Available online at http://scik.org
Commun. Math. Biol. Neurosci. 2015, 2015:35
ISSN: 2052-2541

A STUDY OF THE INFECTIOUS DISEASE WITH INCUBATION PERIOD MODEL BASED ON CELLULAR AUTOMATA

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Abstract. Considering the two measures of vaccination to susceptible population and isolation treatment to infectious population, this study builds a SEIQR -V infectious disease model with incubation period, which is based on the principle of cellular automata. According to the random walking principle, it gets an expanded Moore neighbor. For influenza A (H1N1), BP neural network is used to recognize the quarantine intensity parameters of some countries. Furthermore, according to Cellular Automata's simulation to the number of infections under the different vaccination proportion, the article studies the factors about spreading regularity of infectious diseases. Simultaneously, for different countries, the study proposes a better control strategy suited to the country's vaccination.

Keywords: Infectious disease model; Cellular automata; Vaccination; Parameter identification.

2010 AMS Subject Classification: 37B15.

1. Introduction

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Received February 10, 2015

The havoc of infectious diseases threatens mankind. Establishing a model of infection to simulate the propagation pattern will aid prevention and control.

Cellular Automata (referred to as CA hereon) [1], suggested by Von Neumann, is a dynamic system model in which space and time are discrete, and local interactions induce global variations. The characteristics of transmission through individual contact are very similar to that of infectious disease, and visualise the process of propagation. Therefore, CA has become the new method of studying infectious diseases.

G. Ch. Sirakoulis *et al.* [2] studied the effects of population movement and vaccinations on epidemic propagation. Moreover, the model has been used to study the effects of vaccination for the partial population. The study shows that increased population movement distance and moving percentage will accelerate propagation while vaccination will decrease propagation. Aili You *et al.* [3] studied influenza A (H1N1) through CA modeling and indicated quarantine is an effective method of propagation prevention. Lijuan Zhang *et al.* [4] used CA modeling to simulate the propagation process of infectious diseases within a transmission network, and used this as foundation to study effects of the percentage of vaccination, variation rate of the virus and individual response time on propagation. Effective prevention and control strategies were suggested specifically according to propagation characteristic. Chao Guan *et al.* [5] studied the propagation process under medical intervention, and found that vaccination had a level of effect on propagation control. It is especially effective to vaccinate the high risk zone population, and when the vaccinated population reach adequate numbers, outbreak of disease can be prevented.

The majority of infectious disease modelling using CA does not consider quarantine for the ensconced individual as a control measure for disease propagation. Diseases such as Scarlet fever, whooping cough and chicken pox all have a level of infectiousness within the incubation period. Therefore, methods of quarantine should be both applied to the infected and the ensconced. Furthermore, vaccinating the susceptible population is also an important control method, but there are very few studies which take combined consideration of quarantine and vaccination and their effects on propagation. Thus, this paper takes into account vaccinating the susceptible population and quarantine for the infectious population and establishes a SEIQR-V

epidemic model based on CA. In dynamic simulations created by Matlab, effective propagation control strategies for each country is derived from varying the percentage of vaccination population. This will provide government departments with scientific foundations as basis for formulating optimized epidemic prevention and control strategies.

2. Building a SEIQR-V epidemic model based on cellular automata

During the propagation period, the population is classified into seven groups according to their current states: Susceptible (S), Exposure (E), Vaccination (V), Infection (I), Quarantine (Q), Recovery (R) and Death (D). The propagation flow chart is shown as in FIGURE 1.

