



A STOCHASTIC EPIDEMIC MODELING FOR COVID-19 OUTBREAK IN INDIA

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Abstract

Objectives: The Second wave of Covid-19 has been affecting all over the world drastically, especially in India. The main objectives of this paper are illustrated as high incidence states of Basic and Time-depended reproduction number for COVID-19 in India as well as study the dynamic evaluation of pandemic.

Study design: Our study is about the dynamic evaluation of pandemic. Also, characterization and comparison between first and second wave of COVID-19 are explored and vaccination coverage are estimated through a basic reproduction number. Finally, we discussed about the endemic model of COVID-19 outbreak.

Methods: we adapted a simple stochastic epidemic model, attack rate method for basic reproduction number, Time dependent method used for computing the effective reproduction numbers, fit the Exponential regression model on pandemic waves and some mathematical concepts are also presented.

Results: Our study suggested the peak of the current pandemic to occur in October 2021 with approximate daily infection cases more than 0.35 million in India. Therefore, the impact of the next wave on covid-19 could reach its peak in India at October 2021. Massive vaccination coverage may be reduced the COVID-19 attain its peak. Then we observed that the COVID-19 pandemic will be created unprecedented havoc in community and will become an endemic disease in future.

Conclusion: Our study concludes that the spread of COVID-19's second wave is faster than first wave. In spite of COVID-19's next wave depends on the characteristics of previous states and the probabilities for high affective rates is low.

Keywords: SIR Model, Reproduction number, Exponential regression model, Time-dependent method, Endemic model

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DOI: 10.48047/ecb/2023.12.si10.0017

1. Introduction:

The outbreak of COVID-19 spread all over the world. The current study presents an approach for stochastic epidemic model, also mathematical concepts can be used to show susceptible, recovered and deaths of COVID-19 cases, measure of reproduction numbers. In this study, we will propose an improvised three compartment mathematical model (i.e., Susceptible (S)-Infected (I)-Recovered (R) to analyze the progression of COVID-19) and forecast the epidemic peak of COVID-19 pandemic by using some recorded data. Deterministic (or) Stochastic model for the spread of epidemic disease and may involve some factors, Mode of transmission, quarantine periods [9]. The basic reproduction number was estimated using R0 package in R software [12]. Some more details about the SIR –Model predictions [11]. A framework for compute to basic and time dependent reproduction numbers that can be applied to stochastic epidemic model. Multiple epidemic models are presented for infectious disease [16]. The first and second waves were studied about the effective reproduction number as a maker for the decrease (or) surge in infections [19]. [21] Has a many stochastic models discrete time models. The first wave of COVID-19 outbreak was in December 2019 in Wuhan (China) and during the first half of 2020 spread all over the world and the start of the second wave of COVID-19 was on 11-Feb 2021 in India and spreading most of the states by World health organization [25]. To compute the basic reproduction number R0 and define a discrete time stochastic model by [23]. Characterization of the virus spread in the ongoing second wave in India and quantifiable measure of the virus transmissibility [28]. Modeling for the reproduction number and high incidence states in India [29]. The class of mathematical models using forecast the spread of epidemic diseases and include many factors such as infectious agents, mode of transmission, infectious periods and quarantine periods [23]. Comparison of SIR model with recruitment, mortality, parameter with a parallel description through and logistic equation, demography and the total community minus the recovered community (or) population is not constant through time [27]. Prediction through logistic growth model and SIR Model were used for Short-term projection predicts accurately well with the observed number of incidence cases in India and high incidence states [30]. The prediction through the Markov model approach and estimated the attack rate using COVID-19 data [31]. We conducted a theoretical and systematic review of mathematical and epidemiological model for COVID-19 and then we estimated the basic and

real time reproduction numbers for most affected states in India. Further we discussed about the characterization and comparison of first and second wave in India and effect of vaccination coverage on population. Finally, we discussed about the endemic concepts for COVID-19 outbreak.

2. Model descriptions:

2.1 Data Sources:

The online data numbers of daily infected, recovered, deaths are used. The real time data on COVID-19 daily cases of Active, Confirmed, Recovery, Deceased as well as each state are now available on <http://www.covid19india.org>.

2.2 A simple stochastic epidemic model:

The dynamical system of the stochastic epidemic model can be defined by following differential equations. It is assumed that at any point individuals are susceptible (S), infected (I) and recovery (R). Consequences of the assumptions are that individuals can make following moves from S to I and from I to R, the model is said to be an SIR type epidemic Model. The focus of this paper is applying SIR stochastic epidemic model approach. The model assumptions are, constant population size (N) and no demography. Assume that the population is equal to N. Let S(t), I(t) and R(t) are denoted as the number of susceptible, infectious and recovered (or) death respectively. The following differential equations are describing the deterministic general epidemic model:

$$S' \text{ (or) } \frac{dS}{dt} = -\frac{\beta}{N} S(t)I(t) \dots\dots\dots(1)$$

$$I' \text{ (or) } \frac{dI}{dt} = \frac{\beta}{N} S(t)I(t) - \gamma I(t) \dots\dots\dots(2)$$

$$R' \text{ (or) } \frac{dR}{dt} = \gamma I(t) \dots\dots\dots(3)$$

Where the total population size is constant, S(t)+I(t)+R(t)=N for all t≥0. In assumption that the population is complete susceptible (or) disease-free equilibrium is S≈N and I=R=0. An epidemic occurs if the numbers of infected individuals are increases [i.e. $\frac{dI}{dt} > 0$].

