

How the asymptomatic population is influencing the COVID-19 outbreak in India?

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According to the current perception, symptomatic, presymptomatic, and asymptomatic infectious persons can infect the healthy population susceptible to the SARS-CoV-2. More importantly, various reports indicate that the number of asymptomatic cases can be several-fold higher than the reported symptomatic cases. In this article, we take the reported cases in India and various states within the country as the specimen to understand the progression of the COVID-19. Employing a modified SEIRD model, we predict the spread of COVID-19 by the symptomatic as well as asymptomatic infectious population. Considering reported infection primarily due to symptomatic we compare the model predicted results with the available data to estimate the dynamics of the asymptotically infected population. Our data indicate that in the absence of the asymptomatic infectious population, the number of symptomatic cases would have been much less. Therefore, the current progress of the symptomatic infection can be reduced by quarantining the asymptotically infectious population via extensive or random testing. This study is motivated strictly towards academic pursuit; this theoretical investigation is not meant for influencing policy decisions or public health practices.

INTRODUCTION

At the beginning of the outbreak of COVID-19, the general perception was that the transmission of the disease occurred mostly through the infectious persons having influenza-like symptoms. One reason behind this view was the similarities between the SARS pandemic in 2003 caused by SARS-CoV-1 and the current threat COVID-19 caused by SARS-CoV-2. Both SARS and COVID-19 patients show similar influenza-like symptoms, propagate infections through person-to-person contact via respiratory droplets generated when an infected person breathes, coughs, and sneezes. Measures taken to successfully control the SARS in 2003 were majorly based on testing those having symptoms and isolating the positive cases. Nevertheless, a similar guideline has not been very effective in controlling the COVID-19 as the number of infected individuals has gone past 0.2 million in India and 6.4 million worldwide. Despite severe containment measures, these numbers are several orders of magnitude higher than SARS in 2003 that reported 8,422 cases worldwide with a case fatality rate of 11%. In India, even when the nation is under lockdown, we have been observing a recent surge in new COVID-19 positive cases daily (Fig. 1). Initially, when the nationwide lockdown was enforced on March 23, the infection growth showed a gradual slowdown for a few weeks. However, as days passed, the number of daily new confirmed cases increased significantly which prompted us to revisit our earlier work [1] on the COVID-19 outspread in India using the well-known SIRD model [2–9]. Normally, an individual exposed to the disease sufficient to catch the infection goes through an incubation period

of several days (~ 5 days [10]) before showing symptoms, i.e. presymptomatic. However, many reports [11–16] suggested that a large fraction of those who catch the disease do not show any symptoms at all, i.e. they remain asymptomatic (tested positive for SARS-CoV-2 RNA but show no signs of illness). The presence of the virus in presymptomatic or asymptomatic persons means that they can transmit the disease to others. In this study, we investigate whether the trajectory of the recent surge of infections (Fig. 1) can be attributed to the following characteristics of this disease spread: (a) in addition to the symptomatic cases, the abundance of the infected individuals who do not develop any symptoms at all or remain mildly symptomatic, before recovery (asymptomatic) and (b) human-to-human transmission via those asymptomatic carriers. We use a modified version of the well known SEIRD model in epidemiology [17, 18] as a working handle to account for the asymptomatic infections (Fig. 2). The model analysis as per the current data for India and few Indian states shows that the dynamics of the infection spreading is highly influenced by the asymptomatic population. The real data for India and various states within the country are acquired from the repository with an interactive handle hosted at <https://www.covid19india.org>. The purpose of this article is neither to influence policy decisions nor to put forward any quantitative projections that should be used to design public health guidelines.

MODEL

In the standard SEIRD model, the population N is divided into sub-population of susceptible (S), exposed (E), infected (I), recovered (R) and dead (D) for all times t . Thus, $N = S + E + I + R + D$. In our case, in order to account for the asymptomatic population, we introduced several new ‘sub-population’ compartments and modified the corresponding flows between these compartments. The infected population I in SEIRD model is

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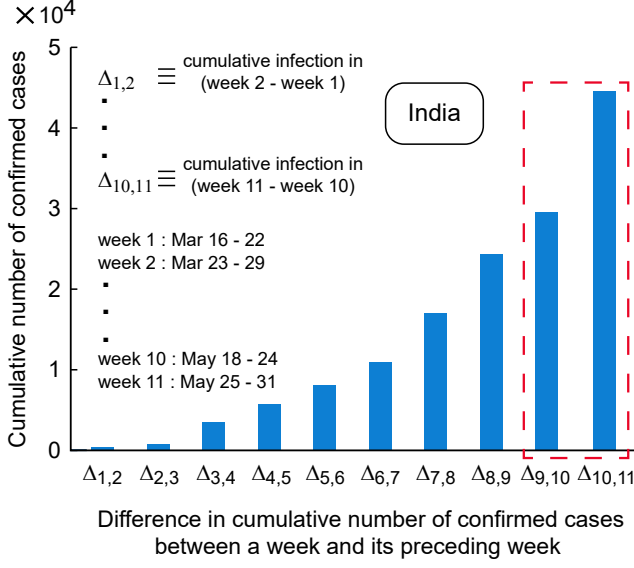


FIG. 1. Increment in the cumulative number of confirmed cases in India. The bars boxed in red highlight the recent surge of infections.

sub-divided into two compartments: (a) infected symptomatic population I_s and (b) infected asymptomatic population I_a (Fig.2A). As per the WHO and the ICMR, India reports, The COVID-19 infected individuals can be divided into two sub-groups: (a) symptomatic carriers and (b) asymptomatic carriers, infected individuals without any symptoms. The asymptomatic population is reported to be several times larger in number compared to the symptomatic population (Fig. 2B). Similarly, the population of recovered R in the SEIRD model is also classified into two new compartments: (a) population recovered from symptomatic infection R_s and (b) population recovered from asymptomatic infection R_a (Fig.2A). The population of dead (D) has inflow from I_s only (Fig.2A); we assumed no death for the asymptomatic individuals due to the disease.

