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Spatial network based model forecasting transmission and control of COVID-19

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A B S T R A C T

The SARS-CoV-2 driven infectious novel coronavirus disease (COVID-19) has been declared a pandemic by its brutal impact on the world in terms of loss on human life, health, economy, and other crucial resources. To explore more about its aspects, we adopted the SEIRD (Susceptible–Exposed–Infected–Recovered–Death) pandemic spread with a time delay on the heterogeneous population and geography in this work. Focusing on the spatial heterogeneity, epidemic spread on the framework of modeling that incorporates population movement within and across the boundaries is studied. The entire population of interest in a region is divided into small distinct geographical sub regions, which interact using migration networks across boundaries. Utilizing the time delay differential equations based model estimations, we analyzed the spread dynamics of disease in India. The numerical outcomes from the model are validated using real time available data for COVID-19 cases. Based on the developed model in the framework of the recent data, we verified total infection cases in India considering the effect of nationwide lockdown at the onset of the pandemic and its unlocking by what seemed to be the end of the first wave. We have forecasted the total number of infection cases in two extreme situations of nationwide no lockdown and strict lockdown scenario. We expect that in future for any change in the key parameters, due to the regional differences, predictions will lie within the bounds of the above mentioned extreme plots. We computed the approximate peak infection in forwarding time and relative timespan when disease outspread halts. The most crucial parameter, the time-dependent generalization of the basic reproduction number, has been estimated. The impact of the social distancing and restricted movement measures that are crucial to contain the pandemic spread has been extensively studied by considering no lockdown scenario. Our model suggests that attaining a reduction in the contact rate between susceptible and infected individuals by practicing strict social distancing is one of the most effective control measures to manage COVID-19 spread in India. The cases can further decrease if social distancing is followed in conjunction with restricted movement.

1. Introduction

The novel coronavirus disease, officially known as 2019-nCoV, or SARS-CoV-2 (severe acute respiratory syndrome coronavirus 2), commonly called COVID-19, has provided the world with an unparallel challenge. The first reported case in
the COVID-19 outbreak appeared in the Wuhan city of China in December 2019, and since then, it has rapidly spread in 222 countries and territories around the world [1]. As of 3 June, 2021, a total of 172,895,701 confirmed cases of the coronavirus and a toll of 3,716,528 deaths has been reported globally [2]. Due to its rapid spreading power and high mortality, it has thrown an unpredictable burden on healthcare systems in the majority of the developed as well as developing countries. With its breakneck spread all across, World Health Organization (WHO) has declared it as a pandemic and to contain the upsurge by breaking its person to person transmission chain involving significant human migration, major steps including partial or complete lockdowns, international travel bans, and social distancing have been widely adopted.

In India, the first case of coronavirus pandemic was identified on 30 January, 2020, originating from China. Since this appearance, there has been a continuous rise in the number of infections with the total number of 28,573,503 cases on 3 June, 2021, of which there are 26,589,759 recoveries and 340,731 deaths [3]. As a preventive measure, India also implemented a strict nationwide lockdown on 22 March, 2020 followed by enforcement of a series of regulations, limiting movement of the entire population to minimize social contacts. The efficiency of such measures is geographically sensitive due to different population densities, social contact networks, and health care facilities. Quantitative projection of the effect of these measures in reducing infection is crucial in outlining social and economic policies. Further, understanding the transmission dynamics of COVID-19 not only provides deep insights into the epidemiological situation to enhance public-health planning, but such investigations can also aid in the layout of alternative breakout control measures.

Knowledge of the early spread dynamics of the infection and figuring out the capability and performance of applied control measures is critical for assessing the extensive outbreak to occur in new regions. Besides medical and biological research, understanding the urgency to develop a predictable mathematical model for the COVID-19 outbreak, few mathematical studies based on statistical reasoning and simulations have been taken up in past months [4–6]. Later, accepting the challenges to explore the efficiency of various control measures since the outbreak, fewer studies adopted more appropriate dynamical equations based on mathematical modeling techniques. Compartment models such as $SI$, $SIR$, $SEIR$ and its variants, which exhibit the change in the category of population among the susceptible ($S$), exposed ($E$), infected ($I$) and recovered ($R$) classes have been developed and studied to understand the spread pattern of COVID-19 in many countries [7–17].

