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The effectiveness of contact tracing in mitigating COVID-19 outbreak: A model-based analysis in the context of India

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\section*{A B S T R A C T}

The ongoing pandemic situation due to COVID-19 originated from the Wuhan city, China affects the world in an unprecedented scale. Unavailability of totally effective vaccination and proper treatment regimen forces to employ a non-pharmaceutical way of disease mitigation. The world is in desperate demand of useful control intervention to combat the deadly virus. This manuscript introduces a new mathematical model that addresses two different diagnosis efforts and isolation of confirmed cases. The basic reproductive number, \( R_0 \), is inspected, and the model's dynamical characteristics are also studied. We found that with the condition \( R_0 < 1 \), the disease can be eliminated from the system. Further, we fit our proposed model system with cumulative confirmed cases of six Indian states, namely, Maharashtra, Tamil Nadu, Andhra Pradesh, Karnataka, Delhi and West Bengal. Sensitivity analysis carried out to scale the impact of different parameters in determining the size of the epidemic threshold of \( R_0 \). It reveals that unidentified symptomatic cases result in an underestimation of \( R_0 \) whereas, diagnosis based on new contact made by confirmed cases can gradually reduce the size of \( R_0 \) and hence helps to mitigate the ongoing disease. An optimal control problem is framed using a control variable \( u(t) \). Projecting the effectiveness of diagnosis based on traced contacts made by a confirmed COVID patient. It is noticed that optimal contact tracing effort reduces \( R_0 \) effectively over time.

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1. Introduction

The Corona-virus diseases 2019 (COVID-19) is an ongoing infectious disease outbreak that originated from the Wuhan city of the Hubei province of Central China in December 2019. The causative virus called severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2). Till the first week of August, 2020, it has spread over 210 countries and international territories, including all continents with a total number of confirmed cases become more than 21 million and, total lethal cases crosses 7.5 lac\textsuperscript{1}. The numbers are still growing with geometric progression. The World Health Organization (WHO) has already declared the disease to be a pandemic on March 11, 2020. With no full proof vaccination, physical distancing is the only precaution response suggested for an individual by the public health officials. Several countries had undergone complete ‘lock-down’ to suppress contact possibilities in the workplace, social gatherings, markets, public transport, etc. As a result, the disease creates a socio-economic burden on an unprecedented scale all over the world. Currently, the globe is in a severe demand for effective control policies to mitigate the pandemic.

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The disease primarily spreads in humans via respiratory droplets discharged by an infected individual during coughing and sneezing while in close contact with a susceptible individual. The human lungs are the most vulnerable organ damaged by this virus. Like most other infections, there is a time lag between the moment of disease and the development of symptoms. Both pre-symptomatic and symptomatic stages are infectious. In the symptomatic stage, the person initially develops flu-like symptoms like fever, cough, sneezing, runny nose. Symptoms such as difficulty in breath, chest pain, vomiting, diarrhea, etc. are noticed in the emergency stage. Some disease may progress to severe pneumonia, multi-organ failure, and death.

Mathematical modeling of transmission of infectious disease is being used to understand the emanation procedure and update intervention policies [35–37]. It is also capable of forecasting future scenarios of an outbreak. With the most basic and straightforward setup, the SIR model proposed by Kermack and McKendrick [7] unlocked a completely new era of Mathematical epidemiology. With further development in computational techniques [40] and associated software, the tool becomes an essential part of public health departments. The primary events of various epidemiological models influenced by the SIR-model are well documented in [6]. Therefore, along with the search for effective vaccination and proper treatment regimen use of mathematical modeling is essential to overcome the current pandemic situation. In recent times, many mathematical models are being proposed to understand the disease transmission and project handful controls [10,15–17,20–25,45]. An early study conducted by Liu et al. [15] demonstrates the effect of the corona virus underlying transmission patterns, both in retrospective and perspective points of view. Prem et al. [16] formulated an age-specific SEIR type model of the disease. They found that physical-distancing can effectively decrease the prevalence and delay the peak of the COVID-19 outbreak. In their work, Hellewell et al. [18], proposed a branching process model to address the use of isolation and contact tracing on the recent outbreak of COVID-19. It is noticed that both of these strategies can effectively reduce the basic reproduction number. Monteiro [42] investigated a compartmental epidemic model for COVID-19. They observed the occurrence of a sequence of peaks in the infected individuals as time progresses. While, Monteiro et al. [43] proposed and simulated an epidemic model by using a probabilistic cellular automaton (PCA) for the spread of SARS-CoV-2. Liu et al. propose another mathematical setup, Liu et al. [20], considering the infectivity of both reported and hidden symptomatic COVID-19 patients. Further, they used their model to predict the future course of the epidemic in South Korea, Italy, and Spain.

During March-April, 2020 the disease COVID-19 has started to affect the European countries like Italy, Spain, Germany, UK etc badly but now the rate of newly disease affected persons has reduced significantly. Thus it may be concluded that, these countries are slowly overcoming the COVID-19 pandemic situation. On the other-hand, India, the second largest populated country has now started to face the hit of COVID-19 and still today it has become second highest COVID-19 affected country just after USA. Due to high population density throughout the whole country, we have seen a new record of becoming newly COVID-19 affected cases almost everyday [13]. Although the first positive COVID-19 case in India has observed in 30th January, 2020 but the disease has started to spread in different parts of India from March 2020 due to international travellers. In this regard, The Ministry of Health and Family Welfare (MHFW), Government of India, has announced complete Lock-down on March 24, 2020, and has extended to May 31, 2020 in four successive steps [5]. Restriction in travel, closure of the educational institute, preventive specifications in various workplaces during this period changes the standard social mixing patterns, which delayed the impact of COVID-19 and delayed the disease onset in uninfected zones of the country. Consequences of human behavioral activity in predictive epidemiological models gained much attention in recent years [26–29]. Alert of a disease outbreak fundamentally results in avoiding unnecessary contact at an individual level, which gives a behavioral immunity in population [8]. In this regard, we follow the recent theoretical setup framed by Mandal et al. [11]. They assumed a portion of susceptible acquires immunity due to the government awareness policy during the outbreak of COVID-19. In a report published by the Ministry of Health of Government of India, it is said that almost 80% of the COVID-19 cases in India are asymptomatic and 20% are symptomatic. So, apart from the public awareness campaigns, tracing out the contacts of a confirmed hospitalized COVID patients is another crucial guideline adopted by public health officials in India [4,5]. Evidence of contact tracing and its impact can be found in [19]. They reported a hospitalized patient who is responsible for 802 new incidence of the disease, and his contact network is also presented in Fig. 1 of [19]. The transmission capacity of a single corona infected individual draws our attention, and we give a particular emphasis on this intervention policy in our study.

