THE HETEROGENEOUS MEAN-FIELD SLEIR PROPAGATION DYNAMICS MODEL ON THE COMPLEX NETWORK

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ABSTRACT. Since the outbreak of the novel coronavirus in early 2020, the epidemic has been affecting our lives. Firstly, a heterogeneous mean-field $SLEIR$ model based on complex networks was established to find disease-free equilibrium points and endemic equilibrium points, and the prediction results in the small-world networks, BA scale-free networks, and ER random networks were compared and analyzed. It was found that the prediction effect of the BA scale-free network using the heterogeneous mean-field model was poor. And most of the prediction results of a single degree are better than the heterogeneous mean-field, while the effect of small-world network and ER random network is the opposite. Through the experiment, it is found that the main reason for this is that the degree distribution of small-world network, ER random network and BA scale-free network is different. Therefore, when conducting predictions using heterogeneous mean-field method, it is preferable to choose the small-world networks as they generally exhibit superior performance compared to other network types.

1. INTRODUCTION

The novel Coronavirus pneumonia ($COVID - 19$), first discovered in Wuhan, China, in January 2020, has now spread throughout the world and will show a tendency of multiple outbreaks in all countries. As time changes, the novel coronavirus is also constantly mutating, leading to increasing difficulties in prevention and control. A variety of forecasting methods are used to predict the epidemic and make useful suggestions to contain the spread of the epidemic. At present, the representative models of infectious disease models include the SIR Model, $SEIR$ model, $SIRS$ model, and other classical infectious disease models. There are also many expansion models based on these classical models. Many people [1–4]predict the time inflection point of the epidemic through an improved SIR model or $SEIR$ model and optimization algorithm, providing good guidance for epidemic prevention and control. By adjusting the parameters of the $SEIR$ model [5], a new model was constructed and a visual analysis system was established. Using nonlinear regression prediction [6] to compare and analyze the development of the epidemic in multiple provinces. The $ARIMA(0,1,0)$ model [7] has a high degree of fit but can only make short-term predictions. Calculate the Spearman

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correlation coefficient [8] between the Baidu index of network-related words and the number of newly confirmed cases using the $ARIMA$ model, $ARDL$ model, and regression model, and demonstrate the consistency of the changes between the two through the $Kendall$ covariance coefficient. The $SLEIR$ model [9,10] takes into account populations that are prone to infection and have low risk of infection, and effectively simulates the epidemic data in this region of India through this model.

The SIR model [11] includes scale-free and stochastic network numerical simulation of novel coronavirus transmission, a dynamic model of SIR model [12] with immune effect, a spatial multi-population model, a network-based the SIS epidemic model [13] with saturation treatment function, an alternative social network model, and growth social network model with local structure [14], Epidemic propagation dynamics models studied through various applications on complex networks, such as $SEIR$ models in heterogeneous mean-fields [15].

Most of the above research content is a prediction based on the mathematical model, and most of the time, it fails to take into account the social network relationships and interpersonal relationships in various regions at present. It is possible to combine the interpersonal connection with the infectious disease model, and consider the influence of different contacts on the infectious disease. The infectious disease model based on the complex network will certainly play a large role in preventing the spread of infectious diseases. The paper mainly combines the $SLEIR$ model and the heterogeneous mean-field method to modify model, and simulates the model using the $RungeKutta$ method.

2. MEAN-FIELD $SLEIR$ MODEL

In the event of an infectious disease, it can be thought of a closed mixed population of N individuals as a complex network, in which individuals can be represented by network nodes and relationships between people can be represented by edges. There is a graph $G = (V, E)$, where V and E represent vertices and edges. Degree is a key property of a node, used to represent the number of edges that the node is connected to other nodes.