Further, as reported, COVID-19 has a latent/incubation period (time from exposure to the development of symptoms), which is estimated to be between 2 and 14 days [18]. Predominantly, the inclusion of the incubation period gives rise to models with the consideration of the difference in time between being exposed to infection and becoming infected (hence, $SEIR$) and in dying the process. So, the consideration of the occurrence of time delay and death during latency period has a crucial biological meaning in epidemic models because the people who are infected at time were exposed at earlier times. This incubation period is very significant as it allows the health authorities to introduce more adequate systems for separating people suspected of carrying the virus to control and prevent the spread of the pandemic [19]. The inclusion of the latent period in compartment models gives COVID-19 time delay models its generalization over the existing model without time delay since, the dynamic behavior of the disease rate of change of the state of the system at a time prior before the delay period $[20,21]$. However, the majority of delay based models assume homogeneity in a large population and ignore numerical variations originating from natural births, deaths, and human migration networks across the regions. The amount that the travels resulting in human interactions readily spread the disease to different places, population and geographic heterogeneities play crucial roles in the infection outbreak process. To look upon the pandemic’s vital characteristics, it is advantageous to include them in the time delay model.

This study presents a mathematical model to analyze the spread of the novel coronavirus within a heterogeneous population and geography. We propose a more realistic $SEIRD$ model by incorporating time delay from exposed to infectious period along with the demographic and stochastic parameters like heterogeneous population, natural births, deaths, and population migration networks within a geographical state (subpopulation in a country) boundaries. Since the disease spread through human contacts, it is most significant to understand the impact of population migrations by means of frequent journeys. In the presented model, predominantly, considering the spatial heterogeneity, the entire population of the broad geographical region of interest is divided into small sub-regions (states), which interact by means of movements across the state boundaries. Epidemic spread on the constructed human migration network is studied. Moreover, there are many inevitable questions related to the spread of the pandemic. How many people are at risk of infection? When will the infection be at its peak and when will it end? Are the existing control measures sufficient to control the outbreak? With the aim to explore more about the transmission of COVID-19 dynamics and to predict its potential tendency, the pandemic is estimated for forwarding time with suitable values for model parameters, which reasonably fit the actual infection cases. The general points of interest, including total infected cases, infection peak, pandemic ending time, are investigated. The most vital parameter, time-dependent effective reproduction number that decides if an originating infectious disease can extend in a population, has been estimated. It is found that restricted population movement along with social distancing are key factors in determining the extent of the epidemic.

2. Material and method

2.1. Generalized $SEIRD$ model with time delay

To estimate the trajectories of COVID-19 transmission, in the proposed approach, a vast geographic region with heterogeneous population distribution (country) is partitioned into $n$ smaller sub-regions (states). To take into account the
Fig. 1. (a) The map of India along with different states (represented by filled dots, numbered from 1 to 32). The solid lines show the connections of a state with its neighboring states resulting in inter state movements. The complete dataset reflecting state wise population distribution is provided in Appendix A.3 in Table 2. *Note that in the study we have not considered a few Indian states and Union Territories including Lakshadweep, Dadra and Nagar Haveli, Daman and Diu, Andaman and Nicobar Islands and Puducherry on account of their comparatively low population density. (b) Within a state, Schematic of SEIRD Model with time delay.

effect of both inter and intrastate infectious population, migration for these states are explicitly incorporated (Fig. 1(a)), using population migration adjacency matrix $\lambda$ (with order $n \times n$). The diagonal coefficients of this matrix represent the migration rate within a state while for any of its $j$th row, $k$th element indicates the migration factor from the $j$th state to the $k$th state. For any two states which share no boundaries migration rate is 0. Within a given state, the transmission is handled according to a deterministic compartmental model dividing the population into five epidemiological classes $S(t)$, $E(t)$, $I(t)$, $R(t)$, $D(t)$ describing at time $t$ the respective proportion of the susceptible cases, exposed cases (infected but not capable of transmitting infection, in a latent period), infected cases (with the infection spreading capacity), recovered cases and deaths owing to virus cases. Fig. 1(b) shows the movement within the classes in model with time delay. Since the latent period ($\tau$) of the COVID-19 is as long as 2 to 14 days [1], the exposed class ($E$) originates because of interactions with the amount $\beta$ (daily contact rate per unit of time) within susceptible ($S$) and infected class ($I$). Only those members of the exposed class who survive the latency period move to the infected class with a rate of $\sigma$. After a course of quarantine treatment, either a part of infected population is discharged with the rate $\delta$ from the hospital ($R$) or encounter death due to underline diseases ($D$) with an estimate $\gamma$. An Appendix A.1 provides complete details of our mathematical model characterized by a group of ordinary differential equations depicting the outbreak at time $t$. The primary model parameters, reasonably fitting the actual infected cases till date, are described in Table 1 in Appendix A.3.