Finally, the above discussions recommend that in the absence of a licensed vaccination and useful treatment guideline for COVID-19, non-pharmaceutical health measures like physical-distancing, hand-washing, using a face mask, etc. become critical strategies to avoid infection. Isolation of a diagnosed person is also essential for disease control and mitigation. Another approach is to trace out the recent contacts of the hospitalized patient and conduct a diagnosis effort to detect new cases among them. Our goal is to formulate a deterministic mathematical model describing the transmission of the COVID-19 with these three intervention strategies. The investigation focuses on determining the usefulness and impact of contact tracing. We have also collected data for six Indian states (which are among most vulnerable COVID-19 states) and fitted to our proposed model.

The rest of this article is presented in the following way: In Section 2, a compartmental mathematical model is formulated describing the COVID-19 transmission and the intervention, as mentioned earlier strategies. The biological feasibility of the model and expression of the basic reproduction number is obtained in Section 3. A qualitative feature of the model system also analyzed in this section. Then in Section 4, we estimate our model parameters by fitting the model to specified
data. An optimal control problem is formulated and solved in Section 5 to understand the efficiency of contact tracing. At last, the findings of our study are discussed in Section 6.

2. Mechanistic model formulation

A compartmental mathematical model is formulated considering different clinical stages of COVID-19 by using a set of ordinary differential equations. The model is built upon some vital transmission characteristics of the disease, including critical non-pharmaceutical prevention strategies used by public health departments. The total population is sub-divided into five sub-classes namely, susceptible \( S(t) \), pre-symptomatic \( I_p(t) \), symptomatic \( I_s(t) \), hospitalized \( H(t) \) and recovered \( R(t) \). The virus is not capable of transmitting vertically and spreads rapidly in contact with corona positive individuals. We assume that the total population size is \( N \) i.e. \( N = S(t) + I_p(t) + I_s(t) + H(t) + R(t) \). The mean life expectancy of a healthy individual is taken as \( \frac{1}{\mu} \) unit of time. The simultaneous flow of the population from susceptible class to recovered class is described below.

**Susceptible individuals \( S(t) \):** A population inflow \( \Pi \) per unit time representing the recruitment rate is taken into a vulnerable class only. With an evolving knowledge about the transmission characteristics, we assumed that all infected individuals undergo an incubation period before developing disease symptoms. Both the pre-symptomatic and symptomatic stages are capable to infect susceptible. But, symptomatic individuals are more infectious than pre-symptomatic person. With these assumption we set the force of infection to be \( \lambda(I_p, I_s) = \beta (I_s + kI_p) \). Here, \( \beta \) is the transmission rate and \( k \) is a fraction which scales the less infectiousness of pre-symptomatic cases. In absence of proper clinical preventive measures, local authority promotes many non-pharmaceutical standards of disease mitigation, including physical distancing, stay away from crowd, full or semi-shutdown of many public or private workplaces etc. As a result, a fraction of the susceptible individuals suppresses the risk of exposor. Theoretically, a constant parameter \( L \) is introduced to represent the effect of these policies with an associated rate \( p \) at which it is implicated \cite{11}. Hence, the total rate at which susceptible becomes immune to the disease due to the government policy is \( pLS \), and they directly move to the recovered class. Therefore, the rate of change in susceptible class is

\[
\frac{dS}{dt} = \Pi - \beta (I_s + kI_p)S - (\mu + pL)S.
\]

**Pre-symptomatic class \( I_p(t) \):** In this clinical stage, the person is infected with the virus but has not grown any symptom yet. However, the person is capable to spread the disease among susceptible. We assume that each infected individual undergoes this pre-symptomatic stage called incubation period with an average duration \( \frac{1}{\sigma} \) time unit. The public health officials are very keen about the contact made by a confirmed diagnosed patient isolated in hospital treatment facility. Special diagnosis effort of these traced individuals reduces pre-symptomatic population at rate \( \xi_1 \) per unit time, and they are being isolated directly in specialized hospitals before developing any disease symptoms. Finally, the governing equation for this sub-class takes

\[
\frac{dI_p}{dt} = \beta (I_s + kI_p)S - (\sigma + \mu)I_p - \xi_1H.
\]

**Symptomatic class \( I_s(t) \):** After incubation period, the person suffers from clinical symptoms of COVID-19. We assume that symptomatic cases are diagnosed at a rate \( \eta \) per unit time. Further, diagnosis guided by contact tracing of hospitalized cases reduces the sub-population at a rate \( \xi_2 \) per unit time. The assumptions lead to the following equation.

\[
\frac{dI_s}{dt} = \sigma I_p - (\eta + \mu)I_s - \xi_2H.
\]

**Hospitalized class \( H(t) \):** After diagnosis, the confirmed active cases of COVID-19 are all treated in a completely isolated ward of specialized hospitals. As a result, hospitalized individuals are not capable to transmit the disease. Another inflow
comes in to hospitals from contact tracing of hospitalized individuals at a rate $(\xi_1 + \xi_2)H$. Further, we assume that this sub-population reduces due to recovery with a rate $\gamma$ and disease induced mortality rated $d$ per unit of time. Hence, we must have
\[
\frac{dH}{dt} = \eta I_s - (\gamma + d + \mu)H + (\xi_1 + \xi_2)H.
\]

Recovered class ($R(t)$): After successful treatment the recovered individuals come into this sub-class and leave only by natural death with a rate $\mu$ per unit time. There is also a direct inflow from susceptible class due to government preventive policies. The possibility of relapse or re-exposer of the recovered is not known till now and negligible cases are recorded [44]. Also, here we are concerned about the short term dynamics of the disease. Therefore, all recovered are assumed to be immune to the disease. The equation monitoring this sub-population is given by
\[
\frac{dR}{dt} = \gamma H - \mu R + pLS.
\]

The above framework of each sub-classes gives the following dynamical system describing the transmission of COVID-19 in human.
\[
\begin{align*}
\frac{dS}{dt} &= \Pi - \beta(I_s + kl_p)S - (\mu + pL)S, \\
\frac{dI_s}{dt} &= \beta(I_s + kl_p)S - (\sigma + \mu)I_s - \xi_1 H, \\
\frac{dI_p}{dt} &= \sigma I_p - (\eta + \mu)I_s - \xi_2 H, \\
\frac{dH}{dt} &= \eta I_s - (\gamma + d + \mu)H + (\xi_1 + \xi_2)H, \\
\frac{dR}{dt} &= \gamma H - \mu R + pLS.
\end{align*}
\]

The initial history are given by
\[
S(0) \geq 0, I_s(0) \geq 0, I_p(0) \geq 0, H(0) \geq 0, R(0) \geq 0.
\]

3. Epidemiological well-posedness and stability analysis

A mathematical model representing transmission dynamics of an infectious disease must be verified on biological ground. The model (1) solutions must be confined in region enclosed in the positive heperocant of the Euclidean space $\mathbb{R}_+^5$. Also, the stability criterion of the exiting steady-states are vital to determine epidemiological consequences. In the following subsections we investigate these basic requirements of our proposed model system (1).

