ISSN 1749-3889 (print), 1749-3897 (online)
International Journal of Nonlinear Science
Vol.34(2022) No.2/3,pp.49-54

Analysis of Epidemic Vaccination Dilemma Considering Pathogen Evolution Based on SVIR Model and Evolutionary Game

Junjie Wei*, Juquan Wang, Xiao Wang
School of Mathematical Sciences, Jiangsu University, Zhenjiang, 212013, P. R. China
(Received October 24 2022, accepted December 8 2022)

Abstract: The global pandemic of COVID-19 warns that pathogens constantly evolve in the epidemic spreading. Therefore, we assume that the pathogens will mutate at a certain probability, the transmission rate of mutant strains increases meanwhile the cost of infection decreases, and the vaccination is only effective for the original strain but ineffective to the mutant strain. Extensive numerical simulations show that in addition to the virus mutation rate, it will lead to more interesting results, with the increase of the transmission rate of the mutant strain and the cost of vaccination, the vaccination rate will gradually decrease.
Keywords: Epidemic spreading; Pathogen evolution; Vaccination game; Evolutionary dynamics

1 Introduction

Plague, cholera, Ebola virus, and other infectious diseases occur frequently around the world. The COVID-19 epidemic since 2020 has also caused serious harm to the safety of people ' s lives and property. The epidemic spreading is often accompanied by mutations in pathogens. What does it mean to have the mutation of the pathogen? For one thing, as the mortality rate of novel coronavirus infection continues to decline, the pathogens will gradually become ' mild ' in the same host for continued transmission. For another, the mutant strain also reminds people that antiviral drugs should be reasonably treated.

We constructed the SVIR epidemic compartment model. Except for the common susceptible(S), infectious (I), and removed (R) compartments [1, 2], we added a new compartment for agents who chose to vaccinate at the onset of the epidemic(V). Heretofore, the interaction between contact mode, behavioral response, and disease dynamics based on game theory has attracted wide attention, and many important results have been achieved[3–7]. The previous studies did not consider the effect of pathogen mutations on disease transmission and vaccination during the epidemic spreading. Therefore, this paper introduces a new parameter δ to represent the mutation rate of the pathogens. Specifically, before the onset of the epidemic season, individuals can choose to vaccinate. In the stage of infectious disease transmission, the pathogen mutated with the probability of δ, and the transmission rate of mutant strains increased, but the infection cost decreased. Furthermore, we assume that the vaccine only has the effect of complete immunization against the original strain but is ineffective against the mutant strain. In other words, the vaccinated individuals are still possible to infect the mutant strain, while the non-vaccinated individuals are susceptible to the original and mutant strains. We only consider once mutation of the pathogen in this paper. Based on the above assumptions, we analyzed the effect of viral mutation on vaccination and the epidemic spreading under different network structures.

The rest of this paper is organized as follows. In Section 2, the SVIR model considering viral mutation rate and an evolutionary model of vaccination strategy based on evolutionary game are established. In Section 3, we present numerical results. Finally, we conclude this paper with summary in Section 4.

2 Epidemic SVIR and evolutionary game model

Considering the mutation of pathogens in the epidemic spreading and the effective limitation of the vaccination, we improved the SIR model. The infection state of the original strain was recorded as I_1, and the infection state of the mutant

