An agent-based model to assess coronavirus disease 19 spread and health systems burden

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Article Info

ABSTRACT

The present pandemic has tremendously raised the health systems’ burden around the globe. It is important to understand the transmission dynamics of the infection and impose localized strategies across different geographies to curtail the spread of the infection. The present study was designed to assess the transmission dynamics and the health systems’ burden of severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2) using an agent-based modeling (ABM) approach. The study used a synthetic population with 31,738,240 agents representing 90.67 percent of the overall population of Telangana, India. The effects of imposing and lifting lockdowns, non-pharmaceutical interventions, and the role of immunity were analyzed. The distribution of people in different health states was measured separately for each district of Telangana. The spread dramatically increased and reached a peak soon after the lockdowns were relaxed. It was evident that the protection offered is higher when a higher proportion of the population is exposed to the interventions. ABMs help to analyze grassroots details compared to compartmental models. Risk estimates provide insights on the proportion of the population protected by the adoption of one or more of the control measures, which is of practical significance for policymaking.

Keywords:
Agent-based model
Coronavirus disease
SARS-CoV-2
Non-pharmaceutical interventions
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1. INTRODUCTION

The first case of coronavirus disease (COVID-19) in India was reported on January 30, 2020, post which “public health emergency of international concern” was declared by the World Health Organization (WHO) considering the impact it could create globally [1]. The epidemic has spread across 221 countries with 228,946,779 reported cases and 4,700,214 mortalities globally as of September 19, 2021 [2]. In India, total infections reported are 1,73,06,420 with 28,07,388 active cases, 1,42,96,703 recoveries and 1,95,118 deaths, till April 25, 2021 [3]. The influx of infections has bothered the countries with a denser population [1]. Several factors such as gender, pollution level, viral load, comorbidities, and others also govern the intensity and duration of infection [4]. A larger proportion of the infected people remaining asymptomatic has further raised serious concerns as they are indistinguishable and act as the potential
sources of transmitting the infection [4], [5]. The healthcare fraternity, researchers, and policymakers from several domains have been trying hard to curtail the transmission of the infection completely [6]. Simulation studies in the past have been successful in addressing issues like preparing evacuation plans for airborne infections [7], devising vaccination strategies for influenza [8], smallpox [9], containing measles [10], and tuberculosis [11]. Agent-based models (ABM) have supported various application areas such as dynamics of transmission [12], tracking contacts [13], scheduling time and geography dependent contacts [12], [14], planning non-pharmaceutical interventions (NPI) [14], [15] such as enforcing lockdowns [12], [13], using face masks, and adopting social distancing [14], and shielding the susceptible population [14], [16].

In India, most researches have employed a compartmental approach based on the susceptible (S), infective (I), and recovered (R) model with modifications such as susceptible (S), exposed (E), infective (I), and recovered (R) (SEIR) [17], susceptible (S), hospitalized or quarantined (H), symptomatic (I), purely asymptomatic (P), exposed (E), recovered (R) and deceased (D) (SIPHERD) [18], and analytical models [19]. Simulations are used to study the real-life systems’ behavior in its existing state and upon implementing modifications without associated risks and investment of time and cost [20], [21]. However, the accuracy is subject to authenticity of data, constraints, and assumptions [21]. Complex and dynamic problems could be effectively addressed using simulations [22]. ABM, discrete event simulation (DES), and system dynamics (SD) are three broad classifications of simulations. ABMs entitles the users to define agent-level details [22], [23] and are capable of reporting details of individual agents while DES and SD provide only collective measures [24]. Each agent in the population can be simulated based on different conditions and can be made to perform different actions. A bottom-up approach is employed by ABM wherein the behavior of each agent contributes to the behavior of the system. Each agent holds a specified state at any instant of the simulation [23]. Technological advancements have improved the capability of systems to handle complex models [22].