The following set of mean-field differential equations dictates the time-dependent dynamics of the population of susceptible (S), exposed (E), symptomatically infected (I_s), asymptomatically infected (I_a), recovered from symptomatic infection (R_s), recovered from asymptomatic infection (R_a) and dead (D), comprehensively capturing the time evolution of the outbreak across the total population.

$$\frac{dS(t)}{dt} = -\beta_s S I_s / N - \beta_a S I_a / N \quad (1)$$

$$\frac{dE(t)}{dt} = \beta_s S I_s / N + \beta_a S I_a / N - \lambda E \quad (2)$$

$$\frac{dI_s(t)}{dt} = \phi \lambda E - (\gamma_s + \delta) I_s \quad (3)$$

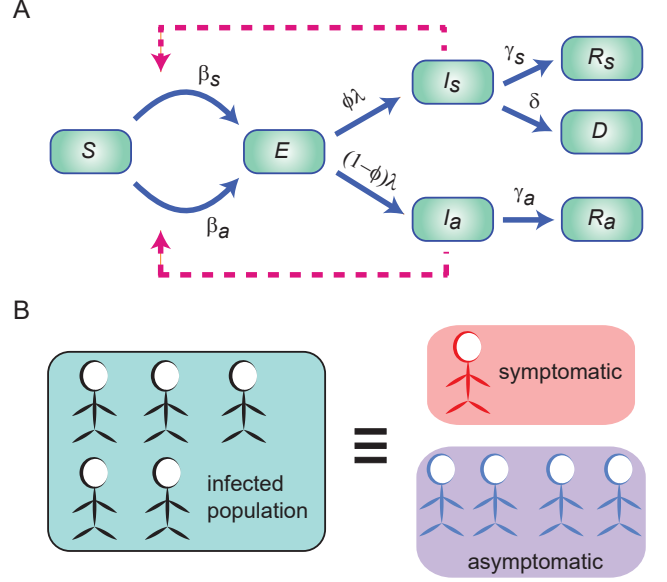


FIG. 2. Schematic representation of the modified SEIRD model used for mapping the current COVID-19 trajectory in India's context. (A) The arrows denote the flux direction between the compartmentalized sub-populations of susceptible (S), exposed (E), symptomatically infected (I_s), asymptomatically infected (I_a), recovered from symptomatic infection (R_s), recovered from asymptomatic infection (R_a) and dead (D). (B) The COVID-19 infected individuals can either develop symptoms or remain asymptomatic throughout before recovery. According to the reports by the WHO and the ICMR, India, the asymptomatic infections can be as large as 4-5 times of the total symptomatic infections.

$$\frac{dI_a(t)}{dt} = (1 - \phi) \lambda E - \gamma_a I_a \quad (4)$$

$$\frac{dR_s(t)}{dt} = \gamma_s I_s \quad (5)$$

$$\frac{dR_a(t)}{dt} = \gamma_a I_a \quad (6)$$

$$\frac{dD(t)}{dt} = \delta I_s \quad (7)$$

The parameters β_s , β_a , λ , ϕ , γ_s , γ_a and δ regulate the temporal flow between different sub-populations of infected, recovered and dead (Fig. 2A). Note that, in the above set of equations, the susceptible population (S), upon interactions with symptomatic and asymptomatic population, becomes exposed (E) to the disease with contact rates β_s and β_a , respectively. The model construction alludes that the individuals belonging to the exposed population are not contagious; hence, they do not transmit the disease by infecting others. The disease transmission from one individual to another occurs when an exposed individual transforms into either a symptomatic

or an asymptomatic carrier of the disease (Fig. 2A-2B). The time-dependent out-flux from the exposed compartment (E) into symptomatic and asymptomatic compartments (I_s and I_a) is governed by the rate λ . The out-flux from the exposed compartment with the rate λ , develops symptomatic infections with a probability ϕ and asymptomatic infection with a probability $(1-\phi)$. The recovery of a symptomatic infected person and an asymptomatic infected are determined by the rates γ_s and γ_a , respectively. An infected individual ceases to transmit the disease once s/he is recovered. Previous reports [10, 19, 20] indicate that, on the average, contagiousness begins to pronounce from 2-3 days before the appearance of symptoms. The contagiousness (disease spreading capability) of a symptomatically infected individual mounts to its peak before the symptoms develop and stays for about 7-9 days after the peak infection is passed. Therefore, a symptomatic individual bears the ability to transmit the disease for nearly about 12 days on average before recovery. However, how long it takes for an asymptomatic individual to recover is hard to ascertain, as a large number of asymptomatic infections remain undetected due to the sheer lack of symptoms. For symptomatic recovery, the time scale of ~ 12 days provides an estimate of the magnitude of the symptomatic recovery rate γ_s . In the preliminary model analysis, the magnitude of the asymptomatic recovery rate γ_a is chosen to be close to the magnitude of symptomatic recovery rate γ_s . Deaths (D) within the symptomatic population occur with a rate δ . We assume that infected, yet asymptomatic individuals do not die due to this disease. Nevertheless, it is imperative to mention that all the relevant rate parameters are varied within a reasonably feasible range to obtain the best fit of the theoretical curves with the real data.

