

Studies of COVID-19 Outbreak Control Using Agent-Based Modeling

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An agent-based model was developed to study outbreaks and outbreak control for COVID-19, mainly in urban communities. Rules for people's interactions and virus infectiousness were derived based on previous sociology studies and recently published data-driven analyses of COVID-19 epidemics. The calculated basic reproduction number of epidemics from the developed model coincided with reported values. There were three control measures considered in this paper: social distancing, self-quarantine and community quarantine. Each control measure was assessed individually at first. Later on, an artificial neural network was used to study the effects of different combinations of control measures. To help quantify the impacts of self-quarantine and community quarantine on outbreak control, both were scaled respectively. The results showed that self-quarantine was more effective than the others, but any individual control measure was ineffective in controlling outbreaks in urban communities. The results also showed that a high level of self-quarantine and general community quarantine, assisted with social distancing, would be recommended for outbreak control.

Keywords: agent-based modeling; COVID-19; control measures; neural network

1. Introduction

In the middle of December 2019, a few cases of pneumonia, caused by a novel coronavirus SARS-CoV-2 (formerly 2019-nCoV) [1], were first reported in Wuhan, China [2]. Since then, there have been 1 610 909 confirmed cases, including 99 690 deaths, in more than 110 countries as of April 11, 2020. On February 11, 2020, WHO announced a name for this new coronavirus disease: COVID-19, an acronym for “coronavirus disease 2019.” Currently, we are in the midst of a global COVID-19 pandemic. Most ongoing research [3] focuses on questions concerning virus transmission, asymptomatic and pre-symptomatic virus shedding, vaccine development, and so on.

In their pioneering work, Andersen et al. [4] discussed the notable features of the SARS-CoV-2 genome and pointed out that this new virus was not manmade but evolved via natural selection in an animal host or humans. No matter where or how COVID-19 started, it is crucial to study COVID-19 spreading in the human population to predict COVID-19 epidemic trends and assess control measures. This will provide the basis for rational recommendations in similar disease crises in the future, especially before vaccines are invented.

SARS-CoV-2 belongs to the coronavirus family, in which there are six other known members, including SARS-CoV and MERS-CoV. According to recent research [5–10], there are two primary ways by which SARS-CoV-2 is transmitted to cause COVID-19: respiratory droplet transmission and contact routes [11]. When a person is in close contact (usually within 1 meter or 3 feet) with an infected person, whose symptoms have developed, droplet transmission can occur. The COVID-19 virus can also be transmitted by direct contact with infected people or indirect contact with objects touched by an infected person. It is worth noting that Nishiura et al. [12] studied a larger dataset of confirmed cases and concluded that pre-symptomatic transmission of the COVID-19 virus was likely to take place and might even occur more frequently than symptomatic transmission. Other research has reported that COVID-19 patients can effectively transmit SARS-CoV-2 [7, 13–15] before symptoms develop. This differs from SARS-CoV, which cannot be transmitted from pre-symptomatic patients [16] instead of symptomatic “super spreaders.”

Many researchers have analyzed the reported data to characterize COVID-19 epidemics. In one of the early works, Li et al. [8] collected information on 425 laboratory-confirmed cases of COVID-19 that had been reported in Wuhan by January 22, 2020, and conducted data analyses to approximate the epidemiologic characteristics of COVID-19. Zhang et al. [17] performed another data-driven analysis to estimate the basic reproductive number of COVID-19 in the early stage of the outbreak on the Diamond Princess cruise ship. Nishiura et al. [12] reviewed available information published in research articles and official reports. They estimated the median serial interval as 4.0 days, which is shorter than the estimation of the mean incubation period (5.0 days) in another study [18]. Additionally, Sun et al. [19] conducted a study on the data for 507 COVID-19 patients reported between January 13 and January 31, 2020. Those patients included 364 from mainland China and 143 from outside of China. They estimated the mean incubation period as 4.5 days, which was consistent with other data-driven works [8, 20–22]. They also provided the age distribution of patients as well as the corresponding estimated relative risk.

It has been reported that simulations are driving the world's response to COVID-19 [23] in addition to data-driven analyses. Some researchers utilized mathematical and statistical models to simulate COVID-19 epidemics, but they needed data to estimate model coefficients. Wu and coworkers [24] used a susceptible-exposed-infectious-recovered (SEIR) metapopulation model to simulate COVID-19 epidemics across all major cities in China. Their model coefficients were based on the data collected from (1) the number of confirmed cases in Wuhan through the end of January 2020; (2) monthly flight bookings from the Official Aviation Guide; and (3) human mobility across more than 300 prefectural-level cities in mainland China from the Tencent database. They estimated that the basic reproduction number was 2.68. Wang et al. [25] used the same SEIR model to assess the non-pharmaceutical interventions' impact on the COVID-19 epidemic in Wuhan. They mainly considered the city quarantine and subsequent interventions, which gradually took place between January 23 and February 1, 2020. They found that the reproduction number dropped from 3.86 before the city quarantine to 0.32 after the quarantine. Also, Sjödin et al. [26] parameterized the SEIR epidemiological model based on the published estimations of the incubation and infectious periods to investigate the extent of physical distancing that was needed to effectively control the COVID-19 outbreak in a lockdown situation in a small town of Italy.