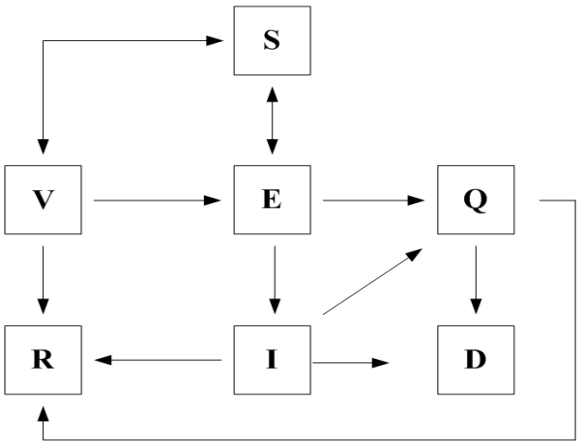

Figure 1: Propagation flow chart

In FIGURE 1, state S individuals are non-infectious and are randomly mobile within neighboring domains. Due to heterogeneity, they will be infected and changed into state E by various probabilities when in contact with state E or state I individuals. State E population are partially quarantined to state Q due to infectiousness, those un-quarantined will be diagnosed after the ensconce period to become either state I or state S. State I is strongly infectious and the population is partially quarantined into state Q. State I individuals not quarantined will either die from disease after the infected period and be extracted from the propagation cycle as state D, or become state R individuals with relatively high immunity levels, and will not be infected during

the immune period. As state Q individuals are isolated from external contact under quarantine, infectiousness is lost, and individuals will either be cured into state R or state D individuals.

When the vaccine is developed and put to use, state S individuals are vaccinated by certain probability and become state V individuals. State V individuals can still be infected into state E before production of antibodies. After this, the individual either fails to be vaccinated and once again becomes state S, or is successfully vaccinated to become state R individuals.

2.1 Expanding Moore neighbourhoods

A two dimensional cellular automaton (CA) usually takes two neighbourhood forms: Von Neumann neighbourhoods and Moore neighbourhoods. These neighbourhoods are static and can be understood as family, neighbours and workmates whom come into direct contact. In reality, there are people who come into contact randomly due to business or travelling. This paper references the random walk cellular automata,see [6-7] references therein, and the extended Moore neighbourhood theories, to produce a neighbourhood form for a cellular $C_{i,j}$ as shown in FIGURE2.

Establish scale of the cellular space as $n \times n$, the percentage of individual random movement as per, thus the number of mobile cellular each time is $N = n \times n \times per$. First, within the cellular network, randomly sweep N non-repeating cellular $C_{i,j}$ (i, j the cellular co-ordinate, of which $i, j \in \{1,2,\ldots n\}$), and produce N sets of discreet random number $(d_{i'}, d_{j'})$(of which $d_{i'}, d_{j'} \in Z$, and $|d_{i'}| \leq n, |d_{j'}| \leq n, i', j' \in \{1,2,\ldots N)$. If $i + d_{i'} < 0$, adjust $i + d_{i'}$ to $i + d_{i'} + n$ according to the CA's periodic boundary condition. If $n < i + d_{i'}$, adjust $i + d_{i'}$ to $i + d_{i'} - n$. Adjust $j + d_{j'}$ in the same way to make $j + d_{j'}$ satisfy $0 \leq j + d_{j'} \leq n$. Finally, randomly exchange cellular $C_{i+d_{i'}, j+d_{j'}}$ with $C_{i,j}$ to complete a random movement.

2.2 Heterogeneous individuals

There is heterogeneity between individuals, thus susceptible individuals have varying immunity $R_{C_{i,j}}$ and infectious individuals have varying infectiousness $f_{C_{m,n}}$. For the average infectious disease, state E individuals have a less infectious than state I individuals. Thus, heterogeneity affects propagation.

