

Review Article

A Literature Review of Social Network Analysis in Epidemic Prevention and Control

Xiaomei Wang, Qi An, Zilong He, and Wei Fang 

School of Management, Northwestern Polytechnical University, Xi'an 710072, China

Correspondence should be addressed to Wei Fang; fwx1998@nwpu.edu.cn

Received 8 May 2021; Revised 22 June 2021; Accepted 3 July 2021; Published 14 July 2021

Academic Editor: Miguel Fuentes

Copyright © 2021 Xiaomei Wang et al. This is an open access article distributed under the Creative Commons Attribution License, which permits unrestricted use, distribution, and reproduction in any medium, provided the original work is properly cited.

Studying the structure and evolution characteristics of social networks is of great significance in assessing and controlling the outbreak of infectious diseases. Therefore, it is necessary to find research trends in this field. In this study, 1,752 documents (2001–2020) related to the relationship between the social network and epidemic published from Scopus, WOS (Web of Science), and CNKI (China National Knowledge Infrastructure) databases were studied to provide a more comprehensive overview of the frontiers of research in this field, including epidemics in social networks, spread of disease, influence of different factors on the spread of the epidemic, prevention and control strategies of the epidemic, and comparison of various strategies. Besides, several new research directions in this field worthy of attention of researchers are discussed.

1. Introduction

Public health is one of the major concerns of governments and international health agencies around the world. In addition to the thousands of new pathogens discovered over the past few decades, the resurgence of infectious diseases such as cholera, plague, and yellow fever is a cause of concern. Lifestyle changes, coupled with environmental and biological changes, have made epidemics of infectious diseases more likely than ever before and spreading farther and faster. The COVID-19 is now wreaking havoc worldwide, causing more than 157.7 million infections and nearly 3.3 million deaths (World Health Organization; “int/emergencies/diseases/novel-coronavirus-2019;” last modified May 8, 2021). The epidemic has seriously affected people’s everyday lives. Therefore, efforts must be made efficiently to research and control infectious diseases and to design effective prevention and mitigation strategies.

On the one hand, the pandemic has a massive impact on the society. The Internet has become an essential thing in our daily lives. It promotes the continuous improvement of modern health systems and reduces the threat of epidemics. On the other hand, the ever-developing social networks have brought closer connections between people, thus

accelerating the outbreak of pandemics, such as SARS in 2003, H1N1 influenza in 2005, H7N9 in 2013, HIV/AIDS in 2015, Ebola epidemic in 2019, and corona virus disease in 2020 which brought considerable losses to the national economy, caused disasters to people’s lives, and brought colossal turmoil to the international community. Therefore, the existence of epidemics is a problem we must solve.

Social networks are one of the most effective and visual tools for measuring and characterizing social relationships. Newman’s [1] previous research found that there seems to be a strong correlation between the network structure and the division of communities perceived by human observers, and it is this correlation that makes community structure analysis a helpful tool for understanding the behavior of network systems. A social network refers to a collection of social actors and their relationships. The fundamental elements include actors, relationships, and groups. All individuals, social entities, or events in a social network can be called actors, all connections between group members are called relationships, and a group is a collection of all actors. Social network analysis (SNA) is based on the interaction between social actors, using points to represent social actors and connections of points to represent a specific social relationship between actors to quantify these social

relationships [2]. SNA has two research orientations. One is the egocentric network analysis method, which takes the individual as the center, analyzes its external relations, and studies the connections between actors and others and the interrelationships between others who are directly related to them. The other is the complete global network analysis method, which studies the direct and indirect relationships between all actors in a group with a clear margin [3]. While epidemiological models can help design and analyze epidemiological surveys, they can identify trends, make general predictions, and estimate uncertainties in predictions based on collecting critical data [4]. With the rapid development of the interdisciplinary fields of computer science, network science, biology, and physics, it is necessary to conduct a comprehensive review of the current state-of-the-art technology and provide a road map to the research community to help organize future research in this field.

In conclusion, social networks' structural and evolutionary characteristics are of great significance for the assessment, control, monitoring, and prevention of epidemic diseases. This research aims to summarize the literature of the past 20 years and the application of manual social network analysis in epidemic prevention and control. At the same time, it looks forward to the future development direction and proposes more detailed research directions. Therefore, the contribution of this research is twofold. First, this article introduces in detail how social network analysis describes the spread of infectious diseases and its application in the prevention and control of infectious diseases, revealing this field's development. Secondly, it puts forward the shortcomings of existing research and new social environment, which hint at future research challenges and opportunities.

The rest of this article is structured as follows. Section 3 will introduce the network model and epidemic spread model designed for the construction of epidemic transmission problems. Section 4 introduces the prevention and control strategies for the spread of infectious diseases combined with social networks. Finally, in Section 5, we propose the deficiencies of existing research and future research directions. Figure 1 enables readers to have a more precise grasp of the structure of this article.

2. Approach to Literature Review

Creating a comprehensive literature review begins with an extensive search of relevant research studies. In order to obtain the best results and to be able to search existing publications consistently, we decided to use the Preferred Reporting Items for Systematic Reviews and Meta-Analyses methodology [5] for meta-analysis (Figure 2). Our literature search can be summarized in Figure 2, where we provide the number of reviewed publications and the screening process followed.

During the search for relevant sources, we used the most popular bibliographic databases: Scopus, Web of Science, and China National Knowledge Infrastructure, and we started with searching for social network analysis in epidemic prevention and control. We started with more generic

keywords, to make sure that we do not oversee any research studies. We used the following set of keywords (i) to describe the social network analysis: complex network, small world network, networked system, social network, scale-free network, adaptive network, network, community structure, heterogeneous network, social network analysis, and SNA (ii) to describe the epidemic spread, prevention, and control: epidemic spreading, contagion spreading, infectious disease spreading, virus spreading, immunization, immunization strategy, and vaccination. We also used the combination of words describing the social network analysis process and the epidemic prevention and control to grasp all possible cases.

After searching through the database, we obtained 1,752 papers, and after preliminary screening, we obtained 279 papers that qualified for the eligibility check. The initial screening excluded papers that were based solely on titles that we can say that they do not fall into the category of "social network analysis" or "epidemic prevention and control."

During the qualification test, we discarded 130 papers that did not fall into the category of "social network analysis" or "epidemic prevention and control," but we did this by reading through the abstract and main text of the paper. For each paper that passed the qualification check, we checked its references (past cross check) and papers citing a given paper (future cross check) to see if any of these papers are eligible to be included in the final Meta-analysis. After that, we reached 149 publications that we included in the final review.

3. Modeling Work

In studying the application of social network analysis in epidemic prevention and control, a very significant point is to study the process of establishing a model. Two aspects need to be considered when establishing the model. (1) What kind of network is used for modeling because the connection modes of different network nodes are different? (2) What kind of infectious disease model is used to simulate the process of disease transmission, which directly affects the complexity of the model? In this article, we have introduced different modeling models used by scholars in the past 20 years, to study the transmission law of infectious diseases based on the social contact network and to solve different infectious disease transmission and prevention and control problems.

3.1. Propagation Modeling

3.1.1. Scale-Free Networks: The Barabási–Albert Model. The scale-free network was first proposed by Barabasi and Albert based on random networks [6]. The degree is the most important index describing the nature of a single node in the network. The degree of a node refers to the number of edges associated with the node and the number of points directly connected to the node [7]. When the degree of each node has a serious uneven distribution (a few nodes in the network called hub points have an extremely large number of connections, and most nodes have only a small number of

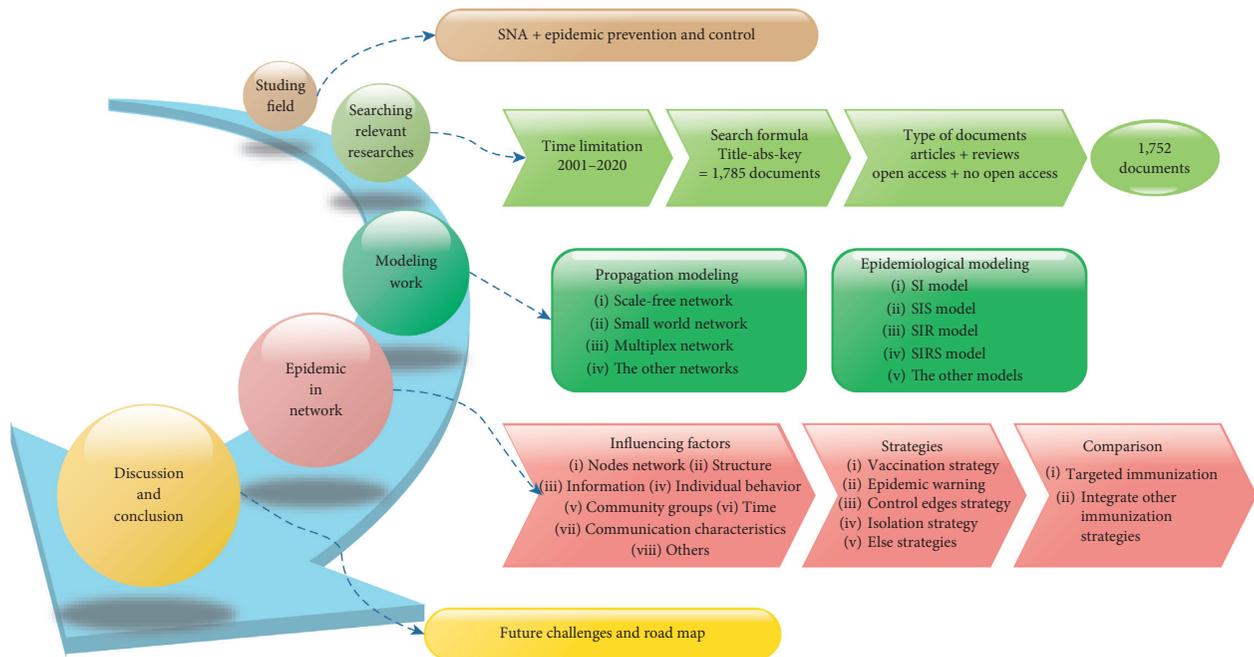


FIGURE 1: Article flowchart of the structure of this article. This review consists of 6 parts: Introduction, Approach to Literature Review, Modeling Work, Epidemic Research Based on Social Networks, Future Challenges and Road Map, and Conclusion.

connections), we call this network a scale-free network, while the BA diagram was introduced as a model of an evolving network (such as the Internet or the World Wide Web). Among them, links to highly connected nodes are successively established with a higher probability. On the Internet and other social networks, this is a fairly intuitive phenomenon. Under this phenomenon, new individuals are often more likely to establish connections with individuals who are already widely known and widely connected. The BA diagram is constructed using the following algorithm [8]. The BA scale-free network model can well reflect the two important characteristics of the network, such as the World Wide Web, router-level network, film cooperation network, and scientific research cooperation network: growth (the network scale continues to expand) and priority connection function (new nodes are more likely to be connected to “large” nodes with higher connectivity) [9]. Table 1 shows the work done by scholars using the BA scale-free network in infectious diseases.

(1) *Analysis of Infective Factors and Their Relationship.* Many factors affect the spread of epidemics, and different factors do not promote or inhibit the spread of epidemics, so different scholars have conducted different studies. In a scale-free network, Barthelemy et al. [10] studied the relationship between the average density of infected individuals and time. Yan [11] and Chu [12] used link weights to indicate the familiarity between two people and studied the detailed epidemic spreading process in scale-free networks. Wang et al. [13] focused on the analysis of epidemic threshold and AOS (average outbreak size). Meloni et al. [14] used analysis and numbers to calculate the outbreak of epidemics in SF networks when infectious diseases are driven by traffic or interactive flows. Cai et al. [15], Shen and

Cao [16], and Yang [17] studied the influence of population density, human immunity, and feedback mechanism on the mechanism of disease transmission.

(2) *Analyze the Spread Mode in Combination with the Infectious Disease Model.* Analyzing the spread of epidemics under social networks will generally be combined with infectious disease models for analysis. For example, Zhou et al. [18] and Lou and Ruggeri [19] used SI models for simulation analysis on scale-free networks; Silva et al. [20], Small et al. [21], and Sun et al. [22] used SIS models to simulate the spread of epidemics and conduct related research and analysis; Chen et al. [23], Liu and Zhang [24], Gong et al. [25], Zhao et al. [26], and Madar et al. [27] combined dynamic SIR epidemiological models to study the spread of epidemics and the impact of immune strategies on the spread of the pathogen in multiple networks; used by Nian et al. [28] and Huo et al. [29], the SIRS epidemic model has been theoretically verified and computer simulated on the scale-free network to establish a more realistic model.

