Assessing the role of voluntary nucleic acid testing with mandatory isolation in the control of COVID-19 using a household epidemic model

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Abstract. The COVID-19 epidemic has had a major impact on people's lives around the world, and many countries and regions have adopted voluntary nucleic acid testing with mandatory isolation for confirmed household to control COVID-19. Based on the method of branching process, this paper analyzes the influence of related factors on the control effect of voluntary nucleic acid testing with mandatory isolation for confirmed household by establishing a specific household model. Through numerical simulation and comparative analysis, we found that increasing the proportion of voluntary nucleic acid testing and shortening the start time of voluntary testing could enhance the epidemic control effect of this measure. At the same time, the proportion of the symptomatic will also have an impact on the effectiveness of the measure.

1. Introduction
Since the end of 2019, the outbreak of novel coronavirus has been surging. Novel coronavirus has high infection rate, strong concealment, and it is difficult to prevent and control, posing a huge threat to the life and health of people all over the world. Different countries and regions have adopted different epidemic prevention and control measures according to their own specific situation. Measures taken so far include quarantine surveillance, travel restrictions, nucleic acid testing and so on. Many studies have focused on COVID-19, and obtained many meaningful conclusions. Several studies aimed to investigate the characteristics of novel coronavirus, such as the determination of fever and nausea as key clinical indicators for COVID-19 treatment [1]. Mario Coccia puted forward index c (integrated represents that the city of contagious disease, population, climate and health risk factors) as infection rates, aiming to quantitative cities/regions’ environmental risk in advance [2]. As to the study of the effectiveness of the prevention and control measures, scholars mainly based on the cabin model, a variety of improvements were made to the SIR model [3-7].

This paper uses a household model which based on the branching process approach, focusing on a control measure which named voluntary nucleic acid testing with mandatory isolation. When the community adopts this measure as epidemic control measures, all people in the community voluntarily undergo nucleic acid testing, and the confirmed patients and their households are subjected to mandatory isolation, while those who do not undergo nucleic acid testing and those who are negative for the nucleic acid test are free to move around the community. After a specific household model was established, the numerical simulation was conducted based on the model to analyze the effects of voluntary nucleic acid testing with mandatory isolation in the control of COVID-19.
2. Methods

2.1. Assumptions and parameters

In order to describe the transmission of novel coronavirus when voluntary nucleic acid testing with mandatory isolation adopted in the community, I made following assumptions.

According to the characteristics of novel coronavirus, the asymptomatic was considered in this paper [8,9]. It is assumed that the infected person presents symptoms at a ratio $\alpha$, and the virus infectivity of the infected person with symptoms is the same as that of the asymptomatic [10]. Assume that the asymptomatic voluntarily undergo nucleic acid testing with probability $\eta_1$, and the symptomatic voluntarily undergo nucleic acid testing with probability $\eta_2$, $\eta_1 \leq \eta_2$. It is assumed that nucleic acid testing begins on the $h$ days after the first generation of infected persons in the household is infected with the virus.

This paper looked at the spread of the epidemic in a community. Assume that the community consists of a large number of households with different sizes. A household refers to a group of people who share the same living facilities under a single shelter structure [11,12]. $k_j$ represents the proportion of the number of households with size $j$ in the total number of households in the community, $\kappa_n = \frac{nk_n}{\sum_{j=1}^{\infty} k_j}$ on behalf of the probability of choosing any person in the community who comes from a household with size $n$. This paper considered household with 2,3,4,5, and 6 members in the numerical simulation. According to a 2019 British population statistics data, the proportion of household with 2,3,4,5,6 members accounted for the community households were 0.295, 0.345, 0.154, 0.139, 0.045, 0.021.

First, considering the situation that no measures are taken to control the epidemic, this paper divides the spread of novel coronavirus into two fields: inside the household and outside the household.