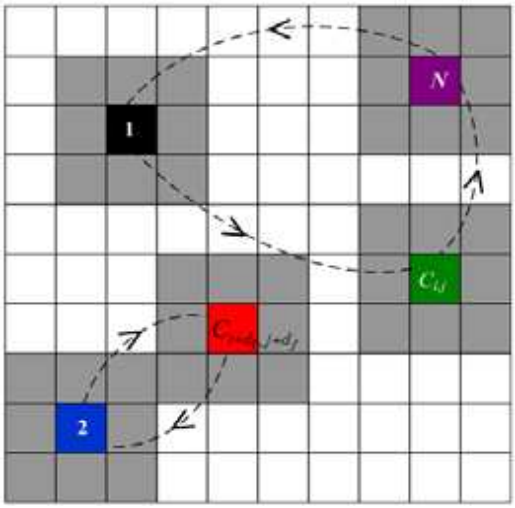

Figure 2: Extended Moore neighborhood form of cellular $C_{i,j}$

Establish the infectiousness of cellular $C_{m,n}$ on cellular $C_{i,j}$ as $f_{C_{i,j}C_{m,n}}$; $C_{i,j}^{'}s$ immunity to disease as $R_{C_{i,j}}$, the Euclidean distance between $C_{i,j}$ and $C_{m,n}$ as $d_{C_{i,j}C_{m,n}}$. Thus the probability $P_{C_{i,j}C_{m,n}}^{t}$ of $C_{i,j}$ being infected by neighboring cellular $C_{m,n}$ at time t can be shown as

$$P_{C_{i,j}C_{m,n}}^{t} = \frac{1}{d_{C_{i,j}C_{m,n}}} \sqrt{f_{C_{i,j}C_{m,n}} \times (1 - R_{C_{i,j}})},\ C_{m,n} \in N_{C_{i,j}} \tag{2.1}$$

Of which, $N_{C_{i,j}}$ represents $C_{i,j}^{'}s$ neighbor set, $f_{C_{i,j}C_{m,n}}$ and $R_{C_{i,j}}$ both follow uniform distribution (0,1).

Take $C_{i,j}^{'}s$ maximum infection probability by all its neighboring cellular as $C_{i,j}^{'}s$ probability of infection $P_{C_{i,j}}^{t}$ of at time t[8]

$$P_{C_{i,j}}^{t} = \max_{(m,n)\neq(i,j)} \{P_{C_{i,j}C_{m,n}}^{t}\},\ C_{m,n} \in N_{C_{i,j}} \tag{2.2}$$

In the simulation, when any state S individual within the cellular network contacts its neighbour, if the neighbour has a state E or I individual, then that cellular will be infected into state E by probability $P_{C_{i,j}}^{t}$ and the above definition.

2.3 Rules of evolution

For convenience of describing the state characteristics of individuals, $S_{i,j}^t = \{0,1,2,3,4,5,6\}$ is used to represent the set of states of $C_{i,j}$ at time t. Seven numbers are in correlation to the seven states D, S, E, V, I, Q and R. The evolution rules for cellular states are as follows:

(1) When $S_{C_{i,j}}^t$=1, calculate infection probability $P_{C_{i,j}}^t$ of $C_{i,j}$ at time t, and use this to determine whether the individual will change to state $S_{i,j}^{t+1}$=2 by $P_{C_{i,j}}^t$, or stay susceptible, where $S_{C_{i,j}}^{t+1}$=1. When vaccines are given in probability v at time T_v, state is changed to $S_{C_{i,j}}^{t+1}$=3.

(2) When $S_{C_{i,j}}^t$=2, within the incubation period T_e, quarantine by probability q_1, state is changed to $S_{C_{i,j}}^{t+1}$=5. After T_e, diagnose by probability p_1 and change into state $S_{C_{i,j}}^{t+1}$=4, otherwise state changes into $S_{C_{i,j}}^{t+1}$=1.

(3) When $S_{C_{i,j}}^t$=3, within the vaccine kick-in time T_μ, calculate the infection probability $P_{C_{i,j}}^t$ of $C_{i,j}$ at time t and determine if the individual changes into state $S_{i,j}^{t+1}$=2 by probability $S_{C_{i,j}}^{t+1}$=6. After T_μ, change state to $S_{C_{i,j}}^{t+1}$=6 at the vaccine protection rate μ, or change state into $S_{C_{i,j}}^{t+1}$=1.

(4) When $S_{C_{i,j}}^t$=4, during the infection period T_i, quarantine by probability q_2 and change state to $S_{C_{i,j}}^{t+1}$=5. After T_i, die by probability d_1 and change state to $S_{C_{i,j}}^{t+1}$=0. Otherwise be cured and change state to $S_{C_{i,j}}^{t+1}$=6.