3.1. Positivity

Clearly, the fundamental theorem of existence and uniqueness assures existence and uniqueness of the model system (1) with the given condition. Since the population can not be negative at any point of time therefore, we intend to examine the positivity of the solution trajectories of the system (1).

**Theorem 3.1.** All the solution trajectories of the model system (1) with non-negative initial conditions remain non-negative $\forall t \geq 0$ whenever $H \leq \min \left[ \frac{\beta(I_s + kl_p)}{\xi_1}, \frac{\sigma I_p}{\xi_2} \right]$.

**Proof.** From the first equation of system (1), we obtain
\[
\frac{dS}{dt} \geq -\beta(I_s + kl_p) - \mu - pL S \Rightarrow S(t) \geq S(0) \exp \left[ -\int_0^t (\beta(l_s(v) + kl_p(v)) + \mu + pL)dv \right] \geq 0.
\]

Now, if we assume that
\[
\beta(I_s + kl_p)S - \xi_1 H \geq 0 \text{ that is, } H \leq \frac{\beta(I_s + kl_p)}{\xi_1}.
\]
then from the second equation of the system (1), we have
\[
\frac{dI_s}{dt} \geq - (\sigma + \mu) I_s \Rightarrow I_s(t) \geq I_s(0) e^{-(\sigma + \mu)t} \geq 0.
\]
Again, by similar argument one can show that from the third equation of the system (1), whenever
\[ H \leq \frac{\sigma I_p}{\xi_2}, \tag{3} \]
then we have
\[ I_s(t) \geq I_s(0)e^{-(\eta+\mu)t} \geq 0. \]
Finally, from the fourth and fifth equation yields
\[ H(t) \geq H(0)e^{-(\gamma+\delta+\mu)t} \geq 0, \]
\[ R(t) \geq R(0)e^{-\mu t} \geq 0, \]
respectively. Therefore, combining conditions (2) and (3) we conclude that all the solution trajectories remain positive as \( t > 0 \) whenever
\[ H \leq \min \left[ \frac{\beta(I_s + kI_p)S}{\xi_1}, \frac{\sigma I_p}{\xi_2} \right]. \tag{4} \]
Hence the theorem follows. \( \square \)

The positivity condition obtained in (4) imposes an upper bound to the hospitalized class. Further, the contact tracing parameters \( \xi_1 \) and \( \xi_2 \) defines the upper bound. Therefore, positive solution trajectories are dependent on the values of \( \xi_1 \) and \( \xi_2 \). Epidemiologically it signifies that rate of contract tracing must be controlled according to the hospital bed capacity and when there is no infection the policy must be terminated. As a result, fixed values of \( \xi_1 \) and \( \xi_2 \) sustain the positive \( I_p, I_s \) trajectories up to a finite time window.

3.2. Boundedness

A biological population must be confined in a region due to its natural constraints. The next theorem establishes this requirement of the model system (1).

**Theorem 3.2.** All the solutions \((S(t), I_p(t), I_s(t), H(t), R(t))\) of the model system (1) initiating in \( \mathbb{R}_+^5 \) are uniformly bounded.

**Proof.** Let us define \( N(t) = S(t) + I_p(t) + I_s(t) + H(t) + R(t) \). Then adding all the equations of the model system (1), we obtain
\[
\frac{dN}{dt} = \Pi - \mu(S + I_p + I_s + H + R) - dH \\
= \Pi - \mu N - dH \\
\leq \Pi - \mu N
\]
that is, \( \frac{dN}{dt} + \mu N \leq \Pi \).

Now, by applying the differential inequality due to Birkoff and Rota [30], we obtain
\[
0 \leq N(t) \leq \frac{\Pi}{\mu} + N(0)e^{-\mu t}.
\]
Thus as \( t \to \infty \), we have \( 0 \leq \limsup_{t \to \infty} N(t) \leq \frac{\Pi}{\mu} \). This implies that all solutions of the system (1) initiating from \( \mathbb{R}_+^5 \) are uniformly bounded in the region
\[
\Omega = \{(S, I_p, I_s, H, R) \in \mathbb{R}_+^5 : 0 \leq S + I_p + I_s + H + R \leq \frac{\Pi}{\mu} + \epsilon\}
\]
for some \( \epsilon > 0 \). Hence the theorem follows. \( \square \)

3.3. Basic reproduction number

The disease free equilibrium point of the system (1) can be obtained by putting \( I_p(t) = 0 \), \( I_s(t) = 0 \) and \( H(t) = 0 \) and finally takes the form \( E^0 = (S^0, 0, 0, 0, R^0) \), where
\[
S^0 = \frac{\Pi}{\mu + pL}, \quad R^0 = \frac{\Pi pL}{\mu (\mu + pL)}.
\]
The basic reproduction number is a central concept in the study of the spread of communicable diseases, the number of secondary infections caused by a single infected person in a population consisting with only of susceptible with the control measures in place (quarantined and isolated class). This dimensionless number is calculated at the disease free state by the next generation operator method and it is denoted by \( R_0 \) [34].
For this, we identify the compartments which are infected from the system (1) as \((l_p, l_s, H)\) and decomposing the right hand side as \(F - V\), where \(F\) is the transmission part denoting the addition of new infection, and the transition part is \(V\), which indicates the change in state. Let us consider the system. Following this technique we re-write the system (1) as

\[
\frac{d\chi}{dt} = F - V,
\]

where \(\chi = (l_p, l_s, H)\),

\[
F = \begin{pmatrix}
\beta (l_s + kl_p) & 0 & 0 \\
0 & 0 & 0
\end{pmatrix},
\]

and

\[
V = \begin{pmatrix}
(\sigma + \mu) l_p + \xi_1 H \\
(\eta + \mu) l_s + \xi_2 H - \sigma l_p \\
(\gamma + d + \mu) H - (\xi_1 + \xi_2) H - \eta l_s
\end{pmatrix}
\]

Now, we calculate the Jacobian of \(F\) and \(V\) at the disease free steady state \(E^0\) as

\[
F = \frac{\partial F}{\partial \chi} = \begin{pmatrix}
\beta kS^0 & \beta S^0 & 0 \\
0 & 0 & 0 \\
0 & 0 & 0
\end{pmatrix},
\]

and

\[
V = \frac{\partial V}{\partial \chi} = \begin{pmatrix}
(\sigma + \mu) & 0 & \xi_1 \\
-\sigma & (\eta + \mu) & \xi_2 \\
0 & -\eta & l_1
\end{pmatrix}
\]

where \(l_1 = \gamma + d + \mu - \xi_1 - \xi_2\).