From equation (2),

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

$$I(t) = I(0)e^{(\beta N - \gamma)t}$$

Epidemic, when $\beta N - \gamma > 0$

$$\therefore \beta N > \gamma$$

$$\frac{\beta}{\gamma} N > 1, \text{ for an epidemic occur in a susceptible.}$$

$\beta S > \gamma$, At the outset of an epidemic, nearly everyone (except the index case) is susceptible. So, we substituting $S=1$, we get, $\frac{\beta}{\gamma} > 1$ (Or) $R_0 > 1$
 (Which is equal to ratio of contact rate and recovery rate) (4)

The basic reproduction number R_0 value is important value of all epidemics, because it is defined as the expected number of secondary infections infected by one individual when introduced into a susceptible population [15]. The ratio denoted by R_0 (or) reproduction number. When $R_0 < 1$ means the number of new cases will decrease overtime, i.e. $\lim_{t \rightarrow \infty} I(t) = 0$ and if $R_0 = 1$ means the cases are stability and if $R_0 > 1$ means the major outbreak, then number of infectious individual increases. But recent studies suggest a

higher R_0 value for second wave of COVID-19. There are several methods to estimate the basic and time dependent reproduction number during an outbreak. We applied attack rate and time dependent method to compute the basic and time dependent reproduction number and these parameters were estimated using R software.

2.2.1 To estimate the basic reproduction number based on Attack rate:

In SIR model of the disease transmission presented between Basic reproduction number along with 95% confidence interval and attack rate [6] by $R_0 = -\log\{(1 - AR/S_0)/AR - (1 - S_0)\}$ where S_0 is the initial percentages of susceptible population. The assumptions are closed population, no more transmission, no change intervention during the pandemic.

Table 1. Estimated the basic reproduction number with 95% confidence interval for the most impacted states and also, over all India.

States	Mid-May-2021	Mid-June-2021	Mid-July-2021
Maharashtra	R : 1.003274[1.00324 , 1.003309]	R : 1.000646[1.000632 , 1.000661]	R : 1.000648[1.000633 , 1.000662]
Karnataka	R : 1.009714[1.009621 , 1.009808]	R : 1.000909[1.000884 , 1.000934]	R : 1.000343[1.000328 , 1.000358]
Kerala	R : 1.00779[1.007705 , 1.007875]	R : 1.002232[1.001639 , 1.002825]	R : 1.002212[1.002175 , 1.002249]
Tamilnadu	R : 1.010907[1.01079 , 1.011024]	R : 1.002488[1.002443 , 1.002533]	R : 1.00478[1.00472 , 1.004841]
Andhra Pradesh	R : 1.008035[1.00793 , 1.008141]	R : 1.00158[1.001539 , 1.001621]	R : 1.000672[1.000646 , 1.000697]
Uttar Pradesh	R : 1.003905[1.003837 , 1.003974]	R : 1.000079[1.00007 , 1.000088]	R : 1.00002[1.000016 , 1.000025]
West Bengal	R : 1.008853[1.008729 , 1.008978]	R : 1.001112[1.001073 , 1.001115]	R : 1.000294[1.000274 , 1.000313]
Delhi	R : 1.002324[1.002267 , 1.002381]	R : 1.00008[1.000069 , 1.00009]	R : 1.000251[1.000233 , 1.00027]
India	R : 1.132854[1.132739 , 1.13297]	R : 1.130064[1.129961 , 1.130168]	R : 1.0006[1.000594 , 1.000607]

From Table 1, Maharashtra, Kerala and Karnataka have higher basic reproduction number as compared to other states. The values of R_0 decreased, because efforts taken by government focused on vaccine, social distancing, wearing masks and strictly adopted lockdown procedures and to minimize the contact between people and also decreased mortality rates. Then the reproduction number for every state has value greater than one.

2.2.2 To estimate the time-dependent reproduction number based on time dependent method:

The Covid-19 outbreak connected with time-dependent reproduction number dynamics. We estimate the time dependent reproduction number R_t and average number of cases (R_j) for all those

cases who show the first symptoms of illness on day t.

$$p_{kj} = w(t_k - t_j / \theta) / \sum_{m=1, m \neq k}^n w(t_k - t_m / \theta) \dots \dots \dots (5)$$

p_{kj} is the probability that the cases k infected by the case j. The time-dependent reproduction number for case j is, $R_j = \sum_{k=1}^n p_{kj}$ and averaged $k=1$,

$$\text{then } R_t = 1 / N_t \sum_{j=1}^{N_t} R_j \dots \dots \dots (6)$$

Where, N_t is the number of cases reported in the unit time 't'. The confidence interval of R_t can be obtained by simulation. From equation (4), R_0 must be a greater than one for an epidemic to occur

in susceptible. This is measured by the R_t (effective reproduction number). We take the serial interval follows gamma distribution with mean (standard deviation) was 4(2) which was given by [15]. The real-time reproduction number provides feedback on the spread of outbreak as the $R_t > 1$, the number of infectious cases will growth infections and if R_t

=1, the disease is endemic and if $R_t < 1$, There will be a decline in the number of cases. Thus our aim is to bring down R_t values below one and close to zero. The average time dependent reproduction number over 7 days with 95% confidence interval for India and most affected states are presented in Table 2. Also, the specific details are presented diagrammatically in Figure 1.

Table 2. Average Time-dependent reproduction number over 7 days and 95% confidence interval using time dependent method.