Estimating the spread of the disease, the reproduction number

The basic reproduction number denoted by R_0 is a crucial parameter in epidemiology that can indicate the pandemic situation of an infectious disease. It is defined as the average number of secondary infections produced by a primary infection seeded into a sea of the susceptible population and its value is suggestive to implement a control intervention for containing the disease. However, in most of the practical situations, it is difficult to realize the single primary infection that has caused the outbreak; besides all contacts may not be susceptible to the infection. Therefore, in the present circumstances, instead of using the term basic reproduction number, we denote this by an effective reproductive number R_e . The effective reproductive number is determined by various rates presented in Equations (1) to (7). In general, an epidemic will begin when $R_e > 1$, so the number of infections increases. Pandemic will become an endemic when R_e becomes 1 and $R_e < 1$ will eventually diminish the number of infections. The effective reproduction number

R_e can be computed from the Equations (1) to (7) using the next generation matrix NGM [21]. An expression for R_e in the pre-lockdown situation is given by:

$$R_e = \frac{\phi\beta_s}{\delta + \gamma_s} + \frac{(1-\phi)\beta_a}{\gamma_a} \quad (8)$$

The mathematical treatment for obtaining the closed-form expression of R_e using NGM is similar to that given in [17].

Accounting for the effects of enforced containment measures

Prior to discussing the effect of containment measures on the infection dynamics, we need to highlight the subtle differences in the connotations of the following terms: (a) lockdown, (b) containment measures, and (c) social distancing. We stress that a lockdown in the model indicates the containment measures enforced across the country. But, even without a countrywide lockdown, containment can be imposed locally in the hotspots of infections (as being implemented during the current unlock phase) to prevent further spread of the disease into a larger region. In a sense, the word ‘lockdown’ bears an essence of universality whereas the implementation of containment can be both local and universal. However, social distancing is not an external norm to be enforced. It is rather a choice of lifestyle where one maintains a ‘good’ habit of physical distancing with other individuals in a public place/crowded environment. Ideally, even if there is no lockdown and/or containment measures in place, strict maintenance of social distancing can significantly reduce the chances of new infections. In the manuscript, in a general sense, where we mention the term ‘lockdown’, we imply that containment measures and/or social distancing are in effect.

Under normal circumstances, the implementation of the containment measures would reduce the interaction of the susceptible population (S) with the infected population (I_s and I_a). As gleaned from the Equation (1), the susceptible population, while interacting with the symptomatically and asymptotically infected population, becomes exposed to the disease with rates β_s and β_a , respectively. We can consider that the direct impact of the enforced containment measures (lockdown in a nationwide sense) and social distancing would be reflected on β_s and β_a in Equations (1) and (2). The susceptible-to-exposed transition rates β_s and β_a should diminish with time as the lockdown is enforced and continued. Hence, as a simple choice, we set the susceptible-to-exposed transition rates $\bar{\beta}_s(t)$ and $\bar{\beta}_a(t)$ in such a way that these rates gradually decline with time as the containment measures are put in place [6, 7]. Prior to the lockdown, β_s and β_a are constant. During the lockdown, the time-dependent $\bar{\beta}_s(t)$ and $\bar{\beta}_a(t)$ are assumed to decrease exponentially as depicted in the following [6]. During the mixing between susceptible population (S) and symptomatically infected

population (I_s),

$$\bar{\beta}_s(t) = \beta_s(1 - \xi_s)e^{-(t-\tau)/T} + \xi_s\beta_s \text{ for } t > \tau \quad (9)$$

$$\bar{\beta}_s(t) = \beta_s \text{ for } t \leq \tau \quad (10)$$

Similarly, During the mixing between susceptible population (S) and asymptotically infected population (I_a),

$$\bar{\beta}_a(t) = \beta_a(1 - \xi_a)e^{-(t-\tau)/T} + \xi_a\beta_a \text{ for } t > \tau \quad (11)$$

$$\bar{\beta}_a(t) = \beta_a \text{ for } t \leq \tau \quad (12)$$

Here, the lockdown (enforcement of the containment measures) begins on the day τ which is calculated from the day 0 (start date or initial time $t = 0$) set in the simulation. The parameters ξ_s and $\xi_a \in [0,1]$ are measures of interaction between the susceptible and infected population (symptomatic and asymptomatic respectively); T denotes the timescale that determines how fast the effect of lockdown on infection transmission becomes prominent. $\xi_s = \xi_a = 1$ means that there is no lockdown; the infected population is freely interacting with the susceptible population and exposing the susceptible individuals to the disease at rates β_s and β_a . $\xi_s = \xi_a = 0$ is the idealized scenario of lockdown where all the infected individuals (both symptomatic and asymptomatic) are isolated/quarantined. Hence, any sort of interaction of the infected individuals with the susceptible population is ruled out.

The time-dependent form of $\bar{\beta}_s(t)$ and $\bar{\beta}_a(t)$ is a non-unique choice consistent with the overall trend of the disease progression and tuned reasonably to arrive at the best fit with the available data. We settled at this particular form of $\bar{\beta}_s(t)$ and $\bar{\beta}_a(t)$, taking cue from the earlier modeling studies on COVID-19 progression [1, 6, 7].

During the lockdown, β_s and β_a are modified as depicted in Equations (9) and (11). Hence, the mathematical form of R_e during the lockdown period stands as

$$R_e = \frac{\phi\bar{\beta}_s}{\delta + \gamma_s} + \frac{(1 - \phi)\bar{\beta}_a}{\gamma_a} \quad (13)$$

In longer time limit, R_e becomes,

$$R_e = \frac{\xi_s\phi\beta_s}{\gamma_s + \delta} + \frac{\xi_a(1 - \phi)\beta_a}{\gamma_a} \quad (14)$$

It is evident from Equation (14) that, the first term in the expression of R_e concerns about the disease transmission via the symptomatic carriers whereas the second term deals with the transmission through asymptomatic carriers. In a population under lockdown, it is plausible to mitigate R_e through the gradual decrease in ξ_s and ξ_a , the interaction parameters. In essence, this is consistent with the default definition of R_e ; diminishing the interaction between the susceptible and the infected reduces R_e and vice-versa.