*Corresponding author. *E-mail address*: weijunjiex@163.com

IJNS.2022.12.15

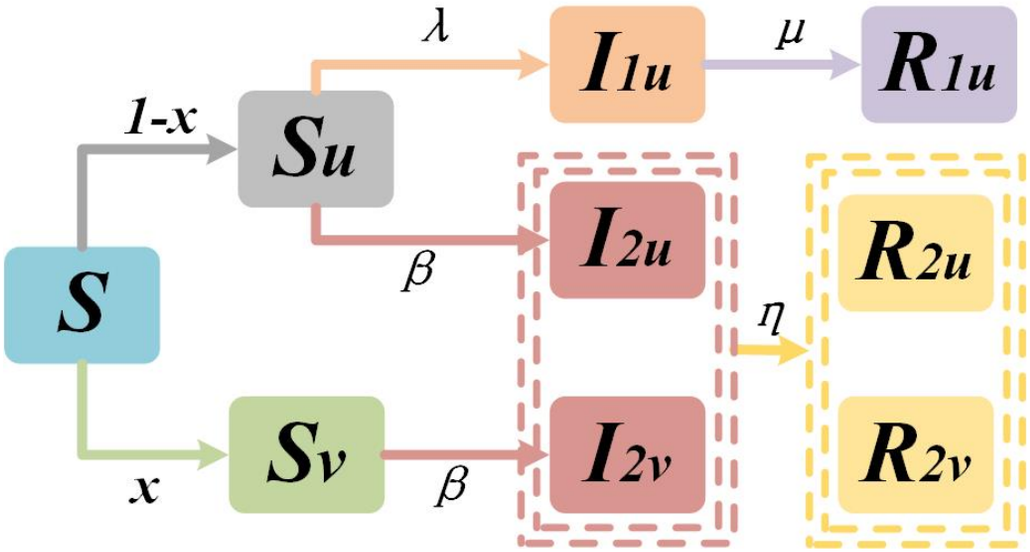

Figure 1: Individual state transition diagram: the initial vaccination rate is x. The vaccinated individuals are still possible to infect the mutant strain, and the infection rate is β. For the individuals without vaccination, the infection rate of the original strain is λ, and the infection rate of the mutant strain is β. The recovery rate of the original strain infection is μ, and the recovery rate of the mutant strain infection is η.

strain was recorded as I_2. The susceptible individuals can choose whether or not to vaccinate the vaccine. The vaccine is completely immune to the original strain, but not immune to the mutant strain. Our SVIR model (Figure 1) is most natural for seasonal influenza-like illness, and vaccination is only given temporary immunization. An epidemic season unfolds on the local time scale, while the global time scale is seasonal. From the perspective of mathematical epidemiology, the SVIR model belongs to a class of compartment infectious disease model, including eight compartments: S_u denotes the susceptible non-vaccinators, S_v denotes the susceptible vaccinators, I_{1u} denotes the non-vaccinators infected with the original strain, I_{2u} denotes the non-vaccinators infected with the mutant strain, I_{2v} denotes the vaccinators infected with the mutant strain, and R_{1u} denotes the recovery of the non-vaccinated individuals infected with the original strain. R_{2u} represents the recovery of non-vaccinated individuals infected with mutant strains, and R_{2v} represents the recovery of vaccinated individuals infected with mutant strains. Under the mean-field approximation, the population density evolution over time is given by the following coupled differential equations.

$$\frac{d_{S_u}}{d_t} = -\lambda S_u(t) I_{1u}(t) - \beta S_u(t)(I_{2u}(t) + I_{2v}(t)) \tag{1}$$

$$\frac{d_{S_v}}{d_t} = -\beta S_v(t)(I_{2u}(t) + I_{2v}(t)) \tag{2}$$

$$\frac{d_{I_{1u}}}{d_t} = \lambda S_u(t) I_{1u}(t) - \mu I_{1u}(t) \tag{3}$$

$$\frac{d_{I_{2u}}}{d_t} = \beta S_u(t)(I_{2u}(t) + I_{2v}(t)) - \eta I_{2u}(t) \tag{4}$$

$$\frac{d_{I_{2v}}}{d_t} = \beta S_v(t)(I_{2u}(t) + I_{2v}(t)) - \eta I_{2v}(t) \tag{5}$$

$$\frac{d_{R_{1u}}}{d_t} = \mu I_{1u}(t) \tag{6}$$

$$\frac{d_{R_{2u}}}{d_t} = \eta I_{2u}(t) \tag{7}$$

$$\frac{d_{R_{2v}}}{d_t} = \eta I_{2v}(t) \tag{8}$$

Here λ is the transmission rate of the original strain and β is the transmission rate of the mutant strain. We consider that the transmission rate of the mutant strain will increase, namely $\beta > \lambda$, the μ and η are the recovery rates of the original strain and the mutant strain, respectively.