Week	Average Time-dependent reproduction number (R_t)							
	Maharashtra	Karnataka	Kerala	Tamilnadu	Andhra Pradesh	Uttar Pradesh	West Bengal	Delhi
(10.05.2021 to 16.05.2021)	5.01 [3.64, 6.15]	4.03 [3.73,5.22]	3.16 [2.11,3.21]	3.03 [2.74,4.32]	5.31 [4.50,6.16]	3.79 [2.68,4.04]	2.95 [2.73,3.15]	3.44 [3.27,3.61]
(17.05.2021 to 23.05.2021)	3.50 [2.01, 4.48]	2.22 [1.11,2.35]	2.24 [1.12,2.35]	1.89 [1.51,2.18]	2.39 [1.00,3.00]	1.97 [1.76,2.20]	1.78 [1.35,2.04]	1.48 [1.31,1.64]
(24.05.2021 to 30.05.2021)	2.99 [1.66, 3.60]	1.53 [1.34,1.72]	1.89 [0.78,2.07]	1.50 [1.42,1.64]	1.52 [1.31,1.70]	1.16 [1.11,1.21]	1.39 [1.00,2.00]	0.93 [0.73,1.15]
(31.05.2021 to 06.06.2020)	2.61 [1.46, 3.13]	1.11 [0.99,1.23]	1.69 [1.34,1.96]	1.32 [1.50,2.51]	1.12 [0.63,1.55]	0.77 [0.66,1.04]	1.20 [1.10,1.57]	0.64 [0.46,1.08]
(07.06.2021 to 13.06.2021)	2.49 [1.5, 3.64]	0.82 [0.34,0.72]	1.60 [1.4, 1.81]	1.21 [0.15,2.51]	0.90 [0.4,1.51]	0.52 [0.31,1.40]	1.09 [0.96,1.22]	0.52 [0.48,1.08]
(14.06.2021 to 20.06.2021)	2.41 [1.16, 3.48]	0.64 [0.23,1.79]	1.61 [1.38,1.79]	1.15 [1.10,1.20]	0.76 [0.63,1.04]	0.36 [0.20,1.02]	1.04 [0.88,1.18]	0.50 [0.37,1.02]
(21.06.2021 to 27.06.2021)	2.40 [1.18, 3.17]	0.54 [0.34,0.72]	1.66 [1.45,1.86]	1.11 [0.99,1.22]	0.66 [0.45,1.06]	0.36 [0.20,1.02]	1.01 [0.81,1.12]	0.45 [0.40,1.05]
(28.06.2021 to 04.07.2021)	2.43 [1.53, 3.79]	0.48 [0.15,0.73]	1.71 [1.02,2.45]	1.08 [0.9, 1.31]	0.61 [0.30,1.08]	0.30 [0.18,1.07]	0.98 [0.50,1.07]	0.32 [0.28,1.02]
(05.07.2021 to 11.07.2021)	2.39 [1.20, 3.61]	0.43 [0.15,0.61]	1.74 [0.63,2.04]	1.06 [0.86,1.29]	0.57 [0.46,1.06]	0.26 [0.17,1.03]	0.95 [0.42,1.05]	0.31 [0.25,1.01]
(12.07.2021 to 18.07.2021)	1.99 [0.99, 2.36]	0.35 [0.32,0.42]	1.58 [1.37,1.78]	1.03[0.71, 1.19]	0.51 [0.34,1.02]	0.18 [0.12,1.05]	0.92 [0.37,1.03]	0.26 [0.20, 1.00]

Table 2, presents the estimated the time dependent reproduction numbers of COVID-19 incidence cases with 95% confidence interval for India and most affected states. The weekly calculation could be useful to measure the effect of virus and also the effectiveness of control measures in different states of India. We studied about the state level; it is always difficult to observe the initial infections in COVID-19 pandemic.

2.3 Covid-19 outbreak in India and high incidence states:

This study has tried to estimate the parameters using daily active cases of COVID-19. Table 2 presents, the average time-dependent reproduction number R_t over 7 days with 95% confidence interval for India and high incidence states such as Maharashtra, Karnataka, Kerala, Tamilnadu,

Andhra Pradesh, Uttar Pradesh, West Bengal, and Delhi. Also diagrammatic representation of Table 2 is presented in Figure 1. The estimated R_t for Maharashtra was 5.01 in the first week, the estimated R_t for Karnataka was 4.03, the estimated R_t for Kerala was 3.16 and observed that increased the values form 14.06.2021, The estimated R_t for Tamilnadu was 3.03, the estimated R_t for Andrapradesh was 5.31, the Uttar Pradesh R_t was 3.79, West Bengal was 2.95 and the estimated R_t for Delhi was 3.44. If the time-dependent reproduction number could be brought down to less than one and high level of control (or) effective intervention of administrative can be aimed with reduce (or) lower level of public

contact tracing. If the value of time-dependent R_t reaches 5.31, the epidemic will be very rapid. Thus,

our aim is to implement social interventions of bring down one ($R_t < 1$) and close to zero.