(3) *Analysis of the Attributes of the Infection Process.* May and Lloyd [30] discussed the properties of the infection process in scale-free networks and associated them with the node connection distribution that characterizes the network. Different social structures in the SF network will significantly affect the transmission characteristics of the epidemic: in an unstructured society, the average proportion of infected individuals increases with the growth of k ; but in a structured community, the proportion of infected individuals decreases as g increases [31]. Under the limit of the unlimited network, the epidemic process in the scale-free network does not have an epidemic threshold, and a major epidemic outbreak or outbreak of an epidemic state cannot be generated below this threshold, which means no matter how small the probability of

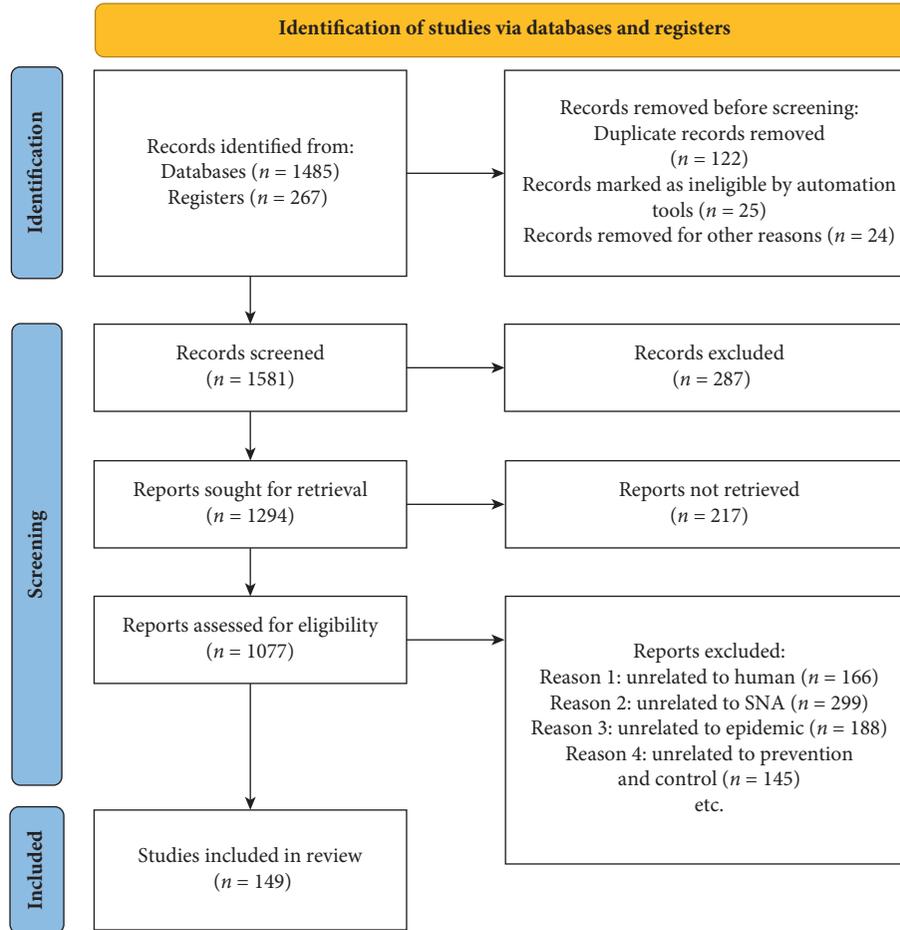


FIGURE 2: The process of screening articles: at the beginning, we retrieved 1752 papers on specific topics, then deleted 388 papers due to repetition, unqualified, or unavailable, and next eliminated 928 less relevant papers through abstract or full-text reading. Finally, we obtained 149 papers for the study.

TABLE 1: The work done on infectious diseases using the BA scale-free network: in the related work column, the research studies performed by researchers using the BA scale-free network are shown, and in the reference column is the relevant literature of the corresponding research.

Related work	Reference
Analysis of infective factors and their relationship	[10–17]
Analysis of the spread mode in combination with the infectious disease model	[18–29]
Analysis of the attributes of the infection process	[19, 24, 30–34]
Simulate the established model	[35–38]
The theoretical support for immunization strategies	[39]
The reliance on developing immune strategies	[8, 40]
Evaluation of immunization strategies	[41–45]

transmission, the disease will continue to spread [32, 33]. For a limited-scale scale-free network, Lou and Ruggeri [19] and Liu and Zhang [24] proved the local stability of disease-free balance and the persistence of the disease on the network. Chen and Zhang [34] studied the spread of the virus on a specific scale-free network under two different artificial immune strategies and simulated how the two immune strategies affect the spread of the virus.

(4) *Simulate the Established Model.* Wu et al. [35] used the Barabási–Albert (BA) scale-free network with degree

distribution to perform Monte Carlo stochastic simulations of epidemic dynamics. Liu et al. [36] simulated the immune strategy in the BA network. Nian and Hu [37] simulated the spread of three immunization programs based on scale-free networks, namely, random immunization, high-risk immunization, and most common friend priority immunization. Alfinito et al. [38] tested the validity of the protocol on various networks from theoretical models to actual networks and considered the classic example of the Barabási–Albert (BA) model at the first level.

(5) *The Theoretical Support for Immunization Strategies.* Models are theoretical support, and researchers will apply different models to support their views. For example, Pastor-Satorras and Espinani [39] concluded in the scale-free network that the lack of epidemic threshold is a key element of epidemiological theory, which opens up different scenarios in the network and rationalizes epidemic events.

(6) *The Reliance on Developing Immune Strategies.* The scale-free network can be considered as a limiting case of heterogeneous systems, and it is natural to find a specially designed immune strategy because the scale-free system does not have any key individual parts. Kuperman and Abramson [8] defined the best immune strategy named total immunity. Xia et al. [40] studied the immunity of highly clustered scale-free networks and proposed an improved local immunity strategy.

(7) *Evaluation of Immunization Strategies.* The evaluation of immunization strategies is inseparable from a specific environment. In the scale-free network, Dezsó and Barabási [41] evaluated random immunity, Shi et al. [42] evaluated directed immunity, Aihara et al. [43] compared immunization strategy of geographical embeddings with uniform or uneven distribution of vertices in a two-dimensional space, and Esquivel-Gomez and Barajas-Ramirez [44] studied the efficiency of isolation policy to control the spread of disease. Besides, Qu and Han [45] compared and analyzed the effects of random immunity and target immunity on BA scale-free networks.

3.1.2. Small World Network. The small world network was first proposed by Watts and Strogatz [46], and then, Newman and Watts [47] applied it to the model of disease transmission. If the average shortest path of the actual network is approximately equal to the average shortest path of the random network and the clustering coefficient of the actual network is greater than the random network, the actual network has the small world attribute. Many networks in the real world have the characteristics of the small world. In other words, the network has a higher clustering coefficient and a shorter average path length [48]. The small world may play an important role in the study of the influence of the network structure upon the dynamics of many social processes, such as disease spreading, formation of public opinion, distribution of wealth, and transmission of cultural traits. In the field of epidemic transmission, prevention, and control, the small world network has provided great help for studying the spread of the pathogen and making targeted immunization measures. Table 2 shows the work done by scholars on infectious diseases using the small world network.

(1) *Research Sites for Propagation Models.* The small world model is very suitable for studying the spread of epidemics. Moore and Newman [49] studied some simple models of disease transmission on small world networks. Kuperman and Abramson [8] observed disordered finite value transitions in a small world model and analyzed infection propagation models with different population structures. Han [50] proposed a susceptibility model with

pandemic alert based on a two-dimensional small world network. Li et al. [51] proposed a dynamic small world network model that can simulate local and mobile connections in real life.

(2) *Analyze the Spread Mode in Combination with the Infectious Disease Model.* In order to use the simplest (minimum parameter) model to accurately simulate the qualitative characteristics of the SARS epidemic, Small and Tse [52] applied the small world model to simulate the spread of SARS in Hong Kong. Verdasca et al. [53] performed long-term stochastic simulations of individual-based cellular automata on a small world network with SIR and SEIR node dynamics.

(3) *The Reliance on Developing Immune Strategies.* Similar to the scale-free network, the small world network is also a platform for proposing immune strategies. For example, Yu et al. [54] proposed an analytical solution for the spread of epidemics and control measures on one-dimensional small world networks by analyzing certain parameters.

(4) *The Place of Simulating, Analyzing, and Verifying Immune Strategies.* Nian and Hu [37] simulated the spread of three immunization schemes based on the small world and scale-free networks. Alfinito et al. [38] tested the validity of the protocol on various networks ranging from theoretical models to actual networks. In order to verify the effectiveness of immunization, Nian et al. [28] conducted theoretical verification and computer simulation on the small world network with the SIRS epidemic model. Based on the UAU-SIS model in multiple networks with heterogeneous infection rates, Yang [17] compared the Monte Carlo simulation with the theoretical results on the proportion of infected nodes.

3.1.3. Multiplex Network. Although the research of Internet epidemiology has made great progress, the traditional single network cannot accurately imitate most real systems, especially in describing the interaction between empirical systems. In this sense, in recent years, multiplexing networks have attracted great attention.

As early as 2006, Jo et al. [55] proposed that a certain type of channel can be separated from the entire network, and a multilayer network model can be constructed in such a way that a different type of information is transmitted through different layers, and only when they are in certain node meets can they interact with each other. In 2014, Chen et al. [56] and Granell et al. [57] described a transmission process involving two competitions: information transmission prevented the spread of disease, and the node infected by the disease can support the information dissemination process by generating new conscious individuals. The abstract model is shown in Figure 3, considering a multiplexing network composed of two layers. The bottom layer is the physical connection network, and the top layer is the representative of the online social network. All nodes represent the same entity in these two layers, but the connectivity between them is different.

In the past four years, the multiplex network model has been further developed. Liu et al. [58] established the system

TABLE 2: The work done on infectious diseases using the small world network: in the related work column, the research studies performed by researchers using the small world network are shown, and in the reference column is the relevant literature of the corresponding research.

Related work	Reference
Research sites for propagation models	[8, 49–51]
Analyze the spread mode in combination with the infectious disease model	[52, 53]
The reliance on developing immune strategies	[54]
The place of simulating, analyzing, and verifying immune strategies	[17, 28, 37, 38]

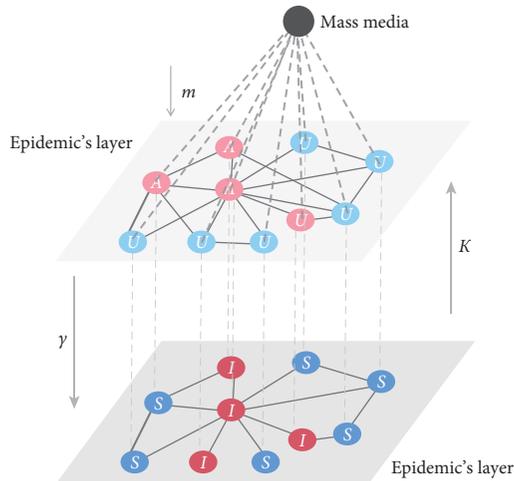


FIGURE 3: Awareness-epidemic model in the presence of mass media: the upper (information) layer is supporting the spreading of awareness, and nodes have two possible states: unaware (U) or aware (A). The lower (epidemic) layer corresponds to the network where the epidemic spreading takes place. The nodes are the same actors as in the upper layer, but here their state can be susceptible (S) or infected (I). The mass media are represented as a top node that provides information to the full system [57].

by mapping the multiplexed network to the two-layer network and combining the individual's risk awareness and explored the interaction between disease transmission and crowd response from the perspective of information dissemination and personal alertness. Li et al. [59] introduced observer nodes (which can identify infected neighbors and enable other neighbors to be vaccinated) into a multinet-work SIR model to study the impact of active immunity on the spread of epidemics. To analyze how the operation of information dissemination affects infected individuals and spreading conditions of epidemics, based on the assumption that the size of the community and individual awareness may affect the infection rate, Lu and Liu [60] proposed a SIR-A (susceptible infection-recovery-active) model to map infection and information dissemination to a two-layer network. Based on the UAU-SIS model in multiple networks with heterogeneous infection rates, Yang [17] compared the ratio of infected nodes to Monte Carlo simulations with theoretical results. Zhao et al. [26] used a multiple Erdős–Rényi (ER) stochastic network and combined it with a dynamic SIR epidemiological model to examine the impact of immune strategies on disease transmission in multiple networks. Buono and Braunstein [61] and Granell et al. [62] studied targeted immunization strategies against epidemics

spreading through multilayer networks. Wang et al. [63] mainly studied the impact of acquaintance immunity on multiple networks. Zuzek et al. [64] used a partially overlapping multiplexing network, considering the SIR model to develop a mitigation strategy. Table 3 shows the work done by scholars on infectious diseases using the multiplex network in recent few years.

3.1.4. The Other Networks. The above models are commonly used or widely popular by scholars in the past 20 years. In order to ensure the scientific nature of this review, we try to exhaustively study the network models of social network analysis used in epidemic prevention and control.