Table 1: payoff matrix

Status	Healthy	Infected
Vaccinated	$-C'_V$	$-C'_V - C'_I$
Non-vaccinated	0	Π_{NI}

Considering the evolution of pathogens at the stage of disease transmission, the mutation rate of pathogens is set to δ. We believe that the variation of pathogens will affect the inoculation cost to increase, and affect the infection cost to reduce. Vaccination cost and infection cost are considered as functions of mutation rate, as follows:

$$C'_V = (1+\delta)C_V \tag{9}$$

$$C'_I = (1-\delta)C_I \tag{10}$$

The fate of individuals during the peak of the epidemic season determines their costs. There is no cost to give up vaccination and keep healthy. The cost of inoculation and infection are shown in the above section. Based on the compensation structure norms so far, the total income of individuals is determined by the group in which state they belong, as summarized in table 1.

It is worth noting that for uninoculated and infected individuals, we assume that they can only infect one of the original or mutant strains, and the corresponding infection cost is set to a function of the corresponding virus transmission rate, as follows:

$$\Pi_{NI} = -\frac{\lambda}{\lambda+\beta}C_I - \frac{\beta}{\lambda+\beta}C'_I \tag{11}$$

The x represents the proportion of individuals who choose to be vaccinated among susceptible populations. f(x) represents the proportion of infected individuals. VH represents individuals vaccinated and healthy. VI represents individuals vaccinated and infected. NH represents individuals unvaccinated and healthy. NI represents individuals unvaccinated and infected. The proportions of the above parts are shown in Table 2.

Table 2: Proportional matrix

Status	Healthy	Infected
Vaccinated	$x[1-f(x)]$	$xf(x)$
Non-vaccinated	$(1-x)[1-f(x)]$	$(1-x)f(x)$

In each round of evolutionary game, individuals gain corresponding benefits according to their strategies and states. Then in the next round of the game, the individual compares his income with the income of the neighbor node to change his strategy. This process is reflected by the Fermi function:

$$P(s_i \leftarrow s_j) = \frac{1}{1+exp[-(\pi_j - \pi_i)/\kappa]} \tag{12}$$

where π_i represents the income of individual i, and π_j represents the income of neighbor node j of individual i. Parameter κ denotes the rational strength of an individual, and $\kappa > 1$indicates that an individual is irrational[8, 9]. $P(s_i \leftarrow s_j)$ represents the probability that individual i adopts the neighbor node j strategy. The probability of state transition between the vaccination strategy and the non-vaccination strategy can be written according to the Fermi criterion. Here we list only one expression :

$$P(VH \leftarrow NH) = \frac{1}{1+exp[-(0-(-C'_V))/\kappa]} \tag{13}$$

For the proportion of inoculated individuals, if an agent imitates its strategy, the proportion will increase, if an inoculated individual imitates the strategy of non-inoculated individuals, the proportion will decrease, therefore, we get

the evolution equation of the proportion of vaccinated individuals over time as follows:

$$\begin{aligned}\frac{d_x}{d_t} =& x(1-x)[1-f(x)]^2[P(NH \leftarrow VH) - P(VH \leftarrow NH)] \\ &+ x(1-x)f(x)[1-f(x)][P(NH \leftarrow VI) - P(VI \leftarrow NH)] \\ &+ x(1-x)f(x)[1-f(x)][P(NI \leftarrow VH) - P(VH \leftarrow NI)] \\ &+ x(1-x)[f(x)]^2[P(NI \leftarrow VI) - P(VI \leftarrow NI)]\end{aligned} \tag{14}$$

3 Numerical simulation

Here, we numerically analyze the SVIR model, first isolated, and then coupled to the evolution dynamics equation. The main parameters concerned include vaccination cost, viral mutation rate, final epidemic scale, and vaccination coverage rate under the steady state. The left figure is ER random network and the right figure is BA scale-free network. The parameters have the following default values: $\lambda = 0.2$,$\beta = 0.35$,$\mu = 0.01$,$\eta = 0.02$,$x = 0.1$, $\kappa = 0.1$.

