2021 6th International Conference on Intelligent Computing and Signal Processing (ICSP) | 978-1-6654-0413-6/20/$31.00 ©2021 IEEE | DOI: 10.1109/ICSP51882.2021.9408970

2021 IEEE 6th International Conference on Intelligent Computing and Signal Processing (ICSP 2021)

Control of COVID-19 Pandemic: Vaccination Strategies Simulation under Probabilistic Node-Level Model

Mengxuan Chen
Intelligent Transportation and Logistics Systems
Laboratory, Tsinghua-Berkeley Shenzhen Institute
Tsinghua University
Shenzhen, P.R China
chenmx19@mails.tsinghua.edu.cn

Chun-Lin Kuo
Intelligent Transportation and Logistics Systems
Laboratory, Tsinghua-Berkeley Shenzhen Institute
Tsinghua University
Shenzhen, P.R China
guojl@mails.tsinghua.edu.cn

Wai Kin Victor Chan*
Intelligent Transportation and Logistics Systems
Laboratory, Tsinghua-Berkeley Shenzhen Institute
Tsinghua University
Shenzhen, P.R China
Wai Kin Victor Chan is the corresponding author (e-mail:
chanw@sz.tsinghua.edu.cn)

Abstract—**This paper aims at constructing a probabilistic node-level time-dependent contagious disease spreading model for coronavirus disease (COVID-19) pandemic which is called *SEINRVseinr* by introducing exposed and asymptomatic infectious state, imperfect vaccination, reinfected possibility and weighted undirected graph for social network into the traditional probabilistic node-level Susceptible-Infectious-Recovered (SIR) network model. This paper simulates the effectiveness of five vaccination strategies (including random base, degree-target base, random acquaintance, first-neighbor and second neighbor strategies) in random network, small world network and scale-free network. Compared with the benchmark model, the results show that random acquaintance strategy is efficient strategy and neighbors' strategies perform better in certain interval.**

Keywords- Probabilistic Node-level Model, Imperfect Vaccination, Numerical Simulation

I. INTRODUCTION

Coronavirus disease 2019 (with COVID-19 as its abbreviation) is a typical type of severe acute respiratory syndrome coronavirus and has been a serious ongoing global pandemic featured with long latent period[1], high ratio of asymptomatic infection and low fatality rate. The longest incubation time from infection to symptoms is almost two weeks. It can be transmitted by human-to-human close contact through air or droplet or surface contact of the contamination. Clinical cases suggest that pre- and asymptomatic infectious group of people may contribute to 80% of the transmission [1].

Along with the outbreak of the disease, network scientists are interested in the spreading of the disease in the social network model. Network simulation [2] is the most commonly researched methodology for the spread of the disease [3], and the contagion network is often regard as the time-dependent adaptive network which could be described through the partial derivative equations (PDEs), e.g., the famous Susceptible-Infectious (SI) model [4] in Gross et al [5] and its later extended version the Susceptible-Infectious-Recovered (SIR) model [6, 7]. In the early stage of this research, the closed form of the node level approximation scheme was come up with by degree-based pair approximation [8] or degree-based MF approximation [7].

Control of COVID-19 varies a lot. Shutdown, segregation and contract tracing are used to control the COVID-19 in the early stage. Firth JA, Hellewell J, Klepac P, Kissler S, Group CC-W, Kucharski AJ, et al employed real-world social network to model the contract tracing and quarantine approach by gather the GPS data from a documentary dataset of BBC [9]. Another common way to control the virus is by vaccine which works by creating an immune memory of the pathogen at the individual level and creates herd immunity at the population level and one of the global strategies to respond to COVID-19 published by World Health Organization (WHO) is to develop safe and effective vaccines and therapies that can be delivered at scale and that are accessible based on need. Especially in macro level, different ways to select nodes to get vaccinated are studies. For example, target strategy which use different measurement of network clustering such as degree, centrality, betweenness. Acquaintance strategy doesn't require the helicopter knowledge about the network since it selects a certain fraction of nodes at random and vaccine its neighbors [10]. Since different strategies meets with different scenarios, a framework of combination of all the strategy has come up by Yang [11]. Also, new vaccination strategy has been tried like a new strategy based on Negative

---

[11] During latent period, individuals can't spread the virus but they get the virus without have any symptoms. During asymptomatic infectious period, individuals can spread the virus but they don't have any symptoms. The incubation period is the time from acquiring the virus to the first symptoms of illness which includes the latent period and the asymptomatic infectious period. See https://www.futurelearn.com/info/courses/ebola-in-context/0/steps/4828 for more information about incubation period and latent period.