(5) When $S_{C_{i,j}}^t$=5, after quarantine period T_q, die by probability d_2 and change state to $S_{C_{i,j}}^{t+1}$=0, otherwise be cured, state changes to $S_{C_{i,j}}^{t+1}$=6.

(6) When $S_{C_{i,j}}^t$=6, during the immune period T_r immunity is high and infection is unlikely, maintaining state $S_{C_{i,j}}^{t+1}$=6.

3. Dynamic simulation and result analysis

3.1 Simulation parameter settings

Assume the cellular network as $n = 100$, initial ratio of state E individuals is 0.0001, the rest are all state S individuals. The proportion of movement for every simulated step is $per = 0.001$. Simulation parameter settings for different epidemics vary, this study use Influenza A (H1N1) as example.

The propagation range of influenza A (H1N1) is quite broad. Assuming population during propagation is constant, that is, the birth rate and death rate are equal, and there are no cases of

relapse due to immunity of cured individuals, take $T_r = 365$. The ensconce period is generally $1 \sim 7$ days, take $T_e = 4$, probability of diagnose as $p_1 = 25\%$. Disease course is approximately 7 days in general, take $T_i = 7$. Hospitalization period are $3 \sim 16$ days[9], take $T_q = 10$. Considering death rate of quarantine is lower than that during the infected period and according to actual epidemic statistics and death rates released by the World Health Organization[10], take $d_1 = 1.0\%$, $d_2 = 0.5\%$.

This paper takes real statistics from actual diagnosed numbers from the period of Influenza A (H1N1) outbreak in China, the US and Mexico (1^{st} May 2009 to 30^{th} June 2009), see [11-12] references therein. As the vaccine for Influenza A (H1N1) was successfully developed in September 2009 and statistics are of before then, in the simulation, initial vaccinated probability is $v = 0.00$.

3.2 Parameter identification

Step 1: Creating a $L_1 96(14^2)$ orthogonal table[13]. Two parameters within $L_1 96(14^2)$ are q_1 and q_2, take fourteen levels for each, which are 0.10, 0.15, 0.20, ..., 0.80 respectively. Considering the quarantine intensity for ensconced individuals will not be greater than that of the infected individuals, as for $q_1 \leq q_2$, only the 120 tests which satisfy $q_1 \leq q_2$ are planned. 120 sets of simulated data are produced by using MATLAB, and based on the simulated parameters above and various levels of variable q_1 and q_2.

Step 2: Calculating the error vector $e_i = [e_{i1}, e_{i2}, e_{i3} \ldots e_{ik}]$ and $i = 1, 2, \ldots, 120$. Real data are selected for May 1 to June 30, 61 days included, that is to say $k = 61$. We can get 120 group's error vector by subtracting down real data from simulation data. Then, we treat the error vector as the input vector of the neural network and the error variance q_1 and q_2 of each group as the output vector.

Step 3: Creating a BP neural network, and the figure of neural network topology is shown in FIGURE 3. In this Figure, the input layer has 61 neurons, two layers are hidden and the neurons of each layer is four, while the output layer has two neurons[14]. The expression of transfer function of neurons in hidden layer is $f(x) = \frac{1}{1+e^{-x}}$; and the transfer function of neurons in output layer is $f(x) = \frac{2}{1+e^{-2x}} - 1$. According to transfer function of hidden layer, if e_i

is acted as network input of input layer neurons, each neurons of hidden layer will produce one output based on weight ϖ and threshold θ of network connections, and this output is looked as network input of next neurons. Finally, the output value q_1 and q_2 were obtained through transfer function of output layer. By calculating error of total output in this network, and transferring the error signal in negative direction to adjust parameter ϖ and θ n this network, until the error reduced to the range of given permissible error beforehand. Therefore, mapping relationship between error e_i and parameter q_1 and q_2 is built.