Now according to the [34], the spectral radius \((\rho)\), i.e., the maximum eigenvalue of the matrix \(FV^{-1}\) gives the basic reproduction number \(R_0\) of the system (1). After some algebraic simplifications, we obtain

\[
R_0 = \rho(FV^{-1}) = \frac{\beta \Pi (kl_2 + \sigma l_1)}{(\mu + pl)(\xi_1 \sigma + (\sigma + \mu) l_2)}
\]

where \(l_2 = l_1(\eta + \mu) + \xi_2\).

3.4. Existence of equilibria

The model system (1) always exhibits a disease free equilibrium \(E^0 = (S^0, l_p^0, l_s^0, H^0, R^0)\) where

\[
S^* = \frac{1}{\beta \left(1 + \frac{kn_1}{\sigma}\right)} \left(\frac{n_1 n_4}{\sigma} + \frac{\xi_1 \eta}{n_3}\right),
\]

\[
l_p^* = \frac{n_1 l_1^*}{\sigma},
\]

\[
l_s^* = \frac{\Pi - (\mu + pl) S^*}{\beta S^* \left(1 + \frac{kn_4}{\sigma}\right)},
\]

\[
H^* = \frac{\eta l_s^*}{n_3},
\]

\[
R^* = \frac{1}{\mu} \left(p l S^* + \frac{\gamma \eta l_s^*}{n_3}\right)
\]

where

\[
n_1 = \sigma + \mu, n_2 = \eta + \mu, n_3 = \gamma + d + \mu - \xi_1 - \xi_2, n_4 = \left(\frac{n_2 + \frac{\xi_2 \eta}{n_3}}{n_3}\right).
\]

It is to be noted that the infected steady state of the model system (1) is feasible provided \(\Pi > (\mu + pl) S^*\) and \(\gamma + d + \mu > \xi_1 + \xi_2\). Now after some algebraic simplifications, we obtain that the condition \(\Pi > (\mu + pl) S^*\) is equivalent to \(R_0 > 1\). Hence we conclude that the model system (1) has a unique endemic steady state \(E^* = (S^*, l_p^*, l_s^*, H^*, R^*)\) when \(\gamma + d + \mu > \xi_1 + \xi_2\) and \(R_0 > 1\).

Now using Theorem 2 in [34], one can establish the following theorem.

**Theorem 3.3.** The disease-free equilibrium of the model system (1) is locally asymptotically stable if \(R_0 < 1\), and unstable if \(R_0 > 1\).
3.5. Local stability of the endemic steady state

In order to study the local asymptotic stability of the infected steady state \( E^* = (S^*, I_p^*, I_s^*, H^*, R^*) \), we calculate the Jacobian matrix of system (1), as given by

\[
J_{E} = \begin{pmatrix}
-m - \mu - pL & -\beta kS^* & -\beta S^* & 0 & 0 \\
0 & \beta kS^* - n_1 & \beta S^* - \xi_1 & 0 \\
0 & \sigma & -n_2 & -\xi_2 & 0 \\
pL & 0 & 0 & \gamma & -\mu
\end{pmatrix},
\]

where \( m = \beta (I_p^* + I_s^*) \), and \( n_1, n_2, n_3 \) are as defined earlier. Now it is easy to observe that one eigenvalue of the above matrix \( J_{E} \) is \(-\mu\). The remaining roots are obtained from the following equation

\[
\lambda^4 + P_1 \lambda^3 + P_2 \lambda^2 + P_3 \lambda + P_4 = 0
\]

(5)

where

\[
P_1 = m + \mu + pL + n_1 + n_2 + n_3 - \beta kS^*,
\]

\[
P_2 = (m + \mu + pL)(n_1 + n_2 + n_3 - \beta kS^*) + n_2n_3 + \xi_2\eta - \sigma \beta S^* - (\beta kS^* - n_1)(n_2 + n_3) + m\beta kS^*,
\]

\[
P_3 = (m + \mu + pL)(n_2n_3 + \xi_2\eta - \sigma \beta S^* - (\beta kS^* - n_1)(n_2 + n_3)) - (\beta kS^* - n_1)(n_2n_3 + \xi_2\eta) + \sigma(\xi_1\eta - \beta S^* n_3) + n(n_2 + n_3)\beta kS^* + \sigma \beta S^* m,
\]

and

\[
P_4 = m\sigma \beta n_1 S^* + m\beta kS^*(n_2n_3 + \xi_2\eta) + \sigma(\xi_1\eta - \beta S^* n_3)(m + \mu + pL) - (m + \mu + pL)(n_2n_3 + \xi_2\eta)(\beta kS^* - n_1).
\]

Now, by applying the well known Routh–Hurwitz criteria, we obtain a set of necessary and sufficient condition for local asymptotic stability of the endemic steady state \( E^* \), which are: \( P_i > 0 \) for \( i = 1, 2, 3, 4 \), \( P_1P_2 > P_3 \) and \( P_1P_2P_3 > P_2^2 + P_4^2 + P_4^2P_4 \).

Based on the above discussions, we may conclude the following result.

**Theorem 3.4.** The endemic equilibrium \( E^* \) is locally asymptotically stable for \( R_0 > 1 \), \( \gamma + d + \mu > \xi_1 + \xi_2 \), \( P_i > 0 \) (\( i = 1, 2, 3, 4 \)), \( P_1P_2 > P_3 \) and \( P_1P_2P_3 > P_2^2 + P_4^2 + P_4^2P_4 \).