978-1-6654-0413-6/21/$31.00 ©2021 IEEE

Key Player Problem which is similar to influencer identification problem in opinion and information spreading [12] or practical ones like first neighbor and second neighbor strategy [13].

In our previous research, we came up with two types of dynamic network for vaccination under SIR model. The former one is discrete vaccination strategy by site percolation [14] which means the vaccination is taken at certain frequency and equivalent to disconnect all the edges for the selected nodes [15]; the latter one is to consider the vaccination as a new state for the disease propagation process and has a new probability to get vaccinated in every timestamp so it is called continuous vaccination strategy [16].

In this paper, we introduce the characteristics of COVID-19 into our model and consider the social network as a weighted undirected graph and extend the five typical vaccination strategies (including random base, degree-target base, random acquaintance, first-neighbor and second neighbor strategies) for the weighted undirected graph and conduct the simulation in scale free network, random network and small world network.

II. MODEL FOR COVID19

In this part, the characteristics of COVID-19 would be introduced into the probabilistic node level disease spreading model.

Here, we defined the parameters used in the model as the following.

TABLE I. DEFINITION OF ALL PARAMETERS

Name	Description
$s_k(t)$	Probability of node k being susceptible at time t.
$e_k(t)$	Probability that node k being exposed at time t.
$i_k(t)$	Probability of node k being infected at time t.
$nsi_k(t)$	Probability of node k being asymptomatic infectious at time t.
$r_k(t)$	Probability of node k being recovered at time t.
$v_k(t)$	Probability of node n being vaccinated at time t.
β	Probability of getting exposed on a contact in a unit time ξ_t. (transmission rate)
θ	Probability of getting infected in a unit time ξ_t.
γ	Probability of getting recovered after infected in a unit time ξ_t. (recovered rate)
η	Probability of getting asymptomatic infectious in a unit time ξ_t.
π	Probability of getting recovered after asymptomatic infectious in a unit time ξ_t.
ε	Probability of getting vaccinated in a unit time ξ_t (vaccination rate)
A	Adjacent matrix for an undirected graph. (symmetric adjacent matrix)

A. *Introduction of Exposed State, Asymptomatic Infectious State*

COVID-19 is featured with long latent period which mean people who get sick without knowledge of it or any symptoms. In this pandemic, many people are asymptomatic which means they could spread the virus but still don't have any symptoms. With these two features and the easy spreading way of the disease, the virus is more powerful compared with other pandemic and we introduce two new state into the original probabilistic node level SIRV model where a deterministic state cannot be obtained in a probabilistic model.

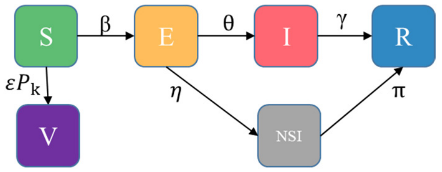

Figure 1 Propagation process for COVID-19 with exposed and asymptomatic states

In the time-dependent probabilistic node-level model, we could write the Partial Derivative Equations (PDEs) considering the state transfer departure of the node. For example, when transferring from exposed state to infectious state, the parameter θ denotes the transfer rate; when transferring from exposed state to asymptomatic infectious state, the term $(1-\theta)\,\eta$ denotes the transfer rate. It's the same for nodes transferring from susceptible state to vaccination state with $(1-\beta)\varepsilon$ as the transfer rate.

