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Analysis of epidemic vaccination strategies on heterogeneous networks: Based on SEIRV model and evolutionary game

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ABSTRACT

Nowadays, vaccination is the most effective way to control the epidemic spreading. In this paper, an epidemic SEIRV (susceptible-exposed-infected-removed -vaccinated) model and an evolutionary game model are established to analyze the difference between mandatory vaccination method and voluntary vaccination method on heterogeneous networks. Firstly, we divide the population into four categories, including susceptible individuals, exposed individuals, infected individuals and removed individuals. Based on the mean field approximation theory, differential equations are developed to characterize the changes of the proportions of the four groups over time under mandatory vaccination. Then through the analysis of the differential equations, the disease-free equilibrium point (DFE) and the endemic disease equilibrium point (EDE) are obtained. Also, the basic reproduction number is obtained by the next-generation matrix method and the stability analysis of the equilibrium points is performed. Next, by considering factors such as vaccination cost, treatment cost and government subsidy rate, differential equations are established to represent the change of vaccination rate over time. By analyzing the final vaccination coverage rate, we can get the minimum vaccination cost to make infectious disease disappear. Finally, the Monte Carlo method is used for numerical simulation to verify the results obtained from the theoretical analysis. Using the SARS-Cov-2 pandemic data from Wuhan, China, the experimental results show that when the effectiveness rate of vaccination is 0.75, the vaccination cost is not higher than 0.886 so that the vaccination strategy can be spread among the population. If mandatory vaccination is adopted, the minimum vaccination rate is 0.146.

1. Introduction

Modeling and analyzing the spreading process of epidemic vaccination strategies is helpful for in-depth analysis of the internal mechanism of epidemic spreading and prediction of spreading range, which provides an important basis for effective epidemic prevention and control [1].

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Notations

Parameter	*Definition*
$s_k(t)$	The density of susceptible individuals with degree k in the network at time t
$e_k(t)$	The density of exposed individuals with degree k in the network at time t
$i_k(t)$	The density of infected individuals with degree k in the network at time t
$r_k(t)$	The density of removed individuals with degree k in the network at time t
i	Node i
j	Adjacent node of node i
x	Vaccination rate
e	Vaccination effectiveness
β	Probability from susceptible state to exposed state
μ	Probability from infected state to removed state
ε	Probability from exposed state to infected state
b	Natural birth rate or natural mortality rate
α	Disease-induced death rate
C_V	Vaccination cost
C_I	Disease treatment cost
d	Government subsidy rate

At present, vaccination is the most effective means of disease prevention. When the number of individuals vaccinated in the population exceeds a certain number, the epidemic cannot be spread in the network, thereby indirectly protecting the unvaccinated individuals and achieving the effect of social group immunity [2]. But in the face of new diseases, people will predict the risk of disease, the risk and cost of vaccination. Individuals tend to have herd mentality and free-riding when choosing vaccination strategies [3]. Individuals' attitudes towards risks and their decision-making payoffs at previous moments will also have a great impact on their vaccination behavior [4–6]. Game theory is an effective means to quantify individual behavioral decisions. Participants maximize their own interests by choosing different strategies [7–10]. Therefore, by combining the traditional epidemic compartment model with the idea of evolutionary game, the evolution mechanism of epidemic vaccination strategies in social networks is analyzed, so as to effectively prevent and control epidemic spreading [11]. Mandatory vaccination means that population is vaccinated at a certain proportion. Voluntary vaccination means that the population voluntarily chooses vaccination strategies without the intervention of external factors.

In network propagation dynamics, researchers regard individuals in a group as nodes and regard the contact between individuals as edges to study the coevolution of network structure and epidemic spreading. Based on different standards, network propagation dynamics models have different classifications. For example, based on different networks forms, the models can be divided into various dynamic networks such as regular networks, random networks and scale-free networks. Based on the heterogeneity of network degree distribution, the model can be divided into homogeneous network model and heterogeneous network model [3,12]. Wan et al. consider the influence of the virus' drug-resistant variation and propose a novel SIVRS (susceptible-infected-variant-recovered-susceptible) epidemic spreading model with variation characteristic on scale-free networks [13]. Recently, spreading of epidemics on weighted scale-free networks and lattice-embedded scale-free networks with nonlinear infectivity has been taken into account [14-17]. In order to investigate the influence of heterogeneity of the underlying networks and quarantine strategy on epidemic spreading, a SIQRS (susceptible-infected-quarantined-recovered-susceptible) model and a SEIRS (susceptible-exposed-infected-removed-susceptible) epidemic model on the scale-free networks are presented [18,19]. Also, Li et al. present a new SIRS (susceptible-infected-removed-susceptible) epidemic model with feedback mechanism on scale-free networks [20]. In addition, researchers also use dynamic networks for risk, resilience assessment and safety support [21-23].

Furthermore, people analyzed the epidemic spreading model and its evolutionary mechanism on the multilayer network. Yang et al. study Suppression of epidemic spreading in time-varying multiplex networks [24]. By means of the quasi-static approximation, Wu et al. derive the condition for the epidemic threshold in a static multiplex network overlapped by the randomly connected subnetwork without clustering [25]. Wang et al. propose a novel epidemic model by using two-layer multiplex networks to investigate the multiple influence between awareness diffusion and epidemic propagation [26]. Influence of geometric correlations and multiple information on epidemic spreading in multiplex networks [27,28]. A two-layered multiplex network model is presented to investigate the spreading property of fatal epidemics [29]. And the interplay between the epidemic spreading and the diffusion of awareness in multiplex networks has been studied [30].

The study of evolutionary game dynamics on complex networks mainly involves the following aspects. The first issue is the selection of strategy types. Different types of games have different strategy sets. The second is the way nodes interact. In this regard, it is usually assumed that individuals only interact with their immediate neighbors and learn their strategies. The third issue is the selection of strategy update dynamics. The policy update can be synchronous or asynchronous. Different update methods may lead to different evolutionary results. What's more, if individual memory is considered or different preference learning methods are introduced, the model can be further complicated [31]. Due to the limitations of the above

factors, it is usually difficult to obtain general results for the evolutionary game research on complex networks. Although analytical explanations can be performed for some simple spatial structures, there are still many restrictions. Therefore, the spatial evolution of the system is usually studied by computer simulation [32]. Besides, charactering and predicting robustness in the networks is also studied [33-35]. For example, Zhang et al. propose the critical threshold of resisting risk as the new indicator of robustness of R&D network [36].

However, most of the previous research work only focused on the vaccination coverage rate under the evolutionary game and analyzed the influence of various factors on the vaccination coverage rate. The traditional epidemic compartment model and the evolutionary vaccination game are not combined to prevent and control epidemic spreading. Meanwhile, the proportion of individuals vaccinated in the mandatory vaccination method remains unchanged in the population. But in reality, the vaccination strategy owned by the individuals in the population is constantly changing, which is an evolutionary voluntary vaccination method.

