

Analysis of Transmission and Evolution of COVID-19 Epidemic based on Cellular Automata

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Abstract

This paper conducts a dynamic evolutionary analysis on the spread of COVID-19 based on cellular automata and the SEIQRD epidemic model. We establish a random-walking cellular automata model to simulate the population mobility. The heterogeneity of individuals (i.e. their individual susceptibility to the virus) is modeled to study the relationship of thorough precautionary measures and the probability of being infected with the coronavirus. The time period of the government's implementation of control measures and its influence on the development of the epidemic is also analyzed in this paper. The experimental results show that reducing the proportion of population movement, adopting precautionary measures, and the timely isolation of patients can significantly reduce the spread of the coronavirus. These results are consistent with the recommendations from the coronavirus experts, which further verify the effectiveness of the model.

Keyword: Cellular Automata, COVID-19, Epidemic Model, Dynamic Evolutionary Analysis

I. Introduction

The outbreak of COVID-19 in December 2019 has caused massive losses and casualties due to its extremely contagious nature. In an attempt to predict the trends of the COVID-19 epidemic in order

to guide optimal prevention and control, many researchers have applied the epidemiological dynamics model such as the SIR model, and its variant the SEIR model [1-2]. However, the SIR model requires many parameters to make predictions, and the evolution of infection is still unknown. Therefore, this paper will utilise the principle of cellular automata, combined with the SEIQRD infectious disease model and Wuhan's official published data, to analyse and demonstrate the spread of COVID-19.

A. Cellular Automata

Cellular automata model is a grid dynamics model with discrete time, space, and states. The spatial interaction and time causality in cellular automata model are local. It can be used to simulate the spatiotemporal evolution process of complex systems. Based on the characteristics of cellular automata, the model can simulate the evolution process of the coronavirus in a certain environment and acquire the visual display of time and space. This is conducive to the formulation of prevention and control measures in different phases.

Cellular automata are mainly composed of the following parts: cell, cell space, neighbors, and state transition rules. The cell is the most basic unit of cellular automata. The cell space is a collection of spatial mesh points distributed by cells. The neighbors are cells that are adjacent to a cell in the space. The area composed of all neighbors of a cell is called a neighborhood. The state transition rule refers to the state transition function that determines the state of the cell at the next moment according to the current states of the cell and its neighborhood [3].

B. SEIQRD infectious disease model

The SEIQRD infectious disease model is a variant of the SIR model. Making use of actual COVID-19 transmission in China, this model divides the population at a certain moment into 6 categories: **Susceptible** (S), which refers to a healthy person not infected by the coronavirus; Latent **Exposed** (E), which refers to a person who has been infected by the virus and has the chance to infect others, but has not developed the symptoms; **Infectious** (I), which refers to a person who has shown certain symptoms with a high chance to infect others; **Quarantine** (Q), which refers to a person who has been diagnosed with COVID-19 and has been isolated and treated in a hospital, and no longer has the chance

to infect others. Yimin et. al. analyzed the impact of isolation measures for the COVID-19 epidemic [4]. They concluded that isolating infected patients immediately can not only avoid large-scale infections, but also enable them to receive medical treatment in time, ultimately increasing the number of cured patients; **Recovered** (R), which refers to a person who has recovered after the medical treatment, gained immunity against the coronavirus, and cannot be re-infected; **Death** (D), which refers to a person who died after being infected with the virus. The infection process of this model is shown in Fig. 1.