2.2. Data source

The epidemic bulletin from the World Health Organization provides us with primary data on epidemiological research. According to the reports by WHO, the incubation period for COVID-19, which is the time between exposure to the virus (becoming infected) and symptom onset, is, on average 8 days; however, it can be up to 14 days [1].

To check how optimal is the fitting between the actual official data for the pandemic spread and the model based obtained numerical approximations, we use the statistical Kolmogorov–Smirnov (K–S) test [22,23]. The K–S goodness-of-fit test is performed on the data to ascertain whether two data series are from the same continuous distribution or not. The null hypothesis implies that data samples are from the same continuous distribution, and the alternative hypothesis states the opposite. The statistic $h$ is 1 if the test rejects the null hypothesis at the 5% level of significance, and 0 otherwise. For the proposed model with retained parameters, the results indicate (with $h = 0$) that both the actual and the projected number of cases are from the same continuous distribution, as desired, showing optimistic estimations.

3. Results

In this section, we conduct a more detailed model analysis to depict outspread for the COVID-19 pandemic. We obtained the numerical solution of the mathematical model discussed in Appendix A.1 for India, established using chosen set of parameters based on the pandemic specifications [1,2,24] and movements within and across the state boundaries during lockdown and unlocking phase. Furthermore, at the initial stage entire population is assumed to be susceptible
Fig. 2. The trajectory for the active infected cases with respect to time (in days) based on the proposed mathematical model for (a) no lockdown scenario (shown in solid red color) (b) scenario with social distancing (shown in dotted yellow color) (c) strict lockdown scenario (shown in green color) since the starting of the COVID-19 cases in India from 30 January, 2020 onwards. The data predicted by the model (shown in black color) is in good agreement with the actual available COVID-19 infected cases for India from 30 January, 2020 to 3 June, 2021 (shown in pink color). The total active infection cases for the extreme scenarios of no lockdown and strict lockdown provides the bound for the number of infections at any time. The parameters are: for validation (intrastate population migration factor, interstate population migration factor, $\beta$) = (0.3–0.75, 0.2–0.45, 2–15), $\tau = 8.8$, $\alpha = 0.0005$, $\sigma = 1/8 - 1/3$, $\delta = 0.6 - 0.97$, and $\gamma = 0.034 - 0.1$; for (a) (intrastate population migration factor, interstate population migration factor, $\beta$) = (0.8, 0.6, 10); for (b) (intrastate population migration factor, interstate population migration factor, $\beta$) = (0.6, 0.5, 4); (c) (intrastate population migration factor, interstate population migration factor, $\beta$) = (0.3, 0.2, 2); $\tau = 8.8$, $\alpha = 0.0005$, $\sigma = 1/3$, $\delta = 0.97$, and $\gamma = 0.1$.

and the infected cases have been considered as per the data available on 30 January, 2020 for India [3]. Using suitably preferred parameters, the same detailing can be obtained for any geographic region. Moving further, we aim at forecasting the infection cases along with the basic reproduction number. It is significant to mention that, at present, due to lack of sufficient diagnostic test for COVID-19, the total number of confirmed active cases for infection in any $j$th state, can be given by $I(t)\alpha N_j$. Here, $N_j$ denotes the population of the $j$th state, and $\alpha$ is considered approximately in the range of $0.01 - 0.1$ in the role of the current testing events [24]. Clearly, the total infected cases in a country with $n$ states can be obtained by the sum of corresponding data from the states.