In this paper, a SEIRV model considering population birth rate and vaccination rate is established firstly based on the mean field approximation theory. The system's disease-free equilibrium point and endemic disease equilibrium point are obtained and the basic reproduction number is analyzed. The model is to vaccinate the population by mandatory vaccination method. Then, an evolutionary model of epidemic vaccination strategy based on evolutionary game is established. Individuals in the network can obtain corresponding payoffs according to their own strategies and learn neighbors' strategies with a certain probability according to strategy update rules. By comparing and analyzing the differences between mandatory vaccination methods in heterogeneous social networks and voluntary vaccination methods based on evolutionary games, theoretically differential equations are used to derive the results. Finally, the theoretical results are verified by constructing a scale-free aggregation network and performing simulations on the network. Our contributions to existing theoretical and practical research are summarized as follows:

- ➢ A SEIRV model considering population birth rate and vaccination rate is established and the basic reproduction number was analyzed.
- ➢ The evolution of vaccination strategies based on evolutionary game on heterogeneous networks is analyzed.
- ➢ The impact of the cost of vaccination and disease treatment on the vaccination coverage rate when the evolution is stable is analyzed.
- ➢ A simulation experiment was carried out using the novel coronavirus pandemic data in Wuhan, China.

The rest of this paper is structured as follows. Section 2 establishes a SEIRV model that considers population birth rate and vaccination rate. The disease-free equilibrium point and endemic disease equilibrium point is obtained and the basic reproduction number is analyzed. Section 3 establishes the evolution model of vaccination strategy based on evolutionary game. Section 4 is the simulation analysis of the above model. We close the paper with Section 5 where conclusion and future research works are discussed.

2. Epidemic SEIRV model for mandatory vaccination strategy

In this section, based on the mean field approximation theory, a SEIRV model considering population birth rate and vaccination rate is proposed to characterize the changes of the proportions of the different groups over time under mandatory vaccination. Then through the analysis of the differential equations, the disease-free equilibrium point and the endemic disease equilibrium point are obtained. Also, the basic reproduction number is obtained by the next-generation matrix method and the stability analysis of the equilibrium points is performed.

2.1. Epidemic SEIRV model on heterogeneous network

In the epidemic SEIRV model on heterogeneous network, the status of N individuals in the population can be divided into the following categories, including susceptible, exposed, infected and removed individuals. Susceptible individuals are in a healthy state and are easily infected. Exposed individuals are infected, but do not show symptoms of infection and do not have the ability to infect other people. Infected individuals have been infected with an epidemic and have a certain degree of contagion. Recovered/removed individuals include people who have gained immunity after illness or people who died after illness.

The idea of epidemic SEIRV model on heterogeneous network is shown in Fig. 1, where

1) $S_k(t)$, $E_k(t)$, $I_k(t)$ and $R_k(t)$ respectively represent the number of susceptible, exposed, infected and recovered individuals with degree k in the network at time t.
2) x represents the proportion of susceptible individuals who receive vaccination strategy.
3) e represents the effectiveness of the vaccine.
4) β represents probability from susceptible state to exposed state.
5) ε represents probability from exposed state to infected state.
6) μ represents probability from infected state to removed state.
7) b represents natural birth rate or natural mortality rate.
8) α represents disease-induced death rate.

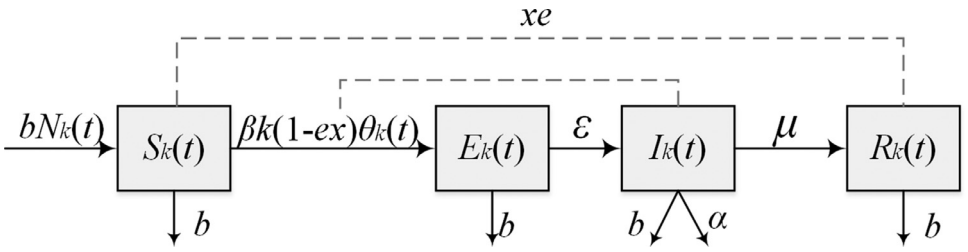

Fig. 1. Epidemic SEIRV model on heterogeneous network.

Mean-field approximation method can be used to study complex multi-agent problems. It converts a huge number of interacting multi-agent problems into a single problem in which each particle is in a weak periodic field. This method is common in statistical physics and biophysics research. The following differential equations can be obtained by the mean-field approximation method.

$$\frac{dS_k(t)}{dt} = bN_k(t) - \beta k[x(1-e) + (1-x)]S_k(t)\theta_k(t) - (xe+b)S_k(t) \tag{1}$$

$$\frac{dE_k(t)}{dt} = \beta k[x(1-e) + (1-x)]S_k(t)\theta_k(t) - (b+\varepsilon)E_k(t) \tag{2}$$

$$\frac{dI_k(t)}{dt} = \varepsilon E_k(t) - (\alpha+\mu+b)I_k(t) \tag{3}$$

$$\frac{dR_k(t)}{dt} = \mu I_k(t) + xeS_k(t) - bR_k(t) \tag{4}$$

$$N_k(t) = S_k(t) + E_k(t) + I_k(t) + R_k(t) \tag{5}$$

where $\theta_k(t) = \sum_l p(l|k)I_l(t)$ represents the probability that the nodes with degree k in the network at time t is connected to the infected nodes. When the degree of the node is not relevant, we have

$$\theta_k(t) = \theta(t) = \frac{\sum_k kp(k)i_k(t)}{\sum_k kp(k)} = \frac{\sum_k kp(k)i_k(t)}{< k >} \tag{6}$$

So the probability that any edge of the network contains the infected individual is equal to the proportion of the total number of edges connected by the infected individuals to the total number of edges in the network. $<k>$ represents the average degree of the network.

Let $i_k(t) = \frac{I_k(t)}{N_k(t)}, e_k(t) = \frac{E_k(t)}{N_k(t)}, i_k(t) = \frac{I_k(t)}{N_k(t)}, R_k(t) = \frac{R_k(t)}{N_k(t)}$. The following differential equations can be obtained.

$$\frac{ds_k(t)}{dt} = b - \beta(1-ex)s_k(t)i_k(t)\frac{< k^2 >}{< k >} - (xe+b)s_k(t) \tag{7}$$

$$\frac{de_k(t)}{dt} = \beta(1-ex)s_k(t)i_k(t)\frac{< k^2 >}{< k >} - (b+\varepsilon)e_k(t) \tag{8}$$

$$\frac{di_k(t)}{dt} = \varepsilon e_k(t) - (\alpha+\mu+b)i_k(t) \tag{9}$$

$$\frac{dr_k(t)}{dt} = \mu i_k(t) + xes_k(t) - br_k(t) \tag{10}$$

where $s_k(t)$, $e_k(t)$, $i_k(t)$ and $r_k(t)$ respectively represent the density of susceptible, exposed, infected and recovered individuals with degree k in the network at time t.

2.2. The disease-free equilibrium point and the endemic equilibrium point

Theorem 1. For a heterogeneous network with an average degree of $\langle k \rangle$, *when the basic reproduction number* $R_0<1$, *the population has a disease-free equilibrium point* $P_1 = (s_1, e_1, i_1, r_1) = (\frac{b}{xe+b}, 0, 0, \frac{xe}{xe+b})$, *where* $R_0 = [\frac{b\beta\varepsilon k_0(1-ex)}{(b+\varepsilon)(b+ex)(\alpha+b+\mu)}]^{\frac{1}{2}}$.

Theorem 2. When the basic reproduction number $R_0>1$, *the population has an endemic equilibrium point* $P_2=(s_2, e_2, i_2, r_2)$.