2. RESEARCH METHOD

From the literature, it was evident that most of the studies to assess the transmission dynamics of infectious diseases employ compartmental models, which fail to incorporate agent-level details. Hence, the present study aims to provide an ABM-based simulation to estimate the spread of COVID-19 by developing a disease model and simulating it using Python. Such simulation studies based on synthetic populations could be helpful for the policymakers and healthcare systems to equip themselves based on the estimates. The present study simulates agents of the synthetic population that represent 90.67% (n=35,003,674) of the overall population of a state. The parameters such as age and geographic information system (GIS) coordinates have been mapped to each individual in the population to ensure exact representation of the state. The incorporation of such agent-level details would help in effectively devising policies locally. Analyzing the NPIs and risk estimates have practical significance in terms of policymaking and governance. In accordance with the Swiss cheese model, the combined effect of multiple interventions on curtailing the spread of infection has been analyzed. Hospitals have been benefited from this approach of setting up multiple defense strategies [25], [26].

2.1. Research design

An ABM approach is employed to assess the outbreak of COVID-19 and its burden on health systems using Telangana state’s synthetic population as shown in Table 1. The code for simulation was developed in python, an object-oriented programming (OOP) language using PyCharm, an integrated development environment. The model was simulated for 365 days for various lockdown strictness as per the Indian scenario [27], [28]. The main functionalities of the code involve creating agents, defining contact networks, developing a disease model, devising interventions, and simulating. Transparency of code, assumptions, variables, and scope of the study are retained throughout in adherence with the ethical good practices in modeling and the International Society for Pharmacoeconomics and Outcomes Research (ISPOR-SMDM) modeling good research practices [29]–[31].

2.2. Agent creation

The main idea to employ an ABM was to represent the population of a state by defining the actual attributes to each of them. Data of 31,738,270 people were taken from the 2011 census of India to generate the synthetic population of Telangana. Unique identifiers for person and household, district codes, and geocoordinates were mapped to the agents. During the data cleansing process, 30 invalid entries were eliminated to obtain 35,003,674 valid records that represent 90.67% of the state’s population as shown in Table 1 [32], [33].
Table 1. Model parameters

<table>
<thead>
<tr>
<th>Parameters</th>
<th>&lt;5</th>
<th>5-59</th>
<th>&gt;59</th>
<th>References</th>
</tr>
</thead>
<tbody>
<tr>
<td>Number of contacts per day</td>
<td></td>
<td></td>
<td></td>
<td>Supplementary [28] [34], [35]</td>
</tr>
<tr>
<td>Probability of getting infected through contact (%)</td>
<td>i) closer circle: (3 to 10); ii) other contacts: (1 to 5)</td>
<td></td>
<td></td>
<td>[34]</td>
</tr>
<tr>
<td>Proportion of people remaining asymptomatic</td>
<td>0.8</td>
<td></td>
<td></td>
<td>[36], [37]</td>
</tr>
<tr>
<td>Average incubation period (in days)</td>
<td>5</td>
<td></td>
<td></td>
<td>[23], [38]</td>
</tr>
<tr>
<td>Average treatment duration (in days)</td>
<td>14</td>
<td></td>
<td></td>
<td>[38]</td>
</tr>
<tr>
<td>Proportion of hospitalized cases in ICU</td>
<td>0.11</td>
<td></td>
<td></td>
<td>[39], [40]</td>
</tr>
<tr>
<td>Treatment duration in ICU (in days)</td>
<td>Triangular (7, 8, 9)</td>
<td></td>
<td></td>
<td>[38], [40]</td>
</tr>
<tr>
<td>Proportion of people moving from ICU to critical illness (Ventilator)</td>
<td>0.88</td>
<td></td>
<td></td>
<td>[40]</td>
</tr>
<tr>
<td>Treatment duration in ventilator state (in days)</td>
<td>Triangular (5, 7, 12)</td>
<td></td>
<td></td>
<td>[38]</td>
</tr>
<tr>
<td>Time between symptom arrival and admission (in days)</td>
<td>3</td>
<td></td>
<td></td>
<td>[41]</td>
</tr>
<tr>
<td>Proportion of people who die</td>
<td></td>
<td></td>
<td></td>
<td>As per Indian statistics [3]</td>
</tr>
<tr>
<td>Risk difference for use of control measures (percentage)</td>
<td>i) Mask: 10.2; ii) Distancing: 14.3</td>
<td></td>
<td></td>
<td>[42]</td>
</tr>
</tbody>
</table>

