Fast Containment of Infectious Diseases With E-Healthcare Mobile Social Internet of Things

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***Abstract*—The infectious disease presents great hazards to public health, due to their high infectivities and potential lethalities. One of the effective methods to hinder the spread of infectious disease is vaccination. However, due to the limitation of resource and the medical budget, vaccinating all people is not feasible in practice. Besides, the vaccinating effects are difficult to be timely observed through traditional ways, such as outpatient services. To tackle the above problems, we propose an e-healthcare mobile social Internet of Things (MSIoTs)-based targeted vaccination scheme to fast contain the spread of the infectious disease. Specifically, we first develop an e-healthcare MSIoT architecture by integrating the e-healthcare system and MSIoTs, whereby the spread status of the infectious disease is timely collected. Furthermore, a graph coloring and spreading centrality-based optional candidate searching algorithm is devised to hunt for the candidates that are powerfully capable of preventing infectious disease. Especially, in order to reduce the vaccination cost, we design an optimal vaccinated target selection algorithm to choose a minimum number of targets whose locations are differentially distributed. Extensive simulations demonstrate that the proposed scheme can effectively prevent infectious disease as compared to conventional schemes.**

***Index Terms*—E-healthcare mobile social Internet of Things (MSIoTs), infectious disease, fast containment, targeted vaccination.**

I. Introduction

INFECTIOUS disease exhibits a serious threat to our lives since the beginning of human civilization. The outbreak of an infectious disease makes a great loss of life and property, and even leads to social instability and riot [1]. Historical records show that the Black Death spreaded across the Europe in the 14th century, killing more than 25% of the European population [2]. The Spanish flu during 1918–1919, induced about 20–50 million deaths worldwide within one year, which is more than the casualties of World War I [3]. In recent years, according to the report of the World Health Organization (WHO), the outbreak of Ebola in 2014 caused high mortalities in many countries, with a fatality rate of 70% [4]. Containing infectious disease is certainly a major concern to save lives and ensure the stable social condition. To minimize the number of casualties and costs for fighting disease, the effective and efficient measure is to timely detect the outbreak of the infectious disease and conduct vaccination in the critical, early stage of disease spreading. For example, smallpox has been worldwide eradicated by the real-time monitoring and vaccination campaign [5].

However, the traditional infection containment approaches have some defects in controlling the spread of infectious disease. On the one hand, the discovery of an infectious disease is mainly through patients visiting doctors with hospital diagnoses and treatments, where it is intractable to predict the outbreak of the infection. On the other hand, the isolation of susceptible persons needs a large amount of the government's health expenses and labor resources, and also incurs the susceptible persons' economic losses. Recently, a promising e-healthcare system based on wearable Internet of Things (IoTs) [6] is proposed to address the above public health crisis, by continuously sensing users' real-time health information, e.g., temperature, heart rate, blood pressure, electrocardiogram, etc. In the e-healthcare system, a server is deployed to collect the health data and detect the abnormal phenomena for providing supporting information of diagnoses [7], [8]. With the analysis on the health data, the medical center can observe the users' health conditions. When the health conditions indicate that some users are infected by an infectious disease, the medical center would execute immune strategies to control the spread of this infectious disease.

In general, the most straightforward immunization strategy is to vaccinate susceptible individuals. Nevertheless, owing to limitations in resources and costs such as vaccine availability, vaccination of all susceptible individuals may be cumbersome in many cases, especially during outbreaks of new infectious disease. Targeted vaccination, vaccinating several people in a community, is an alternative method to control the spread of the infectious disease. Nevertheless, there exist some challenges to hunt for the optimal vaccinated targets. First, the irregular location distribution of infection sources makes the selection of vaccinated targets difficult. Second, as the social contacts and relationships among mobile users are diverse,

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mobile users' abilities on preventing infectious disease are different, where how to select the proper vaccinated targets based on social information is a new challenge. Third, the network dynamic has the effect on the selection of vaccinated targets, such as mobile users' mobility, change of contact frequency, etc.

Fortunately, the e-healthcare system integrated with the mobile social Internet of Things (MSIoTs) [9], [10] is envisioned to realize resource-constrained targeted vaccination. Mobile users' health data collected by the e-healthcare system can be analyzed to track the outbreak of an infectious disease. MSIoTs constructed by mobile users and contact information, offers mobile users' social relationship information by mining users' social data [11]–[13]. The fusion of health data and social data can be utilized to find the specified group of users for targeted vaccination. For example, suppose two mobile users, Bob and Alice, are continuously being tracked during an epidemic outbreak from both health and social perspectives. Through the social data analysis, Bob has frequent contacts with other mobile users including Alice. Once Alice is inferred as an infected patient with the health data, Bob should be vaccinated as soon as possible to slow down the spread of the infectious disease in the early stage.