The epidemiological chain model is used to describe the transmission of virus within a household. Initial cases in household are first-generation infections, second-generation infections are household people infected by the first-generation infections, and so on. The chain of infection shows the number of infected people in each generation, denoted as $I = (I_1, I_2, ...)$, where $I_j$ represents the number of infected people in the $j$-th generation. $P(I|i)$ is the probability of the chain of infection $I$ occurs in the household with $i$ persons. In this paper, we assume that each infected household has only one initial case, i.e., $I_1 = 1$. The description of intra-household infection is based on the Reed-Frost model [11], where $\Theta_j$ represents the probability that a susceptible person is not infected by the $j$-th generation infected person in a household. $P(I|i)$’s specific calculation can be expressed in the binomial distribution with parameter $\Theta_j$, $\Theta_j = e^{-\int_0^t x(t) \, dt}$. $x(t)$ represents the infection level of infected persons at $t$ units of time after infection, which measured by the number of germs carried by infected persons [11]. This paper assumed that the amount of virus carried by an infected person follows a deterministic birth and death process, with a birth rate of $\delta$ and a death rate of $\mu$, and that the autoimmune system begins to function after the infected person is infected $T_I$ days. The values of parameters in the deterministic birth and death process model are shown in Table 1.

| Parameter | Value | Description |
|-----------|-------|-------------|
| $\delta$ | 3 | Birth rate of the virus population. |
| $\mu$ | 4 | Death rate of the virus population. |
| $T_I$ | 5 | The time when the immune system kicks in. |

For the transmission of the virus outside the household, it is assumed that the number of infected persons outside the household infected by the $i$-th generation infected persons in a household is subject to the Poisson distribution with parameter $\lambda_{ii}$ [13]. Because without taking any measures, each
generation of infected people can transmit viruses outside the household in infinite time, so \( \lambda_{11} = \lambda_{11} \pm \lambda \). The probability of i-th generation infected \( m \) people outside their household notes for \( \Phi_{m,i} \).

When voluntary nucleic acid testing with mandatory isolation for confirmed household is taken, the internal and external transmission of the virus would be interrupted.

Thus, for the internal transmission of the virus, it is assumed that the infection rate among household members is \( c_{2h} \) when the k-th generation infected people in the asymptomatic household voluntarily undergo nucleic acid testing. And for the symptomatic household, the infection rate among household members is \( c_{2h} \).

As to the transmission of the virus outside the household, in order to simplify the numerical simulation, it is assumed that only the first generation infected people can infect people outside the household when compulsory isolation of confirmed household is adopted. Before the mandatory household isolation strategy is adopted, the average number of infections outside the household infected by the first generation infected persons is:

\[
\lambda' = \lambda \int_0^{h} \frac{h}{\mu} \frac{e^{\mu t}}{\mu} \ dt = \begin{cases} \\
\lambda \left( \frac{\mu - \delta (\mu + T_i)}{\mu e^{\delta (\mu + T_i)} - \mu} \right) & h \leq T_i \\
\lambda \left( 1 - \frac{\delta e^{(\mu - \delta)h + \mu T_i}}{\mu e^{\delta (\mu - \mu + \delta)}} \right) & h > T_i
\end{cases}
\]

### 2.2. Model and analysis

Under the assumption above, let \( Y \) represent the final number of infected people in the community, and the average of the final number of infected people is denoted as \( EY \). The premise of \( EY \) calculation is that each infected person in the community produces an independent epidemic process and has the same average number of infected people [14]. This method has been used by Becker and Wang [15]. \( EY \) can be expressed as:

\[
EY = \alpha \eta_2 \sum_{i=1}^{\infty} \kappa_i \sum_{l} P(l | i) \sum_{l} I_k c_{2h} + \sum_{i=1}^{\infty} \kappa_i \sum_{l} P(l | i) \sum_{l} I_k \lambda' EY
\]

\[
+ \alpha (1 - \eta_2) \sum_{i=1}^{\infty} \kappa_i \sum_{l} P(l | i) \sum_{l} I_k c_{1h} + \sum_{i=1}^{\infty} \kappa_i \sum_{l} P(l | i) \sum_{l} I_k \lambda' EY
\]

\[
+ (1 - \alpha) \eta_1 \sum_{i=1}^{\infty} \kappa_i \sum_{l} P(l | i) \sum_{l} I_k \sum_{m} \Phi_{m,k} (m EY + 1)
\]