$$\frac{ds_k}{dt} = -\beta s_k \sum_j A_{kj} i_j - (1-\beta)\varepsilon s_k P \tag{1}$$

$$\frac{de_k}{dt} = \beta s_k \sum_j A_{kj} i_j - \theta e_k - (1-\theta)\eta e_k \tag{2}$$

$$\frac{di_k}{dt} = \beta s_k \sum_j A_{kj} i_j - \gamma i_k \tag{3}$$

$$\frac{dnsi_k}{dt} = (1-\theta)\eta e_k - \pi_k nsi_k \tag{4}$$

$$\frac{dr_k}{dt} = \gamma i_k + \pi_k nsi_k \tag{5}$$

$$\frac{dv_k}{dt} = (1-\beta)\varepsilon s_k P_k \tag{6}$$

Here, for (1), it means the node exposed process, and the probability to get exposed is around the multiplication of the transmission rate β and the probability of susceptible and the sum of infectious node around this typical node, which is represented by the adjacent matrix A and the probability of remain susceptible would also be decreased by getting vaccinated. For (2), the probability of explosion could be increased by the exposed process and decreased by the probability of the node to transfer from exposed state to infectious state or asymptomatic infectious state. For (3), the probability to remain infectious would by increased by contacting infectious people and decreased by independent recovery. For (4), the probability to remain asymptomatic infectious could be increased by not getting any symptom but coming from exposed state and decreased by independent recovery. Similarly, the process of recovery and getting vaccinated would be written like (5) and (6).

B. *The Possibility of Reinfection*

The clinical cases of recovered people getting infected again suggest that COVID-19 virus evolved so quickly that the antibody the patients produced lose efficiency in a time period and it is possible to become susceptible even after the patients recovered. Then we consider the recovered state still have a transfer rate as α.

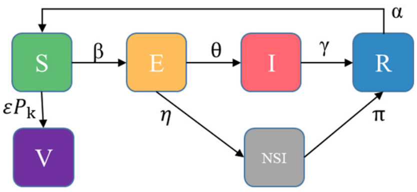

Figure 2 Propagation process for COVID-19 with the possibility of reinfected

Compared with *SEINRV* modle without the possibility of reinfected, the PDEs for s_k and r_k are changed.

$$\frac{ds_k}{dt} = \alpha_r k - \beta s_k \sum_j A_{kj} i_j - (1-\beta)\varepsilon s_k P \tag{7}$$

$$\frac{de_k}{dt} = \beta s_k \sum_j A_{kj} i_j - \theta e_k - (1-\theta)\eta e_k \tag{8}$$

$$\frac{di_k}{dt} = \beta s_k \sum_j A_{kj} i_j - \gamma i_k \tag{9}$$

$$\frac{dnsi_k}{dt} = (1-\theta)\eta e_k - \pi_k nsi_k \tag{10}$$

$$\frac{dr_k}{dt} = \gamma i_k + \pi_k nsi_k - \alpha r_k \tag{11}$$

$$\frac{dv_k}{dt} = (1-\beta)\varepsilon s_k P_k \tag{12}$$

C. *Imperfect Vaccination*

In our previous models, we consider the perfect vaccination which means once get vaccinated all the edges would be disconnected or once vaccinated the state of the node remain in the so-called vaccination state forever. To make the situation more closed to the real situation considering the possibility of the failure of the vaccination even after the injection, we suppose the vaccination state node could be infected but in a much lower probability.

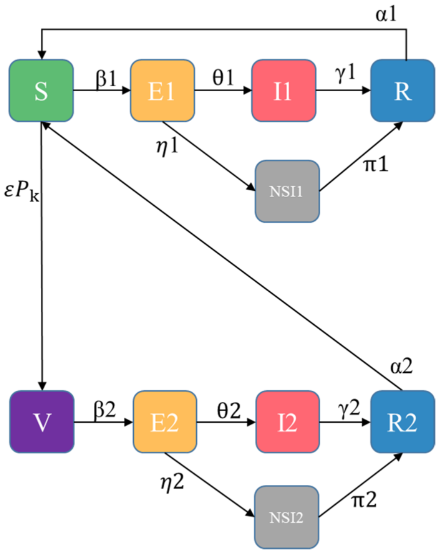

Figure 3 Propagation process for COVID-19 considering imperfect vaccination

Here, the PDEs have ten states and ten equations in total. We called this complicated model *SEINRVseinr*.