Proof. Firstly, we analyze the equilibrium point of the differential Eqs. (7)–(10) and let $\frac{ds_k(t)}{dt}=0$, $\frac{de_k(t)}{dt}=0$, $\frac{di_k(t)}{dt}=0$ and $\frac{dr_k(t)}{dt}=0$. Then we can get

$$b-\beta(1-ex)s_k(t)i_k(t)\frac{<k^2>}{<k>}-(xe+b)s_k(t)=0 \tag{11}$$

$$\beta(1-ex)s_k(t)i_k(t)\frac{<k^2>}{<k>}-(b+\varepsilon)e_k(t)=0 \tag{12}$$

$$\varepsilon e_k(t)-(\alpha+\mu+b)i_k(t)=0 \tag{13}$$

$$\mu i_k(t)+xes_k(t)-br_k(t)=0 \tag{14}$$

For the free-disease equilibrium point, let $e_k(t)=0$, $i_k(t)=0$ and combine Eqs. (11)–(14) to get

$$s_k(t)=\frac{b}{xe+b}, r_k(t)=\frac{xe}{xe+b} \tag{15}$$

It can be seen that in order to make the scale of infection smaller when the evolution is stable, two methods can be adopted, including increasing the proportion of vaccination and increasing the effectiveness of the vaccine.

For the endemic epidemic equilibrium point, directly solving the Eqs. (11)–(14), we can get $P_2=(s_2, e_2, i_2, r_2)$, where

$$s_2=\frac{(b+\varepsilon)(\alpha+b+\mu)}{\beta k_0\varepsilon(1-ex)}$$

$$e_2=\frac{(\alpha+\mu+\varepsilon+ex)b^2+b^3+b(\alpha\varepsilon+\mu\varepsilon-\beta k_0\varepsilon+e\mu x)+ex(\alpha\varepsilon+b\varepsilon+\mu\varepsilon+\alpha b+b\beta k_0\varepsilon)}{\beta k_0\varepsilon(b+\varepsilon)(ex-1)}$$

$$i_2=\frac{(\alpha+\mu+\varepsilon+ex)b^2+b^3+b(\alpha\varepsilon+\mu\varepsilon-\beta k_0\varepsilon+e\mu x)+ex(\alpha\varepsilon+b\varepsilon+\mu\varepsilon+\alpha b+b\beta k_0\varepsilon)}{\beta k_0(b+\varepsilon)(ex-1)(\alpha+b+\mu)}$$

$$r_2=\frac{\mu}{b}i_2+\frac{ex}{b}s_2 \tag{16}$$

And $k_0=\frac{<k^2>}{<k>}$. Then we analyze the stability of the disease-free equilibrium point. From the differential Eqs. (7)-(10), we can get the Jacobian matrix of the equation system.

$$J=\begin{bmatrix} i\beta k(ex-1)-ex-b & 0 & s\beta k(ex-1) & 0 \\ i\beta k(1-ex) & -b-\varepsilon & s\beta k(1-ex) & 0 \\ 0 & \varepsilon & -\alpha-b-\mu & 0 \\ ex & 0 & \mu & -b \end{bmatrix}$$

Let's substitute the disease-free equilibrium point into the Jacobian matrix.

$$J_1=\begin{bmatrix} -b-ex & 0 & \frac{b\beta k(ex-1)}{b+ex} & 0 \\ 0 & -b-\varepsilon & \frac{b\beta k(1-ex)}{b+ex} & 0 \\ 0 & \varepsilon & -\alpha-b-\mu & 0 \\ ex & 0 & \mu & -b \end{bmatrix}$$

We can find the eigenvalues to get

$$\lambda_1=-b-ex, \lambda_2=-b$$

$$\lambda_3=-\frac{\alpha+2b+\mu+\varepsilon}{2}-\frac{(b+ex)(\alpha^2+\mu^2+\varepsilon^2)+2(b+ex)(\alpha\mu-\alpha\varepsilon-\mu\varepsilon)+4b\beta k_0\varepsilon(1-ex)}{\frac{1}{2}(b+ex)^{\frac{1}{2}}}$$

$$\lambda_4=\frac{(b+ex)\left(\alpha^2+\mu^2+\varepsilon^2\right)+2(b+ex)(\alpha\mu-\alpha\varepsilon-\mu\varepsilon)+4b\beta k_0\varepsilon(1-ex)}{\frac{1}{2}\left((b+ex)^{\frac{1}{2}}-2b-\mu-\varepsilon-\alpha\right)}$$

To make the disease-free equilibrium point stable, the four eigenvalues of the Jacobian matrix must be less than 0. It is obvious that $\lambda_1<0$, $\lambda_2<0$ and $\lambda_3<0$. For λ_4, $(b+ex)(\alpha^2+\mu^2+\varepsilon^2)+2(b+ex)(\alpha\mu-\alpha\varepsilon-\mu\varepsilon)+4b\beta k_0\varepsilon(1-ex)=(\varepsilon-\alpha-\mu)^2+4b\beta k_0\varepsilon(1-ex)>0$. So when $(b+ex)^{\frac{1}{2}}<2b+\mu+\varepsilon+\alpha$, the disease-free equilibrium point is stable.

Table 1
Estimated parameters for COVID-19 in Wuhan, China.

Parameter	Estimated mean value	Standard deviation	Definitions
b	2.871×10^{-5}	–	Birth rate of babies per day
β	2.1011×10^{-8} [38]	1.1886×10^{-9}	Probability of transmission per contact
ε	1/7 [38]	–	Transition rate of exposed individuals to the infected class
α	1.7826×10^{-5} [38]	6.8331×10^{-6}	Disease-induced death rate
μ	0.3303 [38]	0.0521	Recovery rate of symptomatic infected individuals

2.3. The basic reproduction number

The basic reproduction number R_0 is the most important parameter that determines the internal transmission rate of epidemic. It refers to the number of individuals who can be infected by a patient on average in an environment where all individuals are susceptible without intervention. R_0 is an index used to describe the rate of infection. And it can reflect the potential and severity of epidemic outbreak. If $R_0>1$ and the epidemic is not controlled, it will show an upward trend. And the larger R_0, the faster the propagation spreading. On the contrary, when $R_0<1$, the epidemic will gradually slow down and even disappear.

In 2002, Driessche and Watmough proposed the next-generation matrix method [37]. By calculating the spectral radius of the next-generation matrix and the asymptotic stability of the disease-free equilibrium point, the basic reproduction number can be obtained. Use the spectral radius of the next-generation matrix to calculate the basic reproduction number as follows.