In another study, Hellewell et al. [27] implemented a branching process model to quantify the potential effectiveness of contact tracing and case isolation for controlling COVID-19 outbreaks. They used the data in some published articles to determine the model parameters, including delays from onset to isolation [8, 28], incubation period [20] and serial interval. They found that case isolation was more effective when there were few pre-symptomatic transmissions and a short delay from symptom onset to isolation. Kucharski et al. [29] fitted a stochastic transmission model [30] to multiple publicly available datasets. They estimated that the median daily reproduction number declined from 2.35 one week before travel restrictions were introduced in Wuhan on January 23 to 1.05 one week after. Additionally, Shao et al. [31] introduced two dynamic models—a time-delay dynamical-novel coronavirus pneumonia (TDD-NCP) model and a Fudan-Chinese Center for Disease Control and Prevention (CCDC) model—to track COVID-19 outbreaks. Using the public data on the cumulative confirmed cases through February 19, 2020, in different regions in China and other countries, these models could clearly illustrate that the containment of the epidemic highly depended on early and effective isolation.

As an alternative approach, agent-based modeling (ABM) simulates an interactive "world" over a certain time range via the rules guiding

the actions of individual agents. Even a simple ABM can elucidate the behavior patterns of complex systems [32] by providing a natural description of the system (i.e., the “world”), such as the aggregate motion of a flock of birds, a herd of land animals, a school of fish or a population of humans. ABM generates stochastic models to describe populations of interacting agents so that it captures emergent phenomena of the whole system from the bottom up. Because the computational structure of ABM is inherently parallel, it is very efficient to conduct ABM simulations via parallel or cloud computing. Assisted by multi-agent programmable tools or environments such as MASON [33] and NetLogo [34], ABM has been widely applied in sociology [35], biology [36], economics [37], physics [38] and many other domains. When studying host-pathogen systems [39] via ABM at different scales, agents can be viruses and/or people. Several ABM-based immune simulators, such as IMMSIM [40], incorporate current knowledge of immunology and allow users to define the interaction rules when studying immune dynamics at the microscale. Additionally, some ABM-enhanced disease simulators, including PathSim [41], provide a general programming framework to model specific diseases such as tumor growth and influenza. At the macroscale level, ABM-based simulations can be used to study the dynamics of disease spread in the human population. For example, Kim et al. [42] conducted ABM simulation to study the super-spreading events of MERS-CoV in the Republic of Korea. Rao et al. [43] presented another ABM simulation to analyze the global epidemiology of avian influenza.

Recently, a few preliminary studies have been conducted to study COVID-19 transmission and control. Bai et al. [44] published the first work on ABM simulation of COVID-19 epidemic trends and discussed the effectiveness of control measures. They used the following parameters to define the rules on behaviors and interaction of agents (i.e., human beings): infection probability, incubation period, recovery time, and close-contact number. However, those parameters were estimated based on a small number (50) of confirmed cases due to the limited resources in the early stage of the COVID-19 epidemic. Chang et al. [45] developed an agent-based model to study COVID-19 transmission and pandemic control in Australia. They used ACEMod, the Australian Census-based Epidemic Model, to generate the probability that a susceptible agent is infected at a given time step. They also considered various intervention strategies, including restriction on international air travel, case isolation and school closures, in addition to social distancing. Cuevas [46] evaluated the COVID-19 transmission risks in facilities via an ABM. In the model, the behavior of each individual is characterized by a set of simple rules that considers their basic interactions inside the facility according to mobility requirements and contagion susceptibility. Also, Wolfram [47] presented an

ABM of COVID-19, considering variable interaction rates between agents as well as the in-person contact network. Other related works include studying the health and economic effects of social distancing interventions [48], investigating the control measure of contact tracing via smartphones [49] and exploring localized non-pharmaceutical interventions to control the pandemic [50].

In this paper, we present a study of COVID-19 spreading in the human population and an assessment of control measures, using ABM simulations. The epidemiological characteristics of COVID-19, including incubation period and recovery time, were estimated from various published works on large datasets to develop the agent-based model. The rule for agent interaction at various interpersonal distances was derived based on previous social studies. Also, an exponential function of the interpersonal distance, which determines the probability that an agent gets infected, was proposed based on the reported attack rate of COVID-19 epidemics. The basic reproduction numbers, calculated from our ABM simulations, were compared to the results from other data-driven analyses or SEIR models. They agreed with each other. In addition to individually assessing the control measures of social distancing, community quarantine and self-quarantine, a neural network model was utilized to study their combined effects on COVID-19 epidemic control. Our simulation results demonstrated that self-quarantine is the most efficient control measure. However, a single control measure has difficulty controlling the COVID-19 epidemics. A combination of various control measures was recommended. Although our studies mainly focused on the COVID-19 epidemics in urban communities, the developed model can be easily extended to study epidemics in suburban or rural communities.