Targeted vaccination has been extensively studied [14]–[22]. For example, the artificial intelligence and simulation methods are jointly utilized to search for mobile users with the highest influence for tracking disease spread [21]. The wireless sensor system is employed to contain the infectious disease in [22], where the connectivity centrality is considered to find the most important mobile users. However, most of the existing works are still intractable to fast prevent infectious disease with e-healthcare MSIoTs. First, the location distribution of infection sources is not sufficient considered in the most of the existing works. Indeed, the infection sources are usually located in different areas, thereby the vaccinated targets with differential locations would induce different effects on preventing the infectious disease. Second, most of the existing works [19], [23] have an implicit assumption that all mobile users are uninfected during the searching of the vaccinated targets, where the infection sources may be selected as vaccinated targets. Third, the overlapping preventing effects of vaccinated targets are not taken into account in some of the related works, i.e., some vaccinated targets have the same effects on controlling the spread of the infectious disease. Therefore, a novel efficient targeted vaccination scheme needs to be devised for preventing infectious disease.

In this article, we extend our previous conference version on the construction of e-healthcare MSIoTs [19] and propose a novel targeted vaccination scheme to contain the spread of the infectious disease. The proposed scheme can timely detect the outbreak of infectious disease and fast find the optimal vaccinated targets by fusing and analyzing the health data and social data. As such, both the infectious ratio and casualty ratio are sharply decreased, where the stable social condition and people's property can be jointly guaranteed. Specifically, we first integrate the e-healthcare system and MSIoTs to develop the architecture of e-healthcare MSIoTs for fast tracking the spread of the infectious disease. Then, we exploit the graph coloring-based optional candidate searching algorithm to find the most widely distributed vaccinated candidates. Especially, taking both mobile users' infecting abilities and infected possibilities into account, a new metric named *spreading centrality* is presented for proper candidate selection. Finally, based on the infectious disease spreading analysis model, we design an optimal vaccinated target selection algorithm to avoid the overlapping containment effects. The main contributions of this article are threefold.

1) We propose a graph coloring and spreading centrality-based optional candidate searching algorithm. The graph coloring theory is exploited to find the most widely distributed mobile users for enlarging the range of immunity. Furthermore, we present a novel concept named spreading centrality by considering both the mobile user's infecting ability and infected possibility, whereby the proper candidates could be hunted for.
2) We develop a dynamic equation-based analysis model to observe the spread of the infectious disease with the consideration of both mobile users' social data and health data. With the analysis model, we can fast observe the number of infected patients over time. Then, we can identify the effect of each mobile user on containing the infectious disease when he/she is vaccinated.
3) Extensive simulations are carried out to evaluate the performance of the proposed scheme. We first evaluate the evolution of the infection ratio over time with different parameters, including the number of vaccinated mobile users, disease spreading rate, and recovery rate. Afterward, we compare the proposed scheme with conventional schemes to show the outperformed performances.

The remainder of this article is organized as follows. The related work is reviewed in Section II. We present the system model in Section III with the design goal. We propose the framework of the targeted vaccination scheme with details in Section IV. The performance is evaluated in Section V, and we conclude this article in Section VI.

II. Related Work

In this section, we review the related works, including social data analysis with MSIoTs, health data analysis with e-healthcare system, and wireless network-based containment of the infectious disease.

A. Social Data Analysis With MSIoTs

Recently, many works extensively studied social data analysis with MSIoTs. Meng *et al.* [24] proposed a non-Bayesian social learning-based high-level distributional state inference scheme for cooperative settings in various crowdsensing tasks. Li *et al.* [25] described a scheme for social-based routing in MSIoTs, and also designed a novel metric to measure the node's capability of forwarding packets to others. Wang *et al.* [26] proposed a dissemination and mobility-aware content replication strategy for edge network area based on the social graph, content dissemination, and user mobility to assign mobile users with social content in the edge network

region. He *et al.* [27] devised a handshake solution framework for cryptography based on hierarchical identity, in which an efficient cross-domain handshake solution is also constructed to achieve symptom matching. Xiao *et al.* [28] proposed two online task assignment algorithms, which separately consider the average makespan and the largest makespan for the crowd-sensing in MSIoTs. However, how to leverage the MSIoTs for tracking the spread of the infectious disease is not deeply investigated in these works. In this article, we construct a novel architecture of e-healthcare MSIoT by integrating the mobile social networks (MSNs) and e-healthcare system, whereby the social data and health data are fused to timely detect the outbreak of the infectious disease and efficiently contain the infectious disease at the early stage.

B. Health Data Analysis With E-Healthcare System

The study of health data analysis with the e-healthcare system was drawn the increasing attention from many related fields. Zhou *et al.* [29] proposed a privacy-preserving holomorphic database aggregation for medical image analysis in cloud-assisted e-healthcare systems. Lee *et al.* [30] devised a healthcare-grade wireless local area network architecture specified for a medical institute that can prioritize medical incidents in accordance with their degree of urgency. Huang *et al.* [31] proposed a healthcare data collection system from the wireless body area network where healthcare data can be securely transmitted over the wireless network. Lomotey *et al.* [32] investigated an efficient synchronicity in the unreliable mobile networks to preserve the electronic health records of patients. Although these works focus on the some aspects of the e-healthcare, most of them do not consider the applications of e-healthcare to prevent infectious disease.