Since the constituting compartments of the model are S , E , I_s , I_a , R_s , R_a and D (Fig. 2), from now on, we can call the model adopted here, with the acronym of $SEI_sI_aR_sR_aD$ model.

All the relevant parameter values are listed in Table S1-S2.

RESULTS

We investigated the role of asymptomatic population propagating COVID-19 infection in India and various states within the country using the $SEI_sI_aR_sR_aD$ model. The results are elucidated in the following and represented in Fig. 3-6. To begin with, we varied the initial susceptible population S_0 within a range of 5-10 million for India (Fig. 3) and explored how the infected population is getting subdivided into two categories: (a) symptomatic population and (b) asymptomatic population; moreover how the asymptomatic population is contributing to the recent surge of infections in India (Fig. 1, Fig. 3-4). Next, we explored how the symptomatic and asymptomatic infection peaks are correlated and whether detecting and quarantining the symptomatic population is sufficient enough to contain the disease spread or the ‘hidden’ carriers without any symptoms make the disease transmission difficult to contain (Fig. 4). Furthermore, we briefly demonstrate how the effective reproduction number R_e computed from the current model behaves under the effect of lockdown/containment measures (Fig. 5). Lastly, we conclude by exploring the symptomatic and asymptomatic infection growth curves for a few Indian states using the $SEI_sI_aR_sR_aD$ model (Fig. 6).

Asymptomatic population and the recent surge of infections: a worrisome affair for India

We first investigated how the infection growth curves would look like in India’s context if we consider the asymptomatic infections. We start with an effective reproduction number $R_e \sim 4$ at the onset of the simulation (Fig. 3). As the lockdown is enforced, R_e plummets to a value ~ 1.75 . The initial susceptible population is varied within a range of 5-10 million. The model analysis shows that the total number of asymptomatic infections is several-fold higher than the symptomatic infections (which is of course subjected to the choice of fitting parameters). As expected, with an increase in the initial susceptible population S_0 , the infection peaks also rise to greater heights. The symptomatic and asymptomatic infection growth curves appear to reach the respective peaks at the end of June or early July. Note that, both the infection peaks may occur at the same time point as depicted in Fig. 3. The cumulative infection curves (inset, Fig. 3) show a flattening signature from the end of July.

The question that intrigues next, is how robustly do

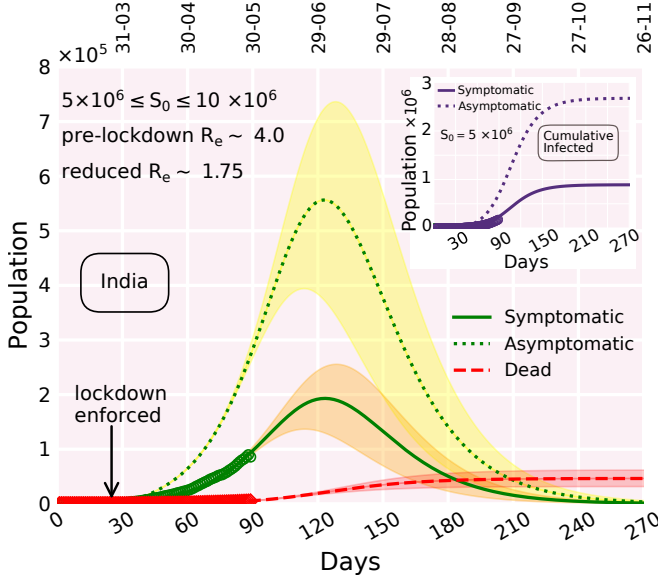


FIG. 3. Time evolution of the population of symptomatically infected (solid curve), asymptotically infected (dotted curve) and dead (dashed curve) in India. The initial susceptible population is varied within a range 5-10 million. During the lockdown period, the interaction parameters are chosen as $\xi_s \sim 0.3$ and $\xi_a \sim 0.5$ for best fit. $\xi_s \sim 0.3$ and $\xi_a \sim 0.5$ imply that the interaction between the susceptible and the symptomatically infected population is reduced to $\sim 30\%$ during the lockdown; similarly, the interaction between the susceptible and the asymptotically infected population is reduced to $\sim 50\%$. The color shades encasing the curves indicate the variation in the initial susceptible population S_0 . (inset) Time evolution of the cumulative population of symptomatic and asymptomatic infections. The cumulative population of symptomatically infected C_s is given by $C_s = I_s + R_s + D$. Similarly, cumulative asymptomatic population C_a is given by $C_a = I_a + R_a$. The real data (plotted as points) are considered from March 2, 2020.

the model predictions zero in on the relative numbers of symptomatic and asymptomatic infections?

