A Flexible Agent-Based Model to Study COVID-19 Outbreak
- A Generic Approach

Anik Burman1, Sayak Chatterjee1, Pramit Ghosh2, and Indranil Mukhokadhyay*1

1Human Genetics Unit, Indian Statistical Institute, India
2Deben Mahata Government Medical College & Hospital, Purulia, India

Abstract

Understanding dynamics of an outbreak like that of COVID-19 is important in designing effective control measures. This study aims to develop an agent based model that compares changes in infection progression by manipulating different parameters in a synthetic population. Model input includes population characteristics like age, sex, working status etc. of each individual and other factors influencing disease dynamics. Depending on number of epicentres of infection, location of primary cases, sensitivity, proportion of asymptomatic and frequency or duration of lockdown, our simulator tracks every individual and hence infection progression through community over time.

In a closed community of 10000 people, it is seen that without any lockdown, number of cases peak around 6th week and wanes off around 15th week. If primary case is located inside dense population cluster like slums, cases peak early and wane off slowly. With introduction of lockdown, cases peak at slower rate. If sensitivity of identifying infection decreases, cases and deaths increase. Number of cases declines with increase in proportion of asymptomatic cases. The model is robust and provides reproducible estimates with realistic parameter values. It also guides in identifying measures to control outbreak in a community. It is flexible in accommodating different parameters like infectivity period, yield of testing, socio-economic strata, daily travel, awareness level, population density, social distancing, lockdown etc. and can be tailored to study other infections with similar transmission pattern.

Keywords: agent-based model, COVID-19, lockdown, asymptomatic stage, sensitivity, simulator

1 Introduction

The world is yet to decipher the riddle called COVID-19. In December 2019, first reported from China and within a few weeks it became the darkest threat looming large over the entire human civilization. Figures are staggering; be it the persons affected, or the death toll or depth of the economic slump. Statistical and mathematical modeling are emerging fast as the tool of the hour, both policy makers and programme managers are eagerly looking for a real-life prediction for the days to come. This would help them in designing future course of action and apportioning resources.

Commonly used model using a set of differential equations like SIR,1 2 describes epidemiological state transition from susceptible to infections to recovered compartments. Mathematical epidemiology is flooded with extensions and sophistications3 6 sprouting out of SIR models that include subdivision of exposed class, hospitalisation, host-pathogen interaction and so on. Undoubtedly incorporation of other compartments would make the disease dynamics model more realistic; on the other hand, SIR involves too many parameters that need to be known and/or estimated a-priori. These models are used for prediction of compartment sizes, impact and severity of the disease etc.7 Hence accurate knowledge about these parameters are essential as performance of such models depends entirely on the parameter values. It might provide good estimates, though initial sizes of different compartments, especially the susceptible class, influence shape and size of the output. Standard estimation procedure based on available data often fails to account for time dependent parameters.8

Interplay of various factors like age, socio-economic strata, occupation of a person along with availability, accessibility and efficiency of testing and treatment would eventually determine the propagation and impact of the disease in a community or country.9 This dynamic and complex nature of the system and society involves many variables that not only shows non-linear behaviour but are also time dependent.9 Inherent stochasticity and spatio-temporal behaviour of the factors involving the disease dynamics might lead to lack of accuracy of deterministic model in tracing the spread of disease over time. Keeping in mind the basic structure of these popular and useful models like SIR, SEIR etc, agent Based model (ABM) becomes another tool10 11 to capture the disease dynamics in presence of several constraints on the parameter values. ABM is a simulation based model and has the potential to capture and produce the spatio-temporal evolution of the system involving different socio-economic variables. It has enough flexibility to incorporate interventions in a specific time period depending on the severity of disease spread. The variables may interact with each other and show non-linear behaviour under complex conditions which is sometimes very hard to describe mathematically. ABM can track the chain of infection depending on population characteristics.12 16 It can be an efficient tool in identifying best possible interventions in a given situation.17 To factor in behavioural or group characteristics along with nature of pathogen transmission, simulation through agent based modeling might be the most useful alternative.