2.3. Contact network

The spread of infection is majorly governed by transmission rates and contact networks. The rate of transmission was varied from 3 to 10% and 1 to 5% for external contacts and household contacts respectively [34]. Contact rates for the present study were assumed to be density-dependent to be varied rationally across districts [15]. The probability with which any two agents meet was assumed to be inversely proportional to the distance between them. Kumar et al. [34] conducted a study in Ballabgarh, India to define contact rates for close-contact infections. This was used in integration with the density-dependent contact rate assumption to determine the contact distributions for all the districts. A multiplication factor (ratio of population density of the district under consideration to that of Ballabgarh) was used to find the proportionate corresponding contact rates for each district [15], [34]. Input analyzer tool of arena that helps to fit datasets into various distributions with corresponding errors was utilized to derive the distributions for contact rates of each district [43].

2.4. Disease model

Disease models depict the progression of any disease through various states that govern the behavior of agents. Each agent exists in one of the states at any point in time which changes based on the conditions presented in the statechart as shown in Figure 1. State chart indicates the state of existence of agents in the simulation.
At any instant, each agent can exist in one of the states mentioned in the statechart. These are governed by the actions that are defined for each agent during the simulation. The interaction of agents drives the transmission of infection from an infected to a healthy agent. Post transmission of infection, agents turn to be either asymptomatic or symptomatic. The latter undergo treatment after the incubation period while the former are untraceable and are not admitted for treatment. However, they spread the infection till recovery. Symptomatic agents further traverse along three states admitted, intensive care unit (ICU) and ventilator during which they either recover or decease. The conditions that govern the progression across states with the period of existence in each state are shown in Table 1.

### 2.5. Model initialization

Various variables that were used to develop the model were obtained from secondary sources including those from the models of infectious disease agent study (MIDAS) [44]. Spatial resolution cannot be attributed as the paths of agents are not considered rather the geo-coordinates are only taken into account. A time step of one day was considered for the simulation.

### 2.6. Model simulation

The Python code was simulated for the six scenarios defined in Table 2 to compare the effects of various NPIs [45]. The variations in strictness of lockdowns were taken care of by altering the contacts of agents at different locations such as home, schools, and work, depending on the place and age. The contacts outside the home were reduced in accordance with the stringency of lockdowns.

### RESULTS AND DISCUSSION

The effects of various NPIs such as lockdowns with varied stringency, adoption of social distancing, and use of face masks along with the impact of immunity on the spread of infection was observed over 365 days by simulation of six scenarios. The six scenarios would be referred to as MD100I90, MD75I90, MD50I90, MD100I180, MD75I180, and MD50I180 in subsequent sections. The numbers after ‘MD’ and ‘I’ indicate the proportion of the population exposed to control measures and immunity period (days) post-recovery respectively. Time-series graphs representing the number of people in asymptomatic and symptomatic states from the overall population are presented in Figure 2. The supplementary file contains time series data of individual districts.

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Figure 2 reveals that the spread of infection has risen sharply after the lifting of lockdowns. The reason for subsequent spikes in Figure 2(a) as compared to Figure 2(b) and also in Figure 2(c) as compared to Figure 2(d) is due to the loss of immunity in Figures 2(a) and 2(c) after 90 days of recovery. Lockdowns prove to be the most effective control measure as the variation in terms of infections reduced relatively lesser even though a higher proportion of the population adopt social distancing and mask. However, there is a decline in the peaks of graphs in scenarios with a larger population exposed to interventions.