At the onset, we used the proposed model to fit actual available COVID-19 infection cases for India up to 3 June, 2021 (Fig. 2). Notably, the officially published data by Ministry of Health and Family Welfare (MoHFW), Government of India from 30 January, 2020 to 3 June, 2021 are marked in pink spots and are considered as a direct validation source. As expected, we can clearly see that the prediction of the exact number of cases diagnosed in the past time by the model is in good agreement with the real value. In the initial phase of the COVID-19 spread, around first wave, we have obtained the qualitative match within the actual cases and the model prediction. The observed variations are primarily due to lesser number of testing owing to government policies at that time. The model predictions agreed very well with second wave of pandemic due to sufficient available data. With an aim to estimate the potential tendency of the COVID-19 pandemic under the impact of the ongoing control measure including social distancing norms and movement within and across the regions, we compared the infection spread in the cases of scenario with relaxed movements and situation with strict social distancing and restricted movements in place.

With parameters in hand, we executed the model forward in time to visualize the progress of the pandemic in range of possible extreme scenarios for India — nationwide no lockdown or strict lockdown. The corresponding results are shown in Fig. 2. The red colored trajectory in Fig. 2 show the effect of no lockdown as per the presented model on the progression of the COVID-19 in India. For this situation, we allowed conventional migration within the states and across the boundaries by setting non zero estimates for diagonal and off diagonal entries in the migration adjacency matrix. Incorporating the effect of the social distancing norm as a control measure to reduce the average contact rate, we choose the interaction rate between susceptible and infected to be approximately ten [24]. Based on these criteria, our model featured yet another infection peak in coming months with the total number of estimated infected to be around 5 million. The outbreak is expected to be nearing its end by 2022 in situation of nationwide no lockdown.

In an alternate scenario, the yellow track in Fig. 2 panel exhibits a rundown for a protocol highlighting the impact of most essential social distancing standards as a step to break or lessen human to human transmission chain of the virus. Considering self awareness within the population, we invoked reduced average contact parameter $\beta$ between susceptible
Fig. 3. Effective reproduction number with respect to time for scenario with (a) no lockdown (solid red line), (b) movement with social distancing (dotted yellow line) and (c) strict lockdown (green line). Corresponding to the infection trajectories in Fig. 2, effective reproduction number is calculated using the relation given in Eq. (7). The value is greater than unity before peak infection and smaller than unity beyond its peak indicating its end. The parameters are (intrastate population migration factor, interstate population migration factor, $\beta$): (a) $(0.8, 0.6, 10)$ (b) $(0.6, 0.5, 4)$ (c) $(0.3, 0.2, 2)$; with common parameters $\tau = 8.8$, $\mu = 0.0005$, $\sigma = 1/3$, $\delta = 0.97$, and $\gamma = 0.1$.

Fig. 4. Contour plot of effective reproduction number for India as on 27 August, 2021 with respect to the average contact rate and interstate population migration factor. With the increase in the value of average contact rate and interstate movement factor, the reproduction number increases significantly, thereby indicating the necessities of both the measures simultaneously in controlling the pandemic. The other parameters are intrastate population migration factor = 0.6, $\tau = 8.8$, $\mu = 0.0005$, $\sigma = 1/3$, $\delta = 0.97$, and $\gamma = 0.1$.

and infected to be approximately four, through social distancing impacts in this case. As likely, this consideration brings the total number of infections to comparatively lower values and slows the spread of the disease to manageable levels. Moreover, peak infections in this scenario decrease significantly in comparison to the situation of the no lockdown. This observation highlights the fact that social distancing is one of several changes that we have to adapt strictly in the coming months. To ensure the distances are well maintained at work or public places, more mature ways of monitoring, including artificial intelligence or machine learning softwares, can be used. Additionally, our model exhibits a further slower growth rate of the pandemic by breaking the cycle of transmission through the combination of restricted movement and social distancing norm, as shown by green curve in Fig. 2. In this situation, we allowed necessary movements within and across the state boundaries for essential activities only, to save the economy along with strict social distancing. Simulations in
Table 1
Quantification of parameters value used in the proposed model.