C. Wireless Network-Based Containment of Infections

The containment of infectious disease with wireless networks was widely studied in the existing works. Sun *et al.* [22] designed a system of wireless sensors to gather social contacts to model the spread of the disease, and a novel metric was devised to find critical nodes of disease containment. Lu *et al.* [33] presented a Markov switching model to recognize infectious disease outbreak patterns in syndromic counting time series, where the disease outbreak statuses were modeled as hidden state variables. Zhou *et al.* [34] designed a monitoring system of symptoms to forecast the epidemic trends related to the Google search algorithm for early detection of epidemic outbreaks. Zhang *et al.* [35] proposed a person-to-person tracking scheme for infections by combining the analysis of social network data and health data from the perspectives of social networks and e-health, respectively. Fan *et al.* [36] proposed a lightweight scheme for the protection of radio-frequency identification medical privacy in the IoT, where the security and privacy of the collected data are guaranteed. However, how to jointly utilize the social data and health data for controlling the spread of the infectious disease needs to be further studied.

The above works have made efforts in some aspects of infections containment with e-healthcare MSIoTs. However, these works focus on the infectious disease that spread in small areas, where the social data and health data are not fully taken advantage to collect the information of infectious disease. Different from them, this article comprehensively investigates the characteristics of the e-healthcare MSIoTs and then proposes a novel targeted vaccination scheme by utilizing both the social data and health data to efficiently control the spread of the infectious disease.

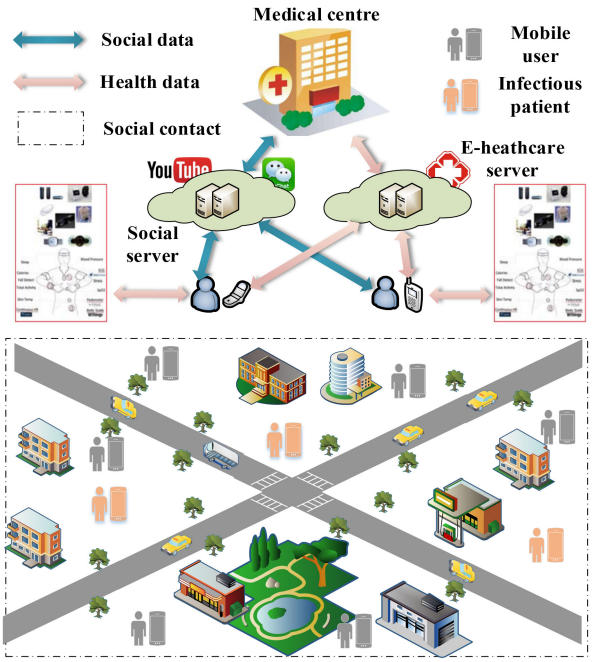

Fig. 1. Illustration of the e-healthcare MSIoTs comprised by multiple mobile users, an e-healthcare server, and a social server.

III. System Model and Design Goals

In this section, we introduce the system model, as shown in Fig. 1, including the network model and social graph. Then, we identify the design goals.

A. Network Model

The e-healthcare MSIoT is composed of mobile users, a social server, and an e-heathcare server.

1) *Mobile Users:* Let $\mathcal{I} = \{1, 2, \ldots, i, \ldots, I\}$ denote the set of mobile users in the system. Every two mobile users may exist a certain social relationships, such as classmates, relatives, colleagues, etc. According to [37], the relationships among mobile users could be divided into five types: a) family relationship; b) friendship; c) neighborship; d) colleague relationship; and e) strangeness. The family relationship indicates that two mobile users are relatives, such as father and son, husband and wife, etc. Friendship means that two mobile users are friends who usually have the common interests. Neighborship means that two mobile users have the similar home addresses, such as the same room, or the same building, etc. Colleague relationship means that mobile users who work for the same company or study in the same

school. Strangeness is that two users have nothing to do with each other. Without loss of generality, the social strengths of the above five relationships are different, which follows $\varpi_1 > \varpi_2 > \varpi_3 > \varpi_4 > \varpi_5$. Here, ϖ_1, ϖ_2, ϖ_3, ϖ_4, and ϖ_5 are strengths of family relationship, friendship, neighborship, colleague relationship, and strangeness, respectively. For mobile user i and mobile user j, we denote a relationship vector $\mathbf{r}_{i,j} = (r^1_{i,j}, r^2_{i,j}, r^3_{i,j}, r^4_{i,j}, r^5_{i,j})$, where $r^k_{i,j} \in \{0, 1\}, k \in \{1, 2, 3, 4, 5\}$. If there exists relationship k between mobile user i and mobile user j, $r^k_{i,j} = 1$. Otherwise, $r^k_{i,j} = 0$. Obviously, the strangeness cannot coexist with other relationships, i.e., if $r^5_{i,j} = 1$, $\sum_{k=1}^{4} r^k_{i,j} = 0$. In addition, for any two mobile users, we have $\sum_{k=1}^{5} r^k_{i,j} > 0$.

2) *E-Healthcare Server:* It is located in the cloud server with powerful computational and storage capabilities. The e-healthcare server has three functionalities. First, the e-healthcare server can collect health data from mobile users. Second, the e-healthcare server can analyze mobile users' health data with guidance from the medical center to detect infectious disease. Third, the e-healthcare server informs mobile users to vaccinate for preventing infectious disease.
3) *Social Server:* The social server is deployed in the cloud server to store mobile users' contact information and analyze each mobile user's social characteristic. The contact information is collected by smartphones in various ways. For example, mobile users can launch their smartphones with the Bluetooth discovery program to search for nearby mobile users within a certain distance. The contact duration is also easy to be recorded by smartphones. The contact information of each mobile user is delivered to the social server via some wireless communication technologies, e.g., cellular, Wi-Fi, etc. The social relationships are extracted through mobile user's social network profiles, including WeChat, Facebook, Twitter, etc. Then, the social server exchanges mobile users' social information with the e-healthcare server for preventing infectious disease.

