Impact of different nucleic acid testing scenarios on COVID-19 transmission

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ABSTRACT

In the past three years, waves of COVID-19 infections have emerged one after another, and may enter a small-scale wave-like recurrent epidemic pattern in the future. When COVID-19 infections occur in small-scale, how to efficiently detect and prevent the disease has become the main problem. In this study, based on the characteristics of the Omicron variant and China's pandemic prevention and control strategies, the following three nucleic acid testing scenarios were simulated: scenario 1 (baseline scenario) included conducting nucleic acid testing at administrative region; scenario 2 included conducting nucleic acid testing at the community; and scenario 3 included conducting nucleic acid testing at the health facility closest to households. The model calibration showed that the baseline scenario was consistent with the actual transmission scenario of the disease. The simulation results revealed that compared with scenario 1, the cumulative cases in scenarios 2 and 3 were reduced by 9.52 % and 46.83 %, respectively. Compared with scenario 2, the cumulative cases in scenario 3 were reduced by 41.23 %. Thus, adopting nucleic acid testing measures at the household level can effectively limit the spread of COVID-19 and should be given a priority when local emergency occurs in the future.

1. Introduction

Since the outbreak of the novel coronavirus (COVID-19) at the end of 2019, the total number of COVID-19 infections worldwide has exceeded 670 million, with a mortality count of over 6.84 million [1]. Moreover, COVID-19 spread to more than 200 countries and caused enormous losses to humanity, economy, and society [1]. In 2022, new rounds of COVID-19 outbreaks occurred in several cities in China, and each city opted for different non-pharmaceutical interventions to limit the spread and infection of COVID-19 [2–6]. Among them, nucleic acid testing was one of the main methods to detect COVID-19 infections. Nucleic acid testing can quickly and accurately detect infected individuals, allowing prompt dispatch to designated hospitals for isolation and allowing the development of corresponding prevention. It additionally helps establish control measures to identify the virus transmission chain, achieve control of the large-scale spread and infection of the pandemic, and minimize losses in all aspects [7]. Although China's current pandemic prevention policies have gradually been completely liberalized, with COVID-19 being classified as an "under Category B management,"

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new cases of COVID-19 occur daily [8], and a recent study also suggests that the COVID-19 would not enter a seasonal pattern of transmission like influenza; instead, it may enter a mini-waves-like recurrent pandemic pattern [9]. It is shown that the number of COVID19 infections has risen again in some regions recently, and new COVID-19 variants (especially the XBB.1.16 spectrum) are replacing older strains in some countries, pushing up the number of cases [10]. Therefore, the risk of localized outbreaks still exists, and implementation of nucleic acid testing, as one of the most effective, economical, and convenient control and preventative measures needs further assessment to deal with potential local emergencies.

Previous studies have primarily examined the role and effectiveness of nucleic acid testing at the administrative-region level. They have focused on factors such as testing frequency, cumulative testing number, and the impact of nucleic acid testing in cities of varying population sizes [7,11–16]. However, there has been limited assessment of nucleic acid testing at the community or household level. The latest "COVID-19 Infection Prevention and Control Program (10th Edition)," issued by the Chinese Center for Disease Control and Prevention (https://www.chinacdc.cn), has introduced an optimized testing strategy. This strategy explicitly discontinues the practice of conducting nucleic acid screening for entire administrative areas and instead emphasizes conducting nucleic acid testing for individuals within communities who are at high risk of severe illness [17]. Hence, there is a compelling need to implement nucleic acid testing on a community and household basis. In this study, we construct an agent-based model to assess the effect of nucleic acid testing measures on the COVID-19 transmission at three different levels: administrative unit, community, and household. We then compare the accumulated number of infected individuals under different scenarios. In closing, we discuss the potential implications of our findings for COVID-19 control.

2. Methods

2.1. Synthetic population

Based on the population structure of Daxing District, Beijing, we established a matched synthetic population dataset of 1.42 million individuals using standardized methods [16]. According to the age group of the population in the region, the synthetic population was classified as students (5–22 years), workers (22–60 years), and others (<5 years and >60 years) based on their occupation. Each individual in the synthetic population was allocated a unique individual ID, social role, and household ID.