| Parameter | Value       | Source (Ref.) |
|-----------|-------------|---------------|
| $\sigma$  | 1/14–1/2    | [1,2]         |
| $\delta$  | 0.6–0.97    | [24]          |
| $\gamma$  | 0.034–0.1   | [1,2]         |
| $\tau$    | 2–14        | [1,2]         |
| $\beta$   | 1–13        | [24]          |
| Entries of $\lambda$ | 0.1–0.85 | [25] |

this scenario indicates with these submissive levels of infections, timely elimination of the ongoing pandemic is possible. Based on the outcomes, as a suggestion, if social distancing along with restricted movement is enforced broadly and is maintained in the coming months, the number of new infections would decrease to a significantly feasible level, and the outbreak could eventually be controlled. Further, the total number of active infection cases in India depends upon the strategies and governance of the states in controlling the pandemic. In case of strict lockdown there interstate travel is minimum except bare essentials while in case of no lockdown there is no restriction on movements. In any other realistic scenario the active infection cases lies within the bounds of the above mentioned extreme plots as shown in the panel of Fig. 2. We call it realistic because owing to the needs of economy movements within and across the regions are impelled to be relaxed.

Additionally, Fig. 3 shows the time-dependent effective reproduction number $R_{eff}(t)$ (discussed in Appendix A.2), corresponding to the infection trajectories in Fig. 2. As hoped for, this value is greater than unity before peak infection and smaller than unity beyond its peak, serving as a useful estimate of the local rate of change of infective at any time. It is noteworthy to mention here that for any state of India, basic reproduction number can be obtained using the relation given in Eqs. (6)–(8) in Appendix A.2. Further, to analyze the impact of social distancing and restricted movement in controlling the COVID-19 spread we draw the contour plot for effective reproduction number with respect to the average contact rate and interstate population migration factor in Fig. 4. Contour plot suggest that with the increase in the value of $\beta$ and interstate movement factor, the reproduction number increases remarkably, which demonstrates that the social distancing measures adopted by the population appear successful, particularly when implemented in association with the restricted movement. The pandemic will persist and spread across the community if the masses will not follow the preventive measures religiously. The model discussed here, could be helpful to health authorities for depicting the total number of infection cases along with the peak infection. The estimated fit values could be made better on a daily base as more data become available.

4. Discussion

We have presented a generalized SEIRD mathematical model with a time delay to analyze the spread of COVID-19 infection in a population. The proposed model incorporates spatial and stochastic parameters like heterogeneous population, natural births, deaths, and population migration networks within geographical state boundaries. We stressed the essential of establishing a framework incorporating population movements in modern times and their effects on epidemics. We demonstrated the main ideas by considering a combined population movement network incorporated by considering population data and movement within and across the state boundaries in India. Based on a detailed analysis of the available public data, we projected COVID-19 pandemic peaks and possible ending time and total infected cases in India within the bounds of no lockdown and strict lockdown. It is significant to mention here that since the real infection cases in India eventually depend upon the spread of the pandemic in its states, the chosen parameters depend crucially on measures like statewide movement patterns, average contacts between people as per the current policies and are not exclusive. Furthermore, we applied our mathematical model to interpret the public data on the total number of infected cases from 30 January, 2020 onwards in two sub regions of India, including Maharashtra and Punjab, as discussed in Appendix A.4. We have chosen Maharashtra since it has a significantly higher number of infections and Punjab since it has a comparatively higher disease mortality rate. Our model suggests a bit restricted movement, followed by an extended period of strict social distancing as one of the most effective control measures to manage COVID-19 spread in days to come.

Owing to significant spatial variations affecting the basic reproduction number, we included spatial heterogeneity by dividing the entire population into smaller sub regions. Based on the technique, effective reproduction number has been estimated at both regional and sub regional levels. The approach helped us to capture sensible COVID-19 infection dynamics over local and global levels.

The proposed model is a general attempt to provide deep insight to analyze the dynamics of COVID-19, helping the involved agencies to arrange and manage crucial resources and design its control strategies. Using suitably chosen parameters, the similar findings can be obtained for any country. Additionally, the proposed work necessarily made some assumptions when framing the model. We ignore the impact of infection spread due to exposed class [1]. Moreover, the work is based on acquired data for a limited duration of time to fit and estimate the spread of COVID-19. With the release of more epidemic data for India, owing to the regional differences on account of government policies, health, education, religion, and per capita income, the key parameters may undergo momentous changes influencing the spread of pandemic among the masses.
CRediT authorship contribution statement

**Natasha Sharma:** Implementation of idea, analysis and method, Prepared the manuscript. **Atul Kumar Verma:** Performed data analysis and validation, Prepared the manuscript. **Arvind Kumar Gupta:** Conceptualized the idea, Designed the methodology and supervised the work.