The paper is organized as follows. Section 2 summarizes the epidemiological characteristics of COVID-19, Section 3 introduces the ABM of COVID-19 spreading in the human population and describes the rules implemented in the model, and Section 4 presents simulations and discussions, including a case study of COVID-19 epidemics in New York City. Finally, Section 5 provides conclusions and future work.

2. Epidemiological Characteristics of COVID-19

The main epidemiological characteristics of a virus-infected disease include the incubation period (i.e., the time between catching the virus and the onset of symptoms of the disease) and the basic reproduction number (i.e., the average number of individuals getting the disease from one infected patient). Li et al. [8] presented the

preliminary conclusion on the epidemiologic characteristics of COVID-19, which has a mean incubation period of 5.2 days and a basic reproduction number of 2.2. Boldog et al. [51] summarized the published estimates of the key epidemiological parameters of COVID-19 while assessing the outbreak risk outside of China after January 23, 2020. Park et al. [52] also conducted a systematic review of studies on COVID-19 outbreaks according to the published literature and preprint archives through February 21, 2020. In addition, Wu et al. [53] collected the available information and aggregated the epidemiology of COVID-19. Tables 1 and 2 are partially based on their summaries. It should be noted that most of the basic reproduction numbers were estimated at the early stage of COVID-19 epidemics without implementing any control measures.

Authors	Basic Reproduction Number
Li et al. [8]	2.2 (1.4–3.9)
Zhang et al. [17]	2.28 (2.06–2.52)
Zhao et al. [21]	2.24 (1.96–2.55)
Wu et al. [24]	2.68 (2.47–2.86)
Kucharski et al. [29]	2.35 (1.15–4.77)
Shen et al. [54]	2.08 (1.99–2.18)
WHO [5]	02.0–2.5
Liu et al. [55]	2.90 (2.32–3.63)
Read et al. [56]	3.11 (2.39–4.13)
Majumder and Mandl [57]	2.0–3.1
Tang et al. [58]	6.47 (5.71–7.23)
Riou and Althaus [59]	2.2 (1.4–3.8)

Table 1. Basic reproduction number (R_0) estimations with uncertainty range (if available).

According to the early studies [60, 63–65], SARS-CoV-2 infection can cause five different outcomes: asymptotically infected persons (1.2%), mild to medium cases (80.9%), severe cases (13.8%), critical cases (4.7%) and death (2.3%). However, the proportion of asymptomatic infection in children under 10 years old could be as high as 15.8% [66]. In addition, the attack rate A , a common way of measuring disease frequency in a population at risk, is defined as

$$A = \frac{\text{number of new cases in the population at risk}}{\text{number of persons at risk in the population}}. \quad (1)$$

An implicit formula $A = 1 - e^{-R_0 A}$ [52, 67] can be used to calculate the final attack rate based on the basic reproduction number. In Table 1, most of the estimated reproduction numbers are between 2.0 and 2.5. We took an average reproduction number of 2.25 and calculated the final attack rate $A = 85.3\%$.

Authors	Incubation Period
Li et al. [8]	5.2 (4.1–7.0)
Linton et al. [18]	5.0 (2.0–14.0)
Sun et al. [19]	4.5 (3.0–5.5)
Backer et al. [20]	6.4 (5.6–7.7)
Lauer et al. [22]	5.1 (4.5–5.8)
WHO [5]	1–14
Liu et al. [55]	2–11
Guan et al. [60]	4.0 (2.0–7.0)
Bai et al. [61]	up to 19
Ki [62]	3.9

Table 2. Incubation period estimations (days) with uncertainty range (if available).

3. Agent-Based Modeling

ABM, also called individual-based modeling, provides a bottom-up approach to understanding complex systems. In NetLogo [34], an ABM platform we used in this study, the interactive environment (i.e., the “world”) is discretized into patches, and the agents (i.e., the people) are randomly located on the patches. At every tick, representing every day, each agent randomly moves to another patch. The agents at the same patch interact with each other, representing socialization and daily events in the real world. Once a SARS-CoV-2 infected agent is introduced, the disease will be spread via the agent interactions. The agents, interaction rules and control measures in ABM of COVID-19 spreading are described below.

3.1 Agents

Agent-based models are composed of agents or computational entities. In our study of COVID-19 spreading in the human population using ABM, the agents are people and have the following state variables and values:

- Infection status: If a person is infected by SARS-CoV-2, the status is true; otherwise, the status is false.

- Incubation period: After a person is infected, the incubation period will be between 4 and 7 days [8].
- Health condition: An uninfected person is healthy. Once a person is infected, there is an 81.9% chance that the person's health condition will be mild [59] after symptoms develop; otherwise, the health condition is critical. We do not consider the asymptomatic condition in this paper.
- Activity level: An uninfected person or an infected person within the incubation period has an activity level of 100%, representing the normal daily activity. Once symptoms develop, the activity level of an infected person will be reduced to 50% and 0% (due to hospitalization) for the mild and critical conditions, respectively. When an infected person has a low activity level, the person has a small chance of interacting with others.
- Sick time: This counts the days that a person has been sick since getting infected.