$$\frac{ds_k}{dt} = \alpha_1 r_{1k} + \alpha_2 r_{2k} - \beta_1 s_k \sum_j A_{kj} i_j - (1-\beta_1)\varepsilon s_k P_k$$

$$(i_j \ includes \ i_{1j} \ and \ i_{2j}) \tag{13}$$

$$\frac{de_{1k}}{dt} = \beta_1 s_k \sum_j A_{kj} i_j - \theta_1 e_{1k} - (1-\theta_1)\eta_1 e_{1k} \tag{14}$$

$$\frac{di_{1k}}{dt} = \beta_1 s_k \sum_j A_{kj} i_j - \gamma_1 i_k \tag{15}$$

$$\frac{dnsi_{1k}}{dt} = (1-\theta_1)\eta_1 e_{1k} - \pi_{1k} nsi_{1k} \tag{16}$$

$$\frac{dr_{1k}}{dt} = \gamma_1 i_{1k} + \pi_{1k} nsi_{1k} - \alpha_1 r_{1k} \tag{17}$$

$$\frac{dv_k}{dt} = (1-\beta_1)\varepsilon s_k P_k - \beta_2 v_k \sum_j A_{kj} s_j \tag{18}$$

$$\frac{de_{2k}}{dt} = \beta_2 s_k \sum_j A_{kj} i_j - \theta_2 e_{2k} - (1-\theta_2)\eta_2 e_{2k} \tag{19}$$

$$\frac{di_{2k}}{dt} = \beta_2 s_k \sum_j A_{kj} i_j - \gamma_2 i_k \tag{20}$$

$$\frac{dnsi_{2k}}{dt} = (1-\theta_2)\eta_2 e_{2k} - \pi_{2k} nsi_{2k} \tag{21}$$

$$\frac{dr_{2k}}{dt} = \gamma_2 i_{2k} + \pi_{2k} nsi_{2k} - \alpha_2 r_{2k} \tag{22}$$

D. *Weighted Undirected Graph*

The classical probabilistic node-level SIR model uses symmetric adjacent matrix where “1” means there are connections in one contract. For COVID-19, it’s suggested that some groups of people get higher possibility to get infected in only one contact, e.g., medial staff, seafood vendors and so on

[17]. Although these groups of people have low degree in the network, they actually have more contact with the virus thus they should be assigned to a higher weight. Here, we consider this factor and use weighted undirected graph in this new model.

The new adjacent matrix is still symmetric but with all the weight of the nodes which follows a power law distribution with the sample mean of 1 for comparability.

$$\begin{bmatrix} 0 & 1 & 0 & 0 & 1 & \dots & 1 \\ 1 & 0 & 1 & 1 & 0 & & 0 \\ 0 & 1 & 0 & 0 & 1 & & 1 \\ 0 & 1 & 0 & 0 & 1 & & 1 \\ 1 & 0 & 1 & 1 & 0 & \dots & 0 \\ \dots & & & & & & \\ 1 & 0 & 1 & 1 & 0 & \dots & 0 \end{bmatrix} \longrightarrow \begin{bmatrix} 0 & w_{12} & 0 & 0 & w_{15} & \dots & w_{1n} \\ w_{12} & 0 & w_{23} & w_{24} & 0 & & 0 \\ 0 & w_{23} & 0 & 0 & w_{35} & & w_{3n} \\ 0 & w_{24} & 0 & 0 & w_{45} & & w_{4n} \\ w_{14} & 0 & w_{35} & w_{45} & 0 & \dots & 0 \\ \dots & & & & & & \\ w_{1n} & 0 & w_{3n} & w_{4n} & 0 & \dots & 0 \end{bmatrix} \tag{23}$$

$$where\ w_{ij} \sim f(x)\ and\ f(x) = kx^{\alpha} where\ \overline{w_{ij}} = 1$$

$$(which\ means\ w_{ij}\ follows\ Power\ Law\ Distribution\ with\ sample\ mean\ equal\ to\ 1)$$

Figure 4 Examples of extension of the adjacent matrix

III. VACCINATION STRATEGIES

By considering the weighted undirected graph, we test the following five vaccination strategies based on *SEINRVseinr.*

A. Benachmark: Random Strategy

Pk in the PDEs is where we set our vaccination strategies. Here, the adjacent matrix doesn't change the random strategies where we randomly take some nodes to get vaccinated so we use $P_k = 1$ as a benchmark for our strategies.