The population was randomly assigned to different residential areas according to the distribution of residential areas and population. Based on the age distribution in the model, the activity locations of students during weekdays were mainly concentrated in schools, while those of workers were mainly concentrated in their homes and workplaces. The activity locations of all other individuals
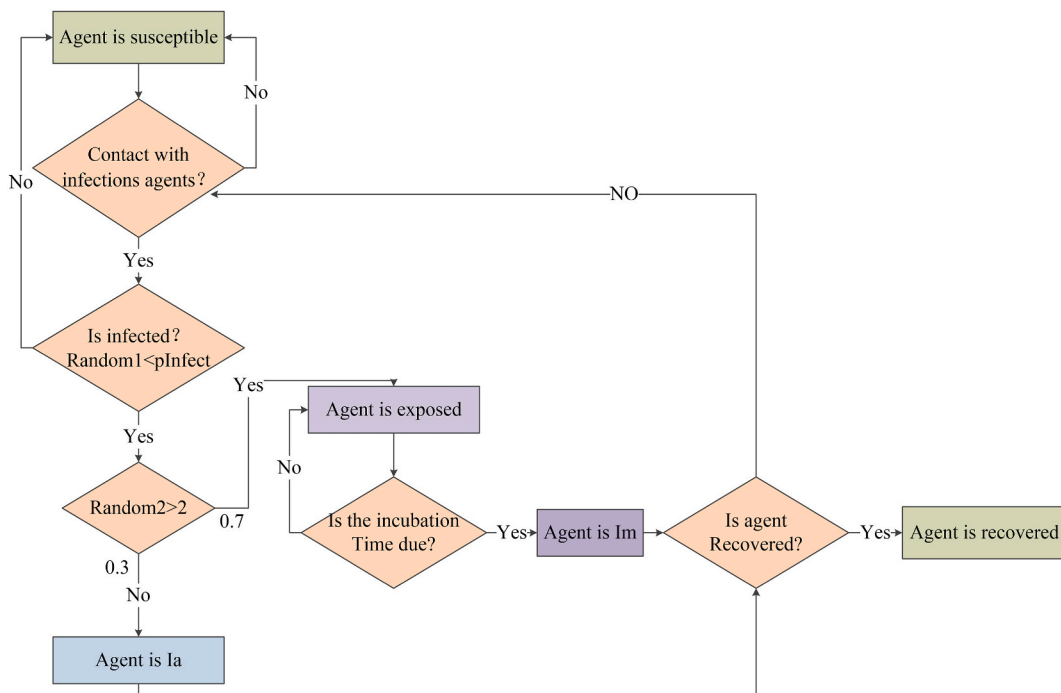
Fig. 1. Individual interaction and state changes in WS small-world networks
pInfect is the infection rate of the disease. Random1 is a random number set in the model to indicate the probability of effective contact between susceptible individuals (S) and infectious individuals (E, I_a, and I_m). Random2 is another random number set in the model to indicate the probability of susceptible individuals (S) being transformed into exposed individuals (E) after being infected. Asymptomatic individuals (I_a), mildly symptomatic individuals (I_m).

were mainly concentrated in homes, entertainment venues, and consumption venues. During weekends, the activity locations of individuals in all groups were mainly concentrated in entertainment and consumption venues. Venues were classified into four interactive venues, each involving various types of locations. According to the distribution of household sizes in Daxing District, five types of households were established: those with one person (89,081 households), two people (98,615 households), three people (64,651 households), four people (26,814 households), and five people (18,770 households).

2.2. COVID-19 transmission model

We developed an agent-based model to assess the impact of various nucleic acid testing measures on the transmission of COVID-19. This model is based on the Susceptible-Exposed-Infectious-Recovered (SEIR) compartmental model, which categorizes individuals into different groups: susceptible (potentially infected after contact with COVID-19 patients), exposed (infected but asymptomatic for a period, later developing mild symptoms), infectious (actively carrying the virus), and recovered (having recovered from infection and do not participate in subsequent infections). Among the infected individuals, two subgroups were considered: asymptomatic (I_a, infected and infectious but always asymptomatic) and mildly symptomatic (I_m, showing symptoms and infectious, converted from exposed individuals). The model's epidemiological classification is detailed in Fig. 1. In this small-world network model [18], susceptible individuals and those with infectivity (exposed, asymptomatic, and mildly symptomatic) were assessed for temporal and spatial intersections, and effective contacts were determined when susceptible individuals had both temporal and spatial intersections with individuals carrying the virus [19]. The model considered five infection locations: households, schools, workplaces, consumption venues, and entertainment venues. The average incubation period for the Omicron variant in the model was 3.1 days [20].