4. The optimal control problem

Our goal in this section is to formulate an optimal control problem using \( u(t) \) as time-dependent control variable representing contact tracing effort both in pre-symptomatic and symptomatic corona patients. In this regard we shall follow the approach taken in [38,39]. After introducing this intervention effort in our model system, the model takes the following form:

\[
\begin{align*}
\frac{dS}{dt} &= \Pi - \beta (I_s + kl_p)S - \mu S - pLS, \\
\frac{dl_p}{dt} &= \beta (I_s + kl_p)S - (\sigma + \mu)l_p - u(t)\xi_1H, \\
\frac{dl_s}{dt} &= \sigma l_p - (\eta + \mu)l_s - u(t)\xi_2H, \\
\frac{dH}{dt} &= \eta l_s - (\gamma + d + \mu)H + u(t)(\xi_1 + \xi_2)H, \\
\frac{dR}{dt} &= \gamma H - \mu R + pLS.
\end{align*}
\]

(6)

The objective of this effort \( u(t) \) is to minimize total disease burden (both in pre-symptomatic and symptomatic classes) together with the associated cost of the employed intervention policy. Also, we should keep in mind that there are some side effects of the contact tracing procedure. It is observed that the health workers engaged in the contact tracing procedure are potentially exposed to the virus and so they are instructed to self-quarantine for 14 days and undergo the COVID-19 test. Here, we also wish to minimize those side effects of the contact tracing procedure. So, we consider a quadratic type control instead of a linear control. Therefore, our objective is to minimize the following cost functional:

\[
J = \int_0^T \left[l_p(t) + l_s(t) + cu^2(t)\right] dt.
\]

(7)
4.1. Existence of optimal control

Our goal in this sub-section is to verify the existence of an optimal solution for the system posed in (6) with the objective functional (7). We have followed the approach taken by Das et al. [27] and hence the results obtained by Fleming and Rishel [41].

Before we proceed, it is required to establish that the solution of the system (6) is bounded above within a finite time frame. The upper bounds on the solutions of (6), that is super-solution \((\bar{S}, \bar{I}_p, \bar{I}, \bar{H}, \bar{R})\) is obtained by the system

\[
\begin{align*}
\frac{d\bar{S}}{dt} &= \Pi, \\
\frac{d\bar{I}_p}{dt} &= \beta \bar{S}, \\
\frac{d\bar{I}}{dt} &= \sigma \bar{I}_p, \\
\frac{d\bar{H}}{dt} &= \eta \bar{I} + (\xi_1 + \xi_2)\bar{H}, \\
\frac{d\bar{R}}{dt} &= \gamma \bar{H} + pL \bar{S}.
\end{align*}
\]

(8)

Clearly, the above system (8) is linear with constant coefficients. Therefore, the super-solutions are uniformly bounded in a finite time window. Now, we are in a position to proceed for verify the existence of an optimal solution for the posed problem. Let us conclude our result due to Fleming and Rishel [41] as the following theorem.

**Theorem 4.1.** There is an optimal control \(u^*(t)\) such that \(J(I_p(t), I(t), u(t)) = \min_u J(I_p(t), I(t), u(t))\) subject to the system of differential Eq. (6) and the objective functional (7).

**Proof.** In order to proof the existence of the optimal control, it is required to check the following five conditions:

1. The optimal control set and the corresponding state variables are non-empty.
2. The set of all admissible controls \(\Theta\) is closed and convex.
3. The right hand side of the state system is continuous and bounded above by a function in state variables and control variable.
4. The integrand of the cost functional is convex over \(\Theta\).
5. There exists constants \(A > 0, B > 0\) and \(\beta > 1\) such that the integrand of the cost functional satisfies \(L(I_p, I, u) \geq A + B|u|^\beta\).

Now, to check the condition 1, we use the result developed by Lukes [32] (Theorem 9.2.1, page 182). Since the system has bounded coefficients and the solution curves are bounded in a compact region within a finite time interval, so the first condition follows from Lukes [32].

From the definition of the control set, it follows the control set \(\Theta\) is closed and convex.

Clearly, the right hand side (RHS) of the system is continuous. Let us consider \(\bar{\Phi}(t, \bar{Y})\) as the RHS of the system (6), except the terms of \(\bar{u}(t)\), and define

\[
\bar{\Phi}(t, \bar{Y}, u) = \Phi(t, \bar{Y}) + \bar{Z},
\]

(9)

where, \(\bar{Y} = [S, I_p, I, H, R]^T\) and \(\bar{Z} = [0, -u\xi_1H, -u\xi_2H, u(\xi_1 + \xi_2)H, 0]^T\). Therefore, using the boundedness of the solutions of (8), we have

\[
|\bar{\Phi}(t, \bar{Y}, u)| \leq \begin{pmatrix} 0 & 0 & 0 & 0 & 0 \\ \beta & 0 & 0 & 0 & 0 \\ 0 & \sigma & 0 & 0 & 0 \\ 0 & 0 & \eta & (\xi_1 + \xi_2) & 0 \\ pL & 0 & 0 & \gamma & 0 \\ \end{pmatrix} + |\bar{Z}|
\]

\[
\leq C_1(|\bar{Y}| + |u|).
\]

(10)

where, \(C_1\) is a constant depending upon the coefficients of the system (6). The above inequality justifies the condition 3.

Next, in order to prove that the integrand of the objective functional (7) i.e. \(\bar{\Phi}(t, \bar{Y}, u) = I_p + I + cu^2\) is convex in the control set \(\Theta\), we have to show

\[
(1 - q) \Phi(t, Y, u) + q \Phi(t, Y, v) \geq \Phi(t, Y, (1 - q)u + qv),
\]

where \(u\) and \(v\) are two controls and \(q \in (0, 1)\). Now,

\[
(1 - q) \Phi(t, Y, u) + q \Phi(t, Y, v) = I_p + I + (1 - q)cu^2 + qcv^2,
\]

and

\[
\Phi(t, Y, (1 - q)u + qv) = I_p + I + Cu\left\{(1 - q)u^2 + q^2v^2 + 2q(1 - q)uv\right\}.
\]
Finally,
\[ [(1 - q) \Phi(t, Y, u) + q \Phi(t, Y, u)] - [\Phi(t, Y, (1 - q)u + qv)] = cq(1 - q)(u - v)^2 \geq 0. \]

Hence the objective function \( \Phi(t, Y, u) \) is convex in the control set \( \Theta \).