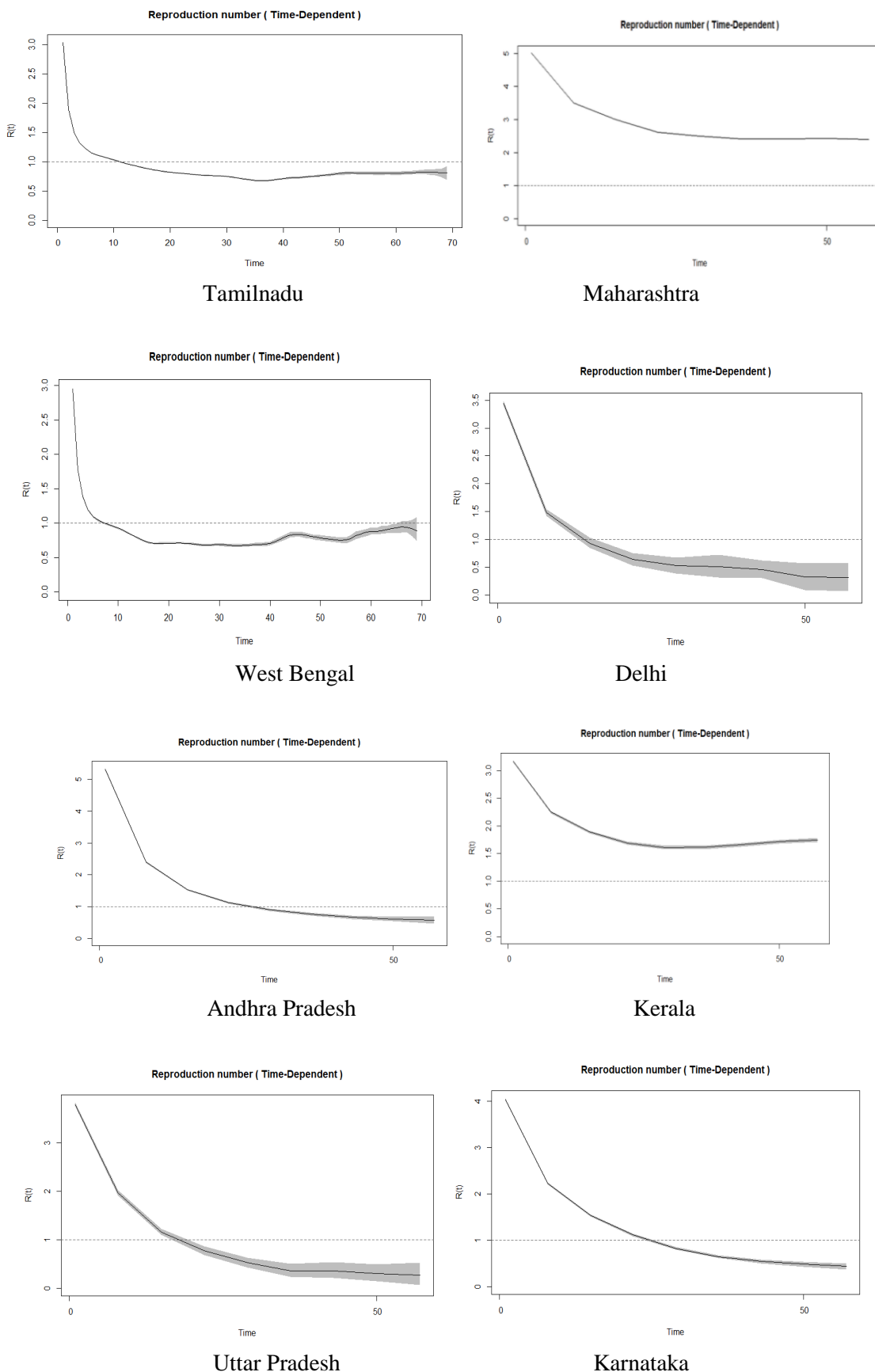
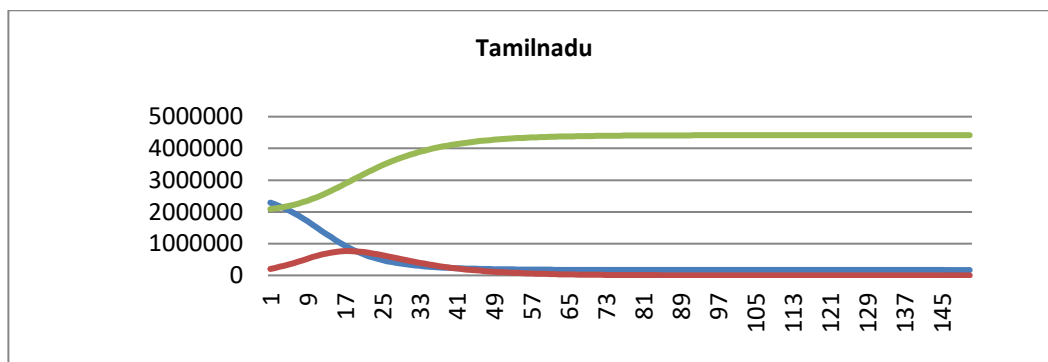
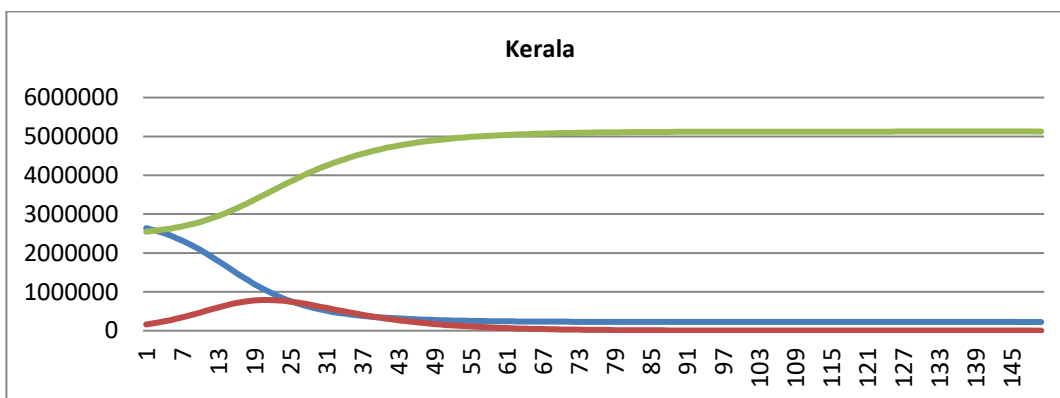
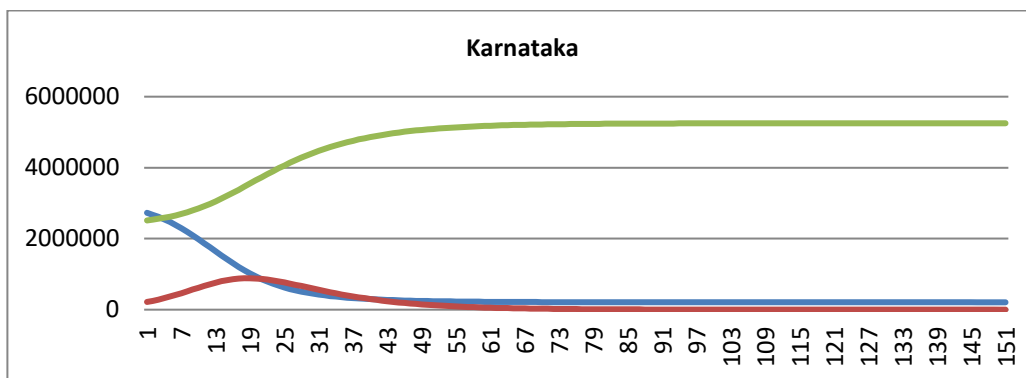
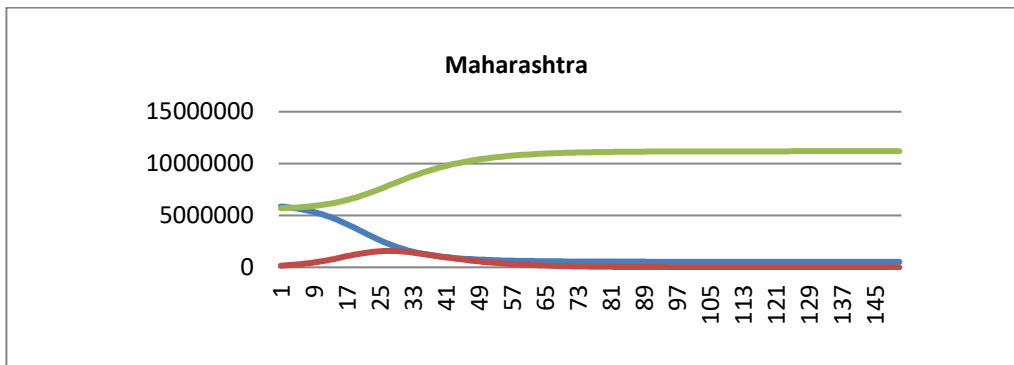