B. Weighted Degree-base Target Strategy

The traditional degree-base target strategy is to take the most highly connected nodes in the network to get vaccinated. In our COVID-19 featured model, the degree-base target strategy is based on the weighted degree which consider the weight of the edges in the network.

$$P_k = \frac{k \sum_j A_{kj}}{\sum_k \sum_j A_{kj}} \tag{24}$$

For example, in the previous probabilistic node level model, the node with high degree would be selected; node with high degree but very low weight wouldn't be selected while nodes with low degree but high weight would be selected in this circumstance. This is realistic in the implementation of vaccination strategy since the government is considering get the medical staff the priority role to get vaccinated since their weights are higher on average although with likely low degree.

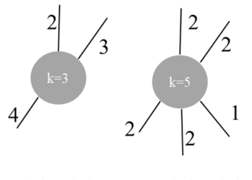

Figure 5 An example for weighted degree(Weighted degree = 9 in these two cases)

C. Important Group's First Neighbor Strategy

Important group's first neighbor strategy is an extension from random acquaintance strategy. Random acquaintance strategy is to randomly take some nodes and select its neighbors to get vaccinated. It's a useful and effective strategy when global information about the network structure is lost(1). In the weighted undirected graph, instead of randomly selecting some nodes and getting their neighbor vaccinated we select the nodes with the most highly average weight and vaccinated their neighbor. Since the weight is considered in the weighted adjacent matrix, their share the same function for P_k.

$$P_k = \frac{k \sum_j A_{kj} \sum_l A_{jl}}{\sum_k \sum_j A_{kj} \sum_l A_{il}} \tag{25}$$

D. Improved First Neighbor Strategy

First neighbor strategy is to get the direct neighbors of the infected node whose degree crosses certain threshold vaccinated. In *SEINRVseinr* model, the nodes with more infected neighbors have a higher probability to get vaccinated. Here, this degree measure has already taken the weight into consideration.

$$P_k = \frac{k \sum_j A_{kj} i_j}{\sum_k \sum_j A_{kj} i_j} \tag{26}$$

E. Improved Second Neighbor Strategy

Second neighbor strategy is to get the neighbors' neighbors of the infected nodes vaccinated. Also, when we considering the neighbor of the infected nodes, the nodes with higher weight would get more attention in our model.

$$P_k = \frac{k \sum_j A_{kj} i_j \sum_l A_{jl} i_l}{\sum_k \sum_j A_{kj} \sum_l A_{il}} \tag{27}$$

IV. SIMUALTION RESULTS

A. Efficiency of different strategies

We conduct 100 times network simulation for 100 nodes in 100 days as the time period of the five original vaccination strategies for each model including the benchmark model (SIRV) and *SEIRNVseinr* in normal adjacent matrix and *SEIRNVseinr* in weighted adjacent matrix in three different networks (scale free network, random network and small world network) respectively. The initialization conditions of the model are listed in TABLE II.

TABLE II. INITIALIZATION CONDITIONS OF THE SIMULATION

Name	**Number**	**Name**	**Number**	**Name**	**Number**
m	5	i_0	1	α_1	0.1
p	0.2	n_0	1	ε_1	0.1
E_0	4	r_0	1	β_2	0.6
I_0	2	β_1	0.3	θ_2	0.2
N_0	2	θ_1	0.7	η_2	0.1
R_0	1	η_1	0.8	γ_2	0.6
V_0	1	γ_1	0.2	π_2	0.7
e_0	1	π_1	0.4	α_2	0.1

Figure 6, 7, 8 are the simulation sensitivity analysis results of the vaccination rate epsilon. The horizontal axis denotes vaccination rate epsilon while the vertical axis denotes the average infectious probability for these 100 nodes and over the 100 days' time period getting rid of infectious nodes in the very beginning. The result of this sensitivity analysis is declining lines since with higher vaccination rate for the whole population the average infectious probability will be lower and the better the vaccination strategy, the quicker the average value will decrease.

Figure 6 shows the result for benchmark SIRV model in random network, scale free network and small world network. For all these three networks, degree base target strategy is best while random acquaintance strategy and random strategy make no distinction of rank while first neighbor strategy and second neighbor strategy fail to beat the random strategy. Theoretically, the remaining strategies should be better than random strategy but the benchmark model shows that these strategies aren't as powerful as we thought in the benchmark condition.