Sensitivity of the model projections on the relative sizes of symptomatic and asymptomatic populations

If we inspect Equations (1) to (4) and Fig. 2 closely, we find that the exposed population is ‘fed’ into the compartments of the symptomatic and asymptomatic population with probability rates $\phi\lambda$ and $(1-\phi)\lambda$ respectively. The choices for the numerical value of ϕ ($\phi \in [0,1]$) regulates the relative size of the symptomatic and asymptomatic populations (since $\gamma_s \sim \gamma_a$, the recovery time for symptomatic and asymptomatic populations are similar). If $\phi \sim 0.5$, the peaks for the symptomatic and asymptomatic infections are likely to have the same height, as per the default model construction (Fig. 4A). The fact that the number of asymptomatic infections likely to be several folds higher than the symptomatic infections [16]

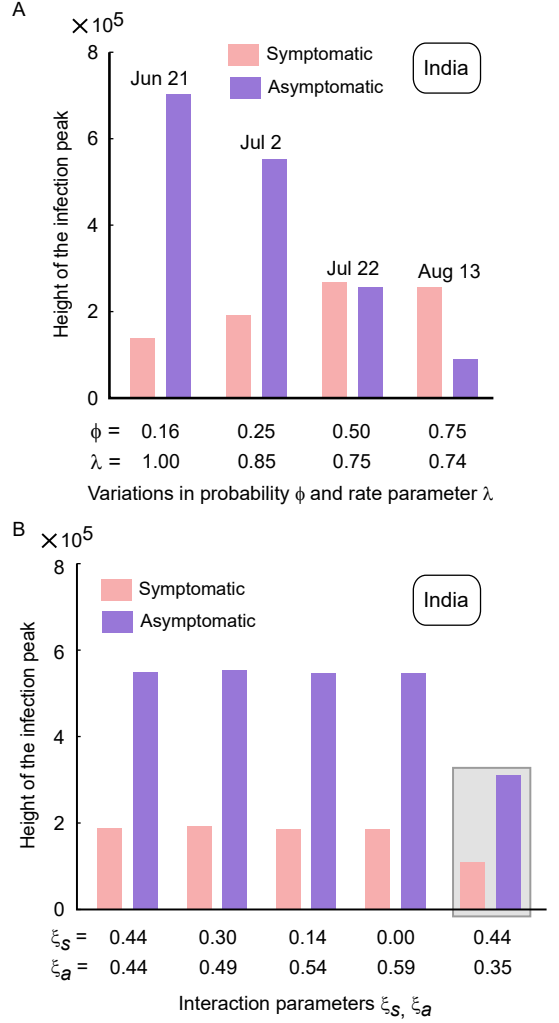


FIG. 4. Additional parameter dependence of symptomatic and asymptomatic infection peaks. (A) Symptomatic and asymptomatic infection peak heights (and tentative time window around which the peaks occur) depend upon the choices of probability ϕ and rate parameter λ . (B) Non-unique choices of symptomatic and asymptomatic interaction parameters ξ_s and ξ_a may yield identical infection curves (not shown) and identical peak heights at the same time. The peak heights of the infection curves are obtained from the best fit with the real data for different values of ξ_s and ξ_a , keeping other parameters fixed at base values. The peak height occurs towards the beginning of July. The last set of bars shaded in grey indicates that the infection peaks would be much lower than the projected trend if the asymptomatic patients are detected and quarantined (manifested through the lower value of ξ_a). For all cases, the initial susceptible population S_0 is chosen to be about 7.5 million. The real data for fitting is considered from March 2.

prompted us to make the current choice of the numerical value of ϕ . The greater size of the asymptomatic population, as suggested in various reports, alludes that it is reasonable to restrict ϕ in the range 0.2-0.4. The best fit with real data shows that, as ϕ increases, the peak of

the symptomatic infections consistently climbs up to a certain value determined by the current trend (Fig. 4A).

The next question is, whether one can attribute the recent surge in the number of symptomatic infections to the largely undetected asymptomatic population.

The recent surge in symptomatic infections: Does the onus fall on the asymptomatic carriers?

To address this question from the current model perspective, we visit the Equations (1) and (2) and Fig. 2. Imagine that all the active cases with symptoms are detected and quarantined. Then, the interaction among the susceptible and the symptomatic population becomes almost null as $\bar{\beta}_s$ effectively falls close to zero. But, even in that scenario, the ‘exposed’ (E) compartment can still be ‘fed’ through the interaction between susceptible and the asymptomatic individuals at a rate $\bar{\beta}_a$. This exposed population, in turn, fluxes into symptomatic and asymptomatic compartments with probability rates $\phi\lambda$ and $(1 - \phi)\lambda$. Thus, it is clear that merely quarantining the symptomatic solely cannot prevent the surge in both symptomatic and asymptomatic infections. The mixing of asymptomatic individuals with the susceptible may lead to new infections which are both symptomatic and asymptomatic. In the Indian context, to date, the testing capacity is mostly dedicated to the detection of symptomatic candidates. Once a positive case with symptoms is detected, the infected person is isolated and quarantined along with others who are traced to come in contact with the infected person. But the cases that show no symptoms are largely undetected. In most of the asymptomatic cases, the person her/himself is unaware of the fact that s/he is transmitting the disease. Thus, even during the lockdown, the mixing of an asymptomatic person with the susceptible cannot be fully filtered and prevented. From the model perspective, this may be reflected in the numerical values of symptomatic and asymptomatic interaction parameters ξ_s and ξ_a , during the lockdown. Extensive detection and quarantining of the cases with symptoms may reduce ξ_s significantly. However, since the asymptomatic population remains largely untapped, ξ_a may not decrease that much compared to ξ_s during the lockdown. In brief, the infection curves will continue to surge if only the symptomatic population is put into quarantine (reflected in significantly suppressed ξ_s) but asymptomatic individuals roam freely (gleaned from the relatively marginal reduction in ξ_a) during the lockdown. Interestingly, we notice that non-unique choices of ξ_s and ξ_a (while other relevant parameters are kept fixed at base values) may lead to identical best fits with the real data. If ξ_s is decreased and simultaneously ξ_a is increased, the combinatorial effect of these two interaction parameters results in identical best-fit curves with precisely the same infection peak height and peak location (Fig. 4B). From a physical perspective, we can argue that even if all the symptomatic

carriers are detected and quarantined, it is not sufficient to suppress the infection growth. A reasonably higher value of ξ_a (asymptomatic carriers mixing with susceptible) can compensate for the isolated symptomatic population (lower ξ_s , symptomatic infections barred to mix with susceptible) and single-handedly keep on fuelling the infection growth at a significant rate (see the first four set of bars, Fig. 4B). It is also evident that if ξ_a is significantly reduced by extensive and/or randomized testing and quarantining patients without symptoms, the infections may be contained at a much lower number (see the last set of bars shaded in grey, Fig. 4B).