In the model, at each time point (8 h), susceptible and infected individuals were allowed to come into contact with each other in four types of environments (school, work, leisure, and home) to allow for COVID-19 transmission. The infection process was allowed to occur in different WS small-world network environments [18]. The interactions between individuals and changes in the individual status in the WS small-world network are shown in Fig. 1. First, it was determined whether there exists a contact between susceptible individuals (S) and infectious individuals (E, I_a, I_m) and then whether the contact is effective. If the randomly assigned random number (Random1) is less than pInfect, the contact is assumed to be effective, and if random number(Random2) is greater than the given probability, the susceptible individual becomes an exposed individual (E), conversely, it is asymptomatic individual(I_a). This study assumed that exposed individuals are infectious [21]. After the incubation period, exposed individuals become mildly symptomatic (I_m). Finally, the study determined whether all infectious individuals had recovered. After recovery, such individuals were assumed to have a certain level of immunity and were thus removed from the model. Otherwise, the model continued to loop until infected individuals recovered.

The simulated nucleic acid testing scenarios were as follows: (1) administrative region (baseline scenario): when a new case is detected, the entire administrative region (Daxing District) undergoes nucleic acid testing for 3 consecutive days; (2) community: after detecting a new case, the community undergoes nucleic acid testing for 3 consecutive days; (3) household: once a new case is detected, households in the community undergo nucleic acid testing for 3 consecutive days at the nearest health facility. For household testing, one test tube is provided per household to reduce crowd gathering and the risk of COVID-19 transmission during testing. We conducted 1000 random simulations for each scenario using the calibrated model.

2.3. Model initialization

Two mildly symptomatic individuals and five asymptomatic individuals were assumed at the initial stage of our model, according to the released data from the Beijing Municipal Health Commission (http://wjw.beijing.gov.cn/). The model was run for 25 days (November 3 to November 27, 2022), and the parameters involved in the model are shown in Table 1.

2.4. Model calibration

The model was calibrated using the daily cumulative confirmed cases from the official website of the Beijing Municipal Health Commission(http://wjw.beijing.gov.cn) in 2022 [22]. In the model, the probability of infection after effective contact with susceptible and infected individuals was assumed to be similar in all five locations. Sensitivity analysis was conducted on both the infection rate (pInfect) and the daily travel ratio (DTratio). The range of pInfect sensitivity analysis values was set at 0.5–0.6 with a step size of 0.05

Table 1
Mean values and sources of the model parameters.

Parameters	Description	Value	Reference
pInfect	Infection rate of effective contact between susceptible and infected persons	0.536	Assumed
incubation period	Time from infection to symptoms of susceptible population	3.1day	DEL AGUILA-MEJIA J [20]
number	Number of exposed individuals during model initialization	5	Beijing local treasure [29]
DTratio	Proportion of migrant population per day	0.004	Derived [24]
interval	Interval between each iteration of the model	8h	Fixed
ticks	Total days of model simulation	25day	Beijing local treasure [28]
nucleic_acid	Nucleic acid detection rate	95 %	China Net [30]
Ia_trans	The proportion of infected individuals who transition to asymptomatic status.	0.3	Oran [31]

[21,23], and the range of DTratio sensitivity analysis values was set at 0.001–0.005 with a step size of 0.001 [24]. Based on root mean square error (RMSE) values, the optimal range of pInfect was determined as 0.53–0.54, and further analysis was conducted with a step size of 0.001 for each combination value. Finally, 500 random simulations were conducted for scenario1(baseline) under each combination value.

2.4.1. Sensitivity analysis of parameters

In this study, two epidemiological parameters were assumed: the virus infection rate (pInfect) and the daily population travel ratio (DTratio). Three sensitivity analyses were conducted on these two parameters, as previously described [25].

The range of parameter combinations in the first sensitivity analysis for pInfect was 0.50–0.60 with a step size of 0.05 and for the DTratio was 0.001–0.005, with a step size of 0.001. The simulation and RMSE results of this combination are shown in Fig. 2(a–f). The results of the first sensitivity analysis showed that when the value of pInfect was between 0.50 and 0.55, the RMSE of the parameter combination was relatively small.

In the second sensitivity analysis, the range of DTratio remained unchanged, but pInfect varied from 0.50 to 0.55 with a step size of 0.01. The RMSE of the second sensitivity analysis are shown in Fig. 3. The results indicate that RMSE is minimized when pInfect is between 0.53 and 0.54.