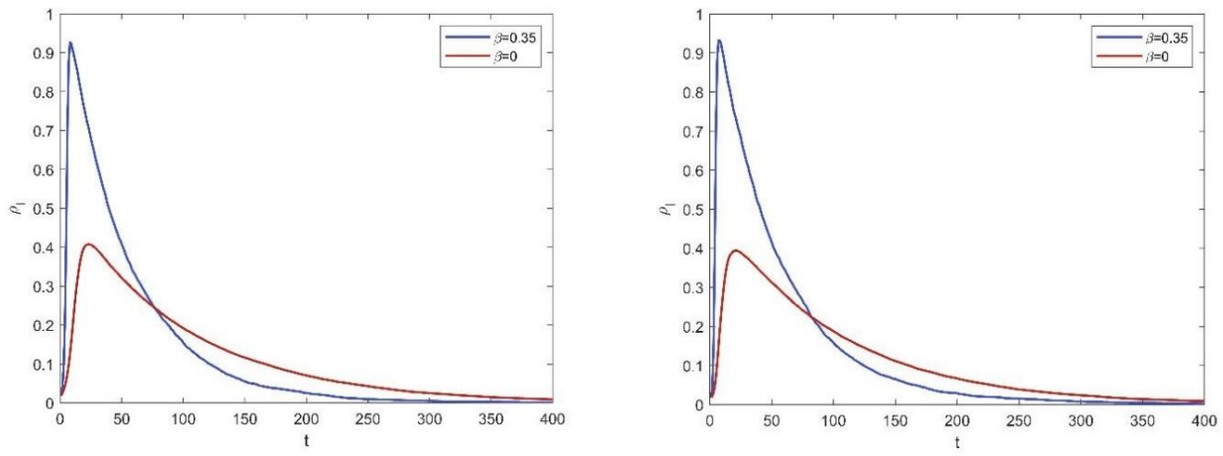

Figure 2: Changes in the density of infected people with time under different network structures without considering virus mutation ($\beta = 0$) and considering virus mutation ($\beta \neq 0$).

First of all, this paper focuses on the impact of virus mutation on the spread of infectious diseases. Therefore, we consider the change of the density of infected people with time when the virus does not mutate, that is, the mutation rate $\delta = 0$, the transmission rate of mutant strain $\beta = 0$ and the virus mutate, namely, $\delta \neq 0$, $\beta \neq 0$. As shown in Figure 2, compared with the virus mutate, that is, $\beta \neq 0$, when the virus does not mutate, the density of infected people will slowly reach the peak, and its value is far lower than the peak value when the virus mutates, which means that the virus mutation will lead to a larger scale of infection and for BA scale-free networks and ER random networks, the scale and process of disease transmission are almost the same.