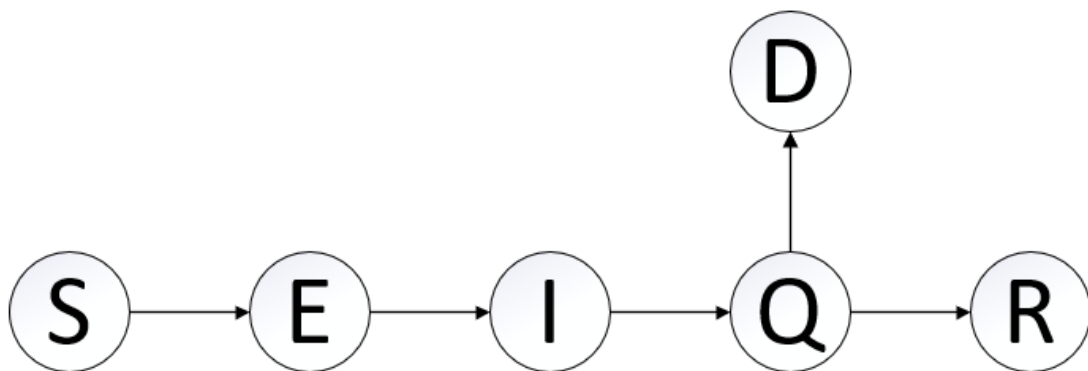


Fig. 1 The spreading process of SEIQRD epidemic model

II. A Hybrid model of random-walking cellular automata and SEIQRD infectious disease model

In this paper, the Moore neighborhood is used. Assuming that the cellular automaton is in a two-dimensional network with $N=n*n$, we choose a central cell A whose position is (i, j) , then the locations of the eight neighbors are shown in Figure 2.

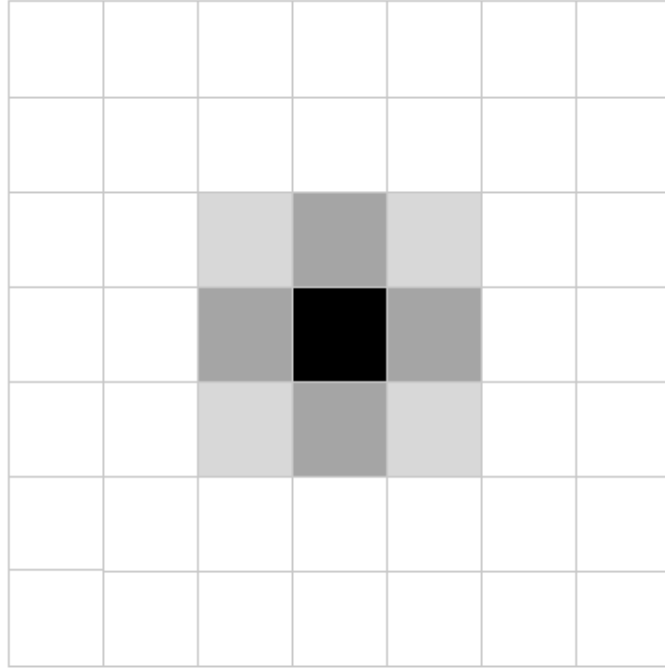


Fig. 2 The Moore neighborhood

In this paper, we set the cell as $C_{i,j}$. $S_{i,j}^t \in \{0, 1, 2, 3, 4, 5\}$, which represents the state of the cell $C_{i,j}$ at time t . The state values of the cells differ accordingly:

- $S_{i,j}^t = 0$: The cell $C_{i,j}$ is a person who is susceptible to infection at time t , and has certain resistance to the virus, but can still be infected by latent and infected persons.
- $S_{i,j}^t = 1$: The cell $C_{i,j}$ is a person who is latent at time t and has no symptoms.
- $S_{i,j}^t = 2$: The cell $C_{i,j}$ is a person who is infected at time t , has some obvious symptoms, has not been isolated or treated, and still has the ability to infect others.
- $S_{i,j}^t = 3$: The cell $C_{i,j}$ is a person who is isolated at time t , has some obvious symptoms, and is being treated in isolation. Assuming that medical staff can achieve 'zero infection rate', the quarantined person no longer has the ability to infect others.
- $S_{i,j}^t = 4$: The cell $C_{i,j}$ is a person who has recovered at time t , has immunity against the coronavirus, and will not be re-infected during the immune period.

- $S_{i,j}^t = 5$: The cell $C_{i,j}$ is a person who is dead at time t , and no longer has immunity and the ability to infect others. This cell will exit the system.