Then, we simulate for the *SEINRVseinr* model and find that except for scale free network where degree base target excel, random acquaintance strategy is better than other strategies which can be illustrated in Figure 7. The simulation result of the *SEINRVseinr* model with weighted indirect graph share the similar conclusion with that with normal adjacent matrix one. For the *SEINRVseinr* model with unweighted indirect graph under scale-free network, when the vaccination rate is larger than approximately 0.55, the neighbors strategies excel the random strategy, while for the *SEINRVseinr* model with weighted indirect graph, when vaccination rate is between 0.28 and 0.65 the neighbors strategies would excel.

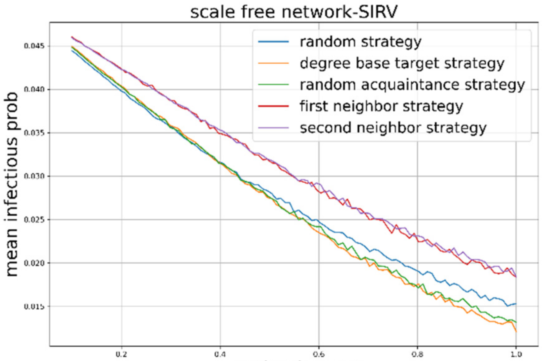

Figure 6 Simulation results for SIRV under scale free network

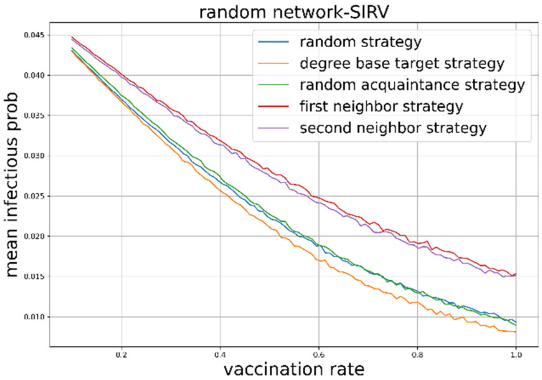

Figure 7 Simulation results for SIRV under random network

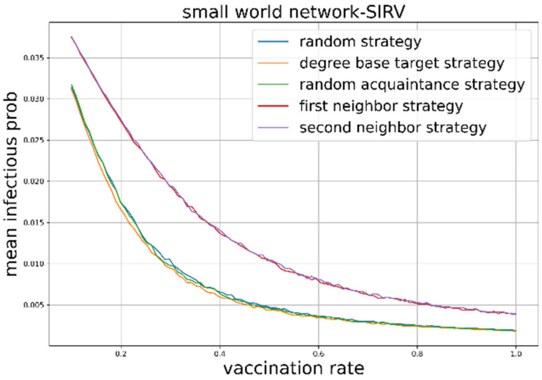

Figure 8 Simulation results for SIRV under small world network

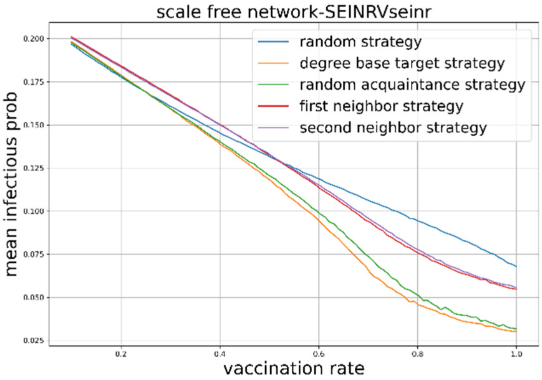

Figure 9 Simulation results for *SEINRVseinr* with unweighted undirected graph under scale free network

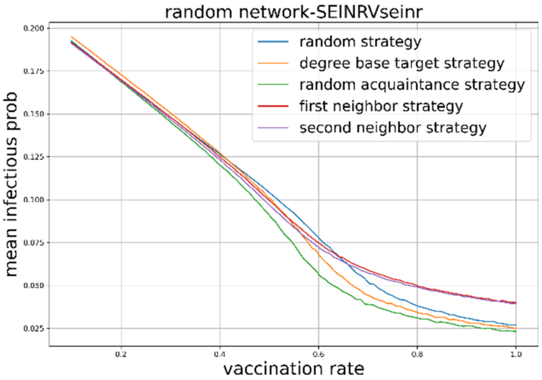

Figure 10 Simulation results for *SEINRVseinr* with unweighted undirected graph under random network