Step1: Divide the variables $\{s_k(t),\ e_k(t),\ i_k(t),\ r_k(t)\}$ into two categories, including infection category $\{e_k(t),\ i_k(t)\}$ and non-infection category $\{s_k(t),\ r_k(t)\}$. For infection category $\{e_k(t),\ i_k(t)\}$, F represents the infection ratio and V represents the transfer ratio.

$$\mathrm{F}=\begin{bmatrix}\beta(1-ex)s_k(t)i_k(t)k_0\\ \varepsilon e_k(t)\end{bmatrix}\qquad \mathrm{V}=\begin{bmatrix}(b+\varepsilon)e_k(t)\\ (\alpha+\mu+b)i_k(t)\end{bmatrix}$$

Step2: Solve the disease-free equilibrium point of the equation system.

$$P_1=(s_1,e_1,i_1,r_1)=\left(\frac{b}{xe+b},0,0,\frac{xe}{xe+b}\right)$$

Step3: Solve FV^{-1} at the disease-free equilibrium point.

$$F=\left[\left.\frac{\partial \mathrm{F}}{\partial(e_k(t),i_k(t))}\right|_{P_1}\right]=\begin{bmatrix}0 & \frac{b\beta k_0(1-ex)}{b+ex}\\ \varepsilon & 0\end{bmatrix}$$

$$V=\left[\left.\frac{\partial \mathrm{V}}{\partial(e_k(t),i_k(t))}\right|_{P_1}\right]=\begin{bmatrix}b+\varepsilon & 0\\ 0 & \alpha+b+\mu\end{bmatrix}$$

Then get the inverse matrix of V and the FV^{-1} matrix as follows.

$$V^{-1}=\frac{1}{(b+\varepsilon)(\alpha+b+\mu)}\begin{bmatrix}\alpha+b+\mu & 0\\ 0 & b+\varepsilon\end{bmatrix}=\begin{bmatrix}\frac{1}{b+\varepsilon} & 0\\ 0 & \frac{1}{\alpha+b+\mu}\end{bmatrix}$$

$$FV^{-1}=\begin{bmatrix}0 & \frac{b\beta k_0(1-ex)}{b+ex}\\ \varepsilon & 0\end{bmatrix}\begin{bmatrix}\frac{1}{b+\varepsilon} & 0\\ 0 & \frac{1}{\alpha+b+\mu}\end{bmatrix}=\begin{bmatrix}0 & \frac{b\beta k_0(1-ex)}{(b+ex)(\alpha+b+\mu)}\\ \frac{\varepsilon}{b+\varepsilon} & 0\end{bmatrix}$$

Step4: The matrix FV^{-1} is the next-generation matrix. The basic reproduction number R_0 is equal to the spectral radius of the next-generation matrix $\rho(FV^{-1})$. So the maximum value of the modulus of the eigenvalue of the next-generation matrix is the basic reproduction number. When $\rho(FV^{-1})<1$, the disease-free equilibrium point is locally asymptotically stable. And when $\rho(FV^{-1})>1$, the disease-free equilibrium point is unstable.

$$R_0=\rho(FV^{-1})=\left[\frac{b\beta\varepsilon k_0(1-ex)}{(b+\varepsilon)(b+ex)(\alpha+b+\mu)}\right]^{\frac{1}{2}} \tag{17}$$

where $k_0=\frac{<k^2>}{<k>}$, $<k>=\int_0^N kP(k)dk=\int_0^N k\cdot k^{-\gamma}dk=\frac{N^{2-\gamma}}{2-\gamma}$, $<k^2>=\int_0^N k^2\cdot k^{-\gamma}dk=\frac{N^{3-\gamma}}{3-\gamma}$. So $k_0=\frac{<k^2>}{<k>}=\frac{N(2-\gamma)}{3-\gamma}$.

The value of b is from the National Bureau of Statistics. Take the total number of people as $N=1.4\times10^9$, $\gamma=1.1$. The specific parameter settings are shown in Table 1.

When the vaccination coverage rate x is equal to 0, it means that no individual in the population is vaccinated. At this time, the basic reproduction number R_0 is equal to 3.6693, as shown in Fig. 2. With the increasement of vaccination coverage

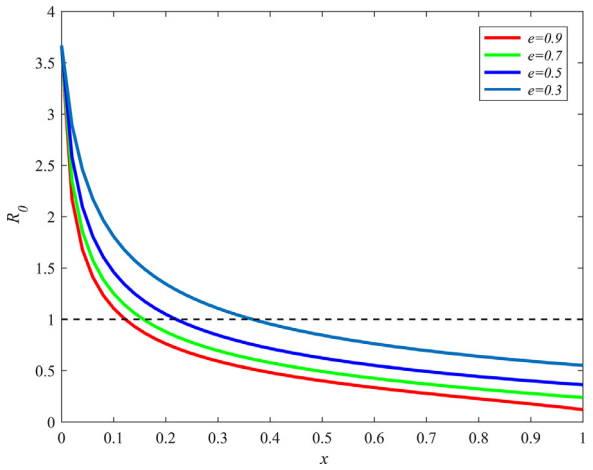

Fig. 2. The curve of the basic reproduction number R_0 with the vaccination coverage rate x (the vaccination effectiveness rates are 0.9, 0.7, 0.5 and 0.3, respectively).

rate, the basic reproduction number gradually decreases. When the value of R_0 is 1, it corresponds to a critical state. When $R_0>1$, the epidemic will spread in the population. When $R_0<1$, the epidemic will gradually disappear. Here, R_0 is a function of the vaccination rate x. It can be seen as mandatory vaccination method for a population and the vaccination ratio is x. In addition, we can get that when the vaccination effectiveness rate is 0.75, the critical value of the vaccination rate for the DFE and EDE is 0.146. Therefore, when the mandatory vaccination method is adopted, the minimum vaccination rate is 0.146.

However, the vaccination rate will change in real life. So the idea of evolutionary game is used to analyze the change of vaccination coverage rate. Each individual in the population has two strategies to choose from, including vaccination strategy and non-vaccination strategy. In the round of each game, each individual will obtain corresponding payoffs according to his own strategy. After each round of the game, each individual will compare the payoff with its neighboring nodes and take the strategy of a high-payoff neighbor with a certain probability as the strategy for the next round of the game. In this case, the problem of voluntary vaccination is analyzed.

3. Evolutionary game model for voluntary vaccination strategy

The evolution of epidemic voluntary vaccination strategy based on evolutionary game is essentially a social dilemma. According to the principle of maximizing self-interest, the non-vaccination strategy for individuals is the optimal strategy. Because when the individual is not vaccinated and is not infected, the individual does not need to pay any costs and the payoff at this time is the greatest compared to the remaining two cases. Therefore, in this case, the vast majority of individuals will not be vaccinated and believe that they will not be infected, called free-riders.

But for the group, if everyone is not vaccinated, then infectious diseases will inevitably spread in the group, causing most people to be infected. The non-vaccination strategy at this time is a bad strategy for the group. Therefore, the vaccination strategy is the optimal strategy for the group. For individuals in the group, non-vaccination strategy is the optimal strategy. But for the group as a whole, vaccination is the optimal strategy, leading to conflicts between individual strategies and group strategies. So, the social dilemmas occur. Furthermore, when an individual is vaccinated, it indirectly reduces the risk of its neighbors being infected. And its neighbor nodes are indirectly protected. In this case, so-called 'herd immunity' occurred. Therefore, from the individual's perception of the risk of infection, its neighboring nodes will adopt a non-vaccination strategy because the risk of infection decreases.

3.1. Evolutionary game model

Here, C_V is used to denote the vaccination cost that an individual needs to pay when vaccinated. And C_I is used to denote the treatment cost paid when the individual is not vaccinated and is infected. What's more, when the individual is not vaccinated and not infected, there is no need to pay any costs and the payoff is zero. Normally, the vaccination cost is less than the treatment cost, namely $C_V<C_I$. Since the vaccination cost is greater than the infection cost, the population tends to be infected. That is meaningless.

In this nonlinear system, the idea of evolutionary game is introduced. The strategy set of the individual i is $s_i=\{V, N\}$. V means vaccination strategy and N means non-vaccination strategy. In each round of the game, each node will obtain the corresponding payoff according to its strategy as shown in the above payoff matrix. Moreover, when the individual i chooses the vaccination strategy and is not infected, only the cost of vaccination needs to be paid. At this time, the individual's payoff is

Table 2
Payoff matrix.