Below are the state transition rules of the cell:

- When $S_{i,j}^t = 0$: the cell $C_{i,j}$ is infected by the latent or infected people (neighbor) with probability $p_{i,j}^t$, and will transform into a latent person.
- When $S_{i,j}^t = 1$: the cell $C_{i,j}$ will turn into an infected person after the incubation period T_1 .
- When $S_{i,j}^t = 2$: the cell $C_{i,j}$ has obvious symptoms and the ability to infect others. We assume that patients will not recover on their own after self-isolation. After self-isolation for T_2 days, the person will be admitted to the hospital for treatment.
- When $S_{i,j}^t = 3$: the cell $C_{i,j}$ is an isolated person at time t who has obvious symptoms. We assume that medical staff will achieve a “zero infection status”. After a treatment period of T_3 days, some patients die with a fatality rate of μ , and others recover with a recovery rate of $(1-\mu)$.
- When $S_{i,j}^t = 4$: the cell $C_{i,j}$ is a recovered person at time t who has immunity against the coronavirus. The immune period is T_4 days and the person will not be re-infected during the immune period. The current COVID-19 data shows that the recovered person will not be infected again, so the immune period is set to be greater than our experimental observation period.
- When $S_{i,j}^t = 5$: the cell $C_{i,j}$ is dead at time t , no longer has immunity and the ability to infect others. This cell will exit the system.

III. Factors for Spreading

A. Uncertain probability of infection

Prior research proposed a cellular automata-based infectious disease model that considered both individual heterogeneity and population mobility, and analyzed the impact of self-resistance and population movement on the spread of infectious diseases [5]. The heterogeneity of individuals

is reflected in three aspects: every individual has a different level of resistance, the latent person and the infected person have different probability of infecting the susceptible person, and the infectivity is restricted by distance factors. Instead, the probability of a cell being infected is therefore influenced by the following factors: self-resistance, self-protection, infectivity of neighbors in different states, and neighbor's location.

Since everyone's physical health and precautionary measures are different, individuals have different resistance levels to the coronavirus $R_{i,j}$. Considering that adopting thorough precautionary measures is more effective than relying on physical health to resist the coronavirus, the experiment sets the individual resistance $R_{i,j}$ to follow the uniform distribution between (0, 0.5) when the individual does not adopt any precautionary measures. The individual resistance is set as $R_{i,j}=1$ when the individual adopts thorough precautionary measures and therefore will not be infected by the coronavirus. The cellular automata in this paper use eight neighborhoods, so the distance between neighboring cells $C_{e,f}$ and cell $C_{i,j}$ in different locations $D_{C_{i,j},C_{e,f}}$ is different. The distance between the top, bottom, left, and right neighbors and the cell $C_{i,j}$ is $D_{C_{i,j},C_{e,f}} = 1$, and the distance with other neighbors $D_{C_{i,j},C_{e,f}} = \sqrt{2}$. Since the infectivity of the latent person and the infected person carrying the coronavirus is different, the infectivity of the latent person to the susceptible person is lower than that the infectivity of the infected person to the susceptible person. We assume that the infectivity of the latent person to the susceptible is 3%, and the infectivity of the infected person to the susceptible is 5%. Combining the individual's personal resistance, the influence of the distance between the neighbors on the cell, and the infectivity of different cells together, the calculation method of the probability that the cell $C_{i,j}$ is infected by the neighbor cell $C_{e,f}$ is calculated as formula (1):

$$p_{C_{i,j},C_{e,f}}^t = \frac{1}{D_{C_{i,j},C_{e,f}}} \sqrt{p * (1 - R_{i,j})} \quad (1)$$

where p represents the infectivity of cell $C_{e,f}$ to cell $C_{i,j}$. When $C_{e,f}$ is a latent person, $p=3\%$; when $C_{e,f}$ is the infected person, $p=5\%$; otherwise, the infectivity of $C_{e,f}$ is 0; then the final probability of infection of the cell $C_{i,j}$ can be calculated by formula (2):

$$p_{i,j}^t = \max_{(e,f) \in N_{C_{i,j}}} \{p_{C_{i,j},C_{e,f}}^t\} \quad (2)$$

where $N_{C_{i,j}}$ represents the neighborhood of cell $C_{i,j}$.