To verify the last condition, note that, \( I_p(t) + I_s(t) + cu^2(t) \geq A + B|u|^\beta \), where \( A \) depends upon the upper bound of \( I_p(t) \) and \( I_s(t) \), \( B = c \) and \( \beta > 1 \). Hence the existence of the optimal control is proved. \( \square \)

### 4.2. Characterization of optimal control

Now we need to find out the value of the optimal control \( u^*(t) \) such that
\[
J(u^*(t)) = \min_{u \in \Theta} J(u) \quad \text{where} \quad \Theta = \{ u \text{ is measurable, } 0 \leq u(t) \leq 1 \text{ for } t \in [0, T] \}. \]

In the objective functional, the weight constants corresponding to the pre-symptomatic and symptomatic populations are taken a unity, where as \( c \) is the positive constant associated with the square of the control. The Lagrangian is given by
\[
L(I_p, I_s, u) = I_p(t) + I_s(t) + cu^2(t). \tag{11}
\]

The Hamiltonian is defined as follows:
\[
H_1(S, I_p, I_s, H, R, u, \lambda_1, \lambda_2, \lambda_3, \lambda_4, \lambda_5) = L(I_p, I_s, u) + \lambda_1(t) \frac{dS}{dt} + \lambda_2(t) \frac{dI_p}{dt} + \lambda_3(t) \frac{dI_s}{dt} + \lambda_4(t) \frac{dH}{dt} + \lambda_5(t) \frac{dR}{dt}, \tag{12}
\]
where the adjoint variables can be obtained as the solution of the following system of differential equations
\[
\begin{align*}
\dot{\lambda}_1(t) &= -\frac{\partial H_1}{\partial S} = \lambda_1(\beta I_p + kl_p) - \lambda_2 \beta (I_s + kl_p) - \lambda_5 p, \\
\dot{\lambda}_2(t) &= -\frac{\partial H_1}{\partial I_p} = \beta k S (\lambda_1 - \lambda_2) + \lambda_2 (\sigma + \mu) - \lambda_3 \sigma - 1, \\
\dot{\lambda}_3(t) &= -\frac{\partial H_1}{\partial I_s} = \beta k S (\lambda_1 - \lambda_2) + \lambda_3 (\eta + \mu) - \lambda_4 \eta - 1, \\
\dot{\lambda}_4(t) &= -\frac{\partial H_1}{\partial H} = \lambda_2 \mu \xi_1 + \lambda_3 u \xi_2 + \lambda_4 (\gamma + d + \mu) - \lambda_4 (\xi_1 + \xi_2) u - \gamma _5, \\
\dot{\lambda}_5(t) &= -\frac{\partial H_1}{\partial R} = \lambda_5 \mu. \tag{13}
\end{align*}
\]

satisfying \( \lambda_i(T) = 0 \), for \( i = 1, 2, 3, 4, 5 \), i.e. the transversality conditions.

Now the following theorem is stated and proved using the Pontryagin’s maximum principle [33].

**Theorem 4.2.** The optimal value of the control variable which minimizes the objective functional \( J \) in the region \( \Theta \) is given as
\[
\bar{u}(t) = \max \{ 0, \min (\bar{u}, 1) \}, \quad \text{where}
\]
\[
\bar{u} = \frac{H}{2c} \{ \xi_1 (\lambda_2 - \lambda_4) + \xi_2 (\lambda_3 - \lambda_4) \}.
\]

**Proof.** The optimal value \( u^* \) of the control variable \( u(t) \) is obtained by using the optimality condition \( \frac{\partial H_1}{\partial u} = 0 \). Using this condition, we obtain \( \bar{u} = \frac{H}{2c} \{ \xi_1 (\lambda_2 - \lambda_4) + \xi_2 (\lambda_3 - \lambda_4) \} \). Again since the control variable is bounded by the upper bound 1 and lower bound 0, so we consider \( u = 0 \) when \( \bar{u} < 0 \) and \( u = 1 \) when \( \bar{u} > 1 \). Therefore, combining these results, we get the optimal value \( u^* \) of the control variable that minimizes the objective functional \( J \). Hence the theorem follows. \( \square \)

Now we intend to show the numerical solutions of the formulated optimal control problem based on some simulated data set. In order to solve the system (13) subject to the system (6), we use the Runge-Kutta method of order 4 and MATLAB software. First the system (6) is solved by using forward Runge-Kutta method of order four and then simultaneously the adjoint system (13) is solved by using backward Runge-Kutta method of order four using the solutions of the state variables and the transversality condition (see [31]). Also, to solve the systems numerically, we take the parameters values as \( c = 1, \quad \Pi = 10, \quad \beta = 0.35, \quad k = 0.78, \quad \mu = 0.3, \quad p = 0.8, \quad L = 0.9, \quad \sigma = 0.1, \quad \xi_1 = 0.1, \quad \xi_2 = 0.1, \quad \eta = 0.2, \quad \gamma = 0.01, \quad d = 0.001. \) The initial size of the state variables, namely susceptible, pre-symptomatic, symptomatic, hospitalized and recovered are taken as 30,25,20,8, and 5 respectively.

The variation of the state variables in presence and absence of control are shown in Fig. 2. It is observed that both the pre-symptomatic and symptomatic population densities decreases significantly due to the use of the control. However, the number of the hospitalized individuals increases due to the contact tracing control measure. Therefore, the real phenomena is justified through the simulation works. Moreover, we have shown the time evolution of the control variable \( u \) in Fig. 3.
Fig. 2. Variation of the state variables in presence and absence of control policy.

Fig. 3. Variation of the control profile $u(t)$. 
Table 1
Global parameters with descriptions and associated magnitudes for the model system (1).

| Descriptions                                      | Symbol used | Magnitude              | Sources |
|--------------------------------------------------|-------------|------------------------|---------|
| Recruitment rate                                 | Π            | -                      | -       |
| Mean life expectancy                             | l            | 68.5 × 365 days        | [2]     |
| Recovery rate of hospitalized                     | γ            | 0.46 day⁻¹             | [1]     |
| Mean incubation-period at pre-symptomatic stage  | l            | 7 days                 | [1]     |
| Death rate of hospitalized COVID-19 patients      | d            | 0.1945 × 10⁻⁴          | [12]    |
| Reduction factor in infectivity of pre-symptomatic| k            | 0.78                   | [9]     |
| Rate of implication of government policy          | p            | 0.8 day⁻¹              | [11]    |
| Awareness level of the susceptible                | L            | 0.9                    | [11]    |

Table 2
State-wise estimated values of the used parameters in the model system 1.