	Healthy	Infected
Vaccination	$-C_V$	$-C_V-(1-d)C_I$
Non-vaccination	0	$-C_I$

Table 3
Proportion matrix.

	Healthy	Infected
Vaccination	$[e+(1-e)(1-f(ex))]x$ (VH)	$(1-e)f(ex)x$ (VI)
Non-vaccination	$(1-x)(1-f(ex))$ (NH)	$(1-x)f(ex)$ (NI)

$-C_V$. In contrast, when an individual chooses the vaccination strategy and is infected, the individual not only needs to pay the cost of vaccination, but also the cost of treatment. But the government will subsidize part of the treatment cost at a certain subsidy rate d. Ultimately, the node's payoff is $-C_V-(1-d)C_I$. When the node adopts the non-vaccination strategy and is not infected, the payoff obtained is 0 and this part of individuals is also called free-riders. Conversely, when a node adopts a non-vaccination strategy and is infected, the payoff obtained is $-C_I$, as shown in Table 2.

x represents the proportion of individuals in the susceptible group who choose to be vaccinated. *VH* refers to individuals who choose the vaccination strategy and maintain a healthy state. It consists of two parts, one is effectively vaccinated individuals and the other is ineffectively vaccinated but not infected individuals. The proportion of these individuals is $[e+(1-e)(1-f(ex))]x$. *VI* represents individuals who have been vaccinated and infected. The proportion of these individuals is $(1-e)f(ex)x$. *NH* refers to individuals who are not vaccinated and remain healthy. The proportion of these individuals is $(1-x)[1-f(ex)]$. *NI* represents individuals who are not vaccinated and are infected. The proportion of these individuals is $(1-x)f(ex)$, as shown in Table 3.

3.2. Femi update rules

In each round of the evolutionary game, the individual will obtain corresponding payoffs according to its strategy and state. Then in the next round of the game, the individual will compare his own payoff with the payoff of neighbor nodes to change his strategy.

$$P(s_i \leftarrow s_j) = \frac{1}{1+\exp[-(\pi_j-\pi_i)/\kappa]}$$

where π_i represents the payoff of individual i and π_j represents the payoff of neighbor node j of individual i. The parameter κ represents the individual's rational strength. $\kappa<<1$ means the individual is rational, while $\kappa>>1$ means the individual is irrational. What's more, $P(s_i \leftarrow s_j)$ represents the probability that individual i adopts the strategy of neighbor node j.

According to the Femi update rule, we can get the probability of each state conversion between the vaccination strategy and the non-vaccination strategy as follows:

$$P(VH \leftarrow NH)=\frac{1}{1+\exp[-(0-(-C_V))/\kappa]} \tag{18}$$

$$P(VH \leftarrow NI)=\frac{1}{1+\exp[-(-C_I-(-C_V))/\kappa]} \tag{19}$$

$$P(VI \leftarrow NH)=\frac{1}{1+\exp[-(C_V+(1-d)C_V)/\kappa]} \tag{20}$$

$$P(VI \leftarrow NI)=\frac{1}{1+\exp[-(-C_I+C_V+(1-d)C_I)/\kappa]} \tag{21}$$

$$P(NH \leftarrow VH)=\frac{1}{1+\exp[-(-C_V)/\kappa]} \tag{22}$$

$$P(NI \leftarrow VH)=\frac{1}{1+\exp[-(-C_I-(-C_V))/\kappa]} \tag{23}$$

$$P(NH \leftarrow VI)=\frac{1}{1+\exp[-(-C_V-(1-d)C_I)/\kappa]} \tag{24}$$

$$P(NI \leftarrow VI)=\frac{1}{1+\exp[-(-C_V-(1-d)C_I+C_I)/\kappa]} \tag{25}$$

Theoretically we analyze the level of cooperation generated by network game behavior. If the system satisfies the mean-field approximation condition, that is, in a very large group, an individual plays a game with a limited number of other individuals randomly selected. Then the mean-field theory can be used to approximate analytical solution. Different from homogeneous networks, the degree of nodes varies greatly in heterogeneous networks. Pastor-Satorras and Vespignani proposed a heterogeneous mean-field approximation (HMF) estimation method, which has the milestone significance for the network spreading of epidemics [39]. They believe that individuals with high degrees have strong statistical importance. Therefore, the strong fluctuations in the degree distribution of the network cannot be ignored.

$$\begin{aligned} x^+ &= x(1-x)(1-f(ex))[e+(1-e)(1-f(ex))]P(NH \leftarrow VH) \\ &+x(1-x)f(ex)[e+(1-e)(1-f(ex))]P(NI \leftarrow VH) \\ &+x(1-e)f(ex)(1-x)(1-f(ex))P(NH \leftarrow VI) \\ &+x(1-e)(1-x)f^2(ex)P(NI \leftarrow VI) \end{aligned} \tag{26}$$

$$\begin{aligned} x^- &= x(1-x)[1-f(ex)][e+(1-e)(1-f(ex))]P(VH \leftarrow NH) \\ &+x(1-x)f(ex)[e+(1-e)(1-f(ex))]P(VH \leftarrow NI) \\ &+x(1-e)(1-x)(1-f(ex))f(ex)P(VI \leftarrow NH) \\ &+x(1-e)(1-x)f^2(ex)P(VI \leftarrow NI) \end{aligned} \tag{27}$$

$$\begin{aligned} \frac{dx}{dt} &= x^+ - x^- \\ &= x(1-x)[1-f(ex)][e+(1-e)(1-f(ex))][P(NH \leftarrow VH) - P(VH \leftarrow NH)] \\ &+x(1-x)f(ex)[e+(1-e)(1-f(ex))][P(NI \leftarrow VH) - P(VH \leftarrow NI)] \\ &+x(1-e)(1-x)(1-f(ex))f(ex)[P(NH \leftarrow VI) - P(VI \leftarrow NH)] \\ &+x(1-e)(1-x)f^2(ex)[P(NI \leftarrow VI) - P(VI \leftarrow NI)] \end{aligned} \tag{28}$$

Because

$$\begin{aligned} P(s_i \leftarrow s_j) - P(s_j \leftarrow s_i) &= \frac{1}{1+\exp\left[-(\pi_j-\pi_i)/\kappa\right]} - \frac{1}{1+\exp\left[-(\pi_i-\pi_j)/\kappa\right]} \\ &= \tanh\left[-\frac{1}{2\kappa}(\pi_i-\pi_j)\right] \end{aligned} \tag{29}$$

So further, we have

$$\begin{aligned} \frac{dx}{dt} &= x(1-x)\Big\{(1-e)f^2(ex)\tanh\left[-\tfrac{1}{2\kappa}(C_V-dC_I)\right] \\ &+(1-f(ex))(1+ef(ex)-f(ex))\tanh\left(-\tfrac{1}{2\kappa}C_V\right) \\ &-f(ex)(ef(ex)-f(ex)+1)\tanh\left[-\tfrac{1}{2\kappa}(C_I-C_V)\right] \\ &+(1-e)(1-f(ex))f(ex)\tanh\left[-\tfrac{1}{2\kappa}(C_V+(1-d)C_I)\right]\Big\} \end{aligned} \tag{30}$$

Carrying out Taylor expansion of the above formula, we can get

$$\frac{dx}{dt} = \frac{1}{2\kappa}x(1-x)[(d+e-de)C_I f(ex) - C_V] \tag{31}$$

When the system evolution is stable, get the equilibrium point x_1=0, x_2=1.$f(ex_3) = \frac{C_V}{(d+e-de)C_I}$, namely $x_3 = \frac{1}{e}f^{-1}(\frac{C_V}{(d+e-de)C_I})$.