B. Population mobility

Over time, with a more developed and convenient transportation system, there is an increased population mobility within China. When the epidemic broke out in China, there was already a spike in population mobility since it coincided with the Spring Festival. To minimize the spread of coronavirus across the country, the Wuhan government announced the closure of the city from 10pm on January 23, 2020. In order to simulate the action of closing the city, we introduce the concept of a random-walking cellular automaton to investigate the impact of the city closure on the spread of the epidemic. The characteristic of random-walking cellular automata is that a certain proportion of cells will walk randomly in the cell space at each time step. In our model, only the susceptible, latent, infected and recovered cells have the ability to randomly wander in the cell space, but the quarantined cells lose the ability to wander due to the isolation, and the dead cells also lose the ability to wander. The experimental model is set as below. At time t , m number of non-repeated cells will be randomly selected to form a wandering set M_1^t . Similarly, another m number of non-repeated cells will be randomly selected to form a wandering set M_2^t . The cells in M_1^t and the cells in M_2^t are made to one-to-one correspondence. If the one-to-one corresponding cells are neither dead nor isolated, the positions of the two cells are exchanged. The experiment assumes that if the city is closed on day T_w , all cells lose the ability to walk randomly.

IV. Simulation Results and Analysis

Based on the SEIQRD epidemic model, this paper analyzes the epidemic situation in Wuhan, sets appropriate experimental parameters, and makes simulations of the spread of the epidemic.

The experiment is completed in MATLAB. We set the cell space as $N=101*101$. The total number of experimental observation days is $T=150$. The lockdown time is $T_w=20$. According to the statistical data analysis of the incubation period and suspected period of pneumonia [5], the incubation period distribution T_1 follows the Weibull distribution with a scale parameter of 8.149554 and a shape parameter of 1.788954. The experiment assumes that the self-isolation period T_2 is close to the suspected period, according to the statistical data by Xiaohui et al [6]. It shows that most of the suspected period is 5-6 days, so we set 5 days for T_2 for the probability of 50% and 6 days for the probability of 50%. According to the analysis on the recovery time of patients with COVID-19 [7], we set the treatment period T_3 to follow a uniform distribution of 14.6 ± 6.7 days. With reference to [8], the mortality rate μ is set to 0.03. The experiment assumes that the survivors infected with the coronavirus will gain lifelong immunity, so the immune period T_4 is set to be greater than the number of observation days in the experiment, $T_4=300$. Lastly, we assume that the initial exposed person is 1.

A. *Basic Model*

In the basic model, the proportion of personally protected cells to all cells is $s=0$, which means that the maximum immunity of all cells in the cell space does not exceed 0.5 and the proportion of cells that walk randomly is $Q = 0$.

Throughout the basic model, the cell state during the experiment was observed. The results of the experiment are shown in Figure 3. Dark blue represents the susceptible cells, blue represents the latent cells, light blue represents the infected cells, yellow represents the quarantined cells, orange represents the recovered cells, and dark red represents the dead cells. In Figure 3(a), at $t = 29$ days, the first death occurred. In Figure 3(b), at $t = 80$ days, large areas of disease and isolation occurred; Figure 3(c) shows that at $t = 150$ days, except for some susceptible people

with good physical health who are not infected by the virus, most of the cells have recovered and only a small portion is dead.