Like any other disease, time, place and person distribution of COVID-19 disease reflects its inherent heterogeneity, depending on genetic nature, host characteristics and environmental correlates. Inter or intra-country variation is common because overcrowding, occupation etc. coupled with urban agglomeration can play a crucial role in fuelling and sustaining the pandemic across the globe.18 Simulation of disease spread using agent-based models can closely mimic this real-life situation.

Our proposed model aims to develop a common digital platform to facilitate simulation over a range of parameters. Although developed for the study of COVID-19 disease dynamics, it would also help in understanding the propagation of infectious disease in a specific community by a pathogen of similar nature which is spread by direct person to person transmission without any intermediary vectors. Our model is a general one as it involves parameters of an SEIR model in a broad sense, population demography, economic status, age, awareness to follow some policies that are expected to contain the disease spread, treatment protocol and other factors and their interactions. Effects of the factors considered in our model might be of immediate nature or can unfold gradually over time as well.

*Corresponding authors, email: ghosh.00@gmail.com, indranil@isical.ac.in
We develop a generic agent-based model (ABM) for COVID-19 that may be applicable to any geographical location and socio-economic structure. Parameters involved in our ABM are given as input that are specific to a community or country or locality.

Input includes both population characteristics and other factors influencing disease dynamics. Susceptible population is stratified based on age, sex, working status, type of work etc. These are all potential determinants for natural history of the disease. Risk of infection and transmission potential are thought to vary with education, occupation, scope of social interaction, stage of infection etc. Agents or individuals with varying attributes behave differently and simulation over time reflects the propagation pattern.

Figure 1 describes various states through which a person moves during the course of the disease. Infected individuals can either remain asymptomatic throughout the 4-week period or manifest disease at some point of time albeit with varying potential. For symptomatic individuals, shedding of virus starts in pre-symptomatic phase, increases till first 3-4 days of manifestation and slowly wanes off in next 2-3 weeks. Force of infection, can be considered as an interplay of rate of contacts among individuals, probability of a contact being with an infectious host and the probability of that contact giving rise to an infection.

Considering all possible combinations of parameters as depicted in Table 1, we have 72 simulation models. To observe the average behaviour for each scenario, every model is run 1000 times over a period of 150 days in 20 sq unit area with 10000 population. Depending on the population density, we can vary its size and/or population size so as to mimic the actual population density. Local population density itself is a function of multiple socio-economic parameters. This also dictates the pace of disease transmission in any community. Social distancing is promoted to increase physical distancing so that virus could not get transmitted to a susceptible host. We assume that once recovered, a person will not be re-infected during the course of simulation. The movement from one stage to other may be considered as a continuum through which a person or agent traverses in unidirectional pattern, once infected. It is not necessary that all agents in the population will be infected; certain percentage may remain uninfected in the community throughout the course of simulation.

The model starts with an assumption that in a virgin community when the first infected person enters, all others are susceptible. We restrict ourselves to a closed population assuming that no one will leave the population during the time period of simulation. Since spread of disease depends on population density, we assume 2- and 3- cluster models for population and varying number of epicentres and their locations. Within a cluster, population density is very high compared to other parts. Epicentres may lie within and/or outside a cluster. We also consider different periods of initiation, duration of lockdown and varying degree of precision for identifying an infected person. Our simulator incorporates the information on age and occupation distribution of the population in the region.

Every individual, known as ‘agent’, is tracked over each day in the entire time period since the inception of infection till it subsides significantly. Movement or mobility of an agent depends on age, working status, disease status, comorbidity, intention to follow lockdown etc. We also consider varying percentage of asymptomatic individuals that play a major role in disease spread. Once an agent dies, it is removed from the population and simulation continues without that agent. We have used comorbidity that depends on age and other factors. This comorbidity is plugged into the risk probability that indicates the probability that a person at a given stage will live one unit of time.