Lately, India has observed a surge of reverse migration of migrant workers from one part of the country to another. Preliminary thermal screening at the destination of their journey, e.g at rail/bus stations, can diagnose symptomatic patients only. However, a large number of these people are asymptotically infected. Due to a lack of social distancing during their plighted journey, the possibility of infection propagation increases manifold. The rapid increase of infections due to the arrival of migrant workers is visible in the recent state-wise data.

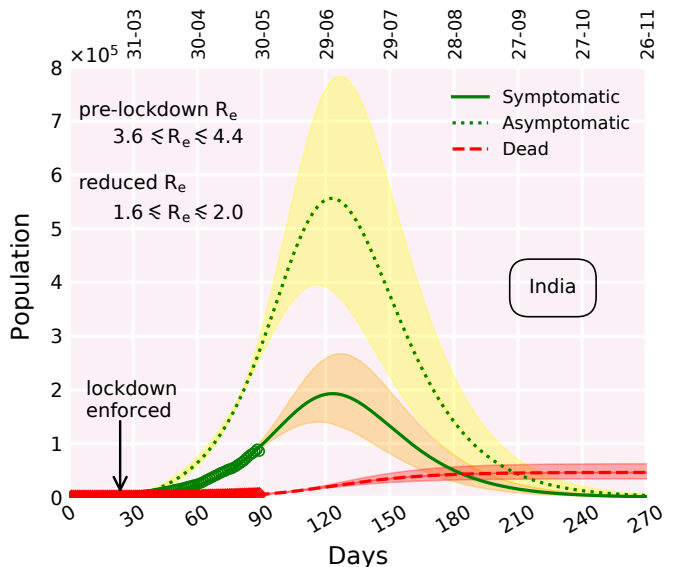


FIG. 5. Best fit of the symptomatic infection and death curves along with the projected asymptomatic infection curve when the pre-lockdown value of the effective reproduction number R_e is tuned within a range 3.5–4.5. The color shades encasing the curves indicate the variation in the effective reproduction number R_e . The initial susceptible population is chosen to be about 7.5 million. The real data (represented as points) are plotted from March 2.

Next, we discuss how the effective reproduction number R_e computed from the current $SEI_s I_a R_s R_a D$ model evolves during the lockdown.