■ 3.2 Rules in Agent-Based Modeling

One of the major rules defined in this study is to determine the interpersonal distance when people interact with each other. Nolan [68] defined the following US American proxemics zones: intimate, personal, social and public. The intimate zone is 0–18 inches, and it is a space that US Americans reserve for their closest friends, lovers and immediate family members. The personal zone includes an “inner” zone (18–24 inches), where close/good friends comfortably interact, and an “outer” zone (2–4 feet), where most of the friendly conversations and easy social interactions take place. The social space is from 4–12 feet, including a cozy distance (4–7 feet) for a cocktail party or reception and a “professional” distance (7–12 feet) for formal gatherings or office arrangements. Sorokowska et al. [69] presented an extensive analysis of interpersonal distances over a large dataset of almost 9000 participants from 42 countries. They estimated the mean value of preferred intimate, personal and social distances for each country; the values for people in the United States were 19 inches, 27 inches and 38 inches, respectively.

Hill and Dunbar [70] theorized that there are several layers of friendship: acquaintances, casual friends, friends and good friends. They also determined that there are cognitive limits to the number of people that we can accommodate in any one layer. We human beings usually are closest to no more than five people, while counting 15 people as good friends and about 50 people as friends. As an important conclusion from their research, most people can only manage up to 150 meaningful relationships. Therefore, combining the above research findings, we determine the interaction probability of an agent with his/her friends of different friendship statuses, as shown in Table 3.

Friendship Status [70]	Love/Best Friends	Good Friends	Casual Friends	Acquaintances
Number of friends [70]	5	15	50	80
Interaction probability	3.34%	43.33%		53.33%
Interpersonal distance [69]	19 in	27 in		38 in

Table 3. Friendship status, interaction probability and interpersonal distances.

Another major rule developed in this study is the probability of an uninfected agent getting infected by SARS-CoV-2 when exposed to the disease without any self-protection interventions. We consider respiratory droplet transmission and develop a relationship between the infectiousness of COVID-19 and the interpersonal distance. The direct/indirect contact transmission can be categorized in the transmission within a very short interpersonal distance. We assume that the infectiousness of COVID-19 follows an exponential function of interpersonal distance as

$$F_{\text{COVID-19}} = e^{-\alpha x^3} \tag{2}$$

where x is the interpersonal distance in inches. According to the estimated reproduction number based on the data at the early stage of the COVID-19 epidemic, the attack rate, calculated as 85% in Section 2, can be viewed as the fraction of the susceptible population who are infected without any control measures. Therefore, taking that 85% of the population at risk was infected by SARS-CoV-2, α can be determined as 4.36×10^{-6} .

Figure 1 illustrates the infectiousness of COVID-19 at different interpersonal distances according to equation (2). It shows that the infectiousness is 19.6% at the interpersonal distance of 72 inches. Although 72 inches is a safe social distance recommended by the

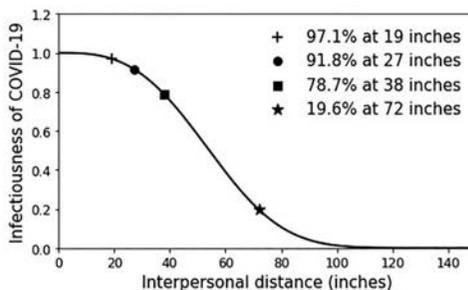


Figure 1. Infectiousness of COVID-19 as a function of interpersonal distance.

Centers for Disease Control and Prevention (CDC), given that peak exhalation (sneezing or coughing) speeds can reach up to 33–100 feet per second (10–30 m/s), the possible presence of a high-momentum cloud could carry the droplets with the virus as far as 23–27 feet or 7–8 meters [71].

The other rules in our ABM simulations include:

- According to the available preliminary data [5], the median time from symptom onset to clinical recovery for the mild cases was approximately 2 weeks and was 3–6 weeks for patients with severe or critical conditions. Among patients who died, the time from symptom onset to outcome ranged from 2–8 weeks. The death rate was reported as 2.3% in all confirmed cases [64]. Therefore, in our ABM simulations, the patients with mild conditions recover and become uninfected after having been sick for 2 weeks. On the other hand, it takes 2–8 weeks for critical-condition patients to either recover or die. The death probability is set as 12.05% among the patients in a critical condition.
- A recovered person is immune to the SARS-CoV-2 and will not get infected again.

3.3 Control Measures on COVID-19 Outbreaks

In this paper, we study the three control measures on COVID-19 outbreaks described below.