Initially at time 0, we assign age, economic and work status randomly to the population. Sizes of different disease status (Figure 1) are \( n_i, i = 1, \ldots, 6 \) such that \( \sum n_i = N \). Since the time unit is one day and time frame is relatively small, we do not assume recruitment and natural death in this population. Moreover, we assume that the population is closed within the region considered as there are some restrictions in the form of lockdown, quarantine etc. Hence in our model inter-region mobility is not allowed. Our main interest is to see the disease transmission and dynamics within a micro environment region.

In the model, the user can select number of clusters and their locations within the region at the start of simulation. Such clusters contain 20% of the total population and the rest 80% population is distributed uniformly over the remaining region. Within clusters, the population is distributed uniformly. Note that it is easy to implement the cluster size in terms of geographical region and assign population accordingly. However, we can safely assume the same population density within clusters which is much more than the population density in rest of the region. This assumption is valid because we know that the population in slums is much denser compared to other areas. This idea of introducing population density is based on the fact that disease is supposed to be transmitted faster in congested areas.

Mobility and hence transmissibility along with other influencing factors also depend on gender and related factors. We assign the gender to an agent using a Bernoulli random variable with probability \( \mu \) as the probability of being male. The value of \( \mu \) can be found for the region; usually it is close to 0.5.

Let \( S_t(x, y) \) and \( I_t(x_0, y_0) \) be a susceptible and an infected agent with location coordinates \((x, y)\) and \((x_0, y_0)\) respectively. Then \( S_t(x, y) \) belongs to the neighbourhood of \( I_t(x_0, y_0) \) if the euclidean distance between the two is less than a preassigned distance \( l_0 \) (say), i.e.\[ S_t(x, y) \in N(I_t(x_0, y_0)) \text{ if } \sqrt{(x-x_0)^2+(y-y_0)^2} \leq l_0 \text{ for all } (x, y) \in \mathcal{R} \text{ and } (x_0, y_0) \in \mathcal{P} \]

where \( \mathcal{P} \) is the entire path covered by \( I_t \) due to its mobility at time \( t \). Note that the circular region with centre at \((x_0, y_0)\) and radius \( l_0 \) must entirely be contained in \( \mathcal{R} \), otherwise an agent may be outside the geographical region violating our model assumption.

So, the proposed ABM incorporates infection timeline, working and economic status, gender, age along with number and duration of lockdown periods. This makes it very flexible and adaptable to any geographical location with varying population density and socio-economic status.

### 2.1 Simulation

We have done extensive simulations to study different scenarios like strict lockdown, relaxed restriction with varying degree of relaxation, number of geographical clusters with higher population density, amount of testing facility etc.

When a susceptible agent comes inside the neighbourhood of an infected agent, either symptomatic or asymptomatic, s/he gets infected with a certain probability. We define this neighbourhood as a circular region centred around the infected
agent. Depending on the movement of an agent, simulation is carried out in a specified area inside the community. Conditional probability of the test being positive given that the agent is actually infected, is taken as the sensitivity of the system in identifying an infected person.

Considering all possible combinations of parameters (Table 1) along with other parameters like population, area of the region, age-sex distribution and occupation strata etc., we have studied 72 simulation models. We report an average curve with a band as given by the standard deviation based on 1000 repetitions of each model over a period of 150 days.

We include two new cases outside the cluster in a virgin community of 10000 population in spite of multiple lockdowns. Let us consider a situation where there are two new cases outside cluster in a virgin community (Figure 2A). We find cases peak around 35 days with cases as high as 600 in a single day; curve gets flattened by 100th day. Cumulative recovered cases are about 1750 and approximately 150 persons expire from the disease.

Then we implement lockdown for 20 days twice, starting at 20th day and 60th day. This drastically altered the shape of the curve (Figure 2C). At the end of first lockdown, there is little dip in active cases, followed immediately by a rise. Active cases peak around 50 days and maximum number of cases is around 450. With introduction of second phase of lockdown, cases decrease fast, and eventually die out by 100th day of outbreak.