(1) *Dynamic Bipartite Graph.* Eubank [65] discussed the use of dynamic bipartite graphs for modeling. He found that the network of connections between people is closely connected, similar to a small world graph, with a clear proportion of degree distribution. However, the location map is not scaled. By placing the sensor in the hub of the location network, efficient outbreak detection can be achieved.

(2) *Local-World Evolving Network.* The basic idea of the model is to retain the growth mechanism in the BA model and use the local priority connection mechanism to replace the global priority connection mechanism in the BA model [66].

(3) *Euclidean Distance Preferred Model.* Guo et al. [67] proposed a novel Euclidean distance preferred (EDP) model, which produces a small world network. In the EDP model, the infection probability of those susceptible individuals to an infected individual depends on the Euclidean distance.

(4) *Community Network Model/Modular Networks.* Wu and Liu [68] constructed a community network model to study the impact of the community structure on the spread of epidemics. The model has a constant degree distribution f_l or different clustering coefficients, and its community degree and clustering coefficient can be adjusted continuously. Min et al. [69] have developed a random weighted community network model that generates networks with different mixed styles under the same modularity. Then, the spread of the pathogen in networks with different mixed patterns is simulated. Masuda [70] focused on a network with a modular structure, that is, by definition, nodes in a network with a modular structure are divided into multiple modules so that the number of links connecting nodes in the same module is relatively large. Ren and Wang [71] proposed a community structure in which the network model changes over time, namely, a time-varying community network.

TABLE 3: The work done on infectious diseases using the multiplex network: in the related work column, the research studies performed by researchers using the multilayer network are shown, and in the reference column is the relevant literature of the corresponding research.

Related work	Reference
Study the relationship between the information layer and the physical layer	[17, 58–60]
The reliance on analyzing and formulating immunization strategies	[26, 61–64]

3.2. *Epidemiological Modeling.* An overall application of infectious disease modeling is the need to evaluate intervention strategies and their impact on emerging and re-emerging pathogens [72]. Here are some common epidemiological models.

3.2.1. *SI Model.* The SI model is the most basic representation of the epidemic spread model. In this model, individuals can be in two discrete states: susceptible (S) or infected (I). A vertex of the network represents each individual. The edges are the connections between individuals, and infection may follow these connections' spread [73]. This model describes the state of individuals or agents who change from susceptible to infected at all times. Therefore, the SI model helps capture the diffusion or penetration process in the entire network and describes the early epidemic stage when no control measures are deployed [74, 75]. Barthelemy et al. [10, 76] applied SI dynamically to each vertex, measuring the evolution of the number of infected individuals and other numbers. The model has not only theoretical significance but also practical significance outside the physical world. For example, Chu et al. [12] used the SI model to study the spread of epidemics and community-weighted networks, trying to understand how weights and social structures affect disease transmission dynamics. Pastor-Satorras and Castellano [77] used the SI model on unweighted and weighted networks to consider the localized phenomenon of the disease and study the local characteristics of disease transmission.

3.2.2. *SIS Model.* The standard SIS model relies on a coarse-grained description of individuals in the population. Individuals can only exist in two states: susceptibility and infection. If every vulnerable node is connected to one or more infected nodes, it will be infected at every time step. At the same time, the infected node may become suspicious again. Individuals randomly go through the cycle of susceptibility \rightarrow infection \rightarrow susceptibility [78]. This model does not consider the possibility of individual evacuation due to death or immunization. It is suitable to describe some epidemics that are not only spread through the vector but also spread between individuals through direct contact [79]. It is mainly used as a model for the study of infectious diseases, that is, the degree of transmission of the infection in the population [39]. The advantage of using the SIS model is that it is relatively simple (similar to the early stage of an epidemic outbreak [21, 80]) and can also be widely used.

The SIS model is widely used. In studying the spread of epidemics in different populations, Joo and Lebowitz [81] analyzed the weights of the edges distributed between two

nodes. Since the weights depend on the connectivity of these nodes, the saturation effect in the SIS model is especially considered. Gross et al. [82] studied the sensitivity to infection susceptibility (SIS) models on adaptive networks. Dan et al. [66] performed a simulation in an epidemic SIS model. Sandro [14] analyzed the SIS model of epidemic infection to study the outcome of the epidemic spreading process driven by transportation rather than reaction events. Ji and Ge [83] used the SIS virus propagation model to test the side-immunity strategy. Taking the SIS model on a scale-free network as an example, Zhang et al. [84] explained that the density of infected individuals $I(t)$ and the number of deleted edges for different strategies have the same expansion rate. Wu et al. [35] and Bansal and Meyers [85] used the SIS kinetic method to study the effect of definitive vaccines. Ren and Wang [71] considered the SIS model and performed numerical simulations to study the effect of mobility on dynamic behavior. Juang and Liang [86] studied a general SIS model with complex network vectors. Guo et al. [67] used the standard SIS model to study the epidemic dynamics on the EDP small world network.

In addition to applying standard models, some scholars have made innovations in the SIS model. In the SIS epidemic model, called MR-SIS (multiple relational susceptibility-infection-susceptibility) epidemic models, the effective transmission rate is calculated by different formulas [87]. Shi et al. [42] proposed and simulated an SIS model of epidemic spread with infected media on a complex network. Yang [17] nested the SIS model in multiple networks using the UAU-SIS model to study the spread of consciousness and epidemics.

3.2.3. *SIR Model.* The agent in the SIR model can access three states S (susceptible), I (infected), and R (recovered). Initially, the state of the node selected for immunization is set to R , and all remaining nodes are in the S state. The infection starts from a random susceptible node and then changes its status to I [88]. At any time, all susceptible (S) individuals are unlikely to be infected (I), and any infected individual may be removed (R): through death, isolation, recovery, or subsequent immunity [52]. These pathogens not only switch between susceptibility and infection (as in the SI model) but also tend to recover in the SIR epidemic model [89]. The dynamics of the SIR model is controlled by two parameters: infection rate β and recovery rate γ : a healthy node may be infected by an infected neighbor with the transmission probability (that is, the infection rate on the link); and, the infected node can also recover with probability γ and never be infected again [66, 90, 91]. The SIR infection process has the following characteristics: (1) all nodes are equally susceptible to infection; (2) infection

always starts from a single location; (3) infectious node can infect any node connected to it with probability p ; (4) the transmission probability is the same; (5) no node is infected twice. Similarly, once a node is infected, it will be infected until it infects one of its neighbors [92]. The SIR model is simple and useful for understanding cascading faults in the network [53]. One disadvantage is the unrealistic assumption of random contact in a large population that is completely mixed [93].

The application of standard SIR dynamics to the social network model is prosperous. Zhang and Xinchu [94] studied the impact of immune function on disease transmission in a complex network with homogeneous properties and then considered the immune function in a complex network with inhomogeneous properties and the impact of inhomogeneous properties on disease transmission. Chu et al. [9] studied the SIR model's dynamic behavior with weighted transmission rate and nonlinear infectivity. Zhao et al. [26] used SIR dynamics as an epidemiological model to examine the impact of immune strategies on disease transmission in multiple networks. The SIR model helps to analyze the spread of epidemics. Chen et al. [23], Gong et al. [25], and Min et al. [69] used the SIR model to simulate the epidemic dynamics in the generated network. To study the effectiveness of community blockade in preventing the spread of epidemics, Gosak et al. [95] simulated a random SIR model on different social networks. The SIR model helps to study immune strategies. Wang et al. [13] used classic and degree-related SIR models to evaluate the effectiveness of incomplete targeted immunity in scale-free networks. Based on the SIR model, Parousis-Orthodox et al. [96] analyzed the spread of infection in the network to introduce vaccination technology; Liu et al. [36] studied the proportion of tuberculosis infection at the end of disease transmission and the time step of disease transmission; Taghavian [87] compared the performance of different immunization methods. Xu and Xu [97] focused on the modeling and control strategy of epidemic spread SIR with the network community structure. To test the immune effect, after immunizing (removing) a certain percentage of nodes, Huang et al. [98] used the classic SIR virus to spread on the remaining network. Vassallo et al. [99] studied the extension of the susceptible infection recovery (SIR) epidemic model using loop vaccination in complex and spatial networks. Buono and Braunstein [61] and Li et al. [59] studied the spread of pathogens and improved immune models based on the SIR infectious disease model in a layer of multiple networks. To understand the influence of overlapping nodes in the epidemic process, Alvarez-Zuzek et al. [100] conducted an empirical evaluation of primary deterministic immunity based on overlapping node strategies. Besides, based on the basic SIR epidemic model in a complex network and the phenomenon that infected individuals have different infection rates, Qu and Han [45] proposed an infectious disease model with two infection rates and transition probability.

3.2.4. SIRS Model. The SIRS model assumes that individuals are always in three discrete states: susceptible (S), infectious (I), and immune (R). The rules for transfer between individuals are susceptible (i.e., healthy). Infected people will be

infected with probability β ; infected people will be cured with probability γ and enter the immune state; immunized people will lose immunity with probability δ , and at the same time, some healthy people can be vaccinated to make them with probability α and directly enter the immune state. When $\alpha=0$, the model is simplified to the standard SIRS infection model [34, 101].

Examples of the application of the SIRS model are as follows. By studying the SIRS epidemiological dynamics, Yan et al. [102] studied the influence of different degrees of the community structure on the dynamics. Based on the Watts–Strogatz (WS) small world network model and the BA model, Nian and Hu [37] established a standard susceptibility to infection recovery susceptibility (SIRS) epidemic model and proposed a new immunization program: “the most common friend’s first immunization.” In the following years, in order to verify the effectiveness of immunization, Nian et al. [28] conducted theoretical verification and computer simulations on different networks with SIRS epidemic models. Huo et al. [29] constructed a more realistic SIRS epidemic model with age of infection and recurrence on the scale-free network. Based on the integrated SIRS model, Cai et al. [15] studied the influence of the feedback mechanism and individual transmission on disease transmission in a scale-free network for population density and artificial immunity.

3.2.5. Other Epidemiological Models. In addition to the infectious disease models introduced above, there are other infectious disease models as follows:

(1) *SEIRS* [24]. Let $S_k(t)$, $E_k(t)$, $I_k(t)$, and $R_k(t)$ be the densities of susceptible, exposed, infected, and recovered vertices of degree k . The infection transmission is defined by the spreading rate λ at which each susceptible individual acquires the infection from an infected neighbor during the one-time step. A susceptible individual first goes through a latent period after infection, before becoming infectious.

(2) *SEIAR* [103]. Based on the transmission process of H1N1, Jin proposed the SEIAR model by dividing the population into susceptibility (S), exposure (E), asymptomatic infection (A), symptomatic infection (I), and removal/immunity (R). Wards with asymptomatic infections include those with no obvious symptoms or mild flu-like symptoms. They have no confirmed cases, but they can spread the infection.

(3) *SIVR (Susceptible-Infective-Variant-Recovery)* [104]. This model considers two different factors in the process of virus transmission: the same virus mutation factors, and it analyzes the steady-state effects of different infection rates, recovery rates, and mutation rates on the dynamic characteristics of the model.

(4) *SEIR*. Since most of the existing epidemiological studies are concentrated in closed areas with fixed population size, Tian et al. [105] proposed a susceptible exposure-infection-recovery model with variable contact rate to describe individuals of the dynamic spread of an epidemic heterogeneous in open limited areas. Different numbers of individuals and dynamic migration rates are considered in

the model. In the case of COVID-19, Medo [106] used an SEIR epidemic model to monitor the spread of disease.

(5) *SIQRS*. To implement isolation as a control measure and analyze its efficiency distribution in different degrees of scale-free networks, Esquivel-Gomez and Barajas-Ramirez [44] constructed the SIQRS model. In this model, each node of the network can only exist in one of four discrete states, namely, susceptible to infection, infected, isolated or removed, and pathogens spread among nodes with the first three states. Besides, Nagatani and Tainaka [107] combined the reaction (SIQRS model) with migration, and the dynamics can be described using the diffusively-coupled SIQRS model.

4. Epidemic Research Based on Social Networks

As we all know, the outbreak of severe infectious disease will not only have a significant impact on social life and medical care but also affect the economy through reduced productivity and high treatment costs. Therefore, it is important to understand the spread of infectious diseases and take relevant measures. Understanding the changes in the network itself and the role of human adaptive behavior in the process of disease transmission can propose effective measures to control the spread of viruses in the real network [108]. In this section, on the one hand, we analyze which factors will affect the spread of the epidemic; on the other hand, we summarize the plans of epidemic prevention and control plans and compare some commonly used plans.