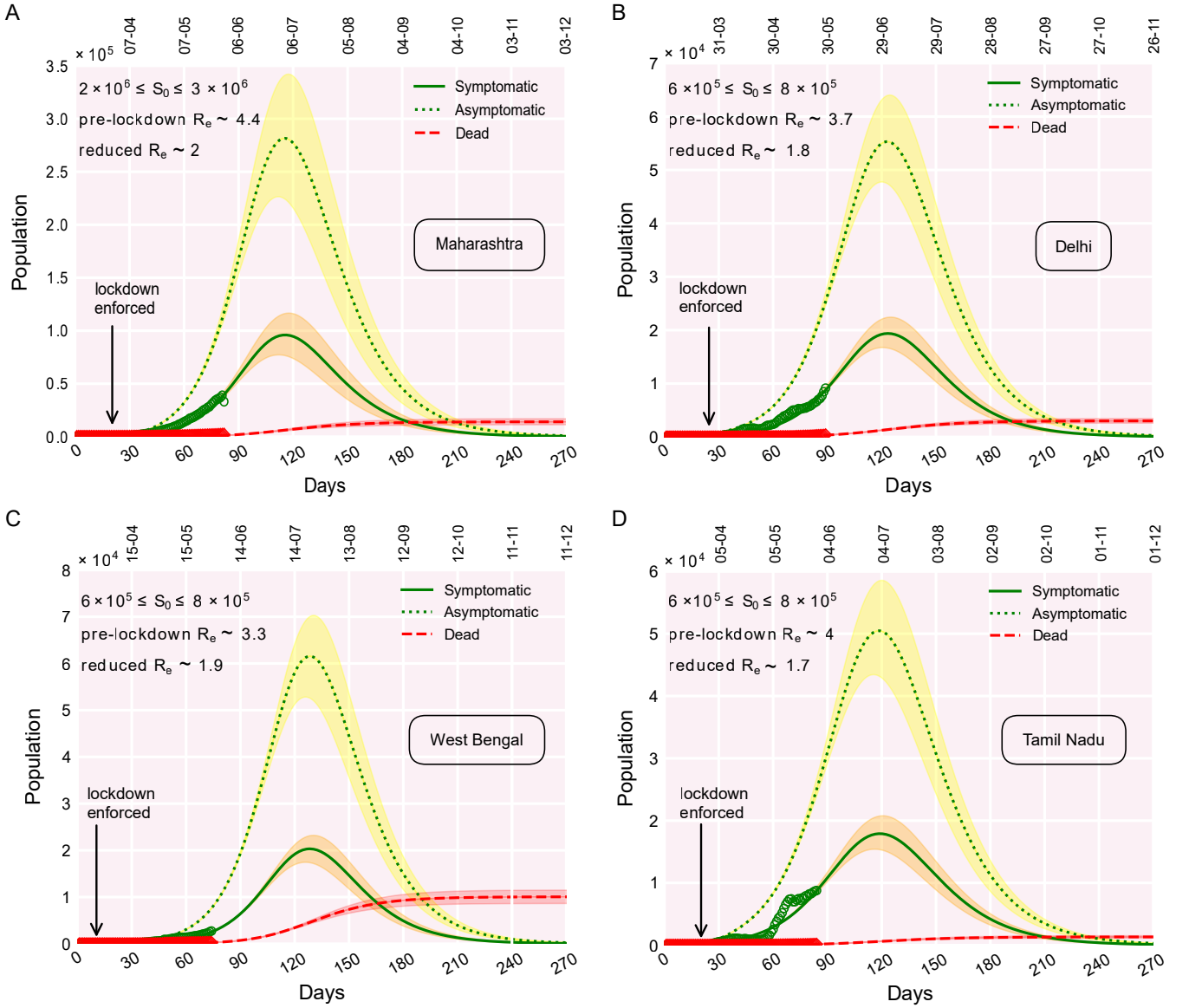


FIG. 6. Best fit of the symptomatic infection and death curves along with the projected asymptomatic infection curves for Indian states Maharashtra (A), Delhi (B), West Bengal (C) and Tamil Nadu (D).

How does the lockdown affect the effective reproduction number R_e ?

During the lockdown, the interaction parameters ξ_s and ξ_a are suppressed because the enforcement of containment measures and social distancing reduces the mixing of infected and susceptible. It is evident from Equation (14) that, as ξ_s and ξ_a decrease, the pre-lockdown R_e should also plummet down to a lower value indicating a relatively slower speed of infection.

In Fig. 5, we observe that the pre-lockdown R_e decreases significantly during the lockdown. Also, in consonance with the definition of R_e [1], we find that higher the value of R_e , greater the number of infections as gleaned from the peak heights (Fig. 5). However, in order to con-

vincingly flatten the infection curve, R_e needs to be taken down to a value below 1. This is a challenge that we have to tackle with utmost priority and sincere policy-making.

Next, we explore the ‘hidden’ asymptomatic influence on the recent surge of infections in a few Indian states using this $SEI_s I_a R_s R_a D$ model.

Asymptomatic carriers and COVID-19 propagation in few Indian States

What we observe from the best fit of the infection curves for Indian states Maharashtra, Delhi, West Bengal, and Tamil Nadu is that in most of the states the infections curves are projected to attain the respective

peaks towards the beginning of July 2020 if the current trend (mapped from the real data) continues (Fig. 6A-6D). Another consistent feature is that the predominantly ‘hidden’ asymptomatic infections may be several folds higher than the symptomatic infections in all the cases.

SUMMARY AND DISCUSSION

The spread of COVID-19 via presymptomatic and asymptomatic cases has been a big concern in recent times as the mobility of people is increasing while lockdown is being relaxed across the country. Since presymptomatic and asymptomatic persons, having no influenza-like symptoms, are not aware of their potential of infecting others, a relaxing lockdown gives ample opportunity to expose a contained population to the virus that effectively increases the number of susceptible. Therefore, the projected trajectories of infections (particularly the infection peaks) largely depend upon the number of susceptible (S_0) in the model. The choice of the initial size of the susceptible population S_0 is a tricky business. Theoretically, in the absence of immunity (acquired or otherwise), an entire population may become susceptible to the COVID-19 outspread. However, in reality, all people will rarely be susceptible to the disease no matter how rapidly it spreads. Various factors like geography, socio-economic characteristics, the demographic landscape can significantly regulate S_0 . The estimation of a ‘ball-park number’ for S_0 is crucial to initiate the modeling analysis. How we have estimated a plausible value of S_0 is described in the following. First, we look at the infection curves for the countries where the cumulative positive cases are have already moved past the peak infection. Dividing the peak infection by the total population of the country under consideration yields a fraction that reflects the average percentage of the population infected by the virus. This fraction turns out to be $\sim 10^{-3}$ for large countries like Germany, USA, Spain, Italy [1]. Thus, an estimate of susceptible can be computed by multiplying this fraction with the total population of a country. For India, the total population is in the order of $\sim 10^9$. Hence, a rough ‘ball-park’ number for the initial susceptible population S_0 would be in the range of $10^9 \times 10^{-3} \sim 10^6$, i.e in the order of millions. We have varied S_0 for India within a range 5-10 million (Table S1, Fig. 2). Note here, that this estimation is a simplistic approximation. After all, it is difficult to comment on the percentage of the population infected by the virus until the pandemic is over. Further details regarding the estimation of S_0 is described in our earlier study ([1]).

In this current study, we have not included the gradual relaxation of lockdown measures (‘unlock 1.0’ plan starting from June 1, laid out by Govt. of India). As the lockdown is being lifted, we expect a considerable surge in the active cases in the upcoming days. We assessed the

COVID-19 progression in the presence of ‘one-time enforcement of containment measures’ where the lockdown and other social distancing norms remain in place for an indefinite time. However, a more realistic reconstruction of the pandemic situation would be to impose ‘intermittent lockdown’ in specific regions where the containment and other social distancing measures are enforced once the number of active infections crosses a threshold determined by the capacity of the regional health-care system. Afterward, the lockdown measures are relaxed/lifted as the active infections fall below a certain threshold (‘unlocking’ the lockdown). This shuttling between the phases of ‘lockdown’ and ‘unlock’ continues until the contagion comes totally under ‘control’ or the threat of an ‘out-of-bound’ infection is eliminated. The nature of intermittent intervention depends on various controlling factors like acquiring ‘herd immunity’, availability of proper vaccines, the capacity of public health facilities where all the patients can be accommodated and treated, etc. A previous study ([16]) in the context of the USA, has discussed these aspects. In the Indian context, it would be interesting to explore further along this avenue as a future venture.