A comparative study of these two graphs provides a good reflection of how effective lockdown is, even in a heterogenous population with variable chance of following the rules, and how it can deter and diminish the rise in active cases. This definitely buys time for community to prepare for the coming onslaught and reduces chance of acute hospital bed crisis.

When cases start from within clusters, then without lockdown, outbreak pattern remains similar to the earlier (Figure 2B). Active cases peak comparatively earlier around 25 days and wane off more slowly, eventually to flatten around 100th day. Number of recovered cases is also similar, around 1750 (Figure 2B). Once we introduce lockdown, cases start to decrease from the beginning of lockdown. Curve rises a bit once first lockdown is lifted, but with introduction of second phase of lockdown, it decreases quickly (Figure 2D). There is another important difference. The curve does not touch x-axis even at 150th day of simulation. Active cases are very few, but cases are still occurring. Cumulative number of recovered cases are around 1450 and graph of recovered cases is yet to plateau.

This indicates, that if started in densely populated areas, the outbreak will have a long-drawn course even in a small community of 10000 population in spite of multiple lockdowns.

In all these situations, we consider asymptomatic proportion as 10% of total cases and chance of detecting infected cases i.e. sensitivity as 95%.

If we lower the sensitivity, number of deaths from the disease increases (Figure 3A) without any lockdown. With 95% chance, cumulative death is around 125, which increases to 175 with 85% and around 225 with 75% chance. So, detecting cases through laboratory testing by escalating availability, accessibility and utilisation of good quality diagnostic kits is critical to reduce mortality.

We consider another situation with 10% asymptomatic proportion and primary cases outside population cluster. We implement two lockdowns and vary the sensitivity (Figure 3B). Graphs shift upwards with decreasing sensitivity; effect appears to be most prominent in number of deaths. Numbers are comparatively less with two lockdowns vis a vis none, keeping other parameters same.

Without any lockdown, when outbreak starts in two epicentres outside cluster and chance of detecting infected cases is 95%, depending on ratio of symptomatic and asymptomatic cases, shapes of curves get altered (Figure 4A). As the asymptomatic proportion increases, total case and deaths come down, without any significant lateral shift of the curves. Lesser proportion of asymptomatic cases means steeper slope of curve for cumulative cases. Similar pattern is seen in situation when primary cases are located inside clusters (Figure 4B).

Once we implement lockdown, curves peak later. Overall cases and deaths come down with rise in proportion of asymptomatic cases (Figure 4C, 4D). When outbreak starts inside population cluster, the course is long-drawn even with lockdown; nevertheless total cases and death are less if asymptomatic infected persons increase.

In spite of having ‘double hump’ of active cases with two lockdowns (Figure 4C) total cases and deaths come down with increase in asymptomatic proportion, even if we keep sensitivity as 95% and both the two primary cases outside cluster. After 150 days of simulation, cumulative recovered cases are around 1500 and 1250 with asymptomatic proportions as 10%

### Table 1: Parameters in our ABM

| No. of epicentres | Location | Sensitivity of identifying an infected person | Percentage of asymptomatics | No. of lockdowns |
|-------------------|----------|---------------------------------------------|-----------------------------|-----------------|
| 2                 | Within cluster | 0.75                                     | 0.10                         | 0               |
| 3                 | Outside cluster | 0.85                                     | 0.25                         | 2               |
and 50% respectively. Number of deaths also comes down from around 125 to around 40. Similar reduction in number of cases and deaths is also seen if primary cases are located inside cluster (Figure 4D). However in neither of situations, cumulative recovered cases plateaued after 150 days.

Hence, the model not only tests the effectiveness of an intervention like lockdown, it also predicts the pattern of outbreak with varying proportion of asymptomatic cases or chance of identifying cases in a specific community. With decreasing sensitivity, number of active cases increase. Even with two lockdowns, failure to detect cases will result in more active cases, as well as number of deaths.
Discussion

Primary impetus to develop an agent-based model is to study the effect of potential interventions on the course of COVID-19 disease in a community. Inter and intra country variation in time, place and person distribution of the disease point towards a complex interplay of multifarious determinants related to individual and societal perspectives.