4.1. Influencing Factors of Network Structure on Disease Transmission

4.1.1. The Impact of Nodes. Identifying the most efficient “communicators” in the network is an essential step in optimizing the use of available resources and ensuring more effective information dissemination [109]. The important influence of the node on the spread of the virus is mainly concentrated on its initial configuration. Volchenkov et al. [31] found that the actual spread of the disease largely depends on the initial distribution of infected individuals on the population, and the process can be manifested as the spread of the disease is short and the cure rate is low. Dan et al. [66] established a comparison between the node with the largest degree and the node with the smallest degree in the initial infection network. With the increase of the parameter M/m , the propagation threshold is on a downward trend. Besides, Buono et al. [110] found that shared nodes’ existence will increase the popularity threshold of isolated networks with lower propagation capabilities.

4.1.2. The Influence of Individual Behavior. The impact of behavioral activities is divided into two parts, one is to promote the spread of the epidemic, and the other is to slow down or hinder the spread of the epidemic. On the one hand, Grabowski and Kosiński [111], Wang et al. [112], Hancean et al. [113], and Mbah et al. [114] believed that human activities have a significant impact on the dynamic processes

in social networks. They found that the activity of an individual (the relative time spent interacting with others each day) is positively related to its degree. Goncalves et al. [115] incorporated social behavior into the key factors for further spread of infection, and through simulations, they proved the impact of different social behaviors on the epidemic threshold. On the other hand, Sun et al. [22] found that individuals’ adaptive behaviors during the spread of disease can quickly reduce the incidence. At the same time, through theoretical analysis and computer simulation, Cai et al. [15], Mirzasoileiman et al. [116], and Yan et al. [89] showed that artificial immunity can reduce the stability ratio of the system and increase the transmission threshold of the system.

4.1.3. The Influence of Communication Characteristics. First of all, we must introduce the concept of the threshold value of the transmission probability, which is a very critical factor in disease transmission. Threshold transmission is defined as a fixed operation for t time steps, and the threshold value is defined as the minimum transmission probability. In the case of the immunological pathogen, the threshold probability is limited [91]. In other words, the higher the threshold, the less likely the disease is to spread; on the contrary, the lower the threshold, the easier the disease is to spread. The second is the infection rate or contagiousness. An increase in the infection rate will lead to more infections [89]. And, the epidemic threshold depends not only on the infectivity of individuals but also on the infectivity between individuals and animals. Shi et al. [42] researched the infectivity between humans and mosquitoes. The next is transmission speed. Chu et al. [12] found that, in the weighted case, the spread of infection in a network with a community is slower than in the unweighted case. Ren and Wang [71] came up with a critical value for the flow rate. In all communities, epidemics with a prevalence rate greater than the critical value broke out, and epidemics with a flow rate less than the critical value died. Meloni et al. [14] proved that the prevalence threshold is determined by the contact flow, and the prevalence is closely related to the emergence of epidemic transmission channels defined and driven by the traffic flow. Besides, the value of the popularity threshold depends on the delivery rate: the smaller the delivery rate, the greater the popularity threshold. Finally, dynamic aggregation is conducive to the spread of infectious diseases. Degree centrality and connectivity centrality can describe infecting ability and infection susceptibility [117].

4.1.4. The Influence of Time. Here, we discuss two-time factors, one is the time of the outbreak and spread of infectious diseases and the other is the time of epidemic detection and vaccination. Through analysis and numerical results, Barthelemy et al. [10] showed that the evolution of the burst time follows precise stratified dynamics. Once it reaches the most closely connected hub, the infection will gradually spread to the entire network at a smaller level. Ren and Wang [71] found that the epidemic can break out in communities where no infected individuals initially existed,

and the outbreak time decreases as the migration rate increases. For the network model, Jin [102] proved that the size of disease-free equilibrium depends on the start time of vaccination. Wang [43] found that reducing detection time is often critical to successful immunization.

4.1.5. Impact of Information. Even if the funds are limited, the network information can be used to monitor and control epidemics [118]. Strona et al. [119] and Yang [120] et al. found that increasing the rate of information dissemination could increase the peak density of information disseminators and the scale of information dissemination at the information layer, which had an inhibitory effect on the spread of the epidemic. Granell et al. [57] studied the influence of multiple network model's three main parameters: immunity, self-awareness, and mass culture. The result shows that although self-awareness has no effect on dynamics after infection, the degree of immunity of conscious individuals and mass media do change the spread of the epidemic in critical areas. Also, through simulation, Wang [43] found that geographic information also plays a role in hindering the spread of epidemics.

4.1.6. Impact of Network Structure. Network structure has a major impact on the dynamics of the epidemic [72, 121]. When there is no immune strategy, the network structure is the key factor that affects the number of all infected vertices under the law of time evolution. For different immunity probabilities and trigger time (time to trigger the control strategy), the percentage of infection using the immunity strategy has different maximum values [54]. The study of Chakraborty et al. [122] and Olinky and Stone [33] indicated that the same pathogen can produce different epidemic dynamics on different networks, so the spread of epidemics depends on infection schemes and network structures. Next, we will illustrate the influence of the network structure on the spread of the epidemic from the weight of the network, the uniformity, and the relevance of the network.

(1) Yan et al. [11] used link weights to express the familiarity between two people and studied the detailed epidemic spreading process in scale-free networks. Numerical studies have shown that nodes with higher strength are preferentially infected, and it is proved that a large dispersion of network weights will cause slower propagation speed. Besides, from the numerical simulation, the global stability of the disease-free state and local balance of the adaptive weighted model with a time delay can be obtained. It can be observed that strong adaptability can suppress the global epidemic to a lower level [22].

(2) Dan et al.'s [66] simulation results showed that the more uneven the network, the smaller the critical value of the virus spreading on it.

(3) Verdasca et al. [53] discovered the long-term characteristic dynamics related to the structure of the network in a quantitative way. In particular, the increase in spatial correlation (i) exacerbates the fluctuations around endemic states, (ii) reduces the effective transmission rate by screening for infectivity and susceptibility, and (iii) increases

the period of incident oscillation due to the lower effective transmission rate. Wang et al. [63] considered the impact of the degree of correlation between network layers and found that the increase of this value is beneficial for reducing the immune threshold based on multinode acquaintance immunity.

4.1.7. Impact of Community Groups. First of all, in real life, the population density will affect the infection rate of the epidemic: the greater the population density, the higher the infection rate of the system and the lower the transmission threshold [15, 123]. Second, the size of the community, the strength of the community structure, and the distance between communities can all affect the spread of epidemics. In the study of Liu et al. [58], the spread of the epidemic has changed significantly after the immunization strategy took effect. More specifically, the final incidence of the disease is higher in large subgroups, while the epidemic disappears in small subgroups, which indicates that the size of the community is affecting individual immune behavior. In other words, the more communities the network has, the fewer the chances of network infection. The study of Liu et al. [124] found that a large family size N and a high intrafamily infection rate β are more likely to cause disease transmission. Wu and Liu [68], Yan [101], and Chu et al. [12] used numerical simulations to demonstrate that the spread of epidemics mainly depends on the extent of the community and decreases as the extent of the community increases. For a fixed level of community, the efficiency will decrease as the clustering coefficient increases. Xu [96] believed that a network with a stronger community structure will be more conducive to the control of infectious diseases than a smaller network. Gupta et al. [125] believed that effective use of the community structure can find influential nodes, thereby achieving target immunity of specific nodes and reducing the probability of epidemics in the entire network. Through simulation and demonstration, Li et al. [51] found that the strong community structure inhibits virus transmission. In the real network, the more frequent the mobile contacts between communities, the higher the probability of healthy individuals being infected and the easier the virus will break out. Xu [73] studied the geographic impact of disease transmission in lattice-free embedded networks and found that the more the geographical restrictions on the network, the smoother the epidemic spread.

4.1.8. Other Influencing Factors. Other epidemics have a weakening effect on the epidemics of current research. Through bond filtration theory and numerical simulation, Wang et al. [126] and Matamalas et al. [127] found that the synergy effect will promote the spread of another disease, thereby increasing the epidemic threshold and reducing the scale of the epidemic. Min et al.'s [69] simulation results showed that, under the same modular conditions, (1) the mixing method significantly affects the size, speed, mode, and immune strategy of the epidemic and (2) the increase in the number of communities magnifies the effect of the mixed style.

4.2. The Prevention and Control Measures of Epidemic

4.2.1. Vaccination Strategy. Vaccination is one of the most important and effective epidemic prevention and control strategies [128]. Vaccination strategies have two core objectives: lower and delay the peak size and reduce the final infected population to limit morbidity [129]. When vaccination coverage is highest, population immunity is greatest because it can increase the critical threshold of disease transmission on complex networks and reduce the spread of infectious diseases [100], so most scholars start researching immunization strategies with vaccines. The common immune control strategies are uniform immunization, proportional immunization, and targeted immunization. However, due to the difficult and uneconomical characteristics of uniform immunization (the strategy of immunizing all nodes in the network), it will not be discussed here. In the following, we will introduce random immunization, proportional immunization, targeted immunization, reactive immunization, and mixed strategies.

(1) *Random Immunization.* Random immunization is to randomly select a part of the entire population for vaccination [72]. Yan's [89] research showed that a significant increase in the system's epidemic threshold will reduce the risk of disease epidemics in the system. Each node can play multiple roles in different topological connections. Inspired by this fact, Zhao et al. [26] proposed immune strategies on multiple networks, including random (target) immunization based on multiple nodes and random (target) immunization based on layer nodes. Interestingly, both types of random immunization strategies show higher efficiency in controlling disease transmission on multiple Erdős–Rényi (ER) random networks. Mirzasoleiman [114] believed that everyone in the network is eager to voluntarily pay for the vaccine and get the immunization. To improve the results of the immunization strategy, he provides the vaccine to the individuals selected by the algorithm at a discount so that most of them could accept it. The simulation results found that the proposed random immunity based on pricing is more influential than target immunization.

(2) *Proportional Immunization.* Proportional immunization requires immunity to a large number of nodes in the network. Guo et al. [67] proposed local immunization and found that there is a key immune radius that can effectively suppress the epidemic. Based on the importance of clustering, Xia et al. [40] proposed an improved local immune strategy, which takes into account the degree of nodes and the clustering coefficient. The strategy involves randomly selecting the initial individual, then selecting his acquaintances (friends) with many friends and scattered friends, and then immunizing the selected acquaintances. This process is repeated by sequentially selecting immunized subjects as the initial input until the number of immunized individuals is reached. Yan [89] proposed a local strategy, which is to vaccinate only at bridge nodes in the community where the epidemic originated. This strategy helps reduce infections at an early stage and may eliminate epidemics in the community. Gupta [122] believed that community centers and bridges are both influential nodes in the network and play a

key role in the spread of epidemics. Therefore, centralized measures need to be taken to mark nodes that have a good balance of internal and external connections in the community as influential.

(3) *Targeted Immunization.* Although a unified mass immunization strategy can help control the prevalence, an established immunization strategy for a specific immune group can better control endemic diseases [102]. Through quantitative analysis, Chu et al. [9] found that controlling individual contact is more important than the infection ability of the disease itself. Therefore, we can protect the entire network from infection by defending a small number of nodes. In addition to random immunization, if the extent of each node is known, an effective immunization strategy can be proposed called targeted immunization, which means the primary vaccination of the largest node [72]. Its advantages are (1) contrary to conventional vaccination, target vaccination has better effects, and there is little demand for vaccines (or antiviral drugs). If new patients are discovered quickly enough, the epidemic can be curbed with relatively few vaccines [110]. (2) It may be of practical significance to establish dynamic control strategies among people with different connectivity patterns. Especially over time, targeted immunization strategies may be particularly effective in controlling epidemics [75]. Through simulation, Chen et al. [23] found that target immunization can effectively control the spread of influenza A H1N1. This is similar to the method of isolating infected patients in real life, cutting off the source of transmission and preventing the continued spread of infectious diseases in the population. Here, we will classify and discuss targeted immunization again: targeted immunization and acquaintance immunization.

The applications of targeted immunization are as follows. According to the weighted network, a "high contact priority" immunization strategy is proposed by Holme [130] and Nian et al [28]. In high contact priority immunity, the nodes that are connected to the infected node and have a high frequency of contact should be inoculated first. Taking into account the development of appropriate vaccination strategies on the dynamic contact network, Shahzamal et al. [131] proposed a strategy based on local contact information, called the individual's movement-based vaccination strategy. Numerical simulations by Yang [17] and Parousis-Orthodox [95] showed that networks with a higher modularity index are more likely to be affected by the central vaccination technology between nodes, so immunization of central nodes is a good way to alleviate epidemics. Based on the concept of independent set, Huang [74] proposed a new immune strategy for complex networks, an immune method with the largest vertex of independent concentration, called independent set target immunity. From the perspective of the network structure, it is clarified that when the sum of degrees of independent centralized immune nodes is equal to the sum of degrees of target immune nodes of the whole network, the target immune strategy of independent sets is more effective than the target immune of the whole network. Liu et al. [132] proposed a new type of immunization strategy that relies on local information. The proposed strategy initializes the score of each node with its

corresponding degree value and then recalculates the score of a specific immune node based on the degree of the two nodes themselves and their nearest neighbors. After that, an immune node tries to find an unimmunized high score neighbor to replace itself. Vassallo's [98] circular vaccination is a mitigation strategy, which involves contacting and vaccinating contacts of sick patients, whose purpose is to provide immunization and stop the spread of the disease. Some scholars have also optimized targeted immunization. Wang et al. [133] used community structure information such as in-degree and out-degree of nodes to select candidate seeds and then selected immune nodes from the candidate set instead of the entire network to narrow the search space. Alfinito et al. [38] used an accurate score based on a local-global hybrid strategy to modify the TI scheme. Specifically, it introduced a modified score that aims to treat the center and people at risk of infection as related to the spread of the epidemic. Jadidi et al. [115] proposed to allocate a limited number of vaccines among different populations and vaccinate the most effective candidate vaccines to disrupt the transmission chain of diseases in each population.