Like the SIRD model used in our previous study [1], this $SEI_s I_a R_s R_a D$ model does not accommodate any spatial information about the infection spread. In other words, there is no spatial degree of freedom in the governing equations of $SEI_s I_a R_s R_a D$ model. The spatial dependence of the disease progression can be executed via simulating this model on a lattice or connected network. The network may feature the following attributes: (a) every node on the network virtually carries the territorial/regional information collected from the map of India; (b) the network connectivity bears the details of human mobility, transmission spread from one region to another. The network nodes also can account for the topology/geography of India in a coarse-grained manner. For example, the nodes representing Himalayan highlands would likely to be attributed lesser human mobility and transmission spread compared to the nodes representing Indian metro cities. This proposed model would enable us to study how the infection spreads from a few initial local pockets to a larger region, thereby rendering a broader picture of the dynamics of the pandemic. A previous study investigating the COVID-19 progression in Italy describes a novel approach using a spatially explicit SEIR model [18]. Future investigation with similar spatial/topological detailing in India’s context would be useful to delve into. Also, note that the current $SEI_s I_a R_s R_a D$ model is a generalized model. It does not contain any specific biological/clinical features of the COVID-19 disease. In this model, COVID-19 enters through the rates and governing parameters in Equations (1) to (12) that are tuned to obtain the best fit of the theoretical curves with the available COVID-19 data.

We observed that the number of asymptomatic cases is several-fold higher than the symptomatic cases. Since the testing is mostly done on individuals showing symp-

toms, this leaves a large fraction of the asymptomatic population untraceable. The infectiousness of an asymptomatic individual may be similar to a person having symptoms. The asymptotically infectious population, mixing freely with the healthy susceptible population, keeps spreading the infection causing a surge in the number of symptomatic as well as asymptomatic cases. To reduce the infection, it is important to trace the source of infection and isolate it from the healthy susceptible population. Currently, there is merely any data available to validate our prediction of the asymptotically infected population. To assess the community spreading and prevalence of asymptomatic cases, India is going to conduct a serology-based (antibody test) survey in select districts. The test aims to find the presence of a specific antibody developed by the immune system of the infected person in response to the viral infection. If the data from the survey is made available in the public domain, the model prediction can be assessed. Irrespective of the testing policy, maintaining social distancing in tandem with prolonged or intermittent containment measures would be crucial. Besides, it is also necessary to use cloth face coverings or mask across the population.

To conclude, ‘indefinite lockdown’ is not a solution to put an end to the COVID-19 outspread. The broader purpose, the lockdown in India served, is the opportunity to buy ‘time’. In a nutshell, the lockdown slows down the infection and the lockdown time window provides us the chance to ramp up the health care facilities, testing capacity, etc. so that when the lockdown is lifted, the COVID-19 does not catch us off-guard. The effect of lockdown can still prevail if social distancing and sanitation protocols are adopted by every individual as the ‘new normal’ of lifestyle.

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Abbreviation	Meaning	Value
Parameters for India		
β_s	rate at which susceptible becomes exposed upon interaction with symptomatic population	0.351 day^{-1}
β_a	rate at which susceptible (S) becomes exposed (E) upon interaction with asymptomatic population	0.351 day^{-1}
λ	rate at which exposed (E) becomes infectious (both symptomatic and asymptomatic)	0.85 day^{-1}
ϕ	probability of being symptomatically infected	0.25
γ_s	rate of recovery for symptomatic individuals	0.083 day^{-1}
γ_a	rate of recovery for asymptomatic individuals	0.09 day^{-1}
δ	rate of death	0.003 day^{-1}
ξ_s	interaction parameter for symptomatic population mixing with susceptible during lockdown	0.30
ξ_a	interaction parameter for asymptomatic population mixing with susceptible during lockdown	0.49
τ	the day from which lockdown begins (counted from day 0, start date of simulation or initial time $t=0$)	30 days
T	delay in number of days before the effect of containment measures on infection propagation becomes visible	9 days
S_0	initial susceptible population	$5-10 \times 10^6$

TABLE S1. List of parameters chosen for the best fit with the real data in Indian context.

Abbreviation	Meaning	Value
Parameters for few Indian states		
β_s	rate at which susceptible becomes exposed upon interaction with symptomatic population	$0.30-0.35 \text{ day}^{-1}$
β_a	rate at which susceptible (S) becomes exposed (E) upon interaction with asymptomatic population	$0.30-0.35 \text{ day}^{-1}$
λ	rate at which exposed (E) becomes infectious (both symptomatic and asymptomatic)	0.81 day^{-1}
ϕ	probability of being symptomatically infected	0.25
γ_s	rate of recovery for symptomatic individuals	$0.07-0.085 \text{ day}^{-1}$
γ_a	rate of recovery for asymptomatic individuals	$0.074-0.091 \text{ day}^{-1}$
δ	rate of death	$0.0009-0.007 \text{ day}^{-1}$
ξ_s	interaction parameter for symptomatic population mixing with susceptible during lockdown	0.29-0.45
ξ_a	interaction parameter for asymptomatic population mixing with susceptible during lockdown	0.45-0.545
τ	the day from which lockdown begins (counted from day 0, start date of simulation or initial time $t=0$)	13-23 days
T	delay in number of days before the effect of containment measures on infection propagation becomes visible	8 days

TABLE S2. List of parameters chosen for the best fit with the real data in few states within India.