The third sensitivity analysis was conducted with the same range of DTratio values and pInfect values ranging from 0.53 to 0.54, with a step size of 0.001. The simulation results of the best pInfect values corresponding to each DTratio value are shown in Fig. 4(a–e), and the RMSE values for all combinations are shown in Fig. 4(f). The results of the final sensitivity analysis show that when the DTratio is 0.004 and pInfect is 0.536, the RMSE of the parameter combination is the lowest, and the model's simulated daily cumulative confirmed cases are most consistent with the observed values.

2.4.2. Basic reproduction number

The basic reproduction number (R_0) is an important indicator in epidemiological studies for measuring virus infectivity. It represents the average number of people without immunity that a positive individual can infect in a population under no external interference [26]. A higher R_0 indicates that the virus can more easily spread and is more difficult to control, while an $R_0 < 1$ indicates lower infectivity of the virus that will gradually disappear over time. To verify the effectiveness of the model, we calculated the R_0 of the proposed model using the relationship between the incubation period, daily cumulative confirmed cases, and recovery period, and compared the calculated results with the observed results of known cases [24]. R_0 was calculated using the following formula:

$$R_0 = (1 + r\overline{T_L})(1 + r\overline{T_I}) \tag{1}$$

$$\overline{T_I} = \overline{SI} - \overline{T_L} \tag{2}$$

Where, in equation (1), r represents the exponential growth rate, which is calculated by simulating daily confirmed cases in the model.
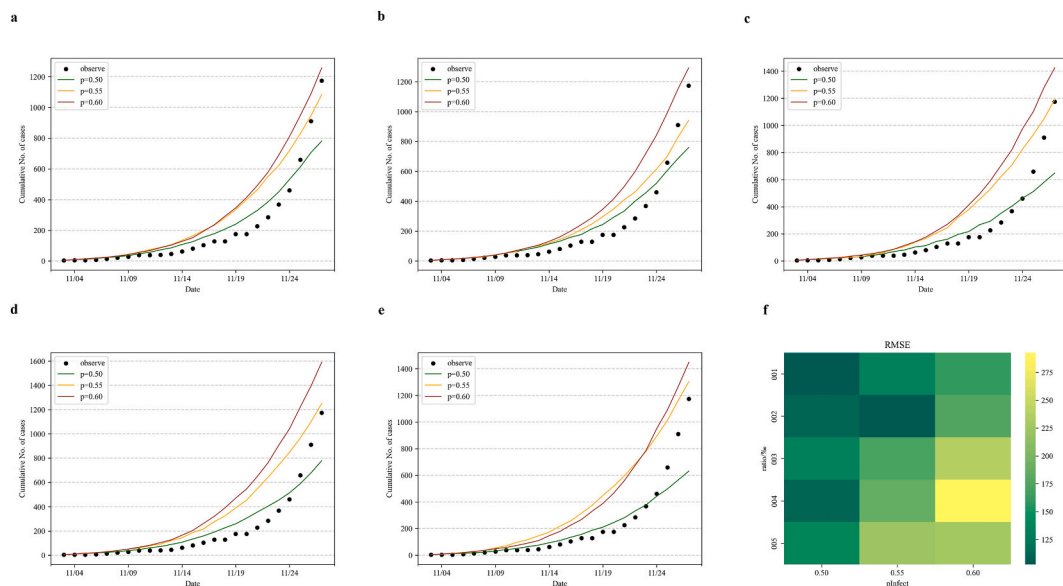