Figure 1. Variations of the time dependent reproduction number for high incidence states in India.

The concept of the epidemic model is that it starts at time $t=0$ and is defined as follows: $S(t)$, $I(t)$, $R(t)$. The number of individuals who have close contact with each other is determined by the contact rate at which it occurs. Each contact is selected uniformly among the individuals from the population (N). All contacts are defined to be mutually independent. A close contact is defined as a contact that is

sufficiently close to cause an infectious disease without affecting others. An infectious period is defined as the period when a contact is not enough to have effect. We consider an infectious period ' I ' are defined to be independent are distributed and having distribution F_I . Then contact processes are also independent.



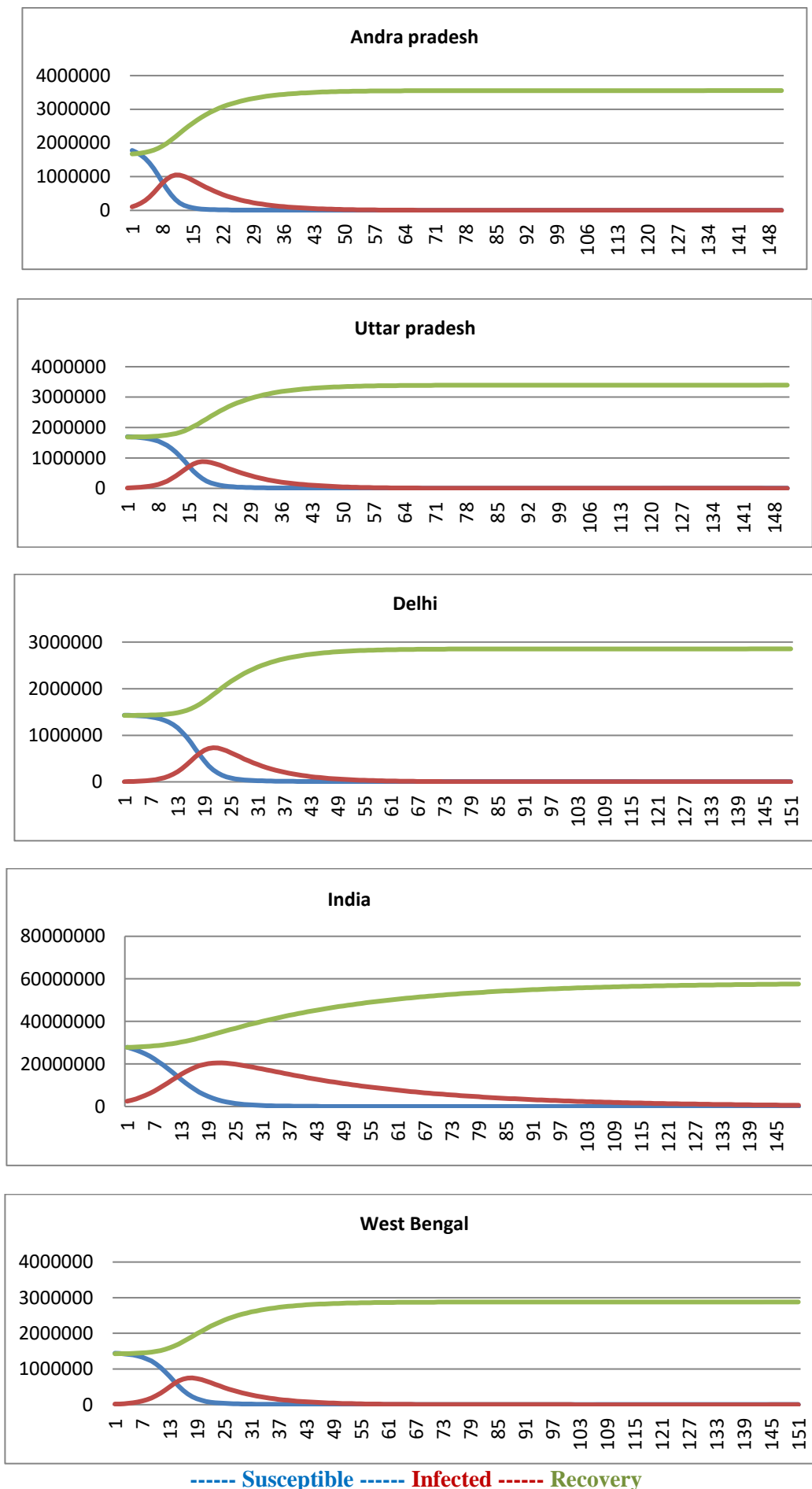


Figure2. Prediction of the Covid-19 trajectory using SIR Model

The above figure shows that the most affected states of COVID-19 trajectory for the next 150 days (up to Oct. 2021) we detected closes approximately. Population size is shown in vertical axes of all graphs and days are shown in horizontal axes. In October 2021 COVID-19 will tends to peak in the states of Maharashtra, Karnataka, Kerala, Tamilnadu, Andhra Pradesh, Uttar Pradesh, West Bengal, and Delhi. Already the first