When the system is stable, we use the final epidemic size to express the infection rate at this time. $R(\infty)$=r_2−$xe(1-s_2)$, $f(ex) = \frac{R(\infty)}{(1-xe)} = \frac{C_V}{(d+e-de)C_I}$. Solve to get the expression of x_3.

$$x_3 = \frac{(b+\varepsilon)(\alpha+b+\mu)}{e\beta k\varepsilon(\frac{C}{d+e-de}-1)} + \frac{1}{e} \tag{32}$$

where $c = \frac{C_V}{(d+e-de)C_I} = \frac{C}{(d+e-de)}$.

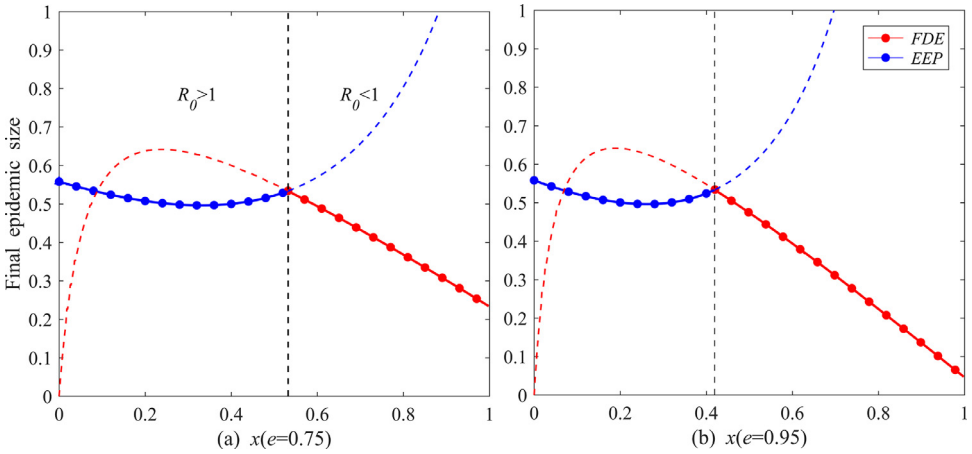

Fig. 3. The change curve of the final infection scale with the vaccination coverage rate x.

4. Numerical simulation

Above the epidemic SEIRV model and the vaccination strategy evolutionary game model are established. Here we perform numerical simulation analysis on the final epidemic size, disease-free equilibrium point, endemic disease equilibrium point and vaccination coverage rate. Finally, by constructing a scale-free aggregation network, the actual simulation is carried out on the network to verify the theoretical results.

4.1. Final epidemic size

When $R_0<1$, the final epidemic size of the population is $FES_1=\frac{xe}{xe+b}-xe(1-\frac{b}{xe+b})$. When $R_0>1$, the final epidemic size of the population is $FES_2=r_2-xe(1-s_2)$. Take b=0.05, β=0.15, ε=0.5, α=0.002, μ=0.1 and the change curve of the final infection scale with the vaccination coverage rate x is obtained.

In Fig. 3, the red curve represents the change curve of DFE with vaccination coverage rate x. And the blue curve represents the change curve of EDE with vaccination coverage rate. In figure (a), when the vaccination effectiveness rate is 0.75, the critical state of R_0=1 is $x = 0.5322$. Therefore, when x>0.5322, R_0<1 can be obtained. Under the circumstances, the system reaches the disease−free equilibrium point when epidemic spreads stably in the population. On the contrary, when x<0.5322, R_0>1 can be obtained. Under the circumstances, the system reaches the endemic equilibrium point when the infectious disease spreads stably. In figure (b), when the vaccination effectiveness rate is 0.95, the critical state of R_0=1 is $x = 0.4202$. Therefore, when x>0.4202, R_0<1 can be obtained. Under the circumstances, the system reaches the DFE when the infectious disease spreads stably in the population. On the contrary, when x<0.4202, R_0>1 can be obtained. Under the circumstances, when infectious disease spreads stably, the system reaches the EDE. In addition, we can find that when the vaccination effectiveness rate increases, the critical vaccination coverage rate of R_0=1 becomes smaller and the final epidemic size is relatively reduced.

4.2. The disease-free equilibrium point

For the DEF, the proportions of susceptible, infected and vaccinated individuals are analyzed. Combining the differential equations (7)−(10), we can get the disease-free equilibrium point as shown in Fig. 4 below.

At the DFE, the disease eventually disappears and the proportion of infected individuals in the population is zero. With the increase in vaccination effectiveness, the proportion of susceptible individuals gradually increases when the evolution is stable. The rate of convergence of the proportion of infected individuals accelerates and the proportion of effectively vaccinated individuals increases. In addition, the peak of the proportional evolution curve of infected individuals becomes smaller and shifts to the left, which means the epidemic spreading is suppressed.

4.3. The endemic disease equilibrium point

For the EDE, the proportion of susceptible, infected and vaccinated individuals is analyzed.

In Fig. 5, at the EDE, the basic reproduction number R_0 is greater than 1. And the proportion of infected individuals is not 0 when the final evolution is stable. With the increase in vaccination effectiveness, the proportion of susceptible individuals and the proportion of vaccinated individuals will increase when the network evolution is stable. However, compared with the DFE, the proportion of vaccinated individuals at the EDE is relatively small. Moreover, when the effective rate of vaccine increases, the peak of the proportion of infected individuals decreases and shifts to the right. In Fig. 6, increasing the

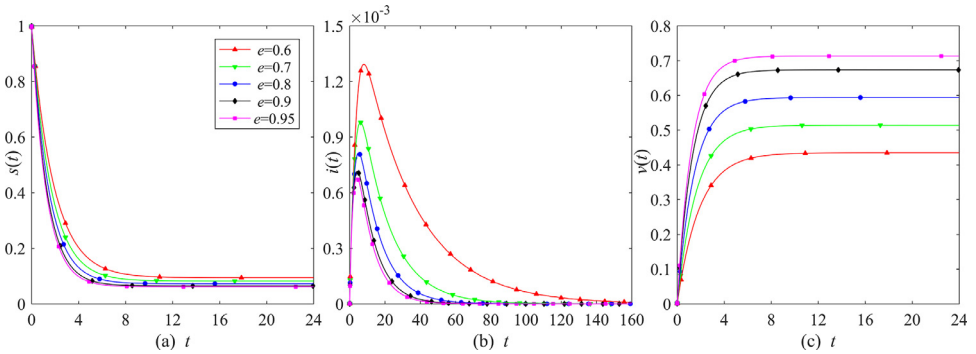

Fig. 4. At the DFE, when the vaccination rate is 0.8, the curve of the proportion of susceptible, infected and vaccinated individuals with time in the population. The effective rate of the vaccine is 0.6, 0.7, 0.8, 0.9 and 0.95 respectively.