| State                  | β    | η    | ξ₁   | ξ₂   |
|------------------------|------|------|------|------|
| Maharashtra            | 0.3156 | 0.0315 | 0.2331 | 0.311 |
| Tamil Nadu             | 0.08857 | 0.01425 | 0.1773 | 0.3773 |
| Andhra Pradesh         | 0.5962 | 0.3264 | 0.05026 | 0.8327 |
| Karnataka              | 0.5045 | 0.225 | 0.02141 | 0.7422 |
| Delhi                  | 0.3179 | 0.2214 | 0.3237 | 0.6049 |
| West Bengal            | 0.4958 | 0.2306 | 0.09899 | 0.6109 |

Table 3
State-wise estimated initial population size used in stimulation for the model system 1. The susceptible, pre-symptomatic and symptomatic initial values are estimated whereas the hospitalized and recovered initial size is obtained from data [3].

| State        | S(0)                  | Iₛ(0) | Iₖ(0) | H(0) | R(0) |
|--------------|-----------------------|-------|-------|------|------|
| Maharashtra  | 8 × 10⁷               | 1 × 10⁵ | 4500  | 107  | 0    |
| Tamil Nadu   | 9.5 × 10⁵             | 3 × 10⁵ | 204000 | 18   | 0    |
| Andhra Pradesh| 1.2 × 10⁶            | 4550  | 400   | 8    | 0    |
| Karnataka    | 1.6 × 10⁶             | 6500  | 950   | 41   | 3    |
| Delhi        | 1.1 × 10⁶             | 19500 | 3100  | 30   | 6    |
| West Bengal  | 1 × 10⁶               | 3500  | 3000  | 9    | 0    |

Table 4
State-wise estimated value of the basic reproduction number R₀ for the model system 1.

| State                | R₀   |
|----------------------|------|
| Maharashtra          | 2.96443 |
| Tamil Nadu           | 1.5177  |
| Andhra Pradesh       | 1.8370  |
| Karnataka            | 1.01891 |
| Delhi                | 1.5809  |
| West Bengal          | 1.6794  |

5. Estimation of parameters in six vulnerable states of India

The proposed model system (1) for COVID-19 is calibrated with weekly reported COVID-19 positive cases of six high-burden states of India namely, Maharashtra, Tamil Nadu, Andhra Pradesh, Karnataka, Delhi and West Bengal from March 24, 2020 till December 15, 2020. During this period, whole India including those six states has undergone through complete lock-down from March 24, 2020 till May 31, 2020 in four consecutive steps. The data source is the India COVID-19 Tracker web page [3], reporting daily registered corona positive cases in Indian states and retrieved on December 15, 2020. Due to high transmission risk of the corona virus, each positive-diagnosed patients is isolated directly in a specialized hospitals as guided by Indian Council of Medical Research [4] and, the total number of cases are reported on daily basis on public domain to elicit healthy practices among population [5]. We employ the least-square fit approach in MATLAB to estimate the parameter magnitude. The parameters with globally accepted values are listed in Table 1 with short description and the state-wise estimated parameters sizes can be found in the Table 2. The best fit initial size are also extracted using the same technique and displayed in the Table 3.

The best-fit curves are plotted with the cumulative weekly observed confirmed cases under treatment in hospitals and displayed in Fig. 4. Further, using these parameter magnitudes we estimated the epidemic threshold quantity, that is, the basic reproduction number R₀ for all six different states (see the Table 4).
Fig. 4. Best fit solution trajectories of the system (1) with the observed data of the six states starting from March 24, 2020 to December 15, 2020.
The accuracy of the employed estimation approach is quantified by two quantities called, Mean Absolute Error ($Q_{\text{MAE}}$) and Root Mean Square Error ($Q_{\text{RMSE}}$). The corresponding definitions are proposed as the followings:

$$Q_{\text{MAE}} := \frac{1}{N} \sum_{i=1}^{N} |\theta(i) - Y(i)|,$$

$$Q_{\text{RMSE}} := \sqrt{\frac{1}{N} \sum_{i=1}^{N} (\theta(i) - Y(i))^2},$$

where, $\theta(i)$ denotes the data reported on $i$th day and $Y(i)$ is the model prediction on the same day with total $N$ number of observations. The quantities give mean error tolerance in measuring the cumulative confirmed corona-positive cases with estimated parameters fitted to the model system (1). These accuracy level indices are reported state-wise in the Table 5.

5.1. Sensitivity analysis

Data collection and estimation of parameters are always uncertain and never error-free. In this situation, it is worthy to list the involved parameters on defining epidemic threshold quantity $R_0$ according to their impact on the size of $R_0$. This investigation will project the most influential parameters in determining the size of $R_0$. The following definition proposed by Chitnis et al. [14] is adapted to list the involved parameters according to their sensitivity in $R_0$.

**Definition 5.1.** The normalized forward sensitivity index of $R_0$ with respect to a parameter say, $\eta$ is defined as the following:

$$\Gamma^R_\eta := \frac{\partial R_0}{\partial \eta} \times \frac{\eta}{R_0}. \quad (14)$$

Clearly, the above definition is well-defined for any positive parametric space. The sensitivity of each associated parameters with $R_0$ for six vulnerable states namely Maharashtra, Tamil Nadu, Andhra Pradesh, Karnataka, Delhi and West Bengal are tabulated in the Table 6. Positive value indicates $R_0$ as an increasing function of that parameter whereas negative indices

### Table 5

| Accuracy indices | Maharashtra | Tamil Nadu | Andhra Pradesh | Karnataka | Delhi | West Bengal |
|------------------|-------------|------------|----------------|-----------|-------|-------------|
| $Q_{\text{MAE}}$ | 24869       | 27468      | 33192          | 17142     | 11346 | 6839        |
| $Q_{\text{RMSE}}$ | 33673       | 33509      | 45171          | 22882     | 13583 | 8908.4      |

### Table 6

Sensitivity indices of the associated parameters with $R_0$ obtained using the Definition 5.1.

| Parameters | Maharashtra | Tamil Nadu | Andhra Pradesh |
|-----------|-------------|------------|----------------|
| $\Pi$     | +1          | +1         | +1             |
| $\beta$   | +1          | +1         | +1             |
| $k$       | +1.2743     | +0.3028    | +2.3084        |
| $\mu$     | $-3.754 \times 10^{-5}$ | $-4.7 \times 10^{-5}$ | $-2.15 \times 10^{-4}$ |
| $\sigma$  | $-1.2741$   | $-0.303$   | $-2.3082$      |
| $\xi_1$   | $-2.06915$  | $-2.6348$  | $-0.442$       |
| $\xi_2$   | $-1.01537$  | $-3.2016$  | $-2.6043$      |
| $\eta$    | +0.2743     | +1.3037    | +1.3086        |
| $\gamma$  | +3.08413    | +0.7835    | +3.0459        |
| $d$       | $+1.3 \times 10^{-4}$ | $+3.3 \times 10^{-4}$ | $+1.29 \times 10^{-4}$ |
| $p$       | $-0.9999$   | $-0.9999$  | $-0.9999$      |
| $L$       | $-0.9999$   | $-0.9999$  | $-0.9999$      |