and second waves of Covid-19 were peaked in September 2020 and May 2021 respectively, and we also know that a maximum of 0.35 million people was affected per day. Therefore, the impact of the next wave on covid-19 will reach its peak in India at October 2021. In this paper the reasons behind why the result is impossible would be discussed.

3. Characterizations and comparison between first and second waves:

Following figure, shown the clear exponential growth pattern between the both waves.

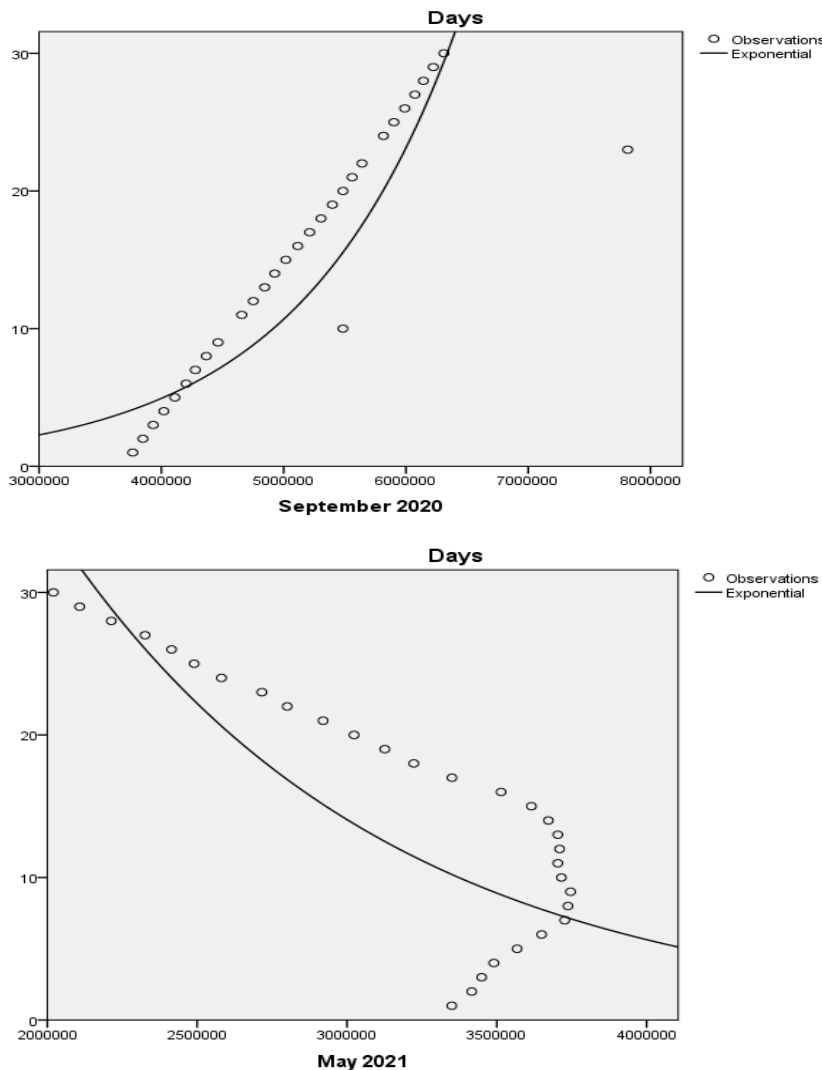


Figure 3. Exponential patterns for first and second wave in India.

[Data for first wave was taken September 2020 and May 2021 for the second wave]

The first wave of COVID-19 in India was steady at value of $R_0 = 1.29$ and beginning of lockdown it was $R_0 = 1.83$. Also, time dependent reproduction value has reached approximately 1.38 duration of first wave. The second wave started slowly near Feb 2021 in Maharashtra but the pandemic quite rapidly in other states start from March. Therefore,

we apply two exponential curves to fit the historical data (daily cases) for COVID-19. Also compared this fit the peak of first wave, when the number of highly infection period was similar to that in the second wave. The peak of the first wave was the daily cases of around 0.1 million in September 2020 and similarly, the peak of the second wave was the daily number of cases crossed 0.2 million in April 2021, also exceeding 0.35 million in mid- May 2021 [28].

Table 3. Fit the Exponential regression model for first and second wave. [$y = a \exp(bt)$].