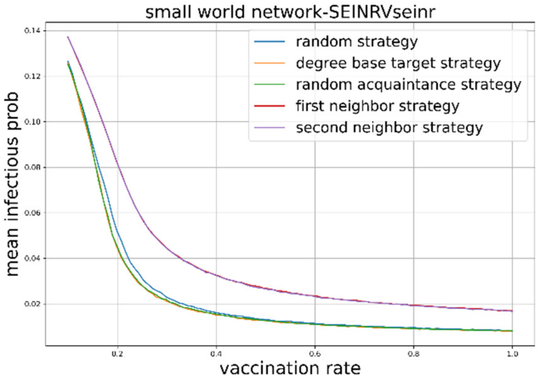

Figure 11 Simulation results for *SEINRVseinr* with unweighted undirected graph under small world network

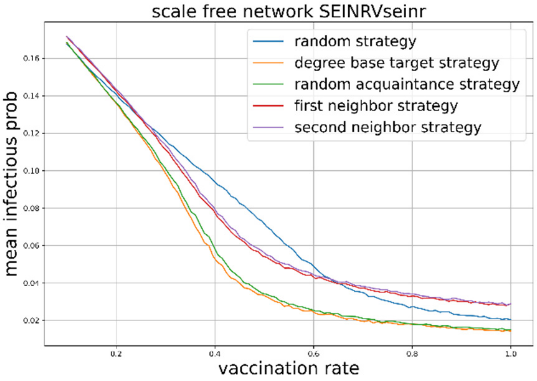

Figure 12 Simulation results for *SEINRVseinr* with weighted undirected graph under scale free network

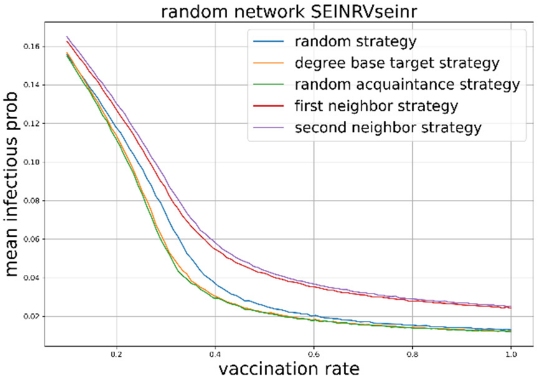

Figure 13 Simulation results for *SEINRVseinr* with weighted undirected graph under random network

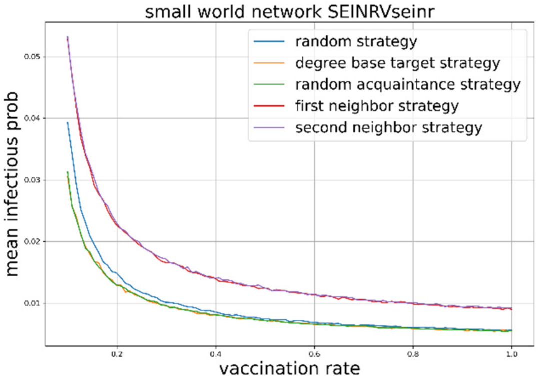

Figure 14 Simulation results for *SEINRVseinr* with weighted undirected graph under small world network

V. CONCLUSIONS AND FUTURE WORKS

We consider the characteristics of COVID-19 into the SIRV model and come up with a more complicated *SEINRVseinr* with weighted undirected graph with latent state, asymptomatic infectious state and reinfected possibility and imperfect vaccination. After conducting the simulation, we know that the SIRV model is too simple as the benchmark model and the degree base target strategy is best neighbor strategies fail to overperform the random strategy. However, for *SEINRVseinr* model random acquaintance strategy is efficient strategy and neighbors' strategies perform better in certain interval.

The main contribution of this paper includes:

1. Introducing the characteristics of COVID-19 into the probabilistic node level disease spreading model, including the exposed state, asymptomatic infectious state, the possibility of reinfection;
2. Considering imperfect vaccination in the *SEINRVseinr* model;
3. Using weighted undirected graph in the social network for disease spreading;
4. Testing five vaccination strategies, rewriting degree-target base, random acquaintance, first-neighbor and second neighbor strategies into weighted degree-base target strategy, important group's first neighbor strategy, improved first neighbor strategy, and improved second neighbor strategy.