Fig. 2. Sensitivity analysis and RMSE results.
figures (a–e) correspond to the simulation results of daily cumulative confirmed cases for different values of pInfect and DTratio ranging from 0.001 to 0.005. Figure f shows the root mean square errors (RMSE) for the combinations of the two epidemiological parameters. The x-axis represents pInfect, the y-axis represents DTratio, and the color gradient from green to yellow represents increasing RMSE values.
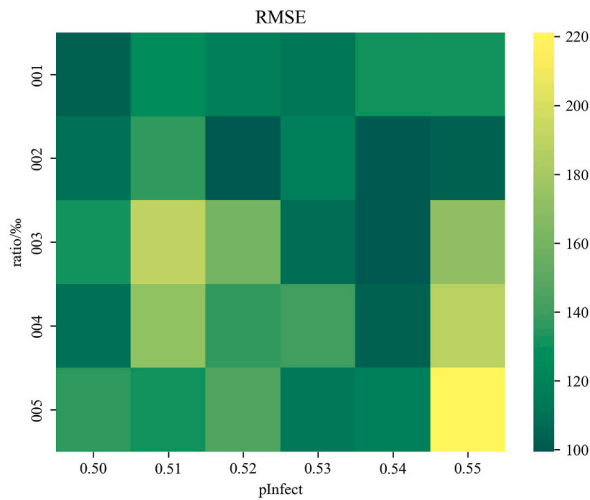
Fig. 3. RMSE results under different parameter combinations
The x-axis represents pInfect with a range of 0.50–0.55 and a step size of 0.01. The y-axis represents a DTratio with a range of 0.001–0.005 and a step size of 0.001. The color gradient from green to yellow indicates increasing RMSE values. (For interpretation of the references to color in this figure legend, the reader is referred to the Web version of this article.)
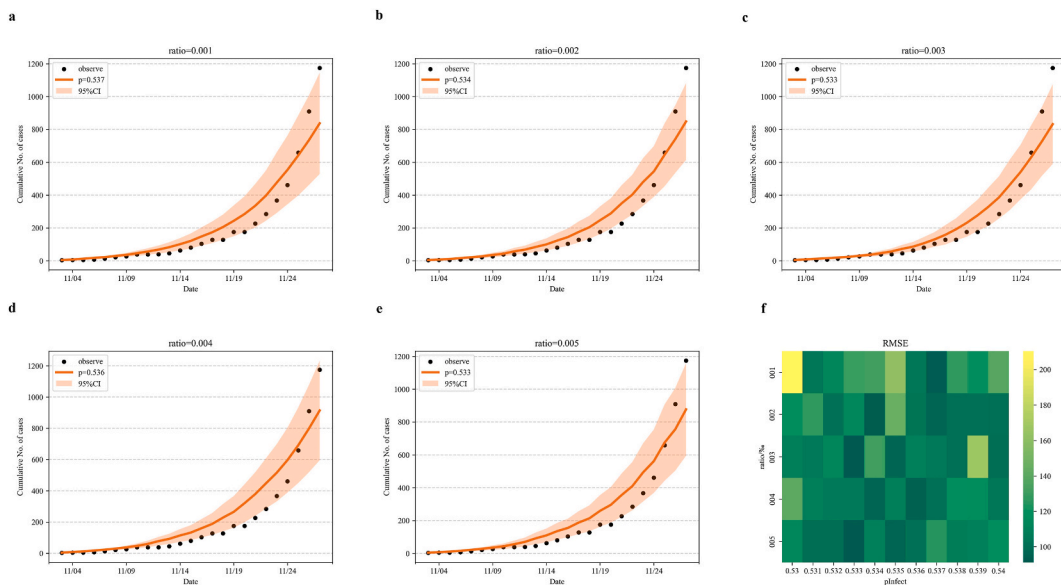
Fig. 4. The optimal simulation results and corresponding RMSE values under different DTratio
The figures (a–e) correspond to the simulation results of daily cumulative confirmed cases using a DTratio of 0.001–0.005 and pInfect values that minimize RMSE. Figure (f) shows the RMSE values for all combinations of the two epidemiological parameters, with pInfect values of 0.53–0.54 and DTratio values of 0.001–0.005, with a step size of 0.001. The color gradient from green to yellow indicates increasing RMSE values. (For interpretation of the references to color in this figure legend, the reader is referred to the Web version of this article.)

$\overline{T_L}$ represents the average latent period of the Omicron variant in infected individuals, with the subscript L indicating latent. $\overline{T_I}$ represents the average recovery period of the Omicron variant in infected individuals, with the subscript I indicating infectious. In equation (2), $\overline{SI}$ represents the average infectious period of the Omicron variant.

The optimum combination of pInfect and DTratio was obtained as (0.536, 0.004) according to sensitivity analyses. Further validation of the model was achieved by calculating the basic reproduction number (R_0). The final R_0 of our model was determined to be 6.4, while the R_0 calculated using the actual daily cumulative confirmed cases from the Beijing Municipal Health Commission was 7.1 [27]. All the model simulation and output results were conducted using Python (version 3.9.7).

3. Results

3.1. Model fitting

The results of simulations performed under Scenario 1, with the optimal parameters of pInfect = 0.536 and DTratio = 0.004, are shown in Fig. 5, which illustrates a reasonably good model fit. The curve for Scenario 1 shows a continuously increasing trend throughout the assessment period. The daily cumulative number of infected people continued to increase with time, and the magnitude of the increase gradually became larger.