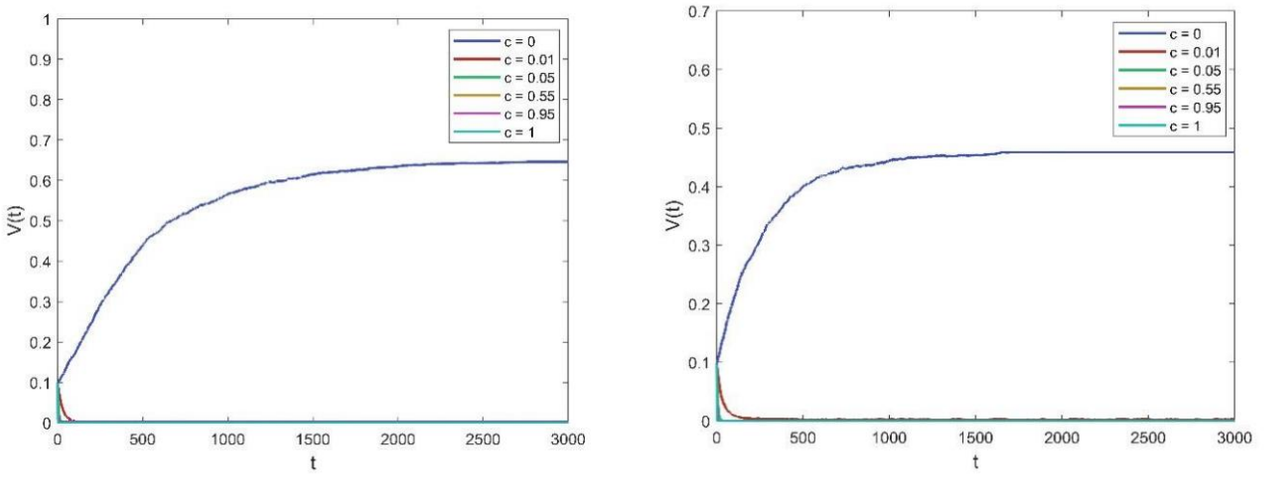

Figure 3: Under different network structure, when vaccination cost takes different value, vaccination coverage rate changes with time t.

Secondly, this paper focuses on the effect of several parameters on the vaccination rate under steady state. Next, we simulate the changes of vaccination rate with time under the influence of different parameters in ER random network and BA scale-free network. All simulations were averaged over 100 times. Figure 3 shows the change of vaccination rate with time for different values of vaccination cost. As shown in the figure, only when the vaccination cost is 0, the vaccination rate will gradually increase and eventually reach the steady-state value. Otherwise, even if the vaccination cost increases slightly to 0.01, the vaccination rate will gradually decrease to the steady-state value of 0. There is almost no difference between the simulation results of the ER random network and the BA scale-free network.

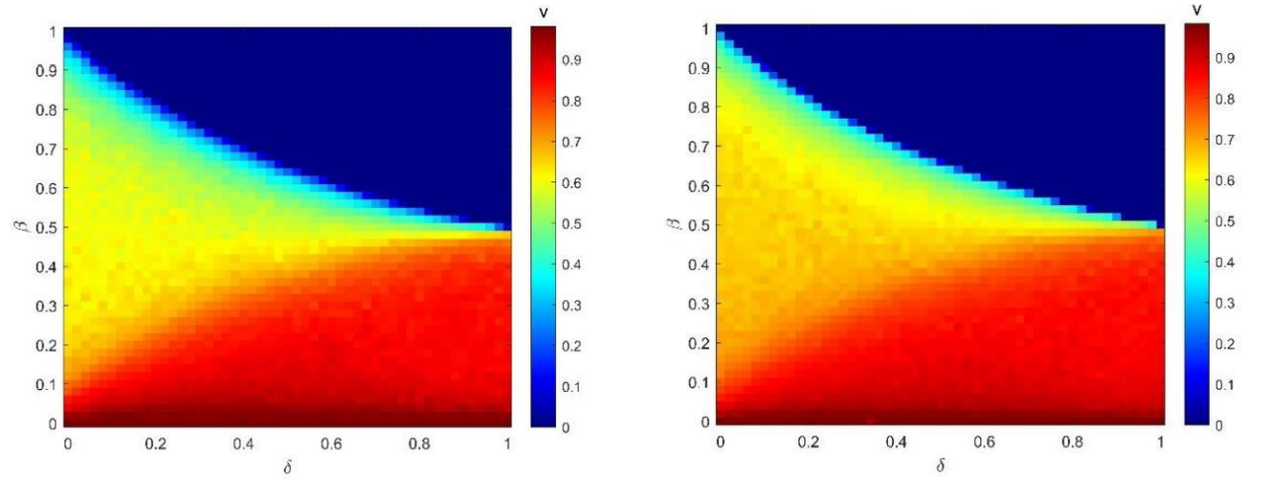

Figure 4: Under different network structures, the coverage rate of vaccination varies with the cost of vaccination and the mutation rate of the virus.