Cohen et al. [134] pointed out that global information is often difficult to collect and may not even have a good definition, so he proposed an immunization strategy that works under low immunization rates and eliminates the need for global information. The advantage of this method is that it can be used before the epidemic begins to spread because it does not require any knowledge of chain infection. Wang et al. [63] proposed immunity to acquaintances who do not need to fully connect information on multiplex networks. According to topological characteristics, this scheme can be divided into two categories: immunity based on multiplexing nodes and acquaintance immunity based on layer nodes. Based on the generating function, it is shown that these two strategies are effective in preventing the spread of the disease, and their theory can accurately predict the immune threshold in the two cases, regardless of the potential interaction topology. Since controlling nodes in the overlapping subnets will help effectively suppress the spread of the epidemic, Nian [86] proposed a more feasible and effective epidemic immunity strategy, which is to use the acquaintances in the overlapping subnets to immunize key nodes in many places as much as possible.

(4) *Reactive Immunization*. Given certain social factors, such as religious beliefs and human rights, immunization is not a mandatory behavior but is determined by the individual. In this case, an individual's vaccination decision depends on the neighbor's strategy (i.e., whether to vaccinate), the neighbor's perceived risk of infection, the perceived safety and efficiency of the vaccine, and the financial costs associated with vaccination and disease infection [72]. Therefore, individual vaccination behavior depends on their local information. For convenience, we call dynamic immunity reactive immunity, which is also called information-driven vaccination or information-dependent vaccination. The impact of reactive immunity on the epidemic threshold and the critical value of the initial epidemic outbreak is negligible, but it can effectively suppress the epidemic outbreak [79]. Wang [123] believed that self-consciousness

control strategies play an important role in suppressing the epidemic of cooperation. In particular, increasing the rate of immunization or isolation can raise the epidemic threshold, reduce the outbreak scale of cooperative epidemics, and lead to the transition from discontinuous to continuous crossover. Through simulation, Wu et al. [35] found that voluntary vaccination based on historical information can effectively control the outbreak of epidemics.

(5) *Hybrid Strategy*. Eubank et al. [65] proposed a combination of vaccination and early detection. Through establishing the large-scale model, he found that the outbreak can be controlled by combining targeted vaccination strategies with early detection without resorting to mass vaccination of the population. Liu et al. [36] proposed to establish a hybrid strategy to slow the spread of infectious diseases. Through three simulations (single target immunization, single acquaintance immunization, and mixed immunization), the following conclusions are drawn: target immunization plays a leading role in the mixed immunization strategy. In these three simulations, the trend curve of the proportion of "deleted" nodes or the time step is close to the curve of single target immunity. Therefore, targeted immunity plays a leading role.

4.2.2. *Epidemic Warning*. Epidemic early warning belongs to the active defense of the pathogen. It includes three aspects: monitoring system, alarm system, and early warning implemented to individuals. First of all, for the monitoring system, Barthelemy et al. [10] suggested that an effective way to contain the epidemic may depend on the deployment of dynamic containment measures, which are focused on gradually changing the categories of the population. More specifically, global surveillance is the main key aspect of epidemic control, and immunization strategies must evolve at different stages of transmission. Li et al. [59] proposed an observer node model that can identify infected neighbors and allow other neighbors to be vaccinated. The simulation results showed that, to maximize the suppression efficiency, we should set up limited observer nodes based on the epidemics' layer. Then, for the alert system, the intuitive solution to limit the damage caused by the infection is to detect it as early as possible. The monitor can be installed on certain network nodes and equipped with the necessary intelligence to detect the infection as soon as it reaches the node. After successful detection, an alarm can be triggered and necessary measures can be taken immediately [135]. Han's [50] model verification shows the impact of pandemic alerts on the spread of the pathogen: first, announcing accurate and timely pandemic alerts can reduce the speed of spread and help control the spread of pandemics. Second, as most health organizations do, there is a need to lead more and more accurate and timely pandemic alerts because accurate and timely pandemic alerts will lead to more decelerating effects on the spread. Finally, Gong et al. [25] found that personal vigilance can effectively slow the spread of the epidemic and delay the arrival of peak infections.

4.2.3. *Control Edge Strategy*. The edge immunity strategy is to delete edges based on the relationship between edges and

important nodes. The first is to sort according to the degree of nodes, select a certain number of nodes from high to low, and delete the edges directly connected to the nodes. In order to reduce the spread of the virus between nodes with large degrees, it is necessary to delete the edges between important nodes and common neighbors. As the average connection distance between nodes with large degrees increases, the threshold for virus spread increases. To effectively immunize the virus, the proportion of a given number of nodes should be gradually increased, and then, edges should be deleted in the same way [82]. The advantage of this strategy is that it can better preserve the integrity of the network during the control of epidemics on the scale-free network [83]. The result of Brethouwer et al. [136] showed that reductions of long-distance transmission are highly efficient for curbing the spread of COVID-19.

4.2.4. Isolation Strategy. According to Barthelemy et al. [10, 75] and Chu et al. [12], we learn that the infection first occurred on a subset of individuals with the largest number of connections and then gradually invaded individuals with a reduced number of connections. Because of the spread of infectious diseases, we can prevent and control the spread of the epidemic through isolation strategies. These strategies, in particular, can reduce the peak of infection and delay the peak time leading to offer ample time for the development of a vaccine and prevent hospitals from reaching their maximum patient capacity [137]. Gosak et al.'s [94] research shows that, in the absence of community lockdowns, only stricter isolation or mobility restrictions can be used to achieve the same effect as mitigating epidemic spreading.

Zheng [93] studied the epidemiological process on the hierarchical social network in the SIR model and proposed that if the spread of the epidemic is to be limited, the "dimension" of the infected node must be at least temporarily reduced. One way to achieve this is to isolate the infected node. Shen and Cao [16] also proposed an efficient new immune strategy from the perspective of weighted networks. This is achieved by reducing the weight of certain edges. Because the formation of tightly linked clusters of susceptible populations at high infection density can make the disease persist, the disease will not last at low infection density [81]; it is very important to reduce infection density or increase isolation. Small and Tse's [52] simulations showed that only by increasing isolation can the exponential growth of the epidemic be prevented. For this reason, they proposed measures such as school suspension, travel restrictions, and improvement of quarantine and public health procedures. Li et al. [51] believed that, in real life, although most people are limited to local activities and there is a relatively little movement across associations, the impact of movement between associations on the spread of the virus cannot be ignored. Strengthening the control of movement between associations is beneficial to suppress the spread of the virus. By comparing the results of different situations, Tian [104] found that the scale of the outbreak depends mainly on the average likelihood of infection of individuals and the number of infected individuals in the area. So,

isolation on highly mobile people and most popular venues are most likely to be effective. Gross [81] proposed that a high rewiring rate can significantly increase the popularity threshold and reduce the popularity rate. And, they have shown that adaptive rewiring can promote the isolation of infected individuals, which can significantly increase the epidemic threshold. So, Givan et al. [138] hoped that epidemic containment based on link outages can be an effective tool that can maintain the network's function and control the epidemic spreading. Wang [43] believed that once the source of infection is detected, the organization responsible for epidemic control must decide which immunization strategy needs to be implemented to prevent the spread of the disease. If the propagation path along the network structure can be predicted, an effective method is to immunologically connect a certain number of vertices to the original source of infection based on the network structure. The prevention and control measures for the apex can be considered from the perspective of the apex (or the individual). Chen and Zhang [34] and Buono and Braunstein [61] found that artificial immunity can effectively reduce the proportion of steady-state infections and increase the transmission threshold of the system, thereby effectively controlling the spread of viruses on complex networks. When an epidemic occurs, collect and release the spread of the epidemic promptly to allow people to actively cut off contact with the infected population; actively carrying out artificial immunization to increase the artificial immunization rate of the group and limiting the frequent flow of social groups and contact with others are all effective measures to control the spread of the pathogen. When the infection rate is large enough that the disease cannot be controlled, the infectious disease may break out in a short time. In this case, we can defend against infectious diseases by improving individual response levels [35]. Self-consciousness control strategies play an important role in restraining the epidemic of cooperation. In particular, it can increase the immunization or isolation rate, raise the epidemic threshold, reduce the outbreak scale of cooperative epidemics, and lead to the transition from discontinuous to continuous crossover [123]. Jose [44] studied the efficiency of isolation in conjunction with the self-protection process and found that increasing the self-protection process can improve the efficiency of curbing the spread of the pathogen. So, raising awareness through social health programs can be a good strategy to reduce the number of people infected during the spread of the pathogen. In addition, prompt intervention played a significant role in mitigating the COVID-19 outbreak, and isolation with a high level of contact tracing and quarantine is the most effective intervention strategy [139].

4.2.5. Other Strategies. As we mentioned in the previous section, other epidemics have a certain impact on the current research epidemic [123]. Zhou et al. [140] investigated the impact of one disease's immunization on the spread of another disease and found that, under some interaction parameters, an increase in the percentage of one disease's

immunization would lead to the mutual damage of another disease. This phenomenon indicates that the control of one disease may lead to the outbreak of other pathogen. Besides, high-risk groups in the network play a decisive role in the spread of the epidemic on the network. Therefore, reducing the number of susceptible and high-risk groups and avoiding the recurrence of displaced persons are effective measures to control the spread of epidemics [29]. At the same time, an increase in the quarantine rate is useful for suppressing the spread of infectious diseases, so establishing an effective quarantine policy is an effective auxiliary means [106].

4.3. Comparison of Various Schemes. Through the introduction in the previous section, we have known some of the epidemic prevention and control strategies, but the application effects of various programs are not very clear. In this section, we will mainly introduce scholars' comparison of the effectiveness of various epidemic prevention and control strategies.

Fu [21] and Lou and Ruggeri [19] discussed proportional immunization and targeted immunization and estimated the threshold of each strategy. By comparing the thresholds of different immunization strategies, it is believed that the targeted immunization strategy is more effective than the proportional strategy. Juang [85] proved that, in scale-free networks, targeted immunization and acquaintance immunization are more effective than uniform immunization and active immunization, and active immunization is the least effective strategy among the four methods. Xia et al. [141] increased the quota for the first round of selection according to the evaluation criteria of degree centrality and then considered another characteristic parameter of the node. Simulation results showed that the proposed strategy based on two rounds of sorting is effective for heterogeneous networks, and its immune effect is better than that of high immunity. In order to find out whether the vaccination target of the targeted immunization strategy is the most connected node in the entire network (global strategy) or the node in the original community where the epidemic began to spread (local strategy), through the use of analysis methods and simulations, Yan [89] observed that the answer depends on how close the communities are. If communities are closely connected, then global strategies will be better than local strategies. When expanding the scope of the investigation from a network of two communities to a network of multiple communities, he studied the patterns of community connection and the location of the community where the epidemic began to spread. Both simulation results and theoretical predictions show that, in most cases, local strategies are a better choice for immunity. However, if the epidemic starts from a core community, then in some cases, the global strategy will be superior. Taghavian [87] and Salathe and Jones [142] evaluated different immunization methods in different synthetic networks and actual networks. The results show that the performance of local methods is far from that of global methods because they are constrained by node-level calculations. Xu's [103] research on preliminary immunization strategy, long-term

immunization strategy, and comprehensive immunization strategy found that, (1) in the early stage of immunization, only susceptible individuals are randomly immunized and the immune cycle is short; (2) the long-term immunization stage has no pre-immune effect, and only the healthy individuals in the network are long-term immunized; (3) the comprehensive immunization strategy is an immune strategy that combines pre-immunity and long-term immunity. Based on the long-term immunization strategy, the immunization targets are healthy groups in the network. Through the comparison of the above three immunization strategies, they found that, under the same immunization intensity, the peak and final steady-state values of the disease population density show a decreasing trend from long-term immunization and pre-immunization to comprehensive immunization. This shows that the comprehensive immunization strategy is superior to other immunization strategies mentioned above.