### Note

The accuracy level indices involving $R_0$ are proposed as the followings:

$$Q_{\text{MAE}} := \frac{1}{N} \sum_{i=1}^{N} |\theta(i) - Y(i)|,$$

$$Q_{\text{RMSE}} := \sqrt{\frac{1}{N} \sum_{i=1}^{N} (\theta(i) - Y(i))^2},$$

where, $\theta(i)$ denotes the data reported on $i$th day and $Y(i)$ is the model prediction on the same day with total $N$ number of observations. The quantities give mean error tolerance in measuring the cumulative confirmed corona-positive cases with estimated parameters fitted to the model system (1). These accuracy level indices are reported state-wise in the Table 5.
specify $R_0$ is a decreasing function of that parameter. For example, $\Gamma_{k}^{R_0} = 1.3292$ indicates that if $k$ is increased by 10% then $R_0$ is also increased by 13.292% and $\Gamma_{p}^{R_0} = -0.9999$ shows that decreasing $p$ by 10% will reduce $R_0$ by 9.9%.

From Table 6, we notice that parameters $\Pi, \beta, k, y, d$ are with positive sensitivity indices and $\mu, \sigma, \xi_1, \xi_2, \eta, d, p, L$ are with negative indices. Bar diagrams are plotted in the Fig. 6 considering the sensitivity indices of the associated parameters with $R_0$ for each six states, here small values associated to the parameters $\mu$ and $d$ are neglected. The list in Table 6 and Fig. 6 shows that the contact tracing rate guided by the contact made by a corona-positive hospitalized patient has negative indices, that is, with increasing contact tracing rate the basic reproduction number decreases gradually. To illustrate this effect pictorially, contour plots are plotted with state-wise estimated parameter values in Fig. 5.

It is to be observed from Table 6 that contact tracing rates both in pre-symptomatic ($\xi_1$) and symptomatic ($\xi_2$) stages of the disease are crucial strategies to reduce the basic reproduction number $R_0$ gradually. The contour plots displayed in Fig. 5 represent the same characteristics of the proposed model system (1). In Figs. 7 and 8 we have plotted expected cumulative weekly confirmed cases for next 4 weeks with variation contact tracing parameters $\xi_1$ and $\xi_2$. We have noticed that disease prevalence is decreasing with increasing value of both $\xi_1$ and $\xi_2$. As India is a highly population density country as well as having almost 1.38 million population therefore to mitigate the disease COVID-19, it is essential to isolate both symptomatic and asymptomatic COVID-19 positive patients. As of still today India has become second highest COVID-19 affected country and looking at the number of population in India, the current data has threaten India may become highest COVID-19 affecting country suppressing USA by upcoming two-three months. Hence contact tracing should be an essential
Fig. 7. State-wise 4 weeks prediction of the disease prevalence. The solid blue curve in each subfigure plotted with estimated parameters values whereas, dashed curves depicts the effects of contact tracing parameters, that is, $\xi_1$ and $\xi_2$ on predicted cumulative weekly confirmed cases.
Fig. 8. State-wise 4 weeks prediction of the disease prevalence. The solid blue curve in each subfigure plotted with estimated parameters values whereas, dashed curves depicts the effects of contact tracing parameters, that is, $\xi_1$ and $\xi_2$ on predicted cumulative weekly confirmed cases.
procedure to minimize the cumulative effect of COVID-19. In this regard, here we have proposed a mathematical model and observed that controlling the parameters related to contact tracing can minimize the positive cases of disease.

6. Discussion and conclusions

Mathematical modeling of infectious diseases is capable of insight into specific characters related to disease transmission or associated control interventions. This current investigation intends to answer the efficacy of the ongoing non-pharmaceutical preventive measures to mitigate the COVID-19 outbreak. The model assumes a homogeneous mixing pattern in the population level; however, a portion keeps themselves out of any contact and acquire behavioral immunity during the outbreak [8]. In this study, two key intervention features are (a) usual diagnosis effort (η) encountered in symptomatic stage η and (b) particular diagnosis effort (ξ1, ξ2) guided by recent contacts made by a confirmed COVID patient. The epidemic threshold key R0 obtained by the next-generation matrix approach. The model dynamics analyzed; and found that R0 < 1 can eliminate the disease from the system. However, with the condition R0 > 1, the infection persists in the population permanently. Moreover, to minimize the effect of the disease, we have considered an optimal control problem considering the parameter u as a time-dependent variable. We have also provided both theoretical and numerical solutions of the formulated optimal control problem. From the solution of the control problem, it has been observed that the system parameter u has a significant contribution in controlling the deadly effect of the pandemic COVID-19.

We have noticed that increasing diagnosis effort (ξ1, ξ2) of a traced individual guided by the recent contacts made by hospitalized COVID patients is crucial to reduce the size of R0. Hence, these two different diagnosis algorithms are vital to determine and control the size of the epidemic threshold of R0. To simulate the theoretical result in a real field, we consider six vulnerable states namely Maharashtra, Tamil Nadu, Andhra Pradesh, Karnataka, Delhi and West Bengal of India, which is right now at the second position, just after USA, in the list of COVID-19 affected countries. The cumulative sum of populations in these six states is more than 400 millions suppressing the cumulative populations of USA by more than 70 million. But the high density in populations of those six states has enabled to spread the disease COVID-19 in a high rate. Hence to eradicate the pandemic COVID-19 in India, it is very much essential to isolate both symptomatic and asymptomatic positive cases. In this regard, in Figs. 7 and 8 we have presented the future predicted profile of the confirmed cases for the upcoming till next four weeks (i.e. till 12/01/2021) for different values of the parameters ξ1 and ξ2. It has been established that, very little changes in these parameters can able to reduce the effect of the disease significantly. Hence, the variety in cases under treatment is the evidence that increasing contact tracing effort can effectively decrease the disease prevalence.

Although we have described only one real world simulation in mitigating the effect of the disease, but we hope that this model can be used to study the dynamics of the disease in other COVID-19 effected regions also.

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