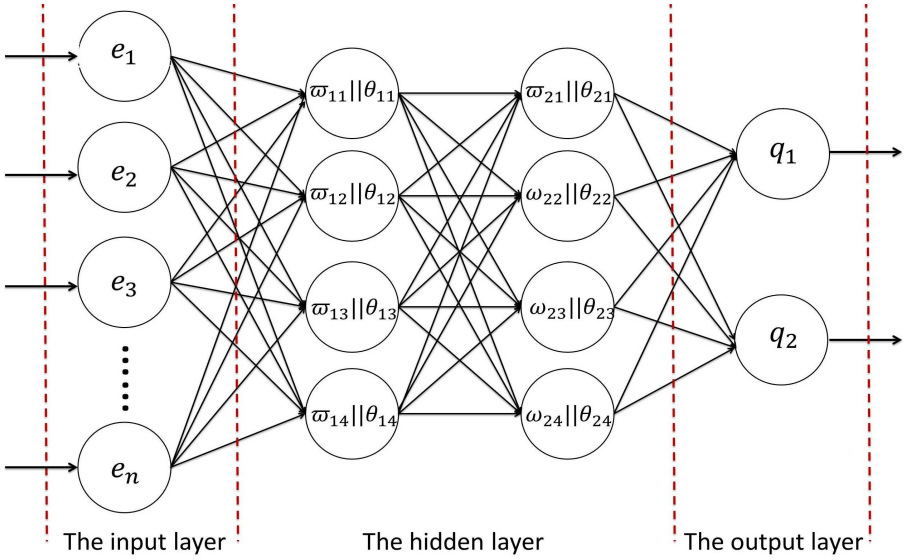

Figure 3: Topological structure of neural network

On the basis of the network structure above, the quarantine intensity which some countries have taken in controlling the spread of the influenza A (H1N1) was obtained after treating error vector $0 = [0,0,0,\ldots,0]_{1\times 61}$ as input vector, and those relationships are shown as in TABLE 1.

Table 1: Quarantine Intensities of Some Countries

	China	US	Mexico
q_1	0.38	0.08	0.37
q_2	0.55	0.70	0.69

Taking China for example, $q_1 = 0.40$, $q_2 = 0.50$ in 120 groups' simulation data are the closest parameter with real data, but neural network simulation's parameters which are $q_1 = 0.38$ and

$q_2 = 0.55$, the result compared with real data are shown in FIGURE 4(a). Using the same process, the comparison diagram between the cumulative number of infections in the US and Mexico and the real data would be got in FIGURE 4(b) and 4(c). FIGURE 4 shows: The simulation result is more closed to real data when simulate quarantine intensity parameters of neural network architecture. Therefore, the study uses neural network simulation parameters q_1 and q_2 as actual quarantine intensity in this country.

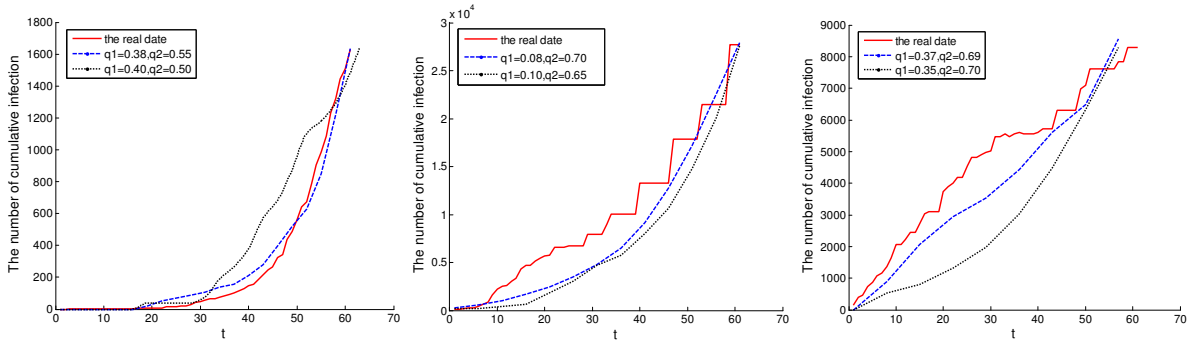

Figure 4: Comparison between simulated data and real data. (1) China (2) US (3) Mexico