Declaration of competing interest

The authors declare that they have no known competing financial interests or personal relationships that could have appeared to influence the work reported in this paper.

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Appendix

A.1. Epidemiological model

We consider a large geographic region with total population $N$, partitioned into $n$ states labeled by $j = 1, 2, \ldots, n$. The population within the $j$th state is partitioned into susceptibles ($S_j$), exposures ($E_j$), infectives ($I_j$), recoveries ($R_j$) and deaths ($D_j$), where $N_j = S_j + E_j + I_j + R_j + D_j$ and $N = \sum_{j=1}^{n} N_j$. The proposed time delay $SEIRD$ system that captures population and geographic heterogeneities is given by:

$$\frac{dS_j}{dt} = -S_j(t) \sum_{k=1}^{n} \beta \lambda_{j,k} \frac{N_k}{N_j} I_k(t) + \mu (1 - S_j(t)). \tag{1}$$

$$\frac{dE_j}{dt} = S_j(t) \sum_{k=1}^{n} \beta \lambda_{j,k} \frac{N_k}{N_j} I_k(t) - e^{-\mu \tau} S_j(t - \tau) \sum_{k=1}^{n} \beta \lambda_{j,k} \frac{N_k}{N_j} I_k(t - \tau) - \alpha E_j(t) - \mu E_j(t). \tag{2}$$

$$\frac{dI_j}{dt} = \sigma E_j(t) + e^{-\mu \tau} S_j(t - \tau) \sum_{k=1}^{n} \beta \lambda_{j,k} \frac{N_k}{N_j} I_k(t - \tau) - \delta I_j(t) - \gamma I_j(t) - \mu I_j(t). \tag{3}$$

$$\frac{dR_j}{dt} = \delta I_j(t) - \mu R_j(t). \tag{4}$$

$$\frac{dD_j}{dt} = \gamma I_j(t). \tag{5}$$

Here $\beta > 0$ is the average rate of contact between susceptible and infected (people exposed at each time step by infected people); $\lambda_{j,k} \in [0, 1]$ denotes the population migration factor for the states $j$ and $k$. The parameter $\sigma \in [0, 1]$ stands for the portion of exposed individuals, which become infectious per time step. We call $\delta \in [0, 1]$ the proportion of infected people who are cured per time step and $\gamma \in [0, 1]$ is the fatality rate due to COVID-19. The parameter $\tau > 0$ is the delay time. Further, without affecting the behavior and general aspects of infection, it is assumed that the population in the $j$th state is born susceptible with the natural birth rate $\mu > 0$ per one individual per time step and the total population remains constant since the natural death rate is considered to be same as the natural birth rate $\mu$.

The first term on the R.H.S. of Eq. (1) represents the fragment of the susceptible individual of $j$th state who have been exposed to the disease by the infected individuals of the same state and by the infected individuals of the other states, who have moved to the former main state, taking into account the average contact rate; migration coefficients for the states; and the relation between the populations of the states.

Those who were exposed to the infection at time $t - \tau$ and survive the latent period $[t - \tau, t]$ with probability $e^{-\mu \tau}$ moves to the infected class at time $t$ [19,26–29]. Moreover, the proportion removed by disease independent mortality for each compartment is given by the last term on R.H.S of each equation.

A.2. Computation of reproduction number

Following the approaches similar to those taken in [19,31,32] with respect to system in Eqs. (1)–(5), let $R_0 = \rho(M_0)$ represents the spectral radius of the matrix $M_0$ with entries $m_0(j, k)$ give by

$$m_0(j, k) = \frac{\beta \lambda_{j,k} \frac{N_k}{N_j} (\sigma + \delta \gamma \mu)}{(\mu + \sigma)(\mu + \delta + \gamma)}, \tag{6}$$
where $1 \leq k, j \leq n$, then the parameter $R_0$ is referred to as the basic reproduction number of the considered geographic region. This number is intended to be an indicator of the transmissibility of COVID-19, the outbreak is expected to continue if $R_0 > 1$ and to end if $R_0 < 1$. Eqs. (6) shows that the basic reproduction number significantly depends on the average rate of contact between susceptible and infected, population migration factor for the states, state population and time delay. Also, the time-dependent effective basic reproduction number, $R_{0e}(t)$, is taken to be

$$R_{0e}(t) = \frac{1}{\delta t (\mu + \delta + \gamma)} \log \left( \frac{I(t + \delta t)}{I(t)} \right) + 1.$$  \hspace{1cm} (7)