Wave	Coefficients	95% CI		Standard Error	t stat	p-value	Adjusted R^2
First	0.01843	0.01559	0.02143	0.001443	12.8131	3.12×10^{-13}	0.849
Second	0.01597	-0.00261	0.03465	0.009074	1.7607	7.67×10^{-38}	0.067

As seen in Figure 3, the comparisons of the first and second waves were separated by about September 2020 and May 2021, fitness statistical data listed in Table 3. The fit of the second wave has a low value of coefficient determination than the first wave. Fits for both waves are statistically significant with adjusted R^2 greater than 0.84. According to the historical data, in first wave in India, Maharashtra and Gujarat had higher reproductive value compared to the other states. Then we study about the second wave, Maharashtra and Karnataka had higher reproductive value compared to the other states in India. Delhi had lower rate of R_0 as compared to the other states during both waves. Also, the recent data indicates that the infection rate is much higher. The effective reproduction number (R_t) rising on Feb 2021 and the second wave to occur in India. The most impact states are Maharashtra, Karnataka, Kerala, Tamil Nadu, Andhra Pradesh, Uttar Pradesh, West Bengal and Delhi. While the recent value of R_t for above the status are reported in Table 2. Already third wave started at the Maharashtra and the much higher infection rates.

4. Estimate the Vaccination coverage for Covid-19 outbreak:

Implications of COVID-19 spread often prevented by wear the mask, social distance, isolation, and several lockdown and travel restriction. These decrease the contact rate, i.e.), to decrease R_0 . However, there is no change in R_0 by taking vaccination, but they create immune in the susceptible population. In this section, we study about modeling impact of vaccination on COVID-19 outbreak. Vaccinations are perfect in the sense that all vaccinated individuals get completely immune to the COVID-19 outbreak. Halloran was described the clinical trials and analysis of vaccine studies during outbreak [17]. Sometimes a vaccine is available previous to the arrival of the pandemic and Consider fraction ‘v’ is vaccinated. For instance, let ‘e’ be a factor of a vaccine reduces susceptibility. So, unvaccinated was as compared with average relative susceptibility (1-e), but has a no implication on infectious individual an infection occurs and new critical vaccine coverage,

$$v_c = \frac{1}{e(1 - \frac{1}{R_0})} \dots\dots\dots (7)$$

We describe the critical vaccination coverage percentages (with approximate) in most affected states in India as listed in Table 4. The equation (7) is true, because all individuals have the same reduction a factor of vaccine susceptibility (e). Therefore, this equation is called leaky vaccines. However, the transmission contact rate equal to a given individuals β/N . So, we get $\beta/N = \beta(1-v)/N$.

$$p_i^{N-m} = \binom{N-m}{k} \left[\phi((N-m-k)\beta/N) \right]^{m+k} - \sum_{i=0}^{k-1} \binom{N-m-i}{k-i} \left[\phi((N-m-k)\beta/N) \right]^{k-i} p_i^{N-m}$$

We apply $dN/dt = N(1-v) = N$ and also, $\beta' = \beta(1-v) = \beta$. Also, the early state of outbreak can be approximated by branching process. We denoted the birth rate, β' and mean $1/\gamma$. Therefore R_v define as,

$$R_v = \beta' / \gamma = \beta(1-v) / \gamma = (1-v) / R_0 \dots\dots\dots (8)$$

From equation (8), the reproduction number R_0 after having vaccinated a fraction v in the population (N).

$R_v = R_0(1-v)$ And $R_v \leq 1$ if a major outbreak is impossible.

$$v = \begin{cases} v \geq 1 - 1/R_0 & \text{If } R_0 > 1 \dots\dots\dots \\ 0 & \text{If otherwise} \end{cases} \dots\dots\dots (9)$$

$$v_c = \begin{cases} v_c \geq 1 - 1/R_0 & \text{If } R_0 \dots\dots\dots \\ 0 & \text{If otherwise} \end{cases} \dots\dots\dots (10)$$

The basic reproduction number for almost every state in India has greater than before one the arrival of the second wave. (See. Table. 1). According to the Table 1, most affected states have very high reproduction number R_0 , the lowest level of vaccination in population (N) by equation (10). Similarly, the severe lockdown measures in the north states while vaccination was increased.

Table 4. Estimate the critical vaccination coverage for most affected states in India.

States	Vaccination coverage with percentage			
	Mid- May 2021	Mid-June 2021	Mid- July 2021	Population in 2021 (N)
Maharashtra	16%	22%	31%	12.2 Cr
Karnataka	17%	26%	40%	6.8 Cr
Kerala	24%	33%	47%	3.5 Cr
Tamilnadu	9%	14%	24%	7.6 Cr
Andhra Pradesh	14%	23%	34%	5.2 Cr
Uttar Pradesh	7%	11%	18%	22.5 Cr
West Bengal	13%	18.6%	26 %	9.7 Cr
Delhi	22%	31%	46%	2 Cr

5. Endemic modeling for COVID-19 outbreak:

In this paper developed the epidemic models for dynamics and transmission of COVID-19 disease and the number of infected people with a contagious illness in closed population (N). i.e., no deaths (or) no births (or) not allow new individuals to enter the population during the outbreak. This section is a model for endemic of COVID-19 disease.

Many public health experts believe that COVID-19 becomes endemic like other infectious diseases that emerged in the past. Some infectious diseases are endemic in many countries (For example, Malaria, Hepatitis B, HIV and etc..) such disease is to understand their dynamics. Given some examples discussed about the stochastic epidemic model for work in the area of endemic diseases [7]. We now briefly define the Markovian SIR epidemic stochastic model with demography [8].

i.The Population Dynamics:

The dynamics are, new individuals (susceptible) are entering the population according to the time, of the homogeneous Poisson process at rate μN . Every individual life for an exponentially distributed time with mean $\frac{1}{\mu}$ [Rate of individuals dies]. So, the population size will around the equal to state N. which hence can be interpreted as “size of population”.

ii.The Disease Dynamics are Similar for the Markovian SIR Epidemic Model:

An infectious individual has close to contacts with each other individual at rate $\frac{\beta}{N}$ and each infectious individual recovers rates (γ). The rate of each individual dies (μ) irrespective of their infectious states.