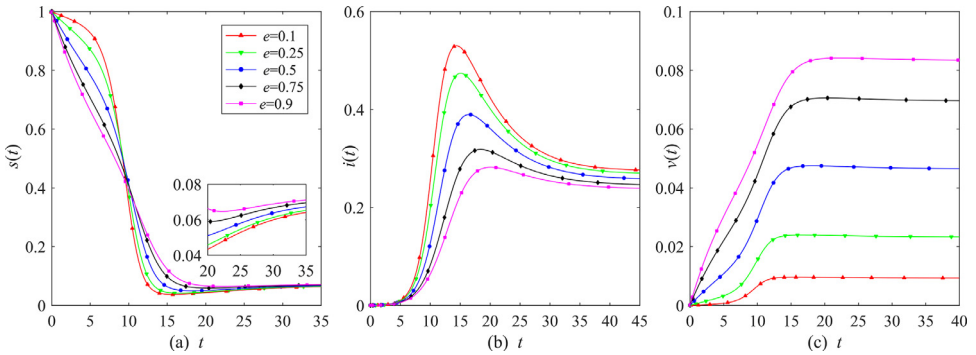

Fig. 5. At the EDE, when the vaccination rate is 0.1, the curve of the proportion of susceptible, infected and vaccinated individuals in the population over time. The vaccination effectiveness rate is 0.1, 0.25, 0.5, 0.75 and 0.9 respectively.

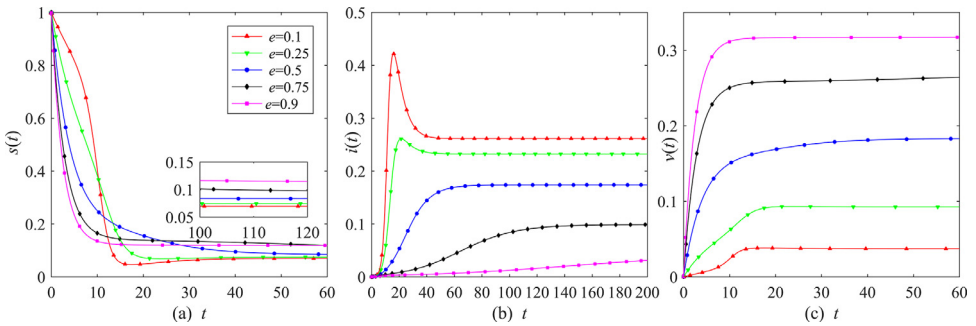

Fig. 6. At the EDE, when the vaccination rate is 0.4, the curve of the proportion of susceptible, infected and vaccinated individuals in the population over time. The vaccination effectiveness rate is 0.1, 0.25, 0.5, 0.75 and 0.9 respectively.

vaccination rate has a very obvious inhibitory effect on the epidemic spreading. And the convergence rate of the curve has accelerated. Because the higher the vaccination rate of the population is, the more possible the realization of herd immunity is. And more individuals are indirectly protected from being infected. Therefore, the higher the vaccination rate is, the smaller the final epidemic size is. For some individuals, even if they are not vaccinated, they will not be infected because they are indirectly protected by the vaccinated population. For the whole population, herd immunity is achieved at this time.

4.4. Vaccination coverage rate based on evolutionary game

We analyze the vaccination coverage rate when the vaccination strategy evolutionary game is stable.

In Fig. 7, by considering the vaccination strategy evolutionary game in the population, when the vaccination effectiveness rate remains unchanged, the vaccination coverage rate decreases with the increase of the vaccination cost. And there is a threshold between the interval [0.45, 0.65]. When the relative cost is greater than the threshold, the final vaccination coverage becomes 0. When the relative cost is zero, the vaccination coverage rate remains the same for different government

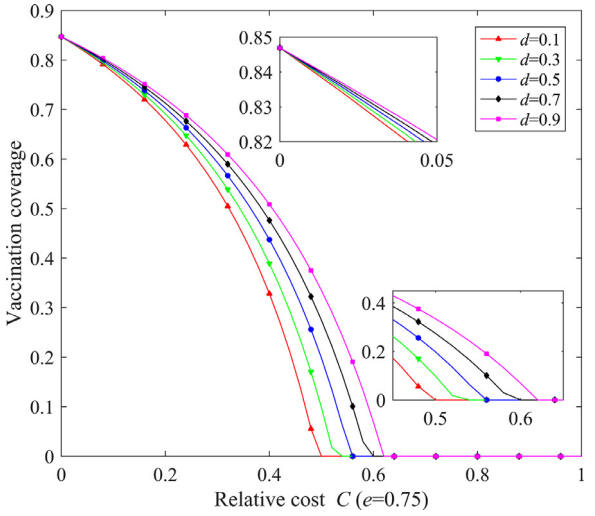

Fig. 7. The variation curve of vaccination coverage rate when the evolutionary game is stable.

Algorithm 1
The epidemic vaccination model based on evolutionary game.

Input: the scale-free network and vaccination strategy
Output: $S(t)$, $I(t)$, $R(t)$, $V(t)$
1. Construct $G(V, E)$ in PCM:
2. $\Pi_i = \frac{k_i}{\sum_{i=1}^{N_0} k_j}$
3. Initialize: parameter set: $\{\beta, \mu, \varepsilon, \alpha, b, \kappa, C_I, C_V, d, e\}$
4. strategy set: $\forall i \in G(V, E) \rightarrow s_i=\{N, V\}$
5. **for** t=1,2,•••,T **do**
6. **if** S_i=S & $rand<\beta$: S_i=E, π_i=-C_I **end if**
7. **if** S_i=E & $rand<\varepsilon$: S_i=I, π_i=-C_I **end if**
8. **if** S_i=I & $rand<\mu$: S_i=R, π_i=-C_I **end if**
9. **if** S_i=V & $rand<e$: S_i=V, π_i=-C_V
10. **else** S_i=S, π_i=-C_V-(1-d)C_I **end if**
11. $\forall i \in G(V, E)$:
12. $P(s_i \leftarrow s_j)=\frac{1}{1+e^{(\pi_i-\pi_j)/\kappa}}$
13. **end for**
14. Construct $G(V+V_0, E+E_0)$ in PCM

subsidy rates. In addition, as the government subsidy rate increases, the vaccination coverage rate increases. The curve of the vaccination coverage rate converges slowly and the threshold point moves to the right.

Next, we build a scale-free network to actually simulate the changes of vaccination rates over time. The network generated by the BA scale-free network model shows a very low aggregation coefficient, which is not consistent with the actual complex network. In view of this, we use the scale-free aggregation network model for analysis. The method of generating scale-free aggregation network is as follows.

Step1: There are m_0 isolated individuals in the initial network.

Step2: Then each time a new individual i with m edges is added to the network and connected to the $m(m<m_0)$ existing individuals in the network.

Step3: The first edge of the m edges is connected to the existing individual by the priority connection mechanism (PCM) in the BA scale-free network model. The remaining m-1 edges are randomly connected to m-1 neighbors of individual j with probability q. If the number of neighbors of individual j is $k_j<m-1$, after individual i has connected all the neighbors of j, the remaining $m-1-k_j$ edges are connected to other individuals by the priority connection mechanism in the network.

The obtained network average degree is 4. We randomly select an initial infection node with the average degree when the spreading originates in a single node. The final vaccination coverage rate is obtained by averaging 100 simulation runs. Synchronous updating rule is adopted, as shown in Algorithm 1.