- **Social distancing:** Also called physical distancing, this maintains enough space between people and avoids mass gatherings. The CDC recommends a social distance of 6 feet (72 inches, or 2 meters), which almost doubles the normal social distance (38 inches) for US Americans. We assess various social distances in this paper and assume that the intimate and personal distances will be correspondingly adjusted as well.
- **Community quarantine:** Community quarantine, or (partial or total) lockdown, is a control measure enacted by closing non-essential businesses, limiting public transportation, issuing stay-at-home orders, replacing school with virtual instruction and so on. Generally, community quarantine will reduce people's mobility, which will in turn slow down the virus transmission. We use a scale of 0–100% to quantitatively estimate the reduction of people's mobility in the community, which can be used to represent various levels of community quarantine. A general community quarantine (GCQ), which includes school closings, dine-in restaurant closings and large-event cancellations, is assumed to be at the level of 30–60%. An enhanced community quarantine (ECQ), when non-essential businesses are closed and public transportation is limited, is considered to be at the level of 60–80%. If a stay-at-home order is issued, there is an extremely enhanced community quarantine (EECQ), which can be up to 100% community lockdown.

- **Self-quarantine:** Self-quarantining people with suspected COVID-19 disease can reduce the chances of uninfected people being exposed to the disease. The degree of self-quarantine depends mainly on law enforcement and public consensus. Both are usually low at the early stage of an epidemic due to poor understanding of COVID-19 infectiousness. We scale the degree of self-quarantine in a range of 0–100%, which approximates the population at risk in the community participating in self-quarantine. In our model, self-quarantine includes self-isolation, in which an infected person with a mild condition is required to be isolated from uninfected people after symptoms develop and COVID-19 disease has been confirmed.

4. Simulations and Discussions

4.1 COVID-19 Outbreaks

We first investigate the COVID-19 outbreaks without any control measures. In our studies, the “world” is discretized as 160 000 patches unless otherwise stated. Various population sizes are considered to study outbreaks in communities with different population densities: 320 000, 160 000 and 80 000, representing urban communities, suburban communities and rural communities/small towns, respectively. Multiple simulations are conducted for each community type. Figure 2 shows the mean numbers (% of the whole population) with 95% confidence interval (CI) of newly infected cases, current infected cases, and cumulative infected cases after one infected case is introduced. It is obvious that COVID-19 spreads slowest in rural communities/small towns and fastest in urban communities. However, without any control measures, all people in urban and suburban communities will be infected eventually. It should be noted that for rural communities with a very low population density, there is a chance that a COVID-19 outbreak will not occur.

The newly infected cases in the population at risk can also be used to calculate the daily attack rate and then the reproduction number. The newly infected cases in the population at risk can also be used to calculate the daily attack rate and then the reproduction number [72]. It is observed that the mean daily reproduction number maintains around a constant during the outbreak: 2.16, 1.74 and 1.51 when the COVID-19 outbreak occurs in urban, suburban and rural communities, respectively. The calculated reproduction number in urban communities, 2.16, agrees with those in Table 1, most of which were estimated based on the data collected in big cities in the early stage of outbreaks. This supports the rules we presented in the previous section.

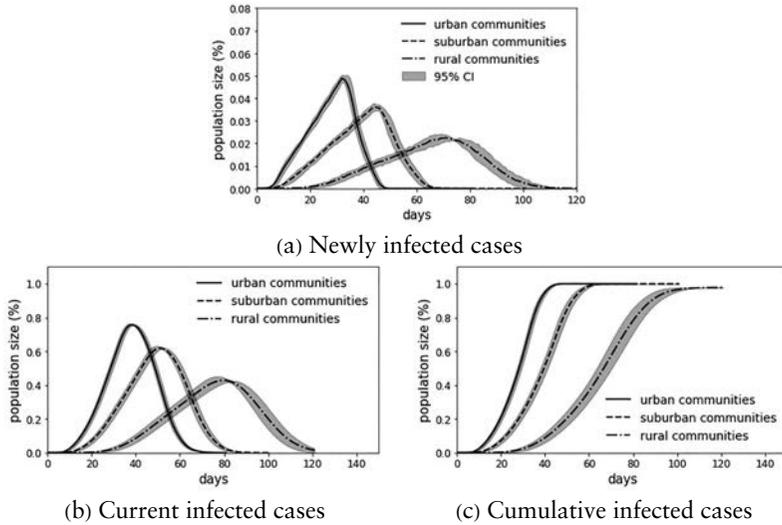


Figure 2. Evolution of the numbers of infected cases in the percentage of the whole population.

4.2 Individual Control Measures

To assess various control measures, we individually study their effects on COVID-19 outbreak control in urban communities only, which have a total of 320 000 people. We mainly consider the scenario in which the control measure is implemented 10 days after the first infected case is introduced. By then, an average of 5000 people have been infected. In our studies, outbreak control [27] is defined as no new infected cases between 12 and 16 weeks after the initial case, with fewer than 10 000 cumulative confirmed cases.