In summary, the targeted immunization is a strategy with more use, more submethods, and better effectiveness. At the same time, if we integrate other immunization strategies, such as the combination of long-term strategies and short-term strategies, the effect of epidemic prevention and control on social networks will be even more surprising.

5. Future Challenges and Road Map

5.1. Future Challenges. It can be seen that there are considerable research bases on the evolution of the social network structure and the control of social network epidemic transmission at home and abroad. While, many scholars considered the factors or scenarios that are a little simple, there were some gaps between the analysis of epidemic spreading in the real world, which may have an impact on subsequent prediction and epidemic prevention research.

In studying the spread of infectious diseases, (1) when studying the evolution model, some authors lack rigorous selection of areas and individuals. In the future, we should further study the theoretical analysis value of the propagation characteristic of the virus in the local world. For example, after fusion analysis with the actual observation data, modify related parameters. (2) Many scholars studied the spread of epidemics in a relatively static state, but many real-life systems will not remain static during the spread of epidemics. At least we should consider the influence of time, such as introducing time-series networks into the propagation model. (3) In the existing model are relatively simple. For example, most studies only consider human-to-human transmission and do not consider the attenuation or mutation of the virus during the transmission process.

In terms of combining research with the real world, (1) the control method in the researchers' model is relatively simple, but in the real world if a certain area is declared as a dangerous area, more health support, such as immunization, can usually be obtained. This will result in a further reduction in the speed of transmission. Therefore, in future research, different analyses can be carried out for different

regions. (2) Many authors have given an ideal assumption in the existing research. However, in actual situations, an infected person will only come into contact with a few susceptible persons within a time step, and there will be differences in the contact pattern and frequency of contact among people. (3) It is a bit difficult to leap from theory to practice. For example, the key to a targeted immunization program is to find specific communicators, but in practice, these communicators, especially supercommunicators, are difficult to identify.

In terms of sets of variables in the model, on the one hand, existing research does not have a sufficient theoretical basis for setting the threshold of node infection. Therefore, in future research, we call on researchers to determine the infection threshold of nodes under specific conditions through investigation. On the other hand, we should also consider the correlation between parameters and the impact of this correlation on the spread of prevention and control strategies.

5.2. Road Map. With the advent of large databases and efficient analysis algorithms, the spread of these pathogens can be better predicted and controlled [143].

In terms of modeling, first, the simple model [32] is very instructive, but many other components should be considered to represent a more realistic real epidemic. It is also necessary to add simple rules to define the network's time pattern, such as the frequency of formation of new connections, the actual length of time the connections exist, or different types of connections. Secondly, it is necessary to consider further the adaptive dynamic behavior on time-varying networks and the corresponding model with double delay [22, 144], such as the delay system's disease freeness and the global asymptotic stability of local equilibrium. Moreover, for large-scale networks with thousands of nodes or more, the algorithm to solve the optimal immunity problem needs to improve the computational efficiency, and the method of calculating the approximate optimal immunity may also require higher accuracy. Finally, considering the synergy may better understand the complex systems of epidemics and human vaccination in future societies. For example, the synergy between mathematical modeling and theoretical exploration and data-driven research, the feedback effect between disease or behavior and vaccination [145], and the combination of adaptive coevolution processes [63].

In terms of scope and environment, first of all, through a secure global immunization organization can the network be optimized for immunization [61]. Unfortunately, the Internet's self-organizing nature does not allow it to figure out how the organization operates quickly. Therefore, in future research, we can study the selective immunity strategy in depth by studying the high-traffic network operation mode. Second, a good immunization strategy should consider many real-life factors, such as politics, economy, culture, and region. Future research can learn more about the different situations in a region through case studies, making network analysis and epidemic prevention and control more practical

here. For example, we want to study the U.S. epidemic prevention and control measures and give valuable suggestions. We can first determine a social network model through field research, questionnaires, and data searching. According to each state's policies, population density, economic development level, and so on, different node characteristics and transmission rate of pathogens between nodes are set to determine each group's attributes in the network. Next, perform simulations to observe the characteristics of the spread and rate of pathogens. Finally, analyze the reasons and adopt effective targeted strategies for the area. Finally, if we want to study a more extensive network structure, such as studying the spread of the pathogen in a country, we can use cities as nodes and the number of infected people as the characteristics of nodes and build the entire network based on the data of population migration between cities.

In terms of prevention and control strategies, first, we can use the existing AI technology to extract a large amount of confidential information and knowledge from data with time series for epidemic prediction. For example, we can learn and analyze a large amount of data with the help of some deep learning algorithms. Second, we can learn how to control the epidemic in practice. Chinese achievements in the prevention of COVID-19 are remarkable. Summarizing the experience of areas with better epidemic prevention and control can make up for the abovementioned theoretical research deficiencies and help to add new ideas for dealing with major public incidents in the region. For example, using the widespread popularity of Internet connections and the miniaturization of equipment to collect epidemiological information with the direct participation of a large number of individuals, the emergence and development of the epidemic can be monitored in near real time, so as to estimate the disease prevalence and vaccination rate and more effectively deploy the epidemic prevention and control work [72]. Finally, we would actively integrate new technologies into network governance. The rise and rapid development of cloud computing and Hadoop technology make it possible to extract and calculate useful information from large-capacity data. If we can use such technology to improve the network's information, our social network analysis will be more efficient and better serve the prevention and control of the epidemic.

6. Conclusion

The research results show that the epidemic prevention work can adopt a multiperspective method for social network analysis and application. Combining the epidemic spread model with the network model can analyze the factors affecting the spread of epidemics. We can conclude that nodes, individual behavior, communication characteristics, time, information, network structure, and community groups are critical factors affecting the spread of epidemics. The analysis of social networks has paramount guiding significance for the prevention and control of epidemics. For example, we can use vaccination strategy, epidemic warning, control edge strategy, isolation strategy, or a combination of several

strategies to control and prevent the spread and occurrence of serious diseases.

Due to the limitations of various technical factors, the previous research results are difficult to avoid defects. However, with the advent of large databases and efficient analysis algorithms, the spread of pathogens can be better predicted and controlled in a more realistic environment. On the one hand, future research can add some simple rules to define the time mode of the network and make the static network dynamic. If supplemented by more accurate and efficient algorithms, it can simulate the spread of viruses in large-scale networks with thousands of points or more. On the other hand, future research can take the COVID-19 pandemic as an example, use cloud computing, Hadoop, and other technologies to extract and calculate useful information from large-volume data, improve network information, and determine social network models and related variable parameters. Then, combined with SNA simulation analysis, we can propose more convenient and effective prevention and control strategies.

Data Availability

The data used to support the findings of this study are included within the article.

Conflicts of Interest

The authors declare that they have no conflicts of interest regarding the publication of this paper.

References

- [1] M. E. Newman, "Fast algorithm for detecting community structure in networks," *Physical Review. E, Statistical, Nonlinear, and Soft Matter Physics*, vol. 69, no. 6, Article ID 066133, 2004.
- [2] W. Fang, S. Dai, and L. L. Tang, "The impact of international research collaboration network evolution on Chinese business school research quality," *Complexity*, vol. 2020, Article ID 7528387, 20 pages, 2020.
- [3] Y. X. Zhu, X. Y. Duan, Y. M. Liu, and B. Qu, "Research progress of social network analysis in AIDS prevention," *Chinese Journal of AIDS & STD*, vol. 26, pp. 787–790, 2020.
- [4] Q. Wu, X. Fu, Z. Jin, and M. Small, "Influence of dynamic immunization on epidemic spreading in networks," *Physica A: Statistical Mechanics and Its Applications*, vol. 419, pp. 566–574, 2015.
- [5] D. Moher, A. Liberati, J. Tetzlaff, and D. G. Altman, "Reprint-preferred reporting items for systematic reviews and meta-analyses: the PRISMA statement," *Physical Therapy*, vol. 89, no. 9, pp. 873–880, 2009.
- [6] A.-L. Barabási and R. Albert, "Emergence of scaling in random networks," *Science*, vol. 286, no. 5439, pp. 509–512, 1999.
- [7] W. Fang, S. Dai, and L. L. Wang, "Evolutionary model and simulation research of collaborative innovation network: a case study of artificial intelligence industry," *Discrete Dynamics in Nature and Society*, vol. 2018, Article ID 4371528, 13 pages, 2018.
- [8] M. Kuperman and G. Abramson, "Small world effect in an epidemiological model," *Physical Review Letters*, vol. 86, no. 13, pp. 2909–2912, 2001.
- [9] X. Chu, Z. Zhang, J. Guan, and S. Zhou, "Epidemic spreading with nonlinear infectivity in weighted scale-free networks," *Physica A: Statistical Mechanics and Its Applications*, vol. 390, no. 3, pp. 471–481, 2011.
- [10] M. Barthélemy, A. Barrat, R. Pastor-Satorras, and A. Vespignani, "Dynamical patterns of epidemic outbreaks in complex heterogeneous networks," *Journal of Theoretical Biology*, vol. 235, no. 2, pp. 275–288, 2005.
- [11] G. Yan, T. Zhou, J. Wang, Z. Q. Fu, and B. H. Wang, "Epidemic spread in weighted scale-free networks," *Chinese Physics Letters*, vol. 22, pp. 510–513, 2005.
- [12] X. Chu, J. Guan, Z. Zhang, and S. Zhou, "Epidemic spreading in weighted scale-free networks with community structure," *Journal of Statistical Mechanics-Theory and Experiment*, 2009.
- [13] Y. Wang, G. Xiao, J. Hu, T. H. Cheng, and L. Wang, "Imperfect targeted immunization in scale-free networks," *Physica A: Statistical Mechanics and Its Applications*, vol. 388, no. 12, pp. 2535–2546, 2009.
- [14] S. Meloni, A. Arenas, and Y. Moreno, "Traffic-driven epidemic spreading in finite-size scale-free networks," *Proceedings of the National Academy of Sciences*, vol. 106, no. 40, pp. 16897–16902, 2009.
- [15] S. H. Cai, D. M. Zhang, G. W. Gong, and C. R. Guo, "Integrated systemic inflammatory response syndrome epidemic model in scale-free networks," *Chinese Physics B*, vol. 20, no. 6, 2011.
- [16] D. Shen and S. Cao, "An efficient immunization strategy based on transmission limit in weighted complex networks," *Chaos, Solitons & Fractals*, vol. 114, pp. 1–7, 2018.
- [17] J. X. Yang, "Epidemic spreading in multiplex networks with heterogeneous infection rate," *EPL*, vol. 124, p. 7, 2018.
- [18] T. Zhou, J. G. Liu, W. J. Bai, G. Chen, and B. H. Wang, "Behaviors of susceptible-infected epidemics on scale-free networks with identical infectivity," *Physical Review. E, Statistical, Nonlinear, and Soft Matter Physics*, vol. 74, Article ID 056109, 2006.
- [19] J. Lou and T. Ruggeri, "The dynamics of spreading and immune strategies of sexually transmitted diseases on scale-free network," *Journal of Mathematical Analysis and Applications*, vol. 365, no. 1, pp. 210–219, 2010.
- [20] S. L. Silva, J. A. Ferreira, and M. L. Martins, "Epidemic spreading in a scale-free network of regular lattices," *Physica A: Statistical Mechanics and Its Applications*, vol. 377, no. 2, pp. 689–697, 2007.
- [21] M. Small, X. C. Fu, D. M. Walker, and H. F. Zhang, "Epidemic dynamics on scale-free networks with piecewise linear infectivity and immunization," *Physical Review E*, vol. 77, p. 8, 2008.
- [22] M. Sun, H. Zhang, H. Kang, G. Zhu, and X. Fu, "Epidemic spreading on adaptively weighted scale-free networks," *Journal of Mathematical Biology*, vol. 74, no. 5, pp. 1263–1298, 2017.
- [23] D. Chen, S. Huang, and M. Shang, "Complex network model and application in epidemic spreading and controlling," *Computer Science*, vol. 38, pp. 118–121, 2011.
- [24] J. Liu and T. Zhang, "Epidemic spreading of an SEIRS model in scale-free networks," *Communications in Nonlinear Science and Numerical Simulation*, vol. 16, no. 8, pp. 3375–3384, 2011.