$$\Theta = \sum_k \frac{kp(k)(I_k + E_k)}{\langle k \rangle}.$$

Θ is the proportion of people in the network who are infectious, including those who are dormant and those who are infected. Where k represents the degree of a node, S_k, L_k, E_k, I_k, R_k respectively represent the proportion of susceptible nodes with degree k, the proportion of low-risk infected nodes with degree k, the proportion of latent nodes with degree k, the proportion of infected nodes with degree k, and the proportion of recovery nodes with degree k, i.e., $S_k(t) + L_k(t) + E_k(t) + I_k(t) + R_k(t) = 1$. $p(k) = \frac{N_k}{N}$ is the proportion of the number of nodes with degree k to the total population. $\langle k \rangle$ represents the average degree of the entire network, $\langle k \rangle = \sum_k kp(k)$. Heterogeneous networks are those with nodes of type greater than 1 or edges of type greater than 1. Now it's presented the basic assumptions for this model:

- Network structure will not change, that is, the complex network is a static network;
- A node represents a person. If two people meet, then the connection of the corresponding node of two people means that there is an edge between the two nodes. The number of people a person meets every day is the number of edges k of a node, also known as the degree of node; $S(t)$, $L(t)$, $E(t)$, $I(t)$, $R(t)$ said five people in t time respectively

accounted for the proportion of the total population, namely $S(t) + L(t) + E(t) + I(t) + R(t) = 1$.

- $S_k(t)$, $L_k(t)$, $E_k(t)$, $I_k(t)$, $R_k(t)$ respectively represents that at time t, the proportion of susceptible nodes with degree k in nodes with degree k, the proportion of low-risk infected nodes with degree k in nodes with degree k, the proportion of latent nodes with degree k in nodes with degree k, the proportion of infected nodes with degree k in nodes with degree k, the proportion of recovering nodes with degree k in nodes with degree k, namely

$$\begin{cases} S_k(t) + L_k(t) + E_k(t) + I_k(t) + R_k(t) = 1, \\ \sum_{k=1}^{n} p(k)(S_k(t) + L_k(t) + E_k(t) + I_k(t) + R_k(t)) = 1, \\ S(t) = \sum_{k=k_{min}}^{k_{max}} p(k)S_k(t), \\ L(t) = \sum_{k=k_{min}}^{k_{max}} p(k)L_k(t), \\ E(t) = \sum_{k=k_{min}}^{k_{max}} p(k)E_k(t), \\ I(t) = \sum_{k=k_{min}}^{k_{max}} p(k)I_k(t), \\ R(t) = \sum_{k=k_{min}}^{k_{max}} p(k)R_k(t). \end{cases}$$

- The population will move in and out for various reasons, but the total number of population will not change in a short time, the migration rate is μ;
- Both the lurkers and the infected can transmit the virus to the healthy population, and the infection ability of the lurkers and the infected person is the same;
- Vulnerable and low-risk infected persons are both healthy people and at risk of infection, but the probability of infection is different between them. The probability of vulnerable infected persons being infected is α, the probability of low-risk infected persons being infected is β, and the number of vulnerable and low-risk infected nodes of degree k being infected per unit time of time t is respectively $\alpha S_k(t)\Theta$ and $\beta L_k(t)\Theta$;
- After infection, both susceptible and low-risk infected persons directly transform into lurkers, with a latent outbreak rate of σ, and the number of infected persons transforming from lurkers to k degrees in t single time is $\sigma E_k(t)$;
- After an outbreak of the virus, the infected person will be treated with a recovery rate of γ, so in t unit time, the infected person of degree k will be treated with the number of recoveries is $\gamma I_k(t)$.

3. Model Establishment

From this definition, it can be seen that the network is a heterogeneous network whose nodes contain five states. The mean-field equation for constructing $SLEIR$ propagation dynamics model based on complex network is shown as follows:

$$\begin{cases} \dfrac{dS_k}{dt} = \mu\rho - \alpha k S_k(t)\Theta - \mu S_k(t), \\[2mm] \dfrac{dL_k}{dt} = \mu(1-\rho) - \beta k L_k(t)\Theta - \mu L_k(t), \\[2mm] \dfrac{dE_k}{dt} = \alpha k S_k(t)\Theta + \beta k L_k(t)\Theta - \sigma E_k(t) - \mu E_k(t), \\[2mm] \dfrac{dI_k}{dt} = \sigma E_k(t) - \mu I_k(t) - \gamma I_k(t), \\[2mm] \dfrac{dR_k}{dt} = \gamma I_k(t) - \mu R_k(t). \end{cases}$$