B. Social Graph

The social graph is denoted as $\mathcal{G} = <\mathcal{I}, \mathcal{E}, \mathcal{W}>$, as shown in Fig. 2, where $\mathcal{E}$ is the set of edges. In graph $\mathcal{G}$, an edge $e_{i,j} = (i, j) \in \mathcal{E}$ exists when there is at least one contact between mobile user i and mobile user j. Since infectious disease spreads bidirectionally, $\mathcal{G}$ is an undirected graph.

In social graph $\mathcal{G}$, we assign each edge $e_{i,j}$ a weight $w_{i,j}$ to describe the disease spreading ability between mobile users i and j. Contact frequency and contact duration are considered to assign the edge weight. For two mobile users who are in frequent contact and often together, if one user becomes a patient, the probability of the other user being infected is high. Hence, the more frequently two nodes encounter each other, the greater the weight of the corresponding edge should be. And, the longer the contact duration they spend, the larger edge weight should be added on the corresponding edge. A further factor affecting the ability to spread disease is the location

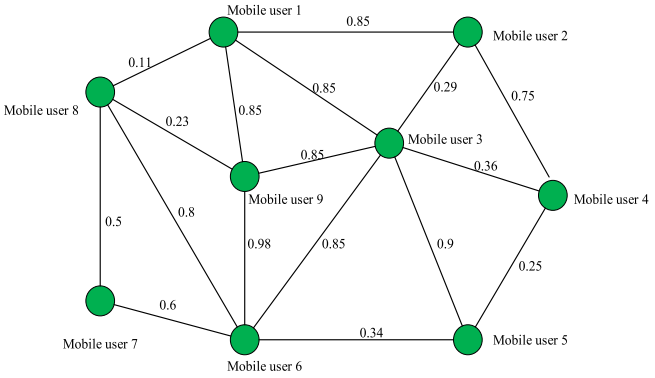

Fig. 2. Illustration of a social graph containing vertices, edges, and weights. The social graph is utilized to model the social contacts among mobile users.

of exposure. Infectious diseases such as influenza can spread faster indoors than outdoors [38]. Similarly, contacts that happen indoor should be assigned larger weight than contacts that happen outdoor. In addition, the social relationships among mobile users also have influences on the spread of infectious disease. For two mobile users with close relationship, if one is infected, the other also has a high probability to get the disease. Thus, if the relationship of two mobile users is closer, the weight on the corresponding edge should be larger. Here, let $\chi_{i,j}$ denote the number of contacts between mobile user i and mobile user j during time period $[0, T]$. Here, the determination for the time scale of the period $[0, T]$ mainly considers the following two aspects. First, the time period should be large to guarantee the statistical data can contain sufficient connotative social contact information. Second, the statistical data can be continuously updated to indicate the dynamic and flexibility of social contact information, where the time period should not be very large. As such, the time scale of period $[0, T]$ can be half-day or one day. Then, the duration of the $\tilde{n}$th contact is denoted as $\varphi_{i,j,\tilde{n}}$, which follows $\sum_{n=1}^{\chi_{i,j}} \varphi_{i,j,\tilde{n}} \leq T$.

Based on contact frequency, contact duration, contact location, and social relationship, the weight on the edge between mobile user i and mobile user j is calculated by

$$w_{i,j} = \sum_{n=1}^{\chi_{i,j}} \left[\exp\left(\varphi_{i,j,\tilde{n}}\right) - 1\right] \mathbf{r}_{i,j} \cdot \vec{\varpi}^{\,\mathbb{T}} \cdot \eta_{i,j,\tilde{n}} \tag{1}$$

where $\vec{\varpi} = (\varpi_1, \varpi_2, \varpi_3, \varpi_4, \varpi_5)$. $\mathbb{T}$ is the transpose symbol. $\eta_{i,j,\tilde{n}}$ is used to determine whether mobile user i and mobile user j contact indoor or outdoor, which is

$$\eta_{i,j,\tilde{n}} = \begin{cases} 1, & \text{if mobile user } i \text{ and } j \text{ contact indoor} \\ \eta_0, & \text{if mobile user } i \text{ and } j \text{ contact outdoor.} \end{cases} \tag{2}$$

Here, $0 < \eta_0 < 1$. The value of η_0 is determined by the transmission characters of the infectious disease. If there is no edge between two mobile users, the weight is zero. The parameter η_0 is used to show the spreading probability of the infectious disease between two mobile users when they contact outdoor. If the value of η_0 is larger and closer to 1, the infectious disease spreads more easily between these two mobile users.