To accommodate variability that exists in the real-life situation, we consider a community mimicking Indian diaspora. It is difficult to capture the exact flavour of extreme diversity of this country. Here we have used census distribution of 2011 for age and sex distribution in a community.

Occupation of an individual, her/his mobility in connection with daily activities are thought to influence the risk of contracting or transmitting the disease. Intermixing pattern definitely plays a role in spreading of the disease in addition to biological and genetic factors. We factor in individual mobility as a marker of intermixing in this model. In a community this mobility or intermixing is not uniform. It varies with habitation, poverty, gender role, work culture, social customs, availability and access to basic amenities etc. In areas where people need to move to crowded places for basic needs like food, water and sanitation, they are definitely more at risk. Inadequately ventilated housing condition common for slum dwellers may also escalate the risk.

Initially the disease influx was prompted by immigrants returning from endemic countries, followed by concentrated foci in urban pockets, more so in slums with high population density. Gradually the disease started to engulf periurban areas of the country and rural spread appears obvious and ominous.

While designing the model, flexibility to accommodate relevant individual traits is given utmost importance. A person’s health behaviour, risk and vulnerability are influenced by a variety of factors. Her/his personal traits and also the socio-cultural milieu where s/he belongs, both are critical. We thought it intriguing and important to study the role of an agent with a particular mix of personal characteristics in COVID-19 disease spread in her/his community either as a perpetrator of disease spread or its victim.

If we consider a local community as a watertight compartment on its own, we can set some rules of interaction within its members and that exactly has been done here. Once primary case of COVID-19 is introduced, simulation starts to run and from those epicentres, infection propagates based on behavior and personal characteristics of individuals in the community.

Chance of infecting close contacts or getting infected, innate or acquired immunity against the disease, change in the disease occurrence and mortality over time all can be incorporated as parameters in this model. We have developed a platform over which simulation with varying individual and group characteristics can be manipulated to observe the effect on course of the disease over coming months or years. Till date it appears robust enough to allow experimentation till six months of introduction of first infected case in a small community. It would be useful to look for a feasible, practical intervention to curb the epidemic spread.

It can also test for sustainability of interventions. It is generally accepted that work from home, home quarantine and physical distancing or lockdown are beneficial to reduce spread. However, after certain period of time, lock down appears to become counter-productive with disastrous effect on livelihood of millions. Moreover, psychological state of general
people desists lockdown over longer duration. So this model is also useful to study the optimum timing and duration of lockdown on eventual course of the disease. It appears that this pandemic is going to stay for some more years. Upsurge of cases have already noted in some of the European countries, while India or USA is still grappling with onslaught of the first wave. The usual flu season in the coming winter months, if coalesce with COVID-19 pandemic, can bring the countries on the brink of disaster.

We would like to use this simulation to translate lessons learned till date into potent measures prior to upcoming waves.

The evidence pool generated by basic scientists, laboratories, clinicians, social scientists, demographers and programme manager can be incorporated into this robust but flexible simulator. The simulator can definitely help re-searchers and scientists to test a motley intervention. Health managers and policy makers may also utilise this ABM to decide on optimum timing and duration of effective programmatic measures.

Course of a disease can get altered with time owing to factors like genetic diversification, modification of host immune response, increased community awareness, changes in environmental parameters or advanced treatment modalities. An agent with assigned characters behaves in a certain way in terms of acquiring or transmitting the infection. In a population with known distribution of these characteristics, our model can forecast possible shape of disease outbreak like COVID-19, which is transmitted from person to person without any intervening vector.