The above equations can be simplified to give the following formula:

(1)

$$\begin{cases} \dfrac{dS_k}{dt} = \mu\rho - \alpha k S_k(t)\Theta - \mu S_k(t), \\[2mm] \dfrac{dL_k}{dt} = \mu(1-\rho) - \beta k L_k(t)\Theta - \mu L_k(t), \\[2mm] \dfrac{dE_k}{dt} = \alpha k S_k(t)\Theta + \beta k L_k(t)\Theta - \sigma E_k(t) - \mu E_k(t), \\[2mm] \dfrac{dI_k}{dt} = \sigma E_k(t) - \mu I_k(t) - \gamma I_k(t). \end{cases}$$

The right end of the equation set 1 is 0, it can be obtained through calculation the disease-free stable point $E_0 = \{(\rho, 1-\rho, 0, 0)\}_{k=1}^n$ and the local disease stabilization point $E_* = \{(S_{k*}, L_{k*}, E_{k*}, I_{k*})\}_{k=1}^n$, where

$$\begin{cases} S_{k*} = \frac{\mu\rho}{\mu+\alpha k\Theta^*}, \\[2mm] L_{k*} = \frac{\mu(1-\rho)}{\mu+\beta k\Theta^*}, \\[2mm] E_{k*} = \frac{\mu((\alpha k\Theta^*+\mu)\beta k\Theta^*+\mu\rho(\alpha k\Theta^*-\beta k\Theta^*))}{(\alpha k\Theta^*+\mu)(\beta k\Theta^*+\mu)(\sigma+\mu)}, \\[2mm] I_{k*} = \frac{\sigma\mu((\alpha k\Theta^*+\mu)\beta k\Theta^*+\mu\rho(\alpha k\Theta^*-\beta k\Theta^*))}{(\alpha k\Theta^*+\mu)(\beta k\Theta^*+\mu)(\sigma+\mu)(\mu+\gamma)}, \\[2mm] \Theta^* = \sum_{k=1}^n \frac{kp(k)(E_{k*}+I_{k*})}{\langle k\rangle}. \end{cases}$$

By the equations 1 and the regeneration matrix method, we can calculate the spectral radius to obtain the basic reproduction number

$$R_0 = \frac{(\alpha\rho+\beta(1-\rho))(\mu+\gamma+\sigma)}{(\sigma+\mu)(\mu+\gamma)}\frac{\langle k^2\rangle}{\langle k\rangle}.$$

4. EXPRIMENT

According to Figure 1, it can be observed that the corresponding values of different degrees are also different, indicating that the amount of contact an individual has with other individuals is significantly related to the predicted results. The different degrees of nodes will have a large deviation between the predicted values. When solving the traditional dynamic differential equation, the influence of the degrees of nodes on the predicted values is not taken into account, and all of them are a single line.
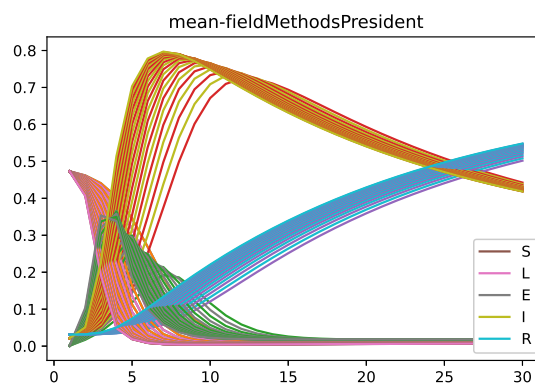

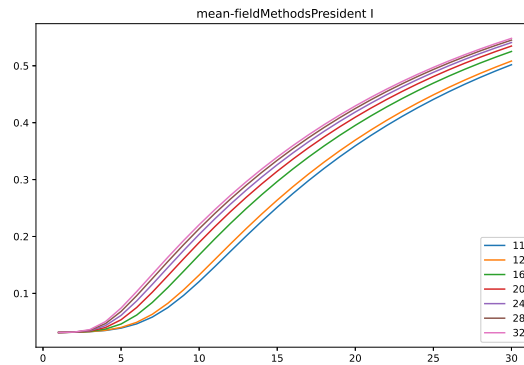FIGURE 1. The evolution of five populations at different degrees

FIGURE 2. Evolution of infected individuals at different levels

It can be observed from Figure 2 that different degrees of infection have different changes. The smaller the degree of infection, the slower the rate of change, and the larger the rate of change, the faster. This indicates that reducing the contact between residents and reducing the degree of nodes will delay the development of the epidemic.