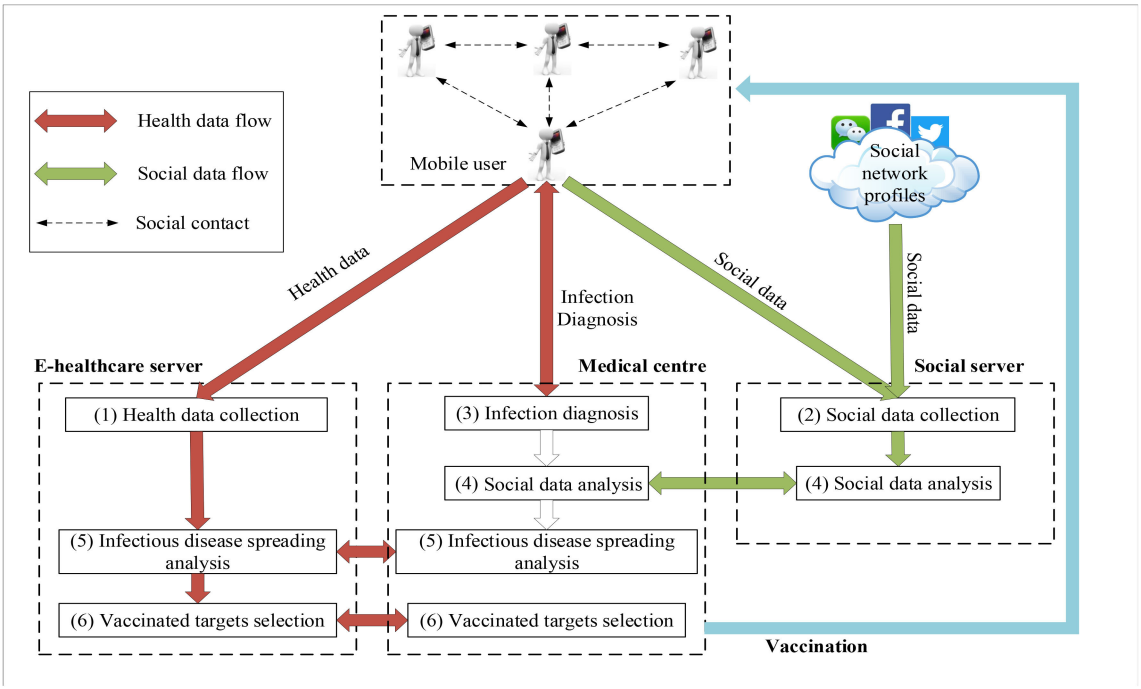

Fig. 3. Illustration of the proposed targeted vaccination scheme. The targeted vaccination scheme is composed of five components: health data collection, social data collection, infection diagnosis and social data analysis, infectious disease spreading analysis, and vaccinated mobile users selection.

Thus, the weight matrix of all edges in the social graph is

$$\mathbf{W} = \begin{bmatrix} w_{1,1}, & w_{1,2} & , \ldots , & w_{1,I} \\ w_{2,1}, & w_{2,2} & , \ldots , & w_{2,I} \\ \vdots & \vdots & \ddots & \vdots \\ w_{I,1}, & w_{I,2} & , \ldots , & w_{I,I} \end{bmatrix}. \tag{3}$$

The network dynamic considered in the proposed scheme includes the following aspects. First, each mobile user's mobility is taken into account, where the locations of mobile users' contact at different time slots are collected, i.e., indoor or outdoor. Besides, the changeable feature of the contact between two mobile users during a time period is considered. In specific, both the number of contacts and the time duration of each contact are both counted by the carried smartphones. Additionally, to indicate the dynamic of contacts and social relationship among mobile users, the social data to construct the social graph is recollected and reanalyzed every time period.

C. Design Goals

The proposed e-healthcare MSIoTs-based targeted vaccination scheme should achieve two goals. First, the system can minimize the number of infected patients during the outbreak of an infectious disease. Second, it takes low resource overhead (e.g., consumptions of labor and electricity resource, etc.) to realize the green system.

IV. Framework of Targeted Vaccination Scheme

In this section, we exploit the social data and health data to prevent infectious disease. We first provide the overview of the proposed targeted vaccination scheme. Then, we present an infectious disease spreading analysis model and a vaccinated mobile users selection algorithm to achieve the design goals.

A. Overview of Targeted Vaccination Scheme

The proposed targeted vaccination scheme fuses the mobile users' health data and social data to prevent infectious disease with a small amount of resource consumption. It consists of five components as shown in Fig. 3.

1) Health Data Collection: According to [35], each mobile user's health data (e.g., temperature, heart rate, ECG, blood pressure, etc.) is collected by on-body sensors and wearable devices, and then sent to the e-healthcare server. Finally, the health data are stored and analyzed in the e-healthcare server.

2) Social Data Collection: As mobile users connect with each other, their smartphones can record details of contact information, including who they are, where they were contacted and when they were contacted. This data can be promptly transferred to social servers for the storage. In particular, by using short-range communication technologies (e.g., Bluetooth, NFC, etc.) and some in-built sensors (e.g., acoustic sensors), the connection between mobile users can be detected when they are in physical proximity. The detailed social data collection procedure can refer to [35].