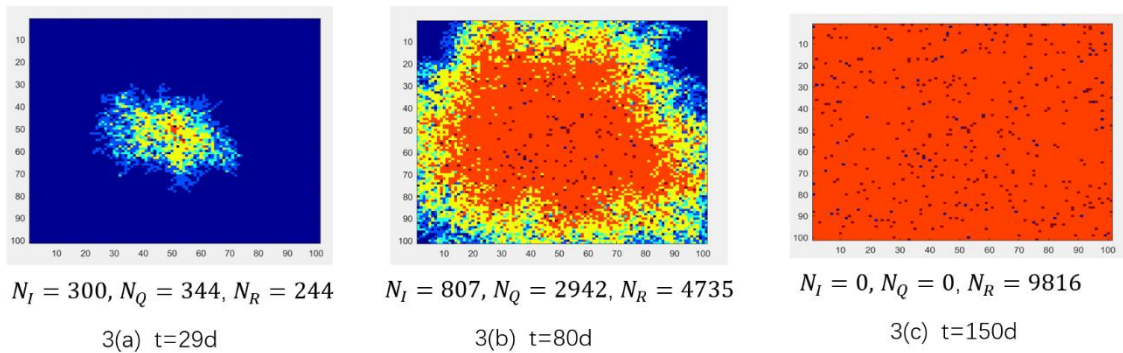


Fig. 3 Dynamic evolutionary analysis diagram of basic model under different days

a. The impact of self-protection on the epidemic

Adopting thorough precautionary measures can effectively minimize transmission of the virus. An Artificial Intelligence (AI) model developed by the University of Cambridge proved that when 80% of the population wears a mask, it will have a significant impact on the epidemic [9]. When a susceptible person adopts thorough precautionary measures, the experiment assumes that the individual’s immunity is 1, which means that the person will not be infected by the coronavirus. When the latent person and the infected person adopt thorough precautionary measures, they will not have the ability to infect others. Isolation treatment is no longer considered. The recovered persons will have antibodies and their immunity to the coronavirus will become 1. The dead will withdraw from the system without gaining immunity or infecting others. In the experimental setting, the proportion of cells adopting precautionary measures is s . The experiment will observe the changes in the cell population with different proportion of adopting precautionary measures when the cells do not walk randomly.

The simulation results of the experiment are shown in Table 1. If the proportion of cells adopting precautionary measures is no more than 50%, the cell space will not have completely stopped evolving when the experiment finishes. However, as the proportion of cells adopting precautionary measures increases, the number of infected cells in the entire cell space is

significantly reduced. When more than 50% of the cells take protective measures, very few cells are infected.

m	Susceptible	Exposed	Infectious	Quarantine	Recovered	Death
0.1	1115	19	33	248	8531	255
0.2	2142	79	84	433	7257	206
0.3	3565	248	247	880	5082	179
0.4	7356	316	205	530	1740	54
0.5	9458	106	43	87	491	16
0.6	10108	0	0	0	90	3
0.7	10199	0	0	0	2	0
0.8	10198	0	0	0	3	0
0.9	10200	0	0	0	1	0
1	10200	0	0	0	0	1

Table. 1 The number of different types of cells at the end of the experiment, with m representing the proportion of cells adopting precautionary measures

b. The impact of reducing random walk ratio on the epidemic

There are cells performing random walks every day. Since the state of the cells needs to be considered when they are walking, most of the cells are susceptible to infection at the beginning of the epidemic and the number of cells that actually walk is relatively large. When the epidemic broke out, some cells were quarantined and some died, so the migration ratio would be greatly reduced. When the epidemic was about to end, most of the infected cells had recovered or might still be susceptible to infection, so the real migration rate will rise again. Considering the proportion of quarantined persons was relatively large when the epidemic broke out, a smaller moving proportion Q was set for observation. The experiment takes Q as 0.05, 0.1, 0.15, 0.2,

and observes the changes of the quarantine under different moving ratios. The experimental results are shown in Figure 4. When the cellular space loses mobility, the outbreak period is longer. However, when the cells in the cell space have mobility, the greater the movement ratio Q , the shorter the outbreak period, and the number of infected persons also increases.