We first consider social distancing with three different distances: 38 inches, which is the normal social distance; 72 inches, recommended by the CDC; and 96 inches as an enhanced social-distancing case. When the social distance elongates, the intimate and personal distances are adjusted correspondingly. Figure 3 shows that social distancing slows down the outbreaks, that is, “flattens the curve.” The reproduction number is reduced from 2.16 to 1.19 and 1.06 when the social distance is elongated to 72 and 96 inches, respectively, during the outbreaks. However, even in an enhanced social distancing case, 90% of the population is infected eventually, and the outbreaks cannot be controlled.

To study the impact of community quarantine on COVID-19 spreading, various levels of quarantine are considered: GCQ (50%), ECQ (70%) and EECQ (90%). Social distancing is not implemented, so that a normal social distance of 38 inches is maintained. Community quarantine reduces people’s mobility so that the COVID-19

outbreaks can be slowed down, as shown in Figure 4. Furthermore, EECQ can dramatically reduce the increment rate of newly infected cases. However, only in an ideal case, when a total community lockdown (100%) is implemented 10 days after an initial infected case is introduced, the number of newly infected cases will be dropped to zero in a week and the COVID-19 outbreaks are controlled.

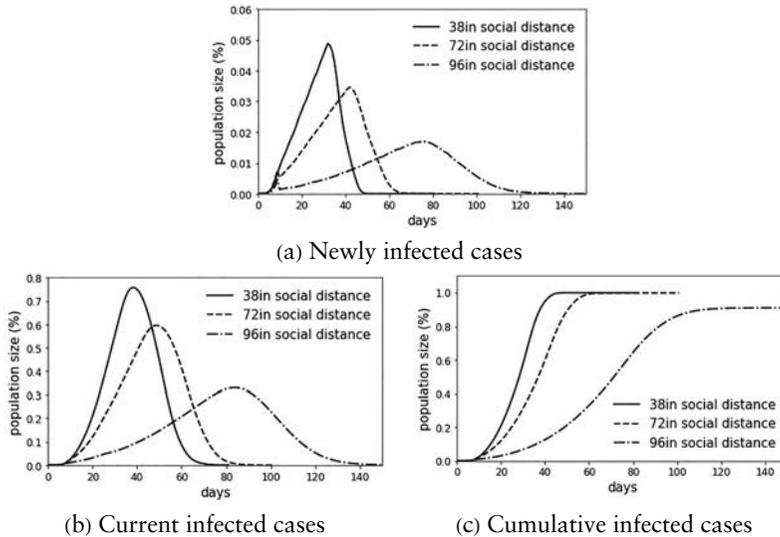


Figure 3. Evolution of the mean numbers of infected cases when social distancing with various distances is implemented 10 days after the first infected case is introduced.

When assessing the control measure of self-quarantine, the normal social distance (38 inches) is maintained, and there is no implementation of community quarantine. Various degrees of self-quarantine are considered: 50%, 70% and 90%, representing how many people in the population at risk will separate themselves from the others, even if they have not developed symptoms or been tested as confirmed cases. It can be seen in Figure 5 that the more people participate in self-quarantine, the more slowly the numbers of infected cases increase. To possibly control the outbreaks, at least 97% of the population at risk should be quarantined if no other control measures are implemented.

The above studies indicate that although it is very difficult to control COVID-19 outbreaks with a single control measure, self-quarantine is more efficient than social distancing and community quarantine. Also, implementing any control measure on its own can slow down the outbreak and allow time for advanced strategies (e.g., a combination of different control measures) and/or vaccine inventions.

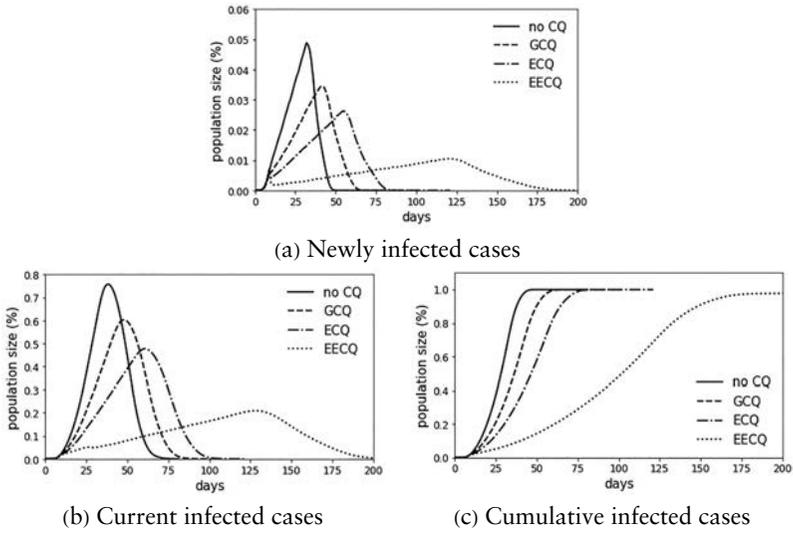


Figure 4. Evolution of the mean numbers of infected cases when community quarantine (CQ) with various levels is implemented 10 days after the first infected case is introduced.