3.2. Impact of community nucleic acid testing

Model simulations under Scenario 2 are shown in Fig. 6. Compared with the results in Scenario 1, the cumulative number of daily confirmed cases increased at a relatively quicker rate in the early stage but gradually slowed down, and the magnitude of the increase became smaller over time. On November 27, the cumulative number of confirmed cases was nearly 100 cases less than those in Scenario 1. Compared with Scenario 1, Scenario 2 was associated with reduced total cumulative confirmed cases by 9.52 %. Compared with Scenario 1 and Scenario 3, on the 5th day, the cumulative confirmed cases in Scenario 2 were the highest (Table 2), this trend continued until the 15th day, however, on the 25th day, the cumulative number of confirmed cases in Scenario 2 was located between Scenarios 1 and Scenario 3.

3.3. Impact of household nucleic acid testing

Model simulations under Scenario 3 were shown in Fig. 6. Compared with Scenario 1, the overall number of daily cumulative confirmed cases was lower, the daily growth rate of cumulative confirmed cases was lower, and the final cumulative confirmed cases were only half of those in Scenario 1. Compared with Scenario 1 and Scenario 2, Scenario 3 were associated with reduced total cumulative confirmed cases (by 46.83 % and 41.23 %, respectively). Compared with Scenario 1 and Scenario 2, on the 5th day, the cumulative confirmed cases in Scenario 3 were the lowest (Table 2), this trend continued until the 15th day, however, on the 25th day, the cumulative number of confirmed cases in Scenario 3 was still the lowest.

4. Discussion

To our knowledge, no study has yet evaluated nucleic acid testing at different levels. In this study, we assessed the efficacy of nucleic acid testing measures conducted at the community, and household level, and compared to that conducted at administrative region. In addition, our study aimed to reduce the spread of infections caused by large-scale population movements during extensive nucleic acid testing, achieve rapid interruption of the transmission chain, and reduce the number of infections by focusing on nucleic acid testing at the community and household levels.

Over time, the COVID-19 strain underwent several mutations [23]; as of 2022, the currently prevalent Omicron variant is highly infectious, with an average basic reproduction number R_0 of 9.5 (5.5–24) [28]. Specifically, large-scale nucleic acid testing in the entire administrative region may cause rapid spread of the virus owing to inadequate personal protective measures and/or failure to wear masks during testing. Such large-scale nucleic acid testing not only increases the risk of viral transmission but also may cause
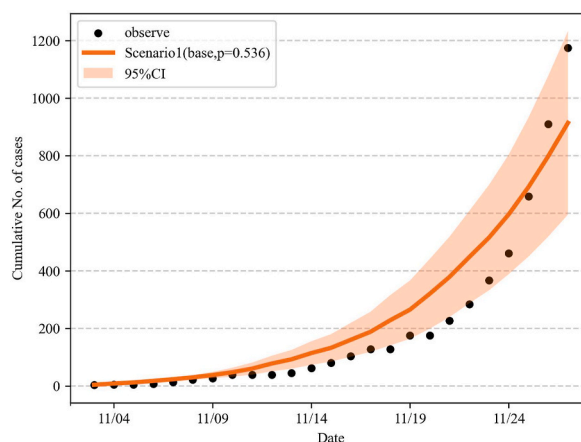
Fig. 5. The daily cumulative confirmed cases determined using routine nucleic acid testing
The black dots represent the actual observed daily cumulative confirmed cases; the orange solid line represents the simulated daily cumulative confirmed cases; the orange shadow represents the 95 % confidence interval of the simulated data. (For interpretation of the references to color in this figure legend, the reader is referred to the Web version of this article.)
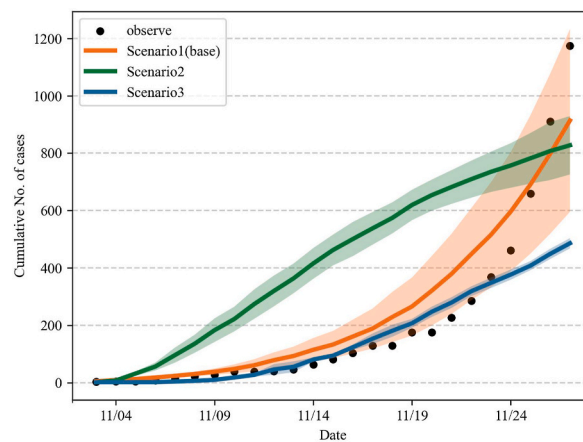
Fig. 6. The daily cumulative confirmed cases of COVID-19 under three scenarios of nucleic acid testing
The black dots represent the actual observed daily cumulative confirmed cases; the solid lines represent the cumulative number of simulated daily confirmed cases; the shaded areas represent the 95 % confidence intervals of the simulated data.