3) Infection Diagnosis and Social Data Analysis: The e-healthcare successively analyzes each mobile user's health data to obtain this mobile user's health condition. The e-healthcare also compares the mobile user's health condition with the guidance from the medicare center, to determine whether this mobile user is infected or not. If the mobile user is determined as the infected one by the e-healthcare server, the e-healthcare sever will send this mobile user's

health data to the medical center for further infection diagnosis. Afterward, the medical center diagnoses the infected disease of the patient. Then, the medical center informs the infected mobile user with the diagnosis result. After diagnosis, the medical center requires the social graph from the social server. Specifically, the medical center and social server analyze the social data of all mobile users within the scopes of the infected mobile user's activities to construct the social graph.

4) Infectious Disease Spreading Analysis: According to the type of infectious disease diagnosed by the e-healthcare server and the medical center, the medical center evaluates the infectious disease spreading parameters (e.g., disease spreading rate, recovery rate, etc.) and the spreading features of the infectious disease, such as susceptible–infected–recovered [39], susceptible–infected–susceptible [40], etc. Then, with the social graph, the medical center and the e-healthcare server construct the infectious disease spreading analysis model to analyze the spreading process of the infectious disease.

5) Vaccinated Mobile Users Selection: With the social graph, the medical center and e-healthcare server first utilize the graph coloring theory to obtain the most widely distributed mobile users to find the optional candidates for vaccination. Then, the spreading centrality integrating the mobile user's infecting ability and infected possibility is exploited to sort the optional mobile users and choose the proper candidates for vaccination. Based on the infectious disease spreading analysis model, the medical center and e-healthcare server then select the optimal vaccinated targets to minimize the number of infected patients. Finally, the medical center informs the vaccinated targets for vaccination through the e-healthcare applications.

B. Infectious Disease Spreading Analysis

After the infection diagnosis, infected mobile users are detected by the e-healthcare server and medical center. These mobile users are called as infection sources. Let $\mathcal{S} = \{1, 2, \ldots, S\}$ denote the set of infection sources. Then, we analyze the spreading process of the infectious disease. Here, we utilize the spreading features of the susceptible–infected–recovered as an example to expound the analysis on the spread of infectious disease. In the spreading process of an infectious disease, there are three states for each mobile user, which are: 1) "susceptible"; 2) "infected"; and 3) "recovered", respectively. The susceptible means that the mobile users are healthy and susceptible to the infectious disease. The infected means that mobile users have been infected and can spread the disease to others. The recovered means that mobile users have returned to be healthy and are immune to the infectious disease. Let $X_i(t)$ denote the state of mobile user i at time t, where $X_i(t) \in \{1,\ 2,\ 3\}$. Let $\theta_i(t)$ denote the probability that the mobile user i is susceptible at time t. $\vartheta_i(t)$ is the probability that the state of mobile user i is infected at time t. $\rho_i(t)$ denotes the probability that the state of mobile user i is recovered at time t. As such, we have

$$\begin{cases} \theta_i(t) = \text{Pro}\{X_i(t) = 1\} \\ \vartheta_i(t) = \text{Pro}\{X_i(t) = 2\} \\ \rho_i(t) = \text{Pro}\{X_i(t) = 3\}. \end{cases} \tag{4}$$

Here, $\theta_i(t) + \vartheta_i(t) + \rho_i(t) = 1$. According to [22], we assume that the infected process of a susceptible mobile user and the recovered process of an infected mobile user are independent Poisson processes with spreading rate β and recovery rate δ, respectively. Thus, we can apply the Markov theory straightaway. The transition rate matrix of the above three-state continuous Markov chain at time t for mobile user i is

$$Q_i(t) = \begin{bmatrix} q_{1,1|i}(t), & q_{1,2|i}(t), & q_{1,3|i}(t) \\ q_{2,1|i}(t), & q_{2,2|i}(t), & q_{2,3|i}(t) \\ q_{3,1|i}(t), & q_{3,2|i}(t), & q_{3,3|i}(t) \end{bmatrix} \tag{5}$$

where $q_{l,l'|i}(t)$ $(l, l' \in \{1, 2, 3\})$ is the transition rate of mobile user i from state l to state l' at time t. The transition rate matrix follows:

$$\begin{cases} q_{1,1|i}(t) + q_{1,2|i}(t) + q_{1,3|i}(t) = 0 \\ q_{2,1|i}(t) + q_{2,2|i}(t) + q_{2,3|i}(t) = 0 \\ q_{3,1|i}(t) + q_{3,2|i}(t) + q_{3,3|i}(t) = 0. \end{cases} \tag{6}$$

The contact strength between mobile users i and j is given by

$$p_{ij} = \frac{w_{i,j}}{(\exp(T) - 1)(||\vec{\varpi}||_1 - \varpi_5)} \tag{7}$$

where $||\vec{\varpi}||_1$ is the 1-norm of vector $\vec{\varpi}$. At time t, the transition rate of mobile user i from state 1 to state 2 is

$$q_{1,2|i}(t) = \beta \sum_{j=1}^{I} \frac{w_{i,j}}{(\exp(T) - 1)(||\vec{\varpi}||_1 - \varpi_5)} \mathbb{1}_{\{X_j(t)=1\}} \tag{8}$$

where $\mathbb{1}_x$ is an indicator function if the event x is true, else it is zero. As a result, the transition rate $q_{1,2|i}(t)$ is a random variable, which essentially makes the process doubly stochastic. We replace the actual random transition rate by an average infection, which is basically a mean-field approximation. Thus, we have

$$\mathbb{E}\big[q_{1,2|i}(t)\big] = \mathbb{E}\left[\beta \sum_{j=1}^{I} \frac{w_{i,j}}{(\exp(T) - 1)(||\vec{\varpi}||_1 - \varpi_5)} \mathbb{1}_{\{X_j(t)=1\}}\right]. \tag{9}$$