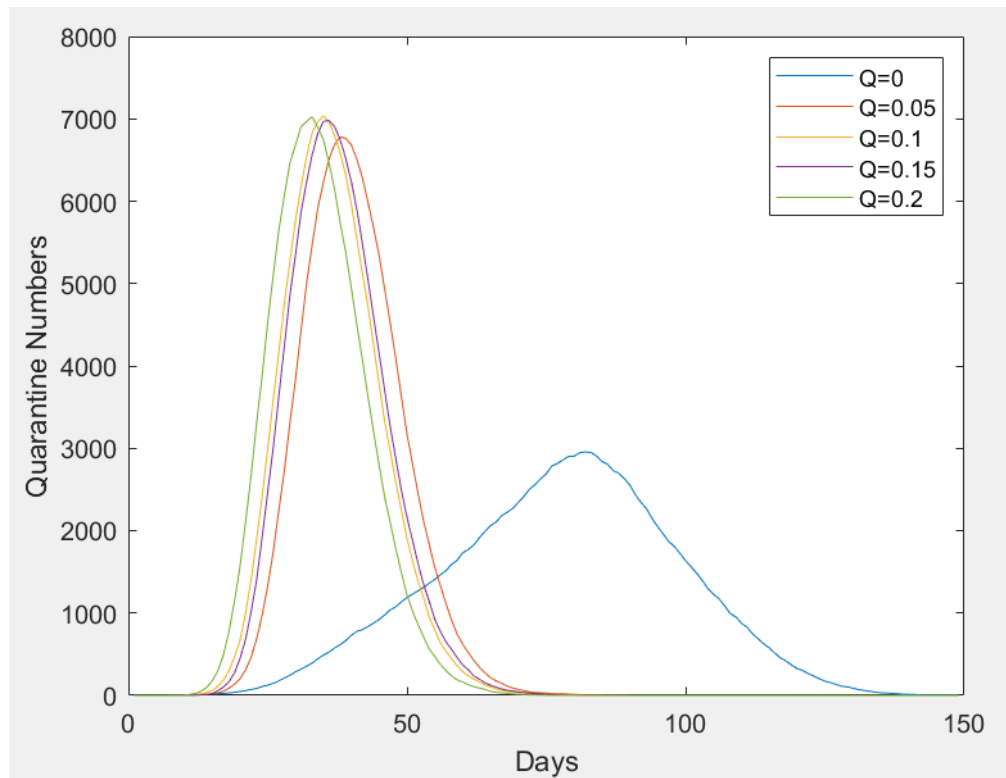


Fig. 4 Changes in quarantine over time under different moving ratios

c. The impact of number of control days and government's early action

We conduct this experiment to observe the impact of governmental control measures at different time points on the spread of the epidemic. In reality, Wuhan announced the closure on February 23, 2020 and the implementation of control measures by wearing masks in public places in Wuhan took place at 10pm on the 22nd. The first case of a COVID-19 patient was first discovered on December 12, 2019. According to the description of the first whistleblower (Dr Li Wenliang) of the epidemic, on December 30, 2019, 7 COVID-19 infections were confirmed. The experiment simulates the control in different time periods. Before the control measures, the cell migration ratio was $Q=0.2$ and after the control measure is implemented, the cell is no longer mobile and 50% of the cells will be protected from the coronavirus. The control time periods are

$t = 10, t = 20, t = 30, t = 40, t = 50, t = 60, t = 70$. We also observe how governmental control measures in different time periods affects the development of the epidemic.

The experimental data is shown in Table 2. The earlier the implementation of the control measures, the fewer the number of people infected at the end of the experiment. When the control measures were taken on the tenth day of the epidemic, the total number of infected people was 4,640. Comparing with the results on the 20th day of the epidemic, about 48.6% of people were free from infection. When the epidemic situation developed 50 days later, the control measures were implemented, but the spread of the epidemic situation will not change significantly.

t	Susceptible	Exposed	Infectious	Quarantine	Recovered	Death
10	5411	0	0	9	4640	141
20	900	0	0	0	9018	283
30	229	0	0	0	9670	302
40	73	0	0	0	9808	320
50	54	0	0	0	9842	305
60	64	0	0	0	9821	316
70	66	0	0	0	9824	311

Table. 2 The number of various types of cells after the end of the test when the control measures are taken on day t

V. Conclusion

Based on the knowledge of epidemiology and the actual transmission characteristics of the coronavirus, this article uses the epidemiological dynamics SEIQRD model to demonstrate the importance of adopting precautionary measures, reducing travel, and for hospitals to accept infected persons for treatment in a timely manner. However, this model also makes several assumptions in the analysis of asymptomatic infections. According to the response from the Chinese Bureau of Disease

Control and Prevention in the "Questions and Answers on the Prevention and Control of Asymptomatic Infections of COVID-19", asymptomatic infections can be classified under two conditions. The first classification of asymptomatic infections is positive nucleic acid test of the infected person. In this case, there were no self-perceived or clinically-identifiable symptoms or signs during the observation of the incubation period, and the infection was always asymptomatic. The second classification is when the infected person has a positive nucleic acid test and no self-perceived or clinically-identifiable symptoms or signs at the time of sampling, but a certain clinical manifestation appeared, that is, a state of "asymptomatic infection" during the incubation period. This paper only considered the second classification of asymptomatic infections during the incubation period in the model and ignored a small number of long-run asymptomatic infections. Additionally, parameters were estimated due to the lack of corresponding literature when setting the infectivity of asymptomatic infections and those with disease. However, in reality, people did not pay enough attention to the epidemic in the early stage, and therefore the epidemic broke out quickly and the human infections were widespread. With the improvement of the governmental control measures, the city was closed in time, the public was required to wear masks, adopt precautionary measures, as well as isolating and treating the infected people. This effectively reduced the transmission of the virus, ultimately winning the battle against the epidemic in Wuhan.

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