By simply computation, we obtain:

\[
EY = \sum_{i=1}^{\infty} \kappa_i \sum_{l} P(l | i) \sum_{l} I_k [\alpha(\eta_2 c_{2h} + 1 - \eta_2) + (1 - \alpha)(\eta_1 c_{1h} + 1 - \eta_1)]
\]

\[
+ EY \sum_{i=1}^{\infty} \kappa_i \sum_{l} P(l | i) \sum_{l} I_k [\alpha(1 - \eta_2 + (1 - \alpha)(1 - \eta_1)] \lambda_1 + [\alpha \eta_2 + (1 - \alpha) \eta_1] \lambda']
\]

Denote:

\[
\Gamma_H = \sum_{i=1}^{\infty} \kappa_i \sum_{l} P(l | i) \sum_{l} I_k [\alpha(\eta_2 c_{2h} + 1 - \eta_2) + (1 - \alpha)(\eta_1 c_{1h} + 1 - \eta_1)]
\]

\[
\Lambda_H = \sum_{i=1}^{\infty} \kappa_i \sum_{l} P(l | i) \sum_{l} I_k [\alpha(1 - \eta_2 + (1 - \alpha)(1 - \eta_1)] \lambda_1 + [\alpha \eta_2 + (1 - \alpha) \eta_1] \lambda'
\]

If I randomly selected an infected household within the community, \( \Gamma_H \) is the mean value of the total number of infected people in the household; \( \Lambda_H \) represents the average of the initial cases produced by the infected people in the selected household, which also called household reproduction number. If \( \Lambda_H < 1 \), we can believe that the epidemic will be under control. \( \Lambda_H \) is the core metric we use.
to measure the effectiveness of control measure. From (3) we can see, \( \lambda_{jk}, \lambda' \) (all related to \( \lambda \)), \( P(I|i) \) (which determined by \( \theta \)), \( \eta_1, \eta_2 \) and \( \alpha \) decide the value of \( \Lambda_H \). \( \eta_1 \) and \( \eta_2 \) show the willingness of people to volunteer for nucleic acid testing. \( \alpha \) represents the percentage of people infected with symptoms. \( \lambda \) and \( \theta \) are all on behalf of the intensity of virus transmission. When there is no effective drug intervention, \( \lambda \) and \( \theta \) are difficult to control. So I choose \( \lambda \) and \( \theta \) as variables to discuss the measures’ epidemic control effect.

3. Results

Under different strategies, curves in the figure below show the relationship between \( \lambda \) and \( \theta \) when \( \Lambda_H = 1 \). For all curves in each figure, the point above the curve satisfies \( \Lambda_H > 1 \), and the point below the curve satisfies \( \Lambda_H < 1 \). The number of infected persons outside the household infected by any generation infected persons in a household is subject to the Poisson distribution with parameter \( \lambda \). \( \theta \) represents the probability that a susceptible person in a household is not infected by any generation infected person in the same household. \( \lambda \) and \( \theta \) can respectively on behalf of the intensity of virus transmission outside and inside the infected household.

3.1. Voluntary detection proportion of the asymptomatic and the symptomatic are the same

From Figure 1, I can conclude that:

- When the proportion of voluntary nucleic acid testing between symptomatic and asymptomatic infected people and the starting time of nucleic acid testing are the same, the proportion of symptomatic infected people has no effect on epidemic prevention and control.
- The higher the proportion of voluntary nucleic acid testing, the better the epidemic prevention and control effect.