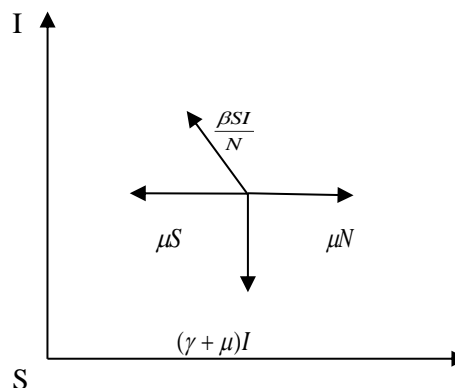


Figure 4, Jump rates for stochastic epidemic model (SIR) with demography.

The following differential equations model for endemic COVID-19:

$$\frac{dS}{dt} = \mu - \beta S(t)I(t) - \mu S(t) \dots\dots\dots (11)$$

$$\frac{dI}{dt} = \beta S(t)I(t) - \gamma I(t) - \mu I(t) \dots\dots\dots (12)$$

$$\frac{dR}{dt} = \gamma I(t) - \mu R(t) \dots\dots\dots (13)$$

The epidemic process $\{S(t), I(t), R(t); t \geq 0\}$ is initial by $(S(0), I(0), R(0))$. We assume that $I(0) > 0$. Figure 4 describe the jump rate for stochastic epidemic model are given in the (S, I) plane. According to differential equations and equating all derivatives into zero. We get the equilibrium state ‘S’ (Susceptible), show that $(S(t), I(t), R(t)) = (1, 0, 0)$ is always a point of equilibrium. The basic reproduction number R_0 , equals to $\frac{\beta}{(\gamma + \mu)}$.

Since, now there are two possible reasons for leaving the recovery and dying. Further, conditions are derived for endemic diseases free equilibrium. A threshold significant parameter R_0 is exists, also greater than one. Then

$$(S(t), I(t), R(t)) = (\hat{S}, \hat{I}, \hat{R}) = \left[\frac{1}{R_0}, \frac{R_0 - 1}{R_0/\delta}, \frac{1 - 1/\delta + R_0 - 1}{R_0/\delta} \right] \dots\dots\dots (14)$$

Where $\delta = \frac{\mu}{\gamma + \mu}$ and this is called endemic equilibrium. [Here 'I' being the endemic level] Some countries, such as New Zealand, have pursued an elimination strategy, keeping COVID-19 infections close to zero, but at the expense of heavy travel restrictions and snap lockdowns when outbreaks are detected. Others, including the UK, have taken the view that SARS-CoV-2 is endemic, meaning it will continue to circulate in the global population and trigger outbreaks, but that a certain number of infections and deaths are tolerable, provided they don't spiral out of control and overwhelm the health system, as they have done during peak periods of the pandemic.

Similarly, there is a chance of COVID-19 disease, changes to endemic in India. Because Table 1 and Table 2 show that all states in India the R0 value has been greater than one and the population size N is large. Therefore, from the differential equations (1), (2), and (3) S(t), I(t) and R(t) became $(N \hat{S}, N \hat{I}, N \hat{R})$ moving towards, and it's demonstrated that COVID-19 virus flare-up changes to endemic. Although, in the end eventually extinct, but require more days. This type is called Quasi-stationary.

Discussion:

We have developed a stochastic epidemic model for dynamics and transmission of Covid-19 disease. With the incidence data about the COVID-19 second wave, the SIR model is used to predict COVID-19 will be peaking in October-2021 (with approximate) (see Figure 2). According to our study the COVID-19 has not attain its peak on October 2021. From this we can come to know that which is not acceptable with current situation. So, this result may not be very accurate, because it does not include many factors such as wearing mask, vaccination, isolation, severe lockdown and other social interventions. Basically, Immunity of Indians is high. Since, their food habit is traditional and more nutritional. Among so many reasons like this, vaccine coverage plays the vital role. Also, vaccination has initial role to reduce COVID-19 spread all over the country. More than 118.44 cores of the people in India are vaccinated with the efforts taken by Government of India. So, the attack rate method and time dependent method used in most affective states and overall, India to estimate the basic and time dependent reproduction number. And it is possible to know that the high incidence status of the available values. We explore the transmissibility parameters in the pandemic through R0 package supports. At present almost every state in India, basic and Time

dependent reproduction numbers were greater than one. Next, the characterization, comparisons, spreading speed, and peak rate was discussed by the exponential regression model. The R^2 values are available in this because the first wave is twice higher than the second wave, and we observed that the propagation rate of the second wave is higher than the first wave. Therefore, from the historical data, we compare to the first and second waves and also analyzed the second wave incidence of COVID-19 in India. Also, we discussed about the vaccination coverage during COVID-19 pandemic. From this, when the R0 value increases (i.e., $R_0 \geq 1$), the vaccination coverage will decrease. At the same time, if the vaccination value is more than the R0 value will be less [28].

Then by the R0 value (basic reproduction number), we calculate the percentage of critical vaccination coverage (mid-May 2021 to mid-July 2021) (see Table 4). Due to the gradual increasing vaccination coverage COVID-19 attain its maximum is impossible. Therefore, next wave is not yet come in India. Finally, we discuss the possibility of COVID-19 disease becoming an endemic disease. We observed that the COVID-19 pandemic will be created unprecedented havoc in community and will become an endemic disease in future.

Conclusion:

This study concludes that the spread of COVID-19's second wave is faster than first wave. So, the transmissibility of third wave depends on characteristics of previous waves.

But, public awareness, effective prevention actions and psychological aspects in India has delayed the next wave. So, the probabilities for high affective rates are low. We explored the prediction and results which may be helpful and effective as guidance for health professionals and Government of India.

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