The possibilities of subsequent peaks are higher in the absence of vaccination, as observed in Figure 3. These graphs could improve the preparedness of the healthcare systems and shed light on the capacity required to treat the admitted infections as shown in Figures 3(a) and 3(b), make arrangements for ICU as shown in Figures 3(c) and 3(d), and ventilators as shown in Figures 3(e) and 3(f). The secondary infections are observed as people start to lose their immunity over time. There is a spike in the number of deceased people post-lockdown with subsequent peaks in accordance with the trend of infections. Prolonged immunity provides an additional time window for planning the capacity and vaccination policies. Figure 4 shows a similar pattern with some temporal offset governed by the duration of existence in the preceding states. The second spike in cumulative infections is earlier in case of Figure 4(a) as compared to that of Figure 4(b) due to shorter immunity. Proportionate spikes are seen in Figures 4(c) and (d) indicating recovery post infections. Despite the high recovery rate, untraceable asymptomatic people pose a major challenge for curtailing the spread as they are highly untraceable to be isolated.

The risk estimates as shown in Table 2 reveal the level of protection offered through various interventions. The interpretation of these estimates are: i) relative risk (RR) is the probability of an event occurring to exposed vs unexposed groups; ii) attributable risk (AR) indicates the excess risk due to a risk factor. A negative value indicates protection offered; iii) population attributable risk (PAR) indicates the percentage of cases in the total population that can be attributed to the risk factor; and iv) PAR% is the proportion of the incidence of disease in the population due to exposure. The first period of 104 days indicates the period after which the first recovered person would lose immunity. Successively, these parameters are calculated for further time intervals to analyze how they vary for different lockdown and intervention scenarios. The RR being lesser than 1 denotes that the exposure offers protection rather than risk
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4. CONCLUSION

Localized research just as the present one provides tailored and accurate insights that are more suitable to be materialized by policymakers for specific geographies. The use of the ABM approach promotes the level of detail offered to individuals in the population. Important factors such as protective factors could provide insights on the proportion of the population that would be shielded by imposing control measures. A total of 31738240 agents that represent 90.67% of Telangana’s population were generated to be used for simulation. The simulation coded in python was run to compare the six different NPI scenarios for 365 days. Time series corresponding to each health state were obtained for each district to get localized measures that could help policymaking. The study also measures the effect of the use of control measures and the role of immunity in the spread of infection. Understanding the variation in the spread of infection with respect to the interventions provide better insights to the policymakers on how to strategize the policies to curtail the spread in different areas. Defining interactions of agents based on GIS coordinates and considering contacts at workspace and closer circle allow us to show variations in the spread of disease during different lockdown setups. This has more practical implications to deliver healthcare services with capacity requirements to more vulnerable people. The ethical good practices in modeling and ISPOR-SMDM modeling good research practices have been adopted throughout the study. As evident from the results, the interventions help to curtail the transmission of the infection which provides more time window for the policymakers to devise apt strategies locally and to research on developing vaccination programs. Lockdown was found to be the most efficient intervention to curtail the spread as its lifting drastically increased the infections in a much shorter
time. The risk estimates further support these as the RR, AR, and PAR% values revealed higher protection during the lockdown period and in scenarios where a higher proportion of the population followed control measures. These values indicated the level of protection offered in each scenario and the proportion of the population that could be shielded by the control measures (exposure). The effect of immunity provides information about possible secondary infections after the loss of immunity. These estimates could be of practical significance to plan the interventions based on the population to be shielded. Limitations to the study include the exclusion of comorbidities, transportation modes, and indirect transmission through suspended particles, which could be considered to improve the accuracy.

DATA AVAILABILITY
The python code, supplementary file, and detailed district-wise estimates files shall be shared by the authors upon request.

REFERENCES
[26] I. Ferwana and L. R. Varshney, “Social capital dimensions are differentially associated with COVID-19 vaccinations, masks, and


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