![Figure 1](image_url)

**Figure 1.** Comparison of the epidemic prevention and control effect when voluntary detection proportion of the asymptomatic and the symptomatic are the same.

3.2. Voluntary detection proportion of the asymptomatic and the symptomatic are different

From Figure 2, I can conclude that:

1. The greater the difference in the proportion of voluntary nucleic acid testing, the greater the difference in the effect of epidemic prevention and control.
(2) The smaller the proportion of symptomatic infected people, the smaller the impact of the difference in the proportion of voluntary nucleic acid testing on the effectiveness of epidemic prevention and control.

(3) When the proportion of asymptomatic infected people is different, the effect of epidemic prevention and control measures under the same proportion of voluntary testing is different.

![Comparison of the epidemic prevention and control effect when voluntary detection proportion of the asymptomatic and the symptomatic are different.](image)

Figure 2. Comparison of the epidemic prevention and control effect when voluntary detection proportion of the asymptomatic and the symptomatic are different.

3.3. Impact of the start time of voluntary nucleic acid testing on the epidemic prevention and control capability

From Figure 3, I can conclude that:

(1) Other conditions being equal, the earlier the start of voluntary testing, the better the epidemic control effect.

(2) For the same proportion of voluntary testing and testing start time, the greater the proportion of symptomatic infected people, the better the epidemic control effect, especially when the nucleic acid testing starts earlier.

(3) When nucleic acid testing started earlier than the peak period of novel coronavirus (5 days in this paper), the prevention and control effect of voluntary nucleic acid testing and mandatory isolation for confirmed households was significantly better than that of the situation when nucleic acid testing started later.

(4) When nucleic acid testing all started earlier (or later) than five days, there was little difference in the epidemic prevention and control effect of the measures.
Figure 3. Comparison of the epidemic prevention and control effect when the start time of voluntary nucleic acid testing are different.

4. Conclusions
In this study, a household model was established by branching process method, and the expression of household reproduction number $\Lambda_H$ was derived. $\lambda$ and $\theta$ were used as graphing variables to analyze the epidemic prevention effect. This paper aims to study the community epidemic prevention and control effect of voluntary testing with mandatory household isolation, and introduced the birth and death process of the virus to describe the infection level of infected people, which is conducive to us to consider the specific impact of time factor in this prevention and control measure. However, the research in this paper takes the community as the scope and the household as the unit, which is conducive to the targeted research of community epidemic prevention and control measures, but there is no community-scale COVID-19 data at this stage, so the model effect cannot be tested with actual data. In addition, this paper only analyzes the measures of voluntary testing and mandatory household isolation. In the future work, I will consider more diversified epidemic prevention measures.

In general, voluntary nucleic acid testing and mandatory isolation of confirmed household has proved effective in COVID-19 control. Its epidemic control effect is related to three factors: the proportion of the symptomatic, the proportion of people volunteering for nucleic acid testing and the time when voluntary nucleic acid testing begins. According to this, we can consider strategies to improve the epidemic control effect of voluntary nucleic acid testing with mandatory isolation through the following aspects. First, the proportion of symptomatic infected people will affect the effectiveness of prevention and control measures, so we need to accurately understand the characteristics of COVID-19. Second, try to increase the proportion of people volunteering for nucleic acid testing. Third, accelerate the time of nucleic acid testing. Thus, I provide advice on health policy below:

1. Increase investment in scientific research on novel coronavirus, and attach importance to the construction of national basic disciplines.
(2) Increase the storage of nucleic acid testing kits, reduce the cost of nucleic acid testing and strengthen the distribution of related medical workers.
(3) Expand publicity, raise people's attention to the prevention of infectious diseases, and popularize the effectiveness of rapid nucleic acid screening.
(4) Emphasis should be placed on the highly mobile members of the community, and mandatory household isolation should be immediately imposed on households with confirmed cases.

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