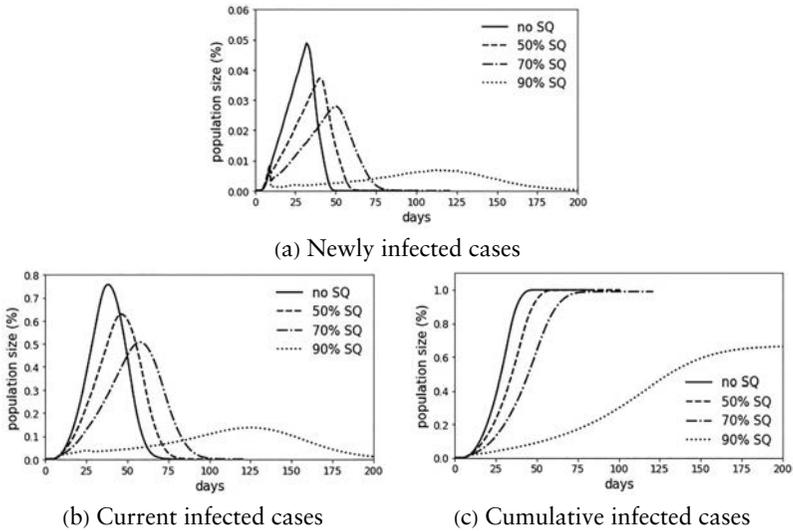


Figure 5. Evolution of the mean numbers of infected cases when self-quarantine (SQ) of various degrees is implemented 10 days after the first infected case is introduced.

4.3 Combined Control Measures

It would be more efficient to control the disease outbreaks if a few different control measures were implemented concurrently. Here we study the effects of combined self-quarantine and community quarantine on the spread of COVID-19 while the CDC-recommended social distance of 72 inches is maintained. As before, we consider the scenario in which the control measures take place 10 days after one infected case is introduced. The controllability of COVID-19 outbreaks is defined as in the previous section as well. Intensive ABM simulations are conducted to generate a set of 6760 data samples. The input variables, that is, features, are the self-quarantine level and the community quarantine level, while the output target is either 0 or 1, representing uncontrolled outbreaks and controlled outbreaks, respectively.

A fully connected artificial neural network (ANN) [73], consisting of an input layer, an output layer and hidden layers, is employed as a machine learning model to classify the controllability of COVID-19 outbreaks based on the collected data. The training of this ANN is iterative between the feedforward process and the backpropagation process. During the feedforward process, every neuron in the hidden layers transforms the outputs from the previous layer into a different representation, which is taken as the input to the next layer. There are two steps in the transformation. First, the data from the previous layer is projected into the neuron via the weights. Then, the projected data is transformed via the activation function. The backpropagation process updates the weight to optimize the neural network model.

In our ANN model, the “relu” activation function is employed in the hidden layers, including three layers with 16, 32 and 32 neurons, respectively. The “softmax” activation function is utilized in the output layer to predict the output target. Tenfold cross-validation is conducted, and the test score (i.e., the accuracy of the test set) is 90.7%. Note that multiple simulations are conducted at a given pair of self-quarantine and community quarantine levels. The data samples with the same input may have different output targets (either “0” or “1”) due to the stochastic characteristics of ABM. Therefore, the accuracy cannot reach 100%. Indeed, we use the well-trained ANN to estimate the outbreak control probability instead of deterministically predicting controlled or uncontrolled outbreaks. Figure 6 shows the probability map of outbreak controllability generated by the ANN predictive model in the self-quarantine and community quarantine space. The white area indicates the outbreak controllability with 0% probability, that is, the uncontrolled outbreaks, while the black area indicates the controllability with 100% probability, that is, the controlled outbreaks. The gray area at the interface of two domains represents the change of the controllability probability.

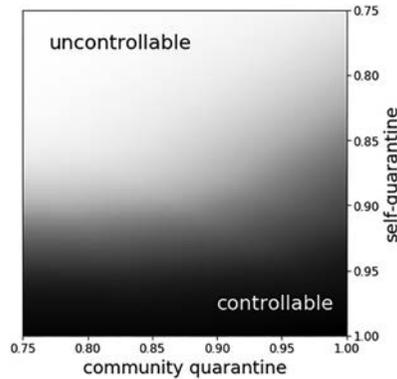


Figure 6. Classification of controllable/uncontrollable outbreaks in the self-quarantine and community quarantine space.

Figure 6 also illustrates that self-quarantine has a more significant impact on outbreak control than community quarantine. This agrees with the conclusion from the studies of individual control measures in the previous section. The outbreaks can be controlled via a total lockdown, that is, a 100% community quarantine, no matter what the self-quarantine level is. However, if the community quarantine level cannot reach 100%, a high-level self-quarantine is required to control the COVID-19 outbreak. For example, a 95% EECQ has no chance to control the outbreak as long as the self-quarantine level is under 85%. In contrast, it is possible that a high-level self-quarantine (90%), combined with an ECQ (60–80%), will control the COVID-19 outbreaks. Considering the impact of control measures on economics, a combination of high-level self-quarantine and general community quarantine, assisted with CDC-recommended social distance, would be a good strategy for COVID-19 outbreak control.