3.3 Implementation of vaccination measures

As the infectious diseases outbreak undergoing large overall, people will take vaccination measures for preventing diffusion of infectious disease. However, people will don't take measure to prevent these infections, such as SARS, influenza A (H1N1) etc, the end of the infectious diseases. In order to prevent and control the spread of infectious disease affectively when it struck again. Considering quarantine measures, this paper will take further discuss about how to take the vaccination.

In this study, the model parameter: vaccination proportion is discretely adjusted and tested, to get how to take vaccination measures can effectively control the spread of infectious disease in different countries. As a result of the limitation of medical conditions, and there are the people not suitable for vaccination such as those with allergies or in early stages of pregnancy, the vaccination proportion $0 \leq v < 1$.

3.4 Simulate and analyze the influence of different vaccination proportion for infectious diseases transmission

This study suppose that the vaccines of influenza A (H1N1) has been the developed and put into use; and because of the inoculants time of influenza A (H1N1) vaccines are in single doses, assuming the general conditions (e.g. waiting room, consulting room, vaccination room) and the number of staff is enough to complete each one dose of vaccine. The works are taken and completed that object of inoculation are inoculated in vaccination proportion v, setting in five days the infections diseases, that is to say $T_v = 5$. Action time of influenza A (H1N1) vaccination is about 15 days, the protection rate of vaccine reach $70\% \sim 90\%$[15], so $T_\mu = 15$, $\mu = 85\%$ in this study.

The simulation for SEIQR-V epidemic model of influenza A (H1N1) in China is based on the parameters above. Changing the values of v, the variation tendency of the cumulative number of infections in different vaccination proportion can be obtained by using MATLAB simulation and the result are shown as in Figure 5.

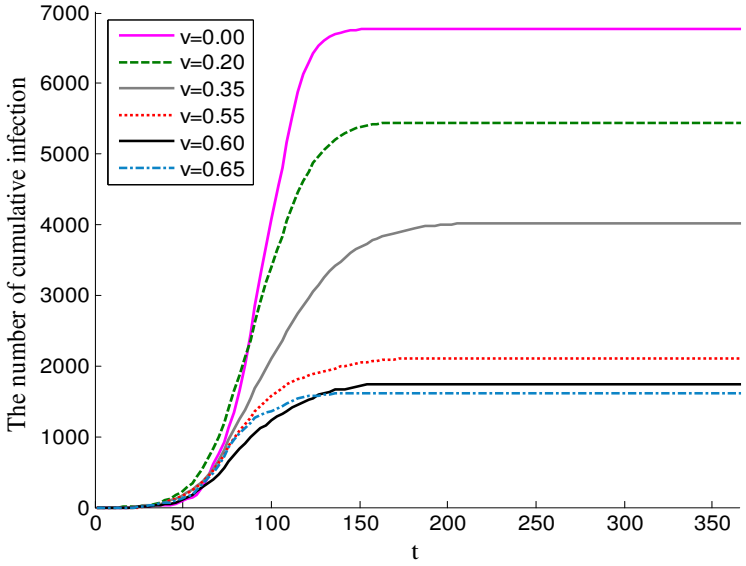

Figure 5: Variation tendency of the cumulative number of infections in china in different vaccination proportion

It can be observed in Figure 5 that the vaccination can control the spread of infectious disease. As proportion of those vaccinated increase, the cumulative number of infections decrease. The

cumulative number of infections decrease reduce by 17.1% when v increase to 0.60, however, the cumulative number of infections only decrease by 8.2% when v increase to 0.65. In reality, when restraining the epidemic propagation, not only the reduction of infected individuals but also cost in implementing vaccinations. As v reach 0.60, both propagation and resources can be significantly restrained.