Generally, we can take the expectation over the spreading rate β, the weight matrix $\mathbf{W}$, and the state $X_j(t)$. Since we assume that both the infection rate β and the weight matrix are constants and given, we only average over the state $X_j(t)$. Using $\mathbb{E}[\mathbb{1}_x] = \text{Pro}[x]$, we replace $q_{1,2|i}(t)$ by

$$\begin{aligned} \mathbb{E}\big[q_{1,2|i}(t)\big] &= \sum_{j=1, j\neq i}^{I} \frac{\beta w_{i,j}}{(\exp(T) - 1)(||\vec{\varpi}||_1 - \varpi_5)} \text{Pro}\big[X_j(t) = 1\big] \\ &= \sum_{j=1, j\neq i}^{I} \frac{\beta w_{i,j}}{(\exp(T) - 1)(||\vec{\varpi}||_1 - \varpi_5)} \vartheta_j(t). \end{aligned} \tag{10}$$

Since mobile user i cannot directly transfer from state 1 to state 3, the transition rate of mobile user i from state 1 to state 3 is zero, i.e.,

$$E\big[q_{1,3|i}(t)\big] = q_{1,3|i}(t) = 0. \tag{11}$$

With the condition in (6), the transition rate of mobile user i from state 1 to state 1 is averaged by

$$E\big[q_{1,1|i}(t)\big] = -\beta \sum_{j=1}^{I} \frac{w_{i,j}}{(\exp(T) - 1)(||\mathbf{v}||_1 - \varpi_5)} \vartheta_i(t). \tag{12}$$

Since mobile user i cannot transfer from state 2 to state 1, the transition rate of mobile user i from state 2 to state 1 at time t is $q_{2,1|i}(t) = 0$. Each infected mobile user cures himself/herself is a Poisson process with recovery rate μ. As such, the transition rate of mobile user i from state 2 to state 3 at time t is $q_{2,3|i}(t) = \mu$. Similarly, with the condition in (6), the transition rate of mobile user i from state 2 to state 2 is averaged by $q_{2,2|i}(t) = -\mu$. When mobile user i reaches to state 3, this mobile user cannot transfer to other states. We can obtain

$$\begin{cases} q_{3,1|i}(t) = 0 \\ q_{3,2|i}(t) = 0 \\ q_{3,3|i}(t) = 0. \end{cases} \tag{13}$$

Therefore, at time t, the transition rate matrix of mobile user i can be rewritten as

$$\mathbb{E}[Q_i(t)] = \begin{bmatrix} -\beta \sum\limits_{j=1}^{I} \frac{w_{i,j}}{\Pi} \vartheta_j(t), & \beta \sum\limits_{j=1}^{I} \frac{w_{i,j}}{\Pi} \vartheta_j(t), & 0 \\ 0, & -\mu, & \mu \\ 0, & 0, & 0 \end{bmatrix}. \tag{14}$$

Here, $\Pi = (\exp(T) - 1)(||\vec{\varpi}||_1 - \varpi_5)$.

Based on Chapman–Kolmogorov equations, the transition probabilities between any two states during time interval $[t, t+\Delta t]$ are

$$\begin{aligned} p_{1,1|i}(t, t+\Delta t) &= \text{Pro}\{X_i(t+\Delta t) = 1 | X_i(t) = 1\} \\ &= 1 + q_{1,1|i}(t)\Delta t + o(\Delta t) \\ &= 1 - \beta \sum_{j=1}^{I} \frac{w_{i,j}}{\Pi} \vartheta_j(t)\Delta t + o(\Delta t) \end{aligned} \tag{15}$$

$$\begin{aligned} p_{1,2|i}(t, t+\Delta t) &= \text{Pro}\{X_i(t+\Delta t) = 2 | X_i(t) = 1\} \\ &= q_{1,2|i}(t)\Delta t + o(\Delta t) \\ &= \beta \sum_{j=1}^{I} \frac{w_{i,j}}{\Pi} \vartheta_j(t)\Delta t + o(\Delta t) \end{aligned} \tag{16}$$

$$\begin{aligned} p_{1,3|i}(t, t+\Delta t) &= \text{Pro}\{X_i(t+\Delta t) = 3 | X_i(t) = 1\} \\ &= q_{1,3|i}(t)\Delta t + o(\Delta t) \\ &= o(\Delta t) \end{aligned} \tag{17}$$

$$\begin{aligned} p_{2,1|i}(t, t+\Delta t) &= \text{Pro}\{X_i(t+\Delta t) = 1 | X_i(t) = 2\} \\ &= q_{2,1|i}(t)\Delta t + o(\Delta t) \\ &= o(\Delta t) \end{aligned} \tag{18}$$