5. MODEL APPLICATION

According to the data, the existing artificial networks include random networks, small-world networks, BA scale-free networks and other networks. Among the structures of so many artificial networks, the network that is most similar to the real human social relationship network structure is the BA scale-free network.

5.1. **Parameter Fitting of Various Artificial Networks.** Three kinds of complex networks, random network, small world network and BA scale-free network, are used for prediction here, and the prediction results are compared with those of the general differential equation. The number of nodes in each kind of network is set to $N = 10000$, and the $SLEIR$ heterogeneous mean-field model is solved by using the minimize function in Python. The parameters obtained for three kinds of networks are shown in Table 1.

name	α	β	γ	ρ	σ	μ	others
ER random network	0.00135	0.00128	0.0160	0.3329	1.0	0.00	$N = 10000, p = 0.001$
BA Scale-free Network	4.2821e-04	3.72199730e-04	1.20998348e-02	2.09494e-01	1.00000e+00	0.00000e+00	$N = 10000, m = 5$
Small World Network	1.980e-03	7.40063601e-03	1.73527228e-02	3.4999e-1	0.0000e+00	1.98628277e-04	$N = 10000, m = 10, p = 0.2$
General differential equation	0.08938	0.0894	0.05266	0.9907	0.02301486	0.499997	

TABLE 1. Parameter values of various networks solved in the heterogeneous mean-field $SLEIR$ model

From Table 1, it can found that the parameters obtained by different complex networks are very different, and the parameters obtained by different networks are not similar.

5.2. **Prediction results and analysis of various artificial networks.** The mean predicted value of I state ($mean\_I$) is shown as follow:

$$(2) \qquad mean\_I = \sum_{k=k_{min}}^{k_{max}} p(k)I_k(t).$$

Through the obtained parameter values of different artificial networks, the epidemic situation in the next 30 days can be predicted. It is good to compare the predicted results with the actual values by the coefficient of standard deviation. Through Table 2, it can be found that the standard deviation coefficients of the final average predicted values of the random networks and the small world networks are smaller than the standard deviation coefficients of the predicted values of general differential equations. While the predicted value of the scale-free network is larger than the standard deviation coefficient of the predicted value of the general differential equation. The reason why this situation occurs is that the heterogeneous mean-field method mainly relies on the degree distribution to calculate. Therefore, it will be discussed from the degree distribution of three kinds of complex networks for the predict effect of the heterogeneous mean-filed method.

name	S	L	E	I	R
ER random network	0.0548883794	0.074561749	32.5060405	1.54024875	0.718464
BA Scale-free Network	0.582704067	0.5878463	40.082686	14.8388333	4.2088276
Small World Network	0.0577953710	0.16183728	32.6868958	1.2232678	0.3743996
General differential equation	0.1193169925	0.1194198452	35.3990665	1.9349754	1.12982

TABLE 2. Coefficient of standard deviation between predicted and actual values of various networks in SLEIR heterogeneous mean-field model