Further, for the $j$th state, the basic reproduction number is given by

$$R_j = \frac{\langle \beta \lambda \rangle (\sigma + e^{-\mu \tau} \mu)}{(\mu + \sigma)(\mu + \delta + \gamma)}.$$  \hspace{1cm} (8)

A.3. Model parameters

The first case of the 2019−20 coronavirus pandemic in India was reported on January 30, 2020. We gathered the dataset for COVID-19 in India from the Ministry of Health and Family Welfare (MoHFW), Government of India from 30 January, 2020 to 3 June, 2021 including the number of active infected cases, the cumulative number of people in recovery and the cumulative number of deaths due to virus [3]. Simultaneously, we collected the state wise total population data for India (projected 2019) from Unique Identification Authority of India (UIDAI), Government of India and migration data to capture the movement of population in different parts of the country from Ministry of Home Affairs, Government of India [25,30]. The preliminary estimated parameters that reflect the primary situation of the pandemic in India at the present stage are summarized in Table 1. State wise population for India is summarized in Table 2 in order of states as appeared in the map of India in Fig. 1.

A.4. Impact on the Indian states

We apply our pre-described mathematical model to interpret the public data on the total number of infected cases from 30 January, 2020 onwards in sub regions of India, which are published daily by Ministry of Health and Family
Fig. 5. The trajectory for the active infected cases with respect to time (in days) based on the proposed mathematical model for (a) no lockdown scenario (shown in solid red color) (b) scenario with social distancing (shown in dotted yellow color) (c) strict lockdown scenario (shown in green color) since 30 January, 2020 for (i) Maharashtra (ii) Punjab. The data predicted by the model (shown in black color) is in good agreement with the actual available COVID-19 infected cases for both the states from 30 January, 2020 to 3 June, 2021 (shown in pink color). The total active infection cases for the extreme scenarios of no lockdown and strict lockdown provides the bound for the number of infections at any time. The parameters are: for validation (intrastate population migration factor, interstate population migration factor), \( \beta = (0.3–0.75, 0.2–0.45, 2–15) \), \( \tau = 8.8 \), \( \mu = 0.0005 \), \( \sigma = 1/8 – 1/3 \), \( \delta = 0.6 – 0.97 \), and \( \gamma = 0.034 – 0.1 \); for (a) (intrastate population migration factor, interstate population migration factor, \( \beta = (0.8, 0.6, 10) \); for (b) (intrastate population migration factor, interstate population migration factor, \( \beta = (0.6, 0.5, 4) \); (c) (intrastate population migration factor, interstate population migration factor, \( \beta = (0.3, 0.2, 2) \); \( \tau = 8.8 \), \( \mu = 0.0005 \), \( \sigma = 1/3 \), \( \delta = 0.97 \), and \( \gamma = 0.1 \).

Welfare (MoHFW), Government of India. Our analysis includes two different regions (states), that is, Maharashtra and Punjab. It is significant to mention here that we have chosen Maharashtra since it has a significantly higher infection cases. Additionally, we have chosen Punjab since it is India’s state with comparatively higher disease related mortality rate. In Fig. 5(a) and (b), the estimated number of active infected cases is plotted for both the states based on model predictions with dotted black lines and actual COVID-19 infection data from 30 January, 2020 to 3 June, 2021 is marked by circles. Here also, the reasonable agreement is observed between real and forecasted data. We then run the proposed model for chosen parameters in forwarding time and performed detailed analysis on similar lines for the no lockdown, strict lockdown and scenario assuming relaxed movement with social distancing, as discussed in Results, Section 3. From the numerically obtained outcomes, with the implementation of social distancing along with current movement patterns, the peak infection witnessed a significant fall (shown by dotted yellow lines in Fig. 5(a) and (b)). Further, as expected, the situation improves much better if social distancing is enforced strictly along with restricted movement (Fig. 5(a) and (b)). Based on the outcomes, as suggested, if social distancing and restricted movement are followed rigorously, the outbreak could eventually be controlled. Using suitably selected parameters, the pandemic transmission patterns can be obtained for any other state of India on similar lines.

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