This model forecasts disease spread over time in a specific community with known values for certain parameters. It also provides an idea on best possible measures to reduce the spread and control the outbreak in a community. It can be useful in estimating value of R0 over time. The model is quite flexible in accommodating 20 different parameters like infectivity period, yield of testing, socio-economic strata, daily travel, awareness level, population density, social distancing, lockdown etc. The same simulation can be used in a synthetic population to study other infections disease spread. With time as more effective treatment and vaccines will hopefully reduce both infectivity period as well as the pool of susceptible population, further refinement can be done easily to this simulator. We have given a demonstration video as supplementary material.

References
[1] Huang Y, Yang L, Dai H et al. Epidemic situation and forecasting of covid-19 in and outside china. *Bull World Health Organ* 2020; 10.
[2] Leonardi M, Horrie AW, Vincent K et al. Self-management strategies to consider to combat endometriosis symptoms during the covid-19 pandemic. *Human Reproduction Open* 2020; 2020(2): hoaa028.
[3] Mwalili S, Kimanthi M, Ojiambo V et al. Seir model for covid-19 dynamics incorporating the environment and social distancing. *BMCResNotes* 2020;.
[4] Ghosh P, Bashee S, Paul S et al. Increased detection coupled with social distancing and health capacity planning reduce the burden of covid-19 cases and fatalities: A proof of concept study using a stochastic computational simulation model. *medRxiv* 2020;.
[5] Yang Z, Zeng Z, Wang K et al. Modified seir and ai prediction of the epidemics trend of covid-19 in china under public health interventions. *Journal of Thoracic Disease* 2020; 12(3): 165.
[6] Das S, Ghosh P, Sen B et al. Critical community size for covid-19: a model based approach for strategic lockdown policy. *Statistics and Applications* 2020; 12(1): 181–196.
[7] Roberts M, Andreassen V, Lloyd A et al. Nine challenges for deterministic epidemic models. *Epidemics* 2015; 10: 49–53.
[8] Lakshmi Priyadarshini S and Suresh M. Factors influencing the epidemiological characteristics of pandemic covid 19: A tisim approach. *International Journal of Healthcare Management* 2020; 13(2): 89–98.
[9] Cuevas E. An agent-based model to evaluate the covid-19 transmission risks in facilities. *Computers in Biology and Medicine* 2020; : 103827.
[10] Hoertel N, Blancher M, Blanco C et al. A stochastic agent-based model of the sars-cov-2 epidemic in france. *Nature Medicine* 2020; 26(9): 1417–1421.
[11] Epstein B. Agent-based modeling and the fallacies of individualism. *Models, simulations, and representations* 2012; 9: 115–144.
[12] Kumar S, Grefenstette J, Galloway D et al. Policies to reduce influenza in the workplace: Impact assessments using an agent-based model. *Am J Public health* 2013; 103(8).
[13] Liu F, Enanoria W, Zipprich J et al. The role of vaccination coverage, individual behaviors, and the public health response in the control of measles epidemics: an agent-based simulation for california. *BMCPublicHealth* 2015; 15.
[14] Kumar S, Piper K, Galloway D et al. Is population structure sufficient to generate area-level inequalities in influenza rates? an examination using agent-based models. *BMCPublicHealth* 2015; 15.
[15] Espana G, Grefenstette J, Perkins A et al. Exploring scenarios of chikungunya mitigation with a data-driven agent-based model of the 2014?2016 outbreak in colombia. *Sci Rep* 2018; 8.
[16] Guchu H, Kumar S, Galloway D et al. An agent-based model for addressing the impact of a disaster on access to primary care services. *Disaster Med Public Health Prep* 2016; 10(3).
[17] Wong A, Scharcanski J and Fieguth P. Automatic skin lesion segmentation via iterative stochastic region merging. *IEEETransactionsonInformationTechnologyinBiomedicine* 2011; 15(6): 929–936.
[18] Desai D. Urban densities and the covid-19 pandemic: Upending the sustainability myth of global megacities. *ORFOccasionalPaper* 2020; 244.
[19] World Health Organization. *Advice on the use of masks in the context of COVID-19: interim guidance, 5 June 2020, 2020.*