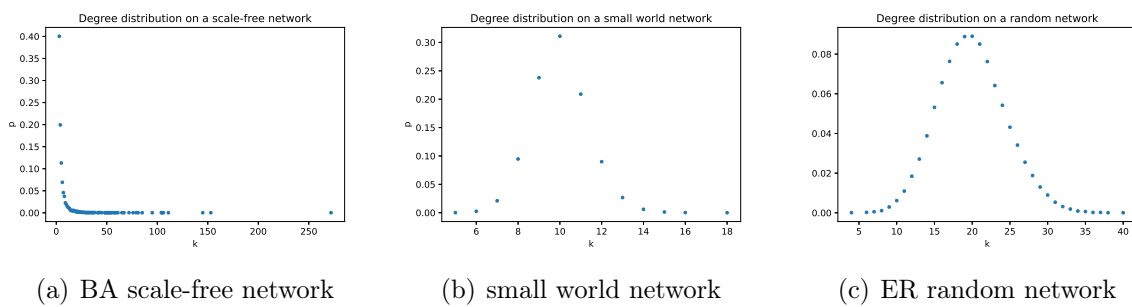(a) BA scale-free network   (b) small world network   (c) ER random network

FIGURE 3. Degree Distribution on Different Networks

From Figure 3, it can be clearly found the largest degree k_{max} of BA scale-free network is obviously much larger than ER random network and small-world network, and the images of ER random network and small-world network are very similar to the images of the normal distribution, both of which are degree distribution with higher probability in the middle and degree probability on both sides is smaller, while the degree distribution image of BA scale-free network is more similar to the power law distribution image, and the probability of smaller degree is larger. As the degree increases, the corresponding probability monotonically decreases and approaches 0, with fewer maximum degrees. The degree of BA scale-free network is relatively concentrated in the range of $0 \sim 100$, and there are only a few scattered degrees of distribution between 100 and 250, while the degree of ER random network and small-world network will exist evenly between the minimum degree and the maximum degree, regardless of the high or low distribution probability.

(a) BA scale-free network   (b) small world network   (c) ER random network
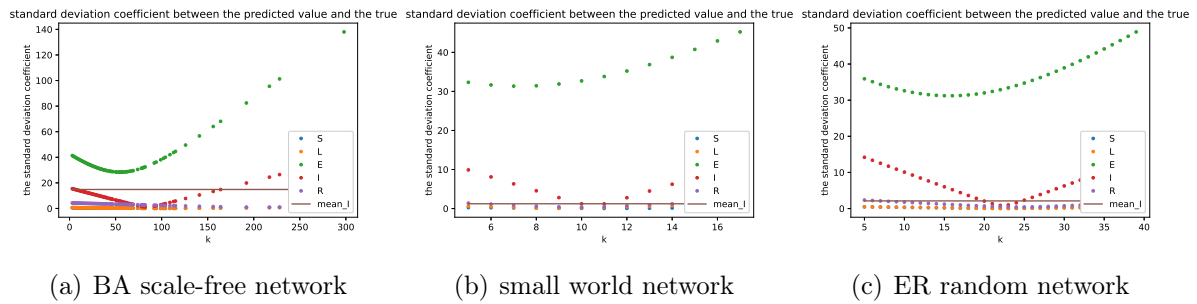
FIGURE 4. Influence of Degree distribution on epidemic prediction

It can be clearly observed from Figure 4 that similarities are exhibited by the three graphs in terms of the small errors and minimal changes observed in the S, L, R states. However, for the E, I states, the errors undergo an initial decrease followed by an increase. It is worth noting that in Figure 4 (a), the predicted values for most individual degree values are consistently lower than the mean predicted value $(mean\_I)$, whereas in Figures 4 (b) and Figures 4 (c), the majority of individual degree values exceed the mean predicted value $(mean\_I)$. Furthermore, the predicted value distributions in Figures 4 (b) and Figures 4 (c) display a relatively uniform pattern, while the predicted value errors in Figure 4 (a) initially appear dense and subsequently become sparse, resembling the degree value distributions illustrated in Figure 3. As per the formula 2, the prediction outcome of $mean\_I$ is heavily influenced by the degree value distribution. In the BA scale-free network, a significant number of nodes without a scale are located in regions with lower degree values, leading to inadequate prediction performance for nodes with lower degree values. Consequently, the predictive effectiveness of the BA scale-free network is inferior to that of the other two networks.
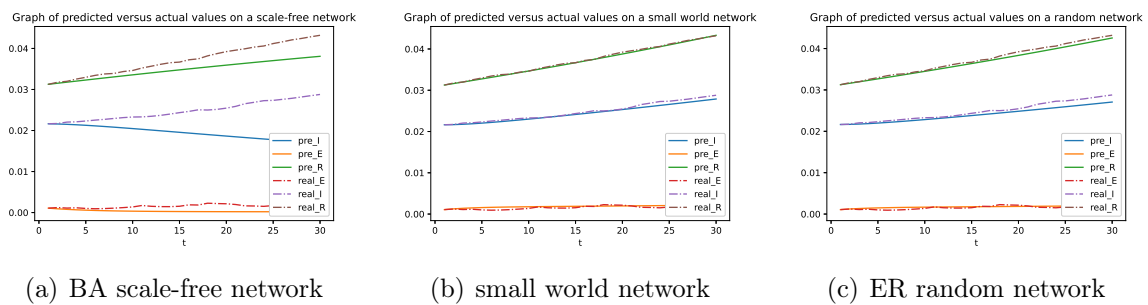