Table 2
Cumulative number of confirmed cases in each stage under three scenarios.

Day	Cumulative No. of cases		
	Scenario1(base)	Scenario2	Scenario3
5 d	24	96	4
10 d	79	320	46
15 d	189	538	153
20 d	448	709	319
25 d	914	827	486

aggregated outbreaks of COVID-19, requiring more social and medical resources [12]. In this study, compared with scenario1, scenario2 significantly reduced the cumulative number of confirmed cases. When the disease transmission occurred under the scenario2, the daily cumulative case number increased gradually at early stage (Table 2), although the growth rate of daily confirmed cases in scenario 2 was higher at the early stage, it gradually decreased at the later stage, as shown in Fig. 6. This is because conducting nucleic acid testing within the community with confirmed cases leads to a cluster of infections in the community. In addition, the missing detection of infected individuals during nucleic acid testing can facilitate transmission in multiple communities, because some of the asymptomatic patients who are not detected would still go out (e.g., purchasing food) and transmit the disease. As infected individuals were moved to a specific hospital for monitoring and isolation, the public's awareness of protection is continuously enhanced, leading to a gradual decrease in confirmed cases at the later stage. Compared with scenarios1 and 2, scenario3 showed an evident decrease in the number of confirmed cases at the early stage and the total cumulative number of confirmed cases. This finding can be explained by the fact that nucleic acid testing within the health facility closest to households would isolate the potential infected individuals from the public, furthermore, most initially diagnosed cases were likely asymptomatic individuals at the early stage, because when they are asymptomatic patients, there will be a certain degree of missed detection during the early testing process, and it will be detected again in multiple rounds of nucleic acid testing afterwards. These asymptomatic individuals then infected household members, resulting in clustered infections within households, which was illustrated by the gradual increase of the cumulative number of confirmed cases in the later period; however, the disease transmission occurred within households. Timely monitoring of these households via multiple rounds of nucleic acid testing can allow more rapid and accurate tracing of close contacts of infected individuals. Therefore, nucleic acid testing conducted at the health facility closest to households level can not only reduce the risk of viral spread but also alleviate the shortage of medical resources.

A limitation of our study needs discussion here. With the emergence of new virus strains, many parameters in the model need to be updated. For example, when the new strain is more infectious than the Omicron variant, it may lead to more population infections, and conversely, it may lead to fewer population infections. As prevention and control policies continue to be adjusted, it may also lead to a large number of population infections when the proportion of population traveling in the city increases. When there is a difference in infectivity between asymptomatic and mildly symptomatic patients, it may also lead to different levels of population infection during subsequent transmission. Therefore, in the future study, we will continuously update these parameters according to the development of the pandemic to make the model simulation results optimal.

5. Conclusion

Our study indicates that, compared with nucleic acid testing at the level of the administrative region (scenario1), testing conducted at community (scenario2) and at the health facility closest to households (scenario3) can reduce number of infected individuals. Of note, at the health facility closest to households nucleic acid testing resulted in a lower daily cumulative number of confirmed cases and total cumulative number of confirmed cases than community testing and should be given a priority when local emergency occurs in the future. In addition, the agent-based model constructed in our study can not only be used for COVID-19 prevention and control, but also be extended to other public health fields to provide reference for the prevention and control of other infectious diseases.

Data availability statement

All relevant data is available in a public repository at https://figshare.com/articles/dataset/Dataset_for_Covid-19_modelling/ 24773340.

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Additional information

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CRediT authorship contribution statement

Xuedong Zhang: Writing - original draft, Validation, Supervision, Funding acquisition. **Bo Chen:** Writing - review & editing, Writing - original draft, Software, Project administration, Methodology, Investigation, Formal analysis, Data curation. **Jiaxu Le:** Validation, Supervision, Formal analysis. **Yi Hu:** Writing - review & editing, Validation, Methodology, Formal analysis, Conceptualization.

Declaration of competing interest

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

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