Likewise, the tendency of the cumulative number of infections the US and Mexico, by numerical modeling for SEIQR-V epidemic model of influenza A (H1N1) about the two countries in the same way, and the results are shown as in FIGURE 6 and FIGURE 7. The two tables show that a better vaccination strategy is vaccination proportion approach 0.45 and 0.65 in the US and Mexico.

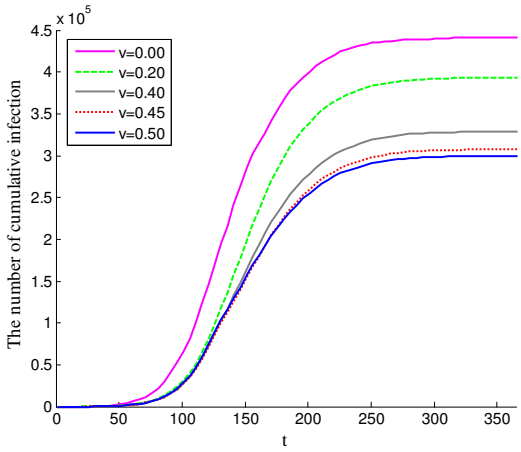

Figure 6: The tendency of the cumulative number of infections in Mexico

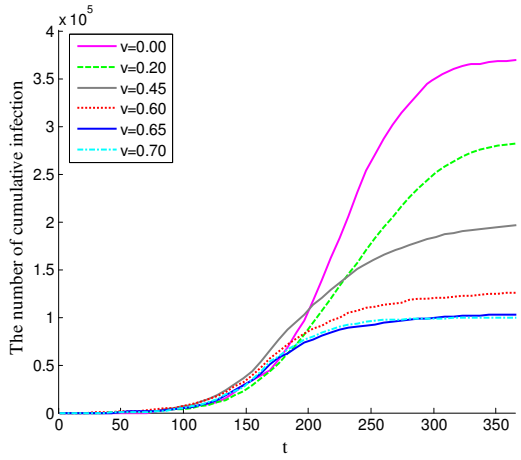

Figure 7: TThe tendency of the cumulative number of infections in the US

4. Conclusion

In this study, the infectious disease in which there is an incubation period. is the research object. Firstly, qualitative analysis the spread of infectious disease; it established SEIQR-V epidemic model based on cellular automata and then take influenza A (H1N1) for example, according to the random walking principle and the expanded Moore neighbor. By assuming reasonable simplifications, this study discuss the impact of vaccination proportion in China, the US and Mexico for the spread of infectious diseases.

Because of lack of the quarantine intensity with real data, and impact of quarantine intensity can't be analyzed directly by the research of real data, quarantine intensities q_1 and q_2 requires parameter identification. Firstly, the error vector e_i is constructed by comparison of the real data and simulation data obtaining by using orthogonal table and MATLAB software. Then, the mapping relationship between the parameters q_1 and q_2 and error vector e_i is established, by BP neural network , back propagation, transfer function and repeated training. Based on this, the simulation parameters q_1 and q_2 are obtained who are the most close to the real data, by zero vector inputting to the artificial neural network. Next, the simulation results based on simulation parameters as the real intensity of the country's isolation. Finally, the cumulative number of infected in China, the US and Mexico in conditions of different vaccination proportion are simulated, based on the intensity values of isolated intensity and so on remain unchanged.

The results show: while keeping other initial parameters constant, the infectious diseases is closely related to vaccination proportion. As vaccination proportion increasing, the tendency of the cumulative number of infections decreases. Thus it is found when the vaccination proportion approaches a certain value without causing significant change to infected individuals. The optimal vaccination proportion for China, the US and Mexico are 0.60, 0.50 and 0.65 to control transmission of influenza A (H1N1). These findings can provide government departments with scientific foundations as basis for formulating optimized epidemic prevention and control strategies.

Conflict of Interests

The authors declare that there is no conflict of interests.

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