- [25] Y. Gong, Y. Song, and G. Jiang, "Epidemic spreading in scale-free networks including the effect of individual vigilance," *Chinese Physics B*, vol. 21, 2012.
- [26] D. W. Zhao, L. H. Wang, S. D. Li, Z. Wang, L. Wang, and B. Gao, "Immunization of epidemics in multiplex networks," *PLoS One*, vol. 9, no. 11, Article ID e112018, 2014.
- [27] N. Madar, T. Kalisky, R. Cohen, D. Ben-Avraham, and S. Havlin, "Immunization and epidemic dynamics in complex networks," *The European Physical Journal B-Condensed Matter*, vol. 38, no. 2, pp. 269–276, 2004.
- [28] F. Z. Nian, L. J. Wang, T. Li, and K. Wang, "High-contact-first immunization strategy on complex networks," *Computer and Medicine*, vol. 59, pp. 476–487, 2017.
- [29] H.-F. Huo, P. Yang, and H. Xiang, "Dynamics for an SIRS epidemic model with infection age and relapse on a scale-free network," *Journal of the Franklin Institute*, vol. 356, no. 13, pp. 7411–7443, 2019.
- [30] R. May and A. Lloyd, "Infection dynamics on scale-free networks," *Physical Review E, Statistical, Nonlinear, and Soft Matter Physics*, vol. 64, Article ID 066112, 2001.
- [31] D. Volchenkov, L. Volchenkova, and P. Blanchard, "Epidemic spreading in a variety of scale free networks," *Physical Review E, Statistical, Nonlinear, and Soft Matter Physics*, vol. 66, Article ID 046137, 2002.
- [32] R. Pastor-Satorras and A. Vespignani, "Immunization of complex networks," *Physical Review E*, vol. 65, 2002.
- [33] R. Olinky and L. Stone, "Unexpected epidemic thresholds in heterogeneous networks: the role of disease transmission," *Physical Review E, Statistical, Nonlinear, and Soft Matter Physics*, vol. 70, Article ID 030902, 2004.
- [34] Q. Chen and Z. Zhang, "Dynamics behavior and immune control strategies of SIRS model with immunization on scale-free complex networks," *Computer Science*, vol. 40, pp. 211–214, 2013.
- [35] Q. Wu, H. Liu, and M. Small, "Dynamical diversity induced by individual responsive immunization," *Physica A: Statistical Mechanics and Its Applications*, vol. 392, no. 12, pp. 2792–2802, 2013.
- [36] B. Liu, S. Yan, and Y. Xue, "Analysis of hybrid immunization strategy in complex networks," *Proceedings of the 2016 4th International Conference on Machinery, Materials and Computing Technology*, vol. 60, pp. 1140–1145, 2016.
- [37] F. Z. Nian and C. S. Hu, "The most common friend first immunization," *Chinese Physics B*, vol. 25, p. 9, 2016.
- [38] E. Alfinito, M. Beccaria, A. Fachechi, and G. Macorini, "Reactive immunization on complex networks," *EPL*, vol. 117, no. 1, 2017.
- [39] R. Pastor-Satorras and A. Vespignani, "Epidemic dynamics and endemic states in complex networks," *Physical Review E*, vol. 63, 2001.
- [40] L. Xia, G. Jiang, Y. Song, and B. Song, "An improved local immunization strategy for scale-free networks with a high degree of clustering," *The European Physical Journal B*, vol. 90, no. 2, 2017.
- [41] Z. Dezsó and A. L. Barabási, "Halting viruses in scale-free networks," *Physical Review E, Statistical, Nonlinear, and Soft Matter Physics*, vol. 65, Article ID 055103, 2002.
- [42] H. Shi, Z. Duan, and G. Chen, "An SIS model with infective medium on complex networks," *Physica A: Statistical Mechanics and Its Applications*, vol. 387, no. 8–9, pp. 2133–2144, 2008.
- [43] K. Aihara, B. Wang, and B. J. Kim, "Comparison of immunization strategies in geographical networks," *Physics Letters A*, vol. 373, no. 42, pp. 3877–3882, 2009.
- [44] J. D. Esquivel-Gomez and J. G. Barajas-Ramirez, "Efficiency of quarantine and self-protection processes in epidemic spreading control on scale-free networks," *Chaos*, vol. 28, no. 1, Article ID 013119, 2018.
- [45] Q. Q. Qu and H. Han, "Analysis of SIR model based on individual heterogeneous infectivity and state transition," *Computer Science*, vol. 46, pp. 327–333, 2019.
- [46] D. J. Watts and S. H. Strogatz, "Collective dynamics of "small-world" networks," *Nature*, vol. 393, no. 6684, pp. 440–442, 1998.
- [47] M. E. J. Newman and D. J. Watts, "Scaling and percolation in the small-world network model," *Physical Review E*, vol. 60, no. 6, pp. 7332–7342, 1999.
- [48] W. Fang and L. M. Xiao, "Simulation of knowledge transfer process model between universities: a perspective of cluster innovation network," *Complexity*, vol. 2018, Article ID 5983531, 13 pages, 2018.
- [49] C. Moore and M. E. J. Newman, "Epidemics and percolation in small-world networks," *Physical Review E*, vol. 61, no. 5, pp. 5678–5682, 2000.
- [50] X.-P. Han, "Disease spreading with epidemic alert on small-world networks," *Physics Letters A*, vol. 365, no. 1–2, pp. 1–5, 2007.
- [51] C. Li, G. Jiang, and Y. Song, "Epidemic spreading in dynamic small-world networks with community structure," *Complex Systems and Complexity Science*, vol. 11, pp. 33–39, 2014.
- [52] M. Small and C. K. Tse, "Clustering model for transmission of the SARS virus: application to epidemic control and risk assessment," *Physica A: Statistical Mechanics and Its Applications*, vol. 351, no. 2–4, pp. 499–511, 2005.
- [53] J. Verdasca, M. M. Telo da Gama, A. Nunes, N. R. Bernardino, J. M. Pacheco, and M. C. Gomes, "Recurrent epidemics in small world networks," *Journal of Theoretical Biology*, vol. 233, no. 4, pp. 553–561, 2005.
- [54] X.-l. Yu, X.-y. Wang, D.-m. Zhang, F. Liang, and X. Wu, "Mathematical expressions for epidemics and immunization in small-world networks," *Physica A: Statistical Mechanics and Its Applications*, vol. 387, no. 5–6, pp. 1421–1430, 2008.
- [55] H.-H. Jo, S. Ki Baek, and H. T. Moon, "Immunization dynamics on a two-layer network model," *Physica A: Statistical Mechanics and Its Applications*, vol. 361, no. 2, pp. 534–542, 2006.
- [56] X. Chen, J. Jiang, T. Jiang, J. Xia, and J. Zhang, "The research of immunization strategy on complex networks," *Information Technology and Computer Application Engineering*, vol. 34, pp. 539–542, 2014.
- [57] C. Granell, S. Gómez, and A. Arenas, "Competing spreading processes on multiplex networks: awareness and epidemics," *Physical Review E, Statistical, Nonlinear, and Soft Matter Physics*, vol. 90, Article ID 012808, 2014.
- [58] T. Liu, P. Li, Y. Chen, and J. Zhang, "Community size effects on epidemic spreading in multiplex social networks," *PLoS One*, vol. 11, no. 3, Article ID e0152021, 2016.
- [59] Z. Li, P. Zhu, D. Zhao, Z. Deng, and Z. Wang, "Suppression of epidemic spreading process on multiplex networks via active immunization," *Chaos (Woodbury, N.Y.)*, vol. 29, Article ID 073111, 2019.
- [60] Y. L. Lu and J. Liu, "The impact of information dissemination strategies to epidemic spreading on complex networks," *Physica A-Statistical Mechanics And Its Applications*, vol. 536, p. 12, 2019.
- [61] C. Buono and L. A. Braunstein, "Immunization strategy for epidemic spreading on multilayer networks," *EPL*, vol. 109, p. 5, 2015.

- [62] C. Granell, S. Gomez, and A. Arenas, "Dynamical interplay between awareness and epidemic spreading in multiplex networks," *Physical Review Letters*, vol. 111, no. 12, 2011.
- [63] Z. Wang, D. W. Zhao, L. Wang, G. Q. Sun, and Z. Jin, "Immunity of multiplex networks via acquaintance vaccination," *EPL*, vol. 112, no. 6, 2015.
- [64] L. G. A. Zuzek, C. Buono, and L. A. Braunstein, "Epidemic spreading and immunization strategy in multiplex networks," *Journal of Physics: Conference Series*, vol. 640, Article ID 012007, 2015.
- [65] S. Eubank, H. Guclu, V. S. Anil Kumar et al., "Modelling disease outbreaks in realistic urban social networks," *Nature*, vol. 429, no. 6988, pp. 180–184, 2004.
- [66] X. U. Dan, L. I. Xiang, and X. Wang, "On virus spreading in local-world complex networks and its immunization control," *Control and Decision*, vol. 21, pp. 817–820, 2006.
- [67] W. P. Guo, X. Li, and X. F. Wang, "Epidemics and immunization on Euclidean distance preferred small-world networks," *Physica A-Statistical Mechanics And Its Applications*, vol. 380, pp. 684–690, 2017.
- [68] X. Wu and Z. Liu, "How community structure influences epidemic spread in social networks," *Physica A: Statistical Mechanics and Its Applications*, vol. 387, no. 2-3, pp. 623–630, 2008.
- [69] Y. Min, X. G. Jin, Y. Ge, and J. Chang, "The role of community mixing styles in shaping epidemic behaviors in weighted networks," *PLoS One*, vol. 8, no. 2, Article ID 57100, 2013.
- [70] N. Masuda, "Immunization of networks with community structure," *New Journal of Physics*, vol. 11, p. 14, 2009.
- [71] G. Ren and X. Wang, "Epidemic spreading in time-varying community networks," *Chaos (Woodbury, N.Y.)*, vol. 24, no. 2, Article ID 023116, 2014.
- [72] Z. Wang, C. T. Bauch, S. Bhattacharyya et al., "Statistical physics of vaccination," *Physics Reports*, vol. 664, pp. 1–113, 2016.
- [73] W.-J. Bai, T. Zhou, and B.-H. Wang, "Immunization of susceptible-infected model on scale-free networks," *Physica A: Statistical Mechanics and Its Applications*, vol. 384, no. 2, pp. 656–662, 2007.
- [74] X.-J. Xu, Z.-X. Wu, and G. Chen, "Epidemic spreading in lattice-embedded scale-free networks," *Physica A: Statistical Mechanics and Its Applications*, vol. 377, no. 1, pp. 125–130, 2007.
- [75] B. Huang, X. Zhao, and C. Wu, "Research on immunization strategies based on independent sets of complex networks," *Journal of Chongqing University*, vol. 37, pp. 138–143, 2014.
- [76] M. Barthélemy, A. Barrat, R. Pastor-Satorras, and A. Vespignani, "Velocity and hierarchical spread of epidemic outbreaks in scale-free networks," *Physical Review Letters*, vol. 92, Article ID 178701, 2004.
- [77] R. Pastor-Satorras and C. Castellano, "Eigenvector localization in real networks and its implications for epidemic spreading," *Journal of Statistical Physics*, vol. 173, no. 3-4, pp. 1110–1123, 2018.
- [78] X. J. Xu, X. Zhang, and J. F. Mendes, "Impacts of preference and geography on epidemic spreading," *Physical Review. E, Statistical, Nonlinear, and Soft Matter Physics*, vol. 76, Article ID 056109, 2007.
- [79] H. Kang and X. Fu, "Epidemic spreading and global stability of an SIS model with an infective vector on complex networks," *Communications in Nonlinear Science and Numerical Simulation*, vol. 27, no. 1–3, pp. 30–39, 2015.
- [80] Q. Wu, H. Zhang, and G. Zeng, "Responsive immunization and intervention for infectious diseases in social networks," *Chaos (Woodbury, N.Y.)*, vol. 24, Article ID 023108, 2014.
- [81] J. Joo and J. L. Lebowitz, "Behavior of susceptible-infected-susceptible epidemics on heterogeneous networks with saturation," *Physical Review. E, Statistical, Nonlinear, and Soft Matter Physics*, vol. 69, Article ID 066105, 2004.
- [82] T. Gross, C. J. D'Lima, and B. Blasius, "Epidemic dynamics on an adaptive network," *Physical Review Letters*, vol. 96, Article ID 208701, 2006.
- [83] P. Ji and H. Ge, "Edges immunization strategy in scale-free network," *Computer Engineering*, vol. 37, pp. 130–132, 2011.
- [84] H. F. Zhang, K. Z. Li, X. C. Fu, and B. H. Wang, "An efficient control strategy of epidemic spreading on scale-free networks," *Chinese Physics Letters*, vol. 26, pp. 296–299, 2009.
- [85] S. Bansal and L. A. Meyers, "The impact of past epidemics on future disease dynamics," *Journal of Theoretical Biology*, vol. 309, pp. 176–184, 2012.
- [86] J. Juang and Y.-H. Liang, "Analysis of a general SIS model with infective vectors on the complex networks," *Physica A: Statistical Mechanics and Its Applications*, vol. 437, pp. 382–395, 2015.
- [87] F. Nian and S. Yao, "The epidemic spreading on the multi-relationships network," *Applied Mathematics and Computation*, vol. 339, pp. 866–873, 2018.
- [88] F. Taghavian, M. Salehi, and M. Teimouri, "A local immunization strategy for networks with overlapping community structure," *Physica A: Statistical Mechanics and Its Applications*, vol. 467, pp. 148–156, 2017.
- [89] A. Chatterjee, G. Ramadurai, and K. Jagannathan, "Contagion processes on urban bus networks in Indian cities," *Complexity*, vol. 21, no. S2, pp. 451–458, 2016.
- [90] S. Yan, S. T. Tang, W. Y. Fang, S. Pei, and Z. M. Zheng, "Global and local targeted immunization in networks with community structure," *Journal of Statistical Mechanics-Theory and Experiment*, vol. 14, 2015.
- [91] J. Zhao, S. M. Wang, Z. X. Zhou, and Z. T. Zhou, "Weighted immunization strategy on real networks," *Proceedings of the 2015 4th National Conference on Electrical, Electronics and Computer Engineering*, vol. 47, pp. 663–667, 2016.
- [92] X. Li and G. Chen, "A local-world evolving network model," *Physica A: Statistical Mechanics and Its Applications*, vol. 328, no. 1-2, pp. 274–286, 2003.
- [93] J. Piccini, F. Robledo, and P. Romero, "Complexity among combinatorial problems from epidemics," *International Transactions in Operational Research*, vol. 25, no. 1, pp. 295–318, 2018.
- [94] H. Zhang and F. U. Xinchu, "Dynamic behavior of SIR epidemic model with immunity on complex networks," *Journal of Shanghai University, Natural Science*, vol. 13, pp. 189–192, 2007.
- [95] M. Gosak, M. Duh, R. Markovic, and M. Perc, "Community lockdowns in social networks hardly mitigate epidemic spreading," *New Journal Of Physics*, vol. 23, pp. 1367–2630, 2021.
- [96] K. J. Parousis-Orthodox, M. M. Stamos, and D. S. Vlachos, "Global vaccination strategies in modular networks," *IC-Msquare 2012: International Conference on Mathematical Modelling in Physical Sciences*, vol. 410, 2013.
- [97] D. G. Xu and X. Y. Xu, "Modeling and control of dynamic network SIR based on community structure," in *Proceedings of the 26th Chinese Control and Decision Conference*, pp. 4648–4653, New York, NY, USA, 2014.