In Fig. 8(a), by analyzing the formula (31), we can get three stable points when the system is stable and these three stable points are related to the vaccination cost C_V. The initial vaccination coverage rate is $x_0=7.5 \times 10^{-5}$ when the time t is 0. What's more, through formula (31), we can obtain the formula of the critical vaccination cost, namely $C^* = \frac{(b+\varepsilon)(\alpha+b+\mu)(d+e-de)}{\beta k\varepsilon(ex_0-1)+1}$, and substitute the value into the formula to get C^*=0.789. When the cost of vaccination is less than 0.789, the vaccination coverage rate in the final system will converge to 1. When the vaccination cost is greater than

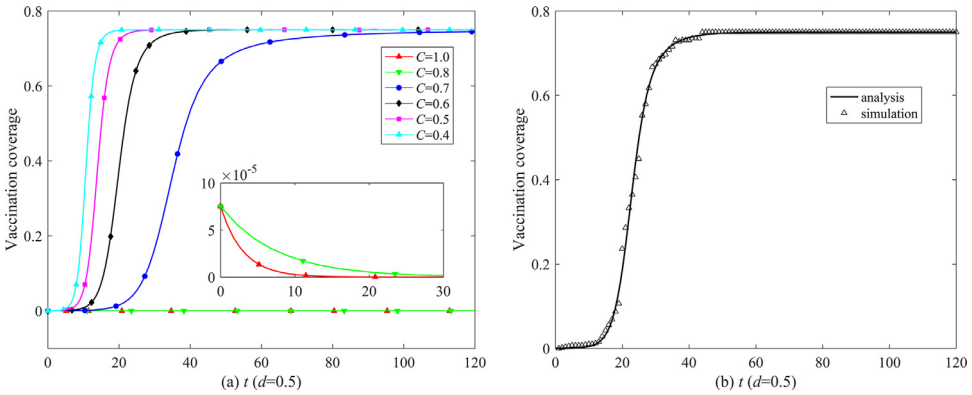

Fig. 8. The variation curve of the vaccination coverage rate with time based on evolutionary game.

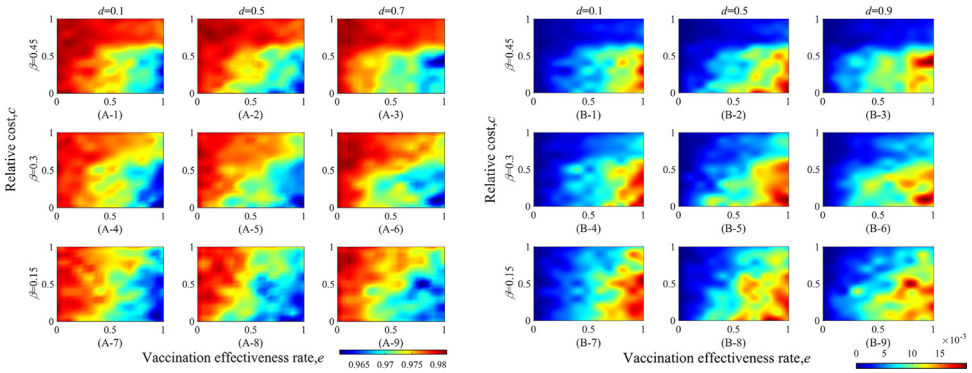

Fig. 9. The final epidemic size (left-hand panels; A-*) and final vaccination size (right-hand panels; B-*) in the case of mandatory vaccination.

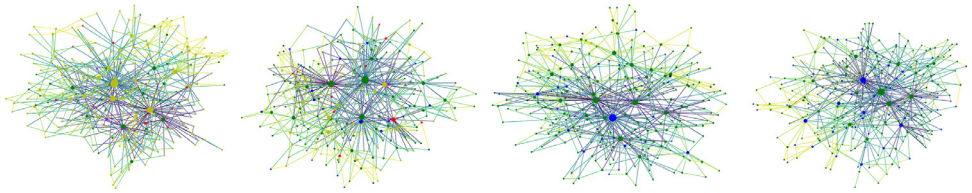

Fig. 10. The epidemic spreading based on evolutionary game.

0.789, the vaccination coverage rate in the final system will converge to 0. In Fig. 8(b), through theoretical analysis and simulation on the scale-free aggregation network, the vaccination coverage rate curves obtained are same.

The heat maps in Fig. 9 shows the influence of factors such as relative cost, vaccination effectiveness, infection rate, and government subsidy rate on the final epidemic size and the final vaccination size. It can be found that different final scales can be obtained under different parameter combinations. In general, smaller relative cost and larger vaccination effectiveness can result in smaller scale of infection and larger scale of vaccination.

In Fig. 10, the scale-free aggregation network composed of 300 nodes is constructed. Each node represents an individual and the edges between nodes represent the interaction between individuals. Yellow, brick red, red, blue, green and black represent susceptible, exposed, infected, removed, vaccinated and dead individuals respectively. We can intuitively see the state transition process of hub nodes. Besides, there are more and more green nodes in the network, indicating that the proportion of individuals vaccinated is increasing.

5. Conclusion and discussion

Based on the mean-field approximation theory, this paper establishes a SEIRV model that considers natural birth rate and vaccination rate. Then the disease-free equilibrium point and endemic disease equilibrium point are obtained in the population and the basic reproduction number is analyzed. This model is aimed for compulsory vaccination method. For a heterogeneous network with an average degree of $< k >$, when the basic reproduction number $R_0<1$, there exists a disease−free equilibrium point in the population $P_1= (s_1, e_1, i_1, r_1) = (\frac{b}{xe+b}, 0, 0, \frac{xe}{xe+b})$. When the basic reproductive number

$R_0>1$, there exist an endemic equilibrium point in the population $P_2=(s_2,e_2,i_2,r_2)$, where $R_0=[\frac{b\beta\varepsilon k_0(1-ex)}{(b+\varepsilon)(b+ex)(\alpha+b+\mu)}]^{\frac{1}{2}}$. Then, an evolutionary game model of epidemic vaccination strategy is established considering various factors such as vaccination effectiveness, vaccination cost, treatment cost and government subsidy rate. Individuals in the network can obtain corresponding payoffs according to their own strategies and learn neighbors' strategies with a certain probability according to the strategy update rules. By comparing and analyzing the differences between mandatory vaccination method and voluntary vaccination method based on evolutionary games in heterogeneous social networks, theoretically we use differential equations to derive the results. Finally, by constructing a scale-free aggregation network and performing actual simulations on the network, the theoretical results are verified. In addition, we use the epidemic parameters in Wuhan, China for analysis. The experimental results show that when the vaccination effectiveness rate is 0.75, the vaccination cost is not higher than 0.886, so that the vaccination strategy can be spread among the population. If mandatory vaccination is adopted, the minimum vaccination rate is 0.146.

Because the parameter values used in the paper are estimated under the background of epidemic prevention and control, the final vaccination rate obtained is smaller than the actual one. In a word, although we have established the evolutionary game model of vaccination strategy from the perspective of evolutionary game and compared it with the mandatory vaccination method, the intimacy between people is different in real life social networks. The intimacy between people in social networks corresponds to the weight of the edges in complex networks. Therefore, it will become more meaningful to study the spreading mechanism of epidemic in weighted networks. Besides, a network is not static in actual situations and its structure will change with the movement of nodes. Therefore, it is necessary to analyze the evolutionary mechanism of infectious diseases in dynamic networks.

Acknowledgments

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