Figure 4 shows the change of vaccination rate under the dual effects of virus mutation rate and mutant strain transmission rate. The two networks still have similar simulation results. We observed that no matter how the mutation rate of the virus changes, the vaccination rate in the steady state will gradually decrease with the increase of the transmission rate of the mutant strain. In addition, we observed an interesting threshold phenomenon. When $\beta < 0.5$, with the increase of virus mutation rate, the steady-state vaccination rate will gradually increase. When $\beta > 0.5$, the steady-state vaccination rate will gradually decrease with the increase of virus mutation rate.

4 Conclusion

Considering the pathogen evolution in epidemic spreading, this paper improves the SIR model and combines it with the evolutionary decision-making model by using game theory. It is assumed that the pathogen will mutate at a certain probability, and the vaccine only has immune effect on the virus that does not mutate. Therefore, even if the individual is vaccinated, there is still a risk to infect the mutant strain. In addition, according to the reality, we assume that the mutation rate of the virus will affect the vaccination cost and increase it, while the infection cost for the mutant strain will decrease, thus studying the impact of virus mutation on the transmission of infectious diseases and the vaccination decision. Through a large number of simulations, we get the following conclusions: with the increase of the transmission rate of the mutant strain and the cost of vaccination, the vaccination rate will gradually decrease. For the virus mutation rate, we observe an interesting phenomenon, that is, when the transmission rate of the mutant strain is less than 0.5, the vaccination rate gradually increases with the increase of the virus mutation rate. When the transmission rate of the mutant strain is greater than 0.5, the vaccination rate gradually decreases with the increase of the virus mutation rate. By comparison, we further find that the simulation results of ER random network and BA scale-free network are the same. We only consider once mutation of the pathogen in this paper. This is not the case in reality. Pathogen evolution will run through the spread of infectious diseases, and the preparation of vaccines will also be improved accordingly. How the co-evolution of pathogens and vaccines will affect the diseases spreading and vaccination decisions is an interesting topic that can be explored in the future.

Acknowledgments

This work was supported by the China Postdoctoral Science Foundation (2019M661731).

References

[1] Kermack, W. O. , and A. G. Mckendrick . Contributions to the mathematical theory of epidemics further studies of the problem of endemicity. ,1991, 53(1-2), 89-118.

[2] Hethcote, Herbert, and W. The Mathematics of Infectious Diseases. The mathematics of infectious diseases. SIAM Rev.,2000, 42(4), 599-653.

[3] Xu, F. , and R. Cressman . Disease Control through Voluntary Vaccination Decisions Based on the Smoothed Best Response. Computational and Mathematical Methods in Medicine,2014,(2014-2-16), 2014, 825734.

[4] Wang, Zhen , et al. Universal scaling for the dilemma strength in evolutionary games. Physics of Life Reviews,2015, 14, 1-30.

[5] Zhang, H. , et al. Hub nodes inhibit the outbreak of epidemic under voluntary vaccination. New Journal of Physics, 2010, 12(2), 023015.

[6] Bauch, Chris T . Imitation dynamics predict vaccinating behaviour. Proceedings of the Royal Society B: Biological Sciences, 2005.

[7] Mbah, Ml Ndeffo , et al. The Impact of Imitation on Vaccination Behavior in Social Contact Networks. Plos Computational Biology, 8(4), 2012,e1002469.

[8] Podobnik, B. , et al. Biological conservation law as an emerging functionality in dynamical neuronal networks. Proc Natl Acad Sci U S A, 2017,05704.

[9] Kuga, K. , J. Tanimoto , and M. Jusup . To vaccinate or not to vaccinate: A comprehensive study of vaccination-subsidizing policies with multi-agent simulations and mean-field modeling. Journal of Theoretical Biology (2019).