- [98] B. Huang, X. Y. Zhao, K. Qi, M. Tang, and Y. H. Do, "Coloring the complex networks and its application for immunization strategy," *Acta Physica Sinica*, vol. 62, no. 8, 2013.
- [99] L. Vassallo, M. A. Di Muro, D. Sarkar, L. D. Valdez, and L. A. Braunstein, "Ring vaccination strategy in networks: a mixed percolation approach," *Physical Review E*, vol. 101, no. 10, Article ID 052309, 2020.
- [100] L. G. Alvarez-Zuzek, M. A. Di Muro, and S. Havlin, "Dynamic vaccination in partially overlapped multiplex networks," *Physical Review E*, vol. 99, 2019.
- [101] X. I. A. Chengyi, L. I. U. Zhongxin, Z. Chen, and Z. Yuan, "SIRS epidemic model with direct immunization on complex networks," *Control and Decision*, vol. 23, pp. 468–472, 2008.
- [102] G. Yan, Z. Q. Fu, J. Ren, and W. X. Wang, "Collective synchronization induced by epidemic dynamics on complex networks with communities," *Physical Review E, Statistical, Nonlinear, and Soft Matter Physics*, vol. 75, Article ID 016108, 2007.
- [103] J. Li, J. Zhong, Y. Ji, and F. Yang, "A new SEIAR model on small-world networks to assess the intervention measures in the COVID-19 pandemics," *Results in Physics*, vol. 25, Article ID 104283, 2021.
- [104] D. G. Xu, X. Y. Xu, and Z. F. Su, "Novel SIVR epidemic spreading model with virus variation in complex networks," in *Proceedings of the 2015 27th Chinese Control and Decision Conference*, pp. 5164–5169, New York, NY, USA, 2015.
- [105] D. Tian, C. Liu, Z. Sheng, M. Chen, and Y. Wang, "Analytical model of spread of epidemics in open finite regions," *IEEE Access*, vol. 5, pp. 9673–9681, 2017.
- [106] M. Medo, "Contact network models matching the dynamics of the COVID-19 spreading," *Journal of Physics A-Mathematical and Theoretical*, vol. 54, no. 3, Article ID 035601, 2021.
- [107] T. Nagatani and K. Tainaka, "Diffusively coupled SIQRS epidemic spreading in hierarchical small-world network," *Journal of the Physical Society of Japan*, vol. 90, no. 1, Article ID 013001, 2021.
- [108] H. Yang, M. Tang, and P. Hui, "Epidemic dynamics on adaptive networks—a short review," *Complex Systems and Complexity Science*, vol. 9, pp. 63–83, 2012.
- [109] L. Hebert-Dufresne, A. Allard, J. G. Young, and L. J. Dube, "Global efficiency of local immunization on complex networks," *Scientific Reports*, vol. 3, no. 1, 2013.
- [110] C. Buono, L. G. Alvarez-Zuzek, P. A. Macri, and L. A. Braunstein, "Epidemics in partially overlapped multiplex networks," *PLoS One*, vol. 9, no. 7, Article ID e92200, 2014.
- [111] A. Grabowski and R. Kosiński, "The SIRS model of epidemic spreading in virtual society," *Acta Physica Polonica A*, vol. 114, no. 3, pp. 589–596, 2008.
- [112] H. Wang, A. Ghosh, J. Ding, R. Sarkar, and J. Gao, "Heterogeneous interventions reduce the spread of COVID-19 in simulations on real mobility data," *Scientific Reports*, vol. 11, no. 1, 2021.
- [113] M. G. Hâncean, M. Perc, and J. Lerner, "Early spread of COVID-19 in Romania: imported cases from Italy and human-to-human transmission networks," *Royal Society Open Science*, vol. 7, no. 7, Article ID 200780, 2020.
- [114] M. L. N. Mbah, J. Z. Liu, and C. T. Bauch, "The impact of imitation on vaccination behavior in social contact networks," *PLoS Computational Biology*, vol. 8, no. 4, Article ID e1002469, 2012.
- [115] S. Gonçalves, M. Kuperman, and M. Ferreira da Costa Gomes, "A social model for the evolution of sexually transmitted diseases," *Physica A: Statistical Mechanics and Its Applications*, vol. 342, no. 1–2, pp. 256–262, 2004.
- [116] B. Mirzasoleiman, M. Babaei, and M. Jalili, "Immunizing complex networks with limited budget," *EPL*, vol. 98, no. 3, 2012.
- [117] M. Jadidi, S. Jamshidiha, I. Masroori, P. Moslemi, A. Mohammadi, and V. Pourahmadi, "A two-step vaccination technique to limit COVID-19 spread using mobile data," *Sustainable Cities and Society*, vol. 70, Article ID 102886, 2021.
- [118] F. Velasquez-Rojas, P. C. Ventura, and C. Connaughton, "Disease and information spreading at different speeds in multiplex networks," *Physical Review E*, vol. 102, 2020.
- [119] G. Strona, C. J. Carstens, P. S. A. Beck, and B. A. Han, "The intrinsic vulnerability of networks to epidemics," *Ecological Modelling*, vol. 383, pp. 91–97, 2018.
- [120] Y. Yang, H. Liu, and J. Zhou, "Epidemic spreading-information dissemination coupling mechanism in heterogeneous areas," *Computers, Materials & Continua*, vol. 67, no. 3, pp. 3311–3327, 2021.
- [121] R. Pastor-Satorras, C. Castellano, P. Van Mieghem, and A. Vespignani, "Epidemic processes in complex networks," *Reviews of Modern Physics*, vol. 87, no. 3, pp. 925–979, 2015.
- [122] D. Chakraborty, A. Singh, and H. Cherifi, "Immunization strategies based on the overlapping nodes in networks with community structure," *Computational Social Networks*, vol. 9795, pp. 62–73, 2016.
- [123] R. B. Schinazi, "On the role of social clusters in the transmission of infectious diseases," *Theoretical Population Biology*, vol. 61, no. 2, pp. 163–169, 2002.
- [124] J. Liu, J. Wu, and Z. R. Yang, "The spread of infectious disease on complex networks with household-structure," *Physica A: Statistical Mechanics and Its Applications*, vol. 341, pp. 273–280, 2004.
- [125] N. Gupta, A. Singh, and H. Cherifi, "Centrality measures for networks with community structure," *Physica A: Statistical Mechanics and Its Applications*, vol. 452, pp. 46–59, 2016.
- [126] Z. Wang, M. Tang, S. Cai, Y. Liu, J. Zhou, and D. Han, "Self-awareness control effect of cooperative epidemics on complex networks," *Chaos (Woodbury, N.Y.)*, vol. 29, no. 5, Article ID 053123, 2019.
- [127] J. T. Matamalas, A. Arenas, and S. Gómez, "Effective approach to epidemic containment using link equations in complex networks," *Science Advances*, vol. 4, no. 12, Article ID eaau4212, 2018.
- [128] C. O. Dorso, A. Medus, and P. Balenzuela, "Vaccination and public trust: a model for the dissemination of vaccination behaviour with external intervention," *Physica A: Statistical Mechanics and Its Applications*, vol. 482, pp. 433–443, 2017.
- [129] R. P. Curiel and H. G. Ramirez, "Vaccination strategies against COVID-19 and the diffusion of anti-vaccination views," *Scientific Reports*, vol. 11, no. 1, 2021.
- [130] P. Holme, "Efficient local strategies for vaccination and network attack," *Europhysics Letters (EPL)*, vol. 68, no. 6, pp. 908–914, 2004.
- [131] M. Shahzamal, B. Mans, F. Hoog, D. Paini, and R. Jurdak, "Vaccination strategies on dynamic networks with indirect transmission links and limited contact information," *PLoS One*, vol. 15, no. 11, Article ID e0241612, 2020.
- [132] Y. Liu, Y. Deng, and B. Wei, "Local immunization strategy based on the scores of nodes," *Chaos (Woodbury, N.Y.)*, vol. 26, no. 5, Article ID 013106, 2016.

- [133] S. Wang, M. Gong, W. Liu, and Y. Wu, "Preventing epidemic spreading in networks by community detection and memetic algorithm," *Applied Soft Computing*, vol. 89, Article ID 106118, 2020.
- [134] R. Cohen, S. Havlin, and D. ben-Avraham, "Efficient immunization strategies for computer networks and populations," *Physical Review Letters*, vol. 91, no. 24, Article ID 247901, 2003.
- [135] Y. Yu and G. X. Xiao, "On early detection of strong infections in complex networks," *Journal of Physics A-Mathematical and Theoretical*, vol. 47, p. 16, 2014.
- [136] J.-T. Brethouwer, A. van de Rijt, R. Lindelauf, and R. Fokkink, "'Stay nearby or get checked:' a Covid-19 control strategy," *Infectious Disease Modelling*, vol. 6, pp. 36–45, 2021.
- [137] Elgazzar and S. Ahmed, "Simple mathematical models for controlling COVID-19 transmission through social distancing and community awareness," *Journal of Biosciences*, 2021.
- [138] O. Givan, N. Schwartz, A. Cygelberg, and L. Stone, "Predicting epidemic thresholds on complex networks: limitations of mean-field approaches," *Journal of Theoretical Biology*, vol. 288, pp. 21–28, 2011.
- [139] H. Ryu, A. Abulali, and S. Lee, "Assessing the effectiveness of isolation and contact-tracing interventions for early transmission dynamics of COVID-19 in South Korea," *IEEE Access*, vol. 9, pp. 41456–41467, 2021.
- [140] S. Y. Zhou, S. Y. Shi, and L. Wang, "Immunizations of interacting diseases," in *Proceedings of the Chinese Control Conference*, pp. 9686–9691, New York, NY, USA, 2018.
- [141] L.-L. Xia, Y.-R. Song, C.-C. Li, and G.-P. Jiang, "Improved targeted immunization strategies based on two rounds of selection," *Physica A: Statistical Mechanics and Its Applications*, vol. 496, pp. 540–547, 2018.
- [142] M. Salathe and J. H. Jones, "Dynamics and control of diseases in networks with community structure," *PLoS Computational Biology*, vol. 6, 2010.
- [143] A. V. Goltsev, S. N. Dorogovtsev, J. G. Oliveira, and J. F. Mendes, "Localization and spreading of diseases in complex networks," *Physical Review Letters*, vol. 109, Article ID 128702, 2012.
- [144] M. Kitsak, L. K. Gallos, S. Havlin et al., "Identification of influential spreaders in complex networks," *Nature Physics*, vol. 6, no. 11, pp. 888–893, 2010.
- [145] Z. Wang, Y. Moreno, S. Boccaletti, and M. Perc, "Vaccination and epidemics in networked populations-An introduction," *Chaos, Solitons & Fractals*, vol. 103, pp. 177–183, 2017.