed models with random intercept and fixed slopes, Sy, Kalra, et al. 2020 have defined the association between population density (used as a proxy for contact rates) and the basic reproduction number of COVID-19 across the U.S. The statistical analysis done by Sy et al. 2020, concludes that regions with greater population density have greater rates of transmission of COVID-19. Mahajan et al. 2020 constructed a SIPHERD model to analyze the impact of lockdown and the number of tests conducted per day on COVID-19 transmission and then predicted the total number of confirmed, active, and death cases. Under the fractional-order derivative, Shaikh et al. 2020 have formulated a compartmental model and applied potential control strategies during Corona virus (CoV) is a challenging problem in front of the world and is a cause of health crises in many countries. Corona viruses are divided into four genus alpha, beta, gamma, and delta. Generally, alpha and beta spread into mammals while gamma and delta mostly infect birds. Many researchers and scientists are studying CoV for their different behaviour and transmission among humans. The incubation period of CoV varies from two-to-fourteen days. The symptoms of Corona viruses are fever with dry cough, shortness of breath, sore throat, and headache. There are four labeled as variants of the corona. As per the WHO survey these variants exist in different continents:

- Beta Variant: The COVID variant that was first detected in South Africa
- Gamma Variant: The COVID variant that was first detected in Brazil
- Delta Variant: The COVID variant that was first detected in India
- Omicron Variant: The COVID variant that was first detected in Western Europe.

Model Description and Formulation for Improved CoV-19 Model:

The Base Model:

W.O. Kendrick et al. (1927) developed a SIR model for the study of epidemiology. The susceptible-infected-recovered model describes the various stages of infectious agents in the population. The base model is defined by the following governing equations:

$$\begin{aligned}\frac{dS}{dt} &= -\beta S I \\ \frac{dI}{dt} &= \beta S I - \alpha I \\ \frac{dR}{dt} &= \alpha I\end{aligned}$$

Where S means the number of susceptible cases, I mean the number of infected cases, R means the number of recovered cases, β means the number of transmission rate and α means the recovery rate.

Improved Model: The fractional SIR Model is given by the following governing equations:

$$\begin{aligned}\frac{dS}{dt} &= \frac{-\beta S I}{N} + \eta R \\ \frac{dI}{dt} &= \frac{\beta S I}{N} - \gamma I \\ \frac{dR}{dt} &= \gamma I - \eta R\end{aligned}$$

Where S means the number of susceptible cases, I mean the number of infected cases, R means the number of recovered cases, β means the transmission rate, γ means death rate and η means the recovery rate.

Important Points for Analysis of the Model:

i. Diseases Free Equilibrium Condition

At the disease-free equilibrium, we have $S' = I' = R' = 0$;

After solving we get,

$$S^* = \left(\frac{N\gamma}{\beta}, 0, \frac{\gamma I}{\eta} \right).$$

ii. Stability of the Model

The Jacobian matrix of the fractional SIR model is given below

$$J = \begin{pmatrix} \frac{-\beta I}{N} & \frac{-\beta S}{N} & \eta \\ \frac{\beta I}{N} & \frac{\beta S}{N} - \gamma & 0 \\ 0 & \gamma & -\eta \end{pmatrix}$$

Now,

$$\begin{aligned}\det(J - \lambda I) &= \begin{vmatrix} \frac{-\beta I}{N} - \lambda & \frac{-\beta S}{N} & \eta \\ \frac{\beta I}{N} & \frac{\beta S}{N} - \gamma - \lambda & 0 \\ 0 & \gamma & -\eta - \lambda \end{vmatrix} = 0 \\ \Rightarrow [C_0 \lambda^3 + C_1 \lambda^2 + C_2 \lambda + C_3] &= 0\end{aligned}$$

$$\text{Where, } C_0 = -1, C_1 = -\left(\gamma + \eta - \frac{\beta S}{N} + \frac{\beta I}{N}\right), \quad C_2 = \frac{\beta S \eta}{N} - \gamma \eta + \frac{\beta I}{N} - \frac{\beta I \eta}{N} - \frac{\beta I \gamma}{N}$$

$$\text{and } C_3 = \frac{2\beta S \gamma}{N} - \frac{\beta I \gamma \eta}{N}.$$

Year wise values	2019-2020	2020-2021	2021-2022
C_0	-1	-1	-1
C_1	0.9266939	0.9267684	0.221352
C_2	0.0000964	0.00009984	0.000001
C_3	0.1396387	0.14073613	0.4296592