We consider the weight of the graph as random variables from power law distribution. In the future work, we tend to study the social ties both the strong ties and weak ties (18) and their influences to the offline contact of the people or even consider dynamic ties (19) and update the method to measure the weight of the network. There were also many researches based on community data or real social network data to conduct simulation analysis (20). Also, we would try to employ some empirical data to validate our model and make the model results closer to the realistic situation.

REFERENCES

[1] Cascella M, Rajnik M, Cuomo A, et al. Features, Evaluation, and Treatment of Coronavirus. [Updated 2020 Oct 4]. In: StatPearls [Internet].

Treasure Island (FL): StatPearls Publishing; 2020 Jan-. Available from: https://www.ncbi.nlm.nih.gov/books/NBK554776/

[2] Granovetter M (1995) Getting a job: a study of contacts and careers. University of Chicago. Press, Chicago

[3] Anderson RM, May RM (1992) Infectious diseases in humans. Oxford University Press, Oxford

[4] R. Pastor-Satorras, C. Castellano, P. V. Mieghem, and A. Vespignani. Epidemic processes in complex networks. arXiv:1408.2701, 2014

[5] Gross T, D'Lima CJD, Blasius B. Epidemic Dynamics on an Adaptive Network. Physical Review Letters. 2006;96(20).

[6] Porter, M. A. and Gleeson, J. P., Dynamical Systems on Networks: A Tutorial,, 2014.

[7] F. Brauer and C. Castillo-Chavez. Mathematical Models in Population Biology and Epidemiology. Springer Verlag, 2nd edition, 2012

[8] M. E. J. Newman. Networks: An Introduction. Oxford University Press, 2010.

[9] Firth JA, Hellewell J, Klepac P, Kissler S, Group CC-W, Kucharski AJ, et al. Using a real-world network to model localized COVID-19 control strategies. Nat Med. 2020;26(10):1616-22.

[10] Madar N, Kalisky T, Cohen R, ben-Avraham D, Havlin S. Immunization and epidemic dynamics in complex networks. The European Physical Journal B - Condensed Matter. 2004;38(2):269-76.

[11] Yang Y, McKhann A, Chen S, Harling G, Onnela J-P. Efficient vaccination strategies for epidemic control using network information. Epidemics. 2019;27:115-22.

[12] S. Lehmann and Y.-Y. Ahn. Complex Spreading Phenomena in Social Systems: Influence and Contagion in Real-World Social Networks. Springer International Publishing, Cham, Switzerland, 2018.

[13] Chun-Lin Kuo, Mengxuan Chen, Wai Kin Victor Chan, Impact of Vaccination Strategies For Epidemic Node-level SVIR Probabilistic Model, International Conference on Public Health and Data Science (ICPHDS2020), (Accepted), Guangzhou, China, Nov 20th-22th, 2020.(EI)

[14] M. E. J. Newman. Networks: An Introduction. Oxford University Press, 2010.

[15] Mengxuan Chen, Chun-Lin Kuo, Wai Kin Victor Chan, Vaccination Strategies by Probabilistic Node-level SIR Model over Dynamic Network, The 8th International Symposium on Project Management(ISPM 2020), (Accepted), Beijing, China, July 18th-19th, 2020.(EI)

[16] Chun-Lin Kuo, Mengxuan Chen, Wai Kin Victor Chan, Impact of Vaccination Strategies For Epidemic Node-level SVIR Probabilistic Model, International Conference on Public Health and Data Science (ICPHDS2020), (Accepted), Guangzhou, China, Nov 20th-22th, 2020.(EI)

[17] Granovetter M (1995) Getting a job: a study of contacts and careers. University of Chicago Press, Chicago

[18] Friedkin N. A test of structural features of granovetter's strength of weak ties theory. Social Networks. 1980;2(4):411-22.

[19] Miritello G, Moro E, Lara R. Dynamical strength of social ties in information spreading. Physical Review E. Physical Review E; 2011;83(4).

[20] Huang C-Y, Chin W-C-B, Wen T-H, Fu Y-H, Tsai Y-S. EpiRank: Modeling Bidirectional Disease Spread in Asymmetric Commuting Networks. Scientific Reports [Internet]. Scientific Reports; 2019;9(1). Available from: https://dx.doi.org/10.1038/s41598-019-41719-8