(a) BA scale-free network   (b) small world network   (c) ER random network

FIGURE 5. Three Different Networks for Epidemic Prediction

It can be clearly observed from Figure5 that the predicted result of BA scale-free network has a large deviation from the actual value, while the predicted result of ER random network and small-world network has a small deviation from the actual value, and the predicted effect of BA scale-free network is almost not feasible compared with the actual value. Through a comprehensive analysis and comparison of Figure 5, it becomes evident that the curve depicting the predicted values and the corresponding real values of the small-world network exhibits a higher level of stability.

(a) BA scale-free network   (b) small world network   (c) ER random network
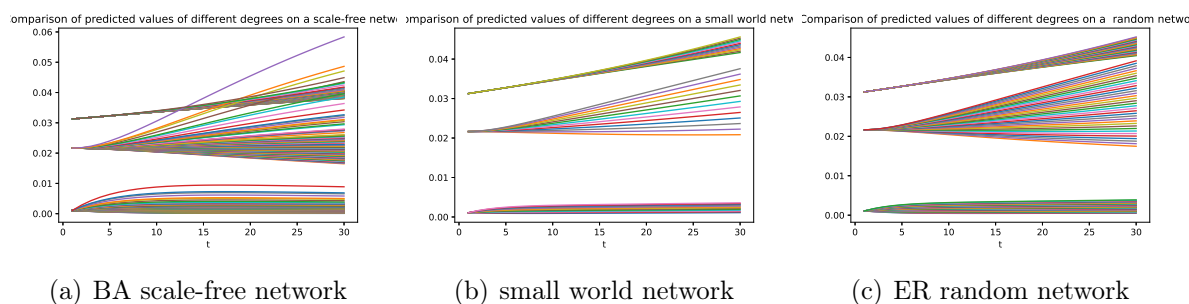
FIGURE 6. Prediction Results of Three Complex Networks at Different Degrees

It can be observed from Figure 6 that under different degree distributions, the prediction of BA scale-free network is the most divergent under different degrees, the second degree of divergence is the predicted result under different degrees of ER random network, and the least degree of divergence is the predicted result under different degrees of small-world network.

6. CONCLUSION

In this paper, the heterogeneous mean field SLEIR model is proposed and the corresponding basic growth number R0 is determined. By considering different degrees of heterogeneity in the mean field, distinct variation trends are observed. To further analyze and compare these trends, three commonly used complex network models are employed. It is found that significant differences in the effects of these models are observed when they are applied to the same dataset. Specifically, superior performance is demonstrated by the ER random network and small-world network, while poor predictive value is exhibited by the BA scale-free network. Experimental results reveal that the predicted values of the BA scale-free network for individual degrees are consistently lower than the overall predicted value, whereas the opposite trend is observed for the ER random network and small-world network. Additionally, it is observed that both the ER random network and small-world network exhibit a degree distribution similar to a normal distribution, while a power law distribution is followed by the BA scale-free network. Consequently, poor predictions are yielded by the BA scale-free network primarily due to the majority of low-degree values and the associated limited predictive effectiveness. Based on these findings, it is recommended to avoid using the BA scale-free network when selecting a heterogeneous mean field model for pre-testing purposes, as better predictive value may be offered by the small-world network.

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