After solving the characteristic equation using MATLAB, we get the following outcomes for the improved model:

Eigenvalues of the year 2019-2020 are for the delta variant of CoV – 19:

$$1.0557 + 0.0000i$$

$$-0.0629 + 0.3587i$$

$$-0.0629 - 0.3587i$$

Eigenvalues of the year 2020-2021 are for the delta variant of CoV – 19:

$$1.0557 + 0.0000i$$

$$-0.0629 + 0.3587i$$

$$-0.0629 - 0.3587i$$

Eigenvalues of the year 2021-2022 are for the delta variant of CoV – 19:

$$0.8357 + 0.0000i$$

$$-0.3079 + 0.6479i$$

$$-0.3079 - 0.6479i$$

After solving the Jacobian matrix, the eigenvectors are seen to be two components eigen spinors, which can be further divided to underlying vector duplets. It means either the complex situation will grow or decay in the future.

Table 1: Numerical values for variables of the model.

S.No.	Variables	Description	Value			Reference
			2019-2020	2020-2021	2021-2022	
1	S_0	Number of susceptible cases at $t = 0$	1396116710	1407361270	1417170099	Estimated
2	I_0	Number of infected cases at $t = 0$	136115	102330	1543	8-9-10
3	R_0	Number of recovered cases at $t = 0$	134302	100242	1531	8-9-10
4	$N(0)$	Total number of Population	1396387127	1407563842	1417173173	8-9-10

Table 2: Numerical values for parameters of the model.

S.No.	Parameter	Description	Estimated Value	Reference
1	β	Transmission rate	$\lambda * N(0)$	Estimated
2	γ	Recovery rate (0.05-0.1)	0.07298	1
3	η	Death rate	0.000035	1

According to above table, the values of all eigen values are negative that is the system will be stable due to vaccination policy in the system. Therefore, vaccination is the best optimal control for the improved model.

iii. Basic Reproduction Number

The basic reproduction number R_0 is defined for SIR fractional model by

$$R_0 = \frac{\text{The transmission rate}}{\text{The recovery rate}}$$

If $R_0 < 1$, then the disease-free equilibrium will be stable and if $R_0 > 1$, then the disease-free equilibrium will be unstable. The basic reproduction number R_0 has important role to measure the rate of infection in the society. Here the value of basic reproduction number is less than 1 so we can conclude that the current situation is stable.

Theorem: The polynomial $P(\lambda) = a_n\lambda^n + a_{n-1}\lambda^{n-1} + a_{n-2}\lambda^{n-2} + \dots + a_1\lambda^1 + a_0$ is stable if and only if its coefficients are positive and all the principal diagonal minors are positive.

Proof: Here, all coefficients are positive or zero, if all the coefficients are positive. Then the system is stable. Also, according to Hurwitz theorem, we have the characteristics equation,

$$a_3\lambda^3 + a_2\lambda^2 + a_1\lambda^1 + a_0 = 0,$$

If $a_1 > 0, a_2 > 0$ and $a_1 \cdot a_2 > a_0$.

Since, the numerical values are satisfying the above conditions, therefore the given system is stable. [Ref. Table 1 and 2 used for numerical measures]

iv. Graphical Representation:

In India, from January 3rd, 2020 to 16th August, 2023, there are 44996599 confirmed cases of COVID – 19 with 531935 deaths, a reported to WHO.

India has detected the Eris sub-variant of COVID-19, which caused concern in the UK, but has not reported any clustering or increase in cases. The Indian SARS-CoV-2 Genomics Consortium (Insacog) held a meeting last week to monitor genomic variations of the coronavirus amid a surge in COVID-19 infections in the UK due to the new variant.