4.4 COVID-19 Outbreak in New York City

We employ the developed ABM to simulate the COVID-19 outbreak in New York City (NYC) starting on March 2, 2020, when the first infected case was reported. Our agent-based model has 250 000 patches and 500 000 agents to minimize the size effect. It is assumed that at the beginning of the COVID-19 outbreak, only 10% or less of the population at risk is willing to be self-quarantined due to a lack of public consensus. Also, the community quarantine was unofficially at a low level (10%) until March 22, when the PAUSE plan (i.e., ECQ) was issued by the New York state government. The normal social distance of 38 inches was maintained before March 22. In our ABM simulations, after March 22, it takes 40 days to improve the percentage of the self-quarantined population to 70% ($\pm 10\%$). This is

mainly because of the gradually increasing public awareness and testing capability. At the same time, due to public practices and law enforcement, the social distance moves from 38 inches to 72 inches (i.e., 6 feet), and the community quarantine level improves from 50% to 80% ($\pm 10\%$).

The evolution of the number of daily new cases with 95% CI from ABM simulations is shown in Figure 7, compared to the reported data, which was assembled by the NYC Department of Health and Mental Hygiene (DOHMH) Incident Command System for COVID-19 Response (Surveillance and Epidemiology Branch in collaboration with Public Information Office Branch). The singular point at day 20 in the ABM simulation result is due to the implementation of the PAUSE plan on March 22. It can be seen that the reported data is lower than the prediction but that the trends agree with each other. The main reasons include insufficient testing capability and testing delays, so that the infected cases could not be totally and promptly confirmed.

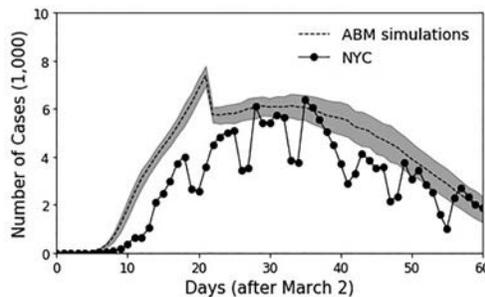


Figure 7. The prediction of daily new cases in NYC via ABM simulations, compared to the reported data.

5. Conclusions and Future Work

In this paper, we presented a study of COVID-19 spreading in the human population by using agent-based modeling (ABM). In ABM simulations, the interactions between the agents (i.e., the people) and the virus transmission followed the rules developed in this research. Based on previous sociology studies on friendship status, we derived the probability of people's interactions at different friendship statuses so that interpersonal distances could be estimated. Also, we proposed the COVID-19 infectiousness as a function of interpersonal distance, including intimate, personal and social distances, according to recent data analyses of the COVID-19 epidemic. The basic reproduction number of COVID-19 outbreaks in urban areas without control

measures was calculated as 2.16 from our ABM simulations. This agrees with many other data-driven studies and susceptible-exposed-infectious-recovered (SEIR) modeling of the COVID-19 outbreaks in big cities. In addition, our case study of the COVID-19 outbreak in New York City provided results that agreed with the real trend based on the reported data.

The control measures considered in this paper include social distancing, self-quarantine and community quarantine. To quantitatively assess their impact on outbreak control, self-quarantine was scaled to represent how much of the population at risk was quarantined, while community quarantine was scaled to represent various community lockdown levels. Our ABM simulations indicated that any of these control measures can slow down the COVID-19 outbreaks to allow time for advanced control strategies and/or vaccine inventions; however, any individual control measure has difficulty controlling the outbreaks in urban communities. We also conducted intensive simulations at various self-quarantine and community quarantine levels assuming the Centers for Disease Control and Prevention (CDC)-recommended social distance of 72 inches. The collected data was used to train an artificial neural network (ANN) model to predict outbreak controllability. Based on the simulation results, it can be concluded that self-quarantine is the most efficient control measure for COVID-19 outbreak control. Furthermore, self-quarantine has much less impact on economics than community quarantine. However, the efficiency of self-quarantine largely depends on testing capability, public consensus, testing delay, quarantine delay, contact tracing and others. A combination of high-level self-quarantine and general community quarantine could be a good strategy, but further research may be needed to assess the impact of community quarantine on economics.

The developed ABM framework can be easily extended to considering more outbreak factors and control measures, including patients' age/gender, COVID-19 testing capability, contact tracing/isolation, self-protection and others. Delays between symptom onset and testing and/or between onset and isolation can be considered as well. Although we focused on studying COVID-19 spreading in urban communities, the developed ABM can be utilized to study outbreaks in suburban and rural communities as well. Expertise in sociology and virology is needed in future studies to improve our ABM by developing more accurate rules for people's interactions and virus infectiousness. In addition to data-driven or ordinary differential equation-based models, ABM simulations provide an alternative approach to potentially predicting the COVID-19 epidemic trend, quantitatively assessing the current control measures and rationally recommending future control strategies.

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