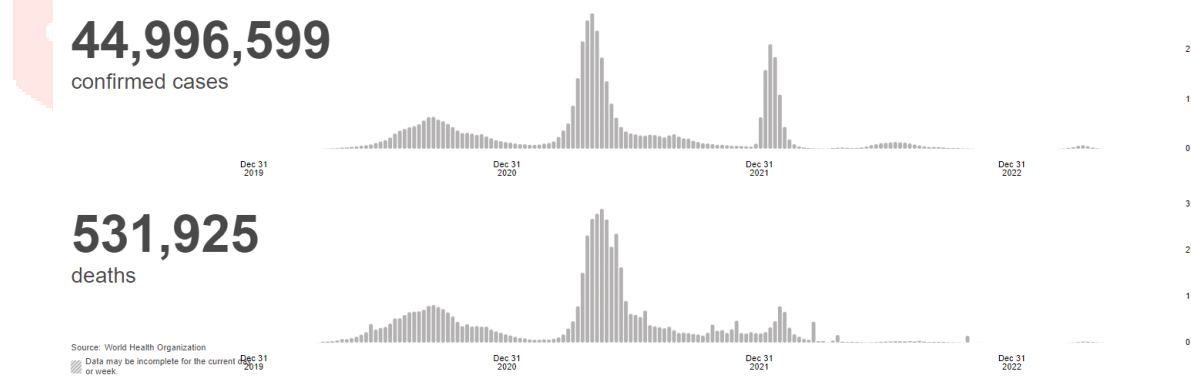


Figure 1: Data based model for sub-variant of COVID-19

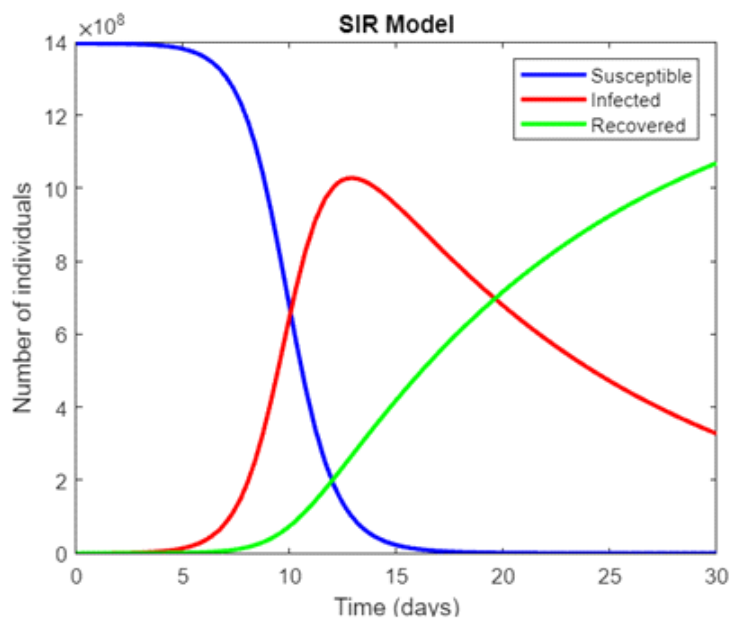


Figure 2: SIR model for the year 2019-2020

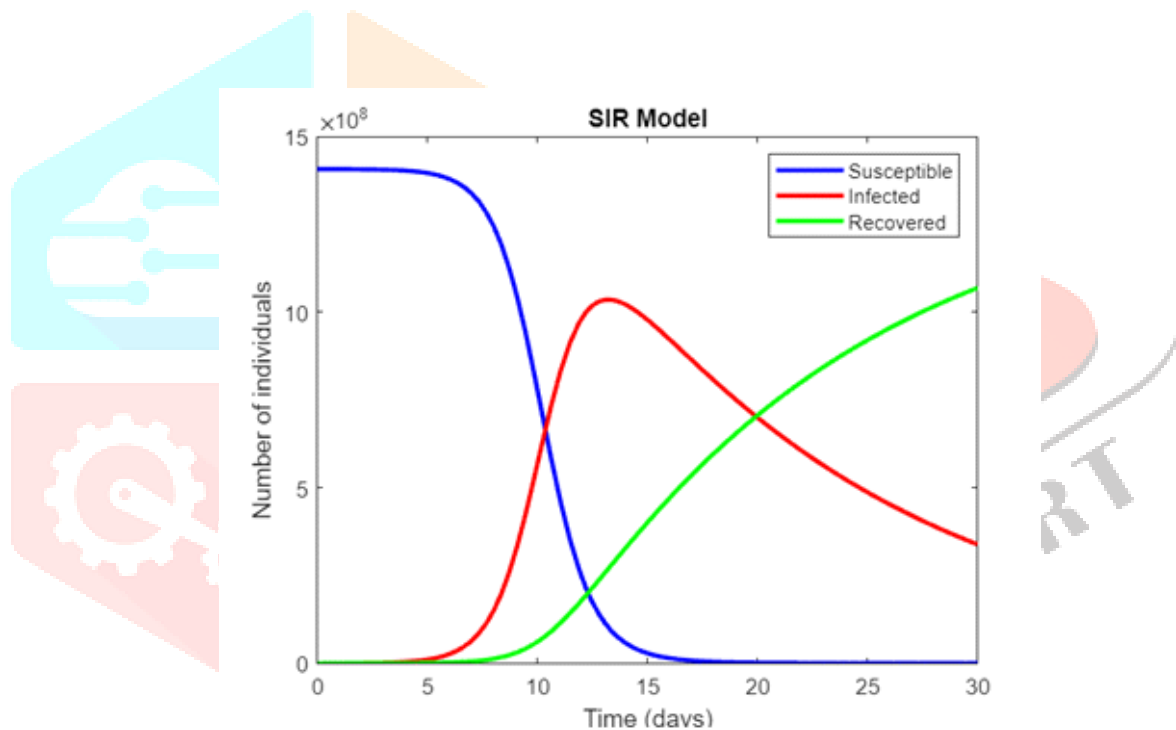


Figure 3: SIR model for the year 2020-2021

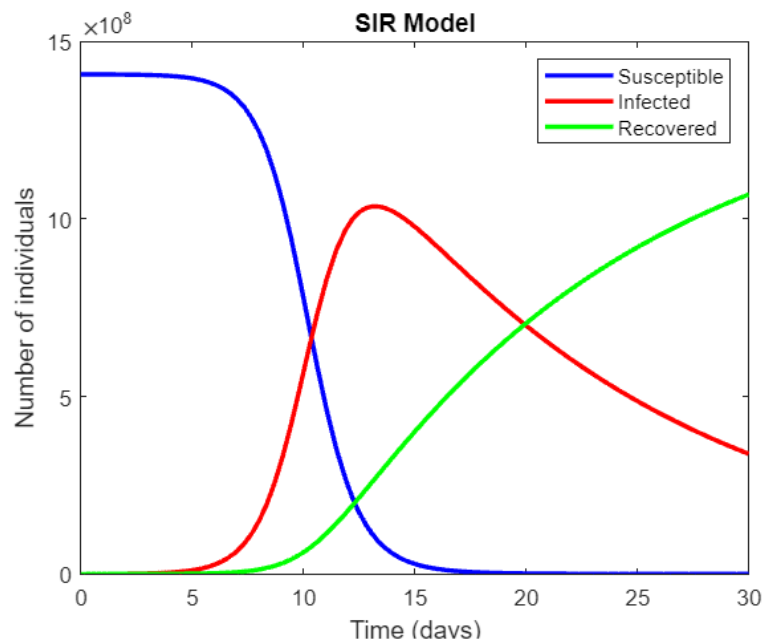


Figure 4: SIR model for the year 2021-2022

Discussion and Conclusion:

Corona virus spreads specially in winter season. The SIR compartmental model explains the transmission mechanism of the novel corona viruses (nCoV) and their serious impact on human society. The basic reproduction number explained the transmission of the nCoV status in the India and world where the range of basic reproduction number is 2.0 to 4.9. Here, we found the value of basic reproduction number is less than one, which shows that the spreading of infection will be very low into the society. Human health department has to publish health related guidelines, in which the important message should be no one interfere or unnecessary experiment with the nature. Presently, the total number of confirmed cases with nCoV is very low in India and other countries respectively. After solving the Jacobian matrix, the eigenvectors are seen to be two components eigen spinors, which can be further divided to underlying vector duplets. It means either the complex situation will decay in the future.

Furthermore, our investigation has practical implication to make some new health related policies. Also, the basic reproduction number shows the outbreak of the nCoV, which has been reported in many continents in the form of serious epidemic.

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