$$\begin{aligned} p_{2,2|i}(t, t+\Delta t) &= \text{Pro}\{X_i(t+\Delta t) = 2 | X_i(t) = 2\} \\ &= 1 + q_{2,2|i}(t)\Delta t + o(\Delta t) \\ &= 1 - \mu\Delta t + o(\Delta t) \end{aligned} \tag{19}$$

$$\begin{aligned} p_{2,3|i}(t, t+\Delta t) &= \text{Pro}\{X_i(t+\Delta t) = 3 | X_i(t) = 2\} \\ &= q_{2,3|i}(t)\Delta t + o(\Delta t) \\ &= \mu\Delta t + o(\Delta t) \end{aligned} \tag{20}$$

$$\begin{aligned} p_{3,1|i}(t, t+\Delta t) &= \text{Pro}\{X_i(t+\Delta t) = 1 | X_i(t) = 3\} \\ &= q_{3,1|i}(t)\Delta t + o(\Delta t) \\ &= o(\Delta t) \end{aligned} \tag{21}$$

$$\begin{aligned} p_{3,2|i}(t, t+\Delta t) &= \text{Pro}\{X_i(t+\Delta t) = 2 | X_i(t) = 3\} \\ &= q_{3,2|i}(t)\Delta t + o(\Delta t) \\ &= o(\Delta t) \end{aligned} \tag{22}$$

$$\begin{aligned} p_{3,3|i}(t, t+\Delta t) &= \text{Pro}\{X_i(t+\Delta t) = 3 | X_i(t) = 3\} \\ &= 1 + q_{3,3|i}(t)\Delta t + o(\Delta t) \\ &= 1 + o(\Delta t). \end{aligned} \tag{23}$$

Therefore, we have

$$\begin{aligned} \theta_i(t+\Delta t) &= \text{Pro}\{X(t+\Delta t) = 1\} \\ &= \sum_{l=1}^{3} \text{Pro}\{X_i(t) = l\} p_{l,1|i}(t, t+\Delta t) \\ &= \theta_i(t)\left(1 - \beta \sum_{j=1}^{I} \frac{w_{i,j}}{\Pi} \vartheta_j(t)\Delta t\right) + o(\Delta t) \end{aligned} \tag{24}$$

$$\begin{aligned} \vartheta_i(t+\Delta t) &= \text{Pro}\{X(t+\Delta t) = 2\} \\ &= \sum_{l=1}^{3} \text{Pro}\{X_i(t) = l\} p_{l,2|i}(t, t+\Delta t) \\ &= \theta_i(t)\beta \sum_{j=1}^{I} \frac{w_{i,j}}{\Pi} \vartheta_j(t)\Delta t + \vartheta_i(t)(1-\mu\Delta t) + o(\Delta t) \end{aligned} \tag{25}$$

$$\begin{aligned} \rho_i(t) &= \text{Pro}\{X(t+\Delta t) = 3\} \\ &= \sum_{l=1}^{3} \text{Pro}\{X_i(t) = l\} p_{l,3|i}(t, t+\Delta t) \\ &= \vartheta_i(t)\mu\Delta t + \rho_i(t) + o(\Delta t). \end{aligned} \tag{26}$$

The Markov differential equations for the probabilities of the above three states can be calculated by

$$\begin{aligned} \frac{d\theta_i(t)}{dt} &= \lim_{\Delta t \to 0} \frac{\theta_i(t+\Delta t) - \theta_i(t)}{\Delta t} \\ &= -\beta\theta_i(t) \sum_{j=1}^{N} \frac{w_{i,j}}{\Pi} \vartheta_j(t) \end{aligned} \tag{27}$$

$$\begin{aligned} \frac{d\vartheta_i(t)}{dt} &= \lim_{\Delta t \to 0} \frac{\vartheta_i(t+\Delta t) - \vartheta_i(t)}{\Delta t} \\ &= \theta_i(t)\beta \sum_{j=1}^{N} \frac{w_{i,j}}{\Pi} \vartheta_j(t) - \vartheta_i(t)\mu \end{aligned} \tag{28}$$

$$\frac{d\rho_i(t)}{dt} = \lim_{\Delta t \to 0} \frac{\rho_i(t+\Delta t) - \rho_i(t)}{\Delta t} = \vartheta_i(t)\mu. \tag{29}$$

Then, at time t, the number of unhealthy mobile users, including the number of infected mobile users and recovered mobile users is

$$\widetilde{I}(t) = \sum_{i=1}^{I} (\vartheta_i(t) + \rho_i(t)). \tag{30}$$

C. Vaccinated Target Selection

The highest objective of the vaccinated target selection in the proposed scheme is to search for the optimal group of mobile users whose vaccinations can maximally mitigate the spread of infectious disease. Nevertheless, as the number of mobile users in the network is considerable, and the social contact behaviors of mobile users are dynamic and heterogeneous, the optimal vaccinated target selection with the constraint of the immune budget is pretty hard to deal with and consumes

Algorithm 1 Optional Candidate Searching Algorithm

Input: $\mathcal{C} = \{c_1, c_2, \ldots, c_O\}$, $\mathcal{G} =< \mathcal{I}, \mathcal{E}, \mathcal{W} >$, F.
Output: Set of proper candidates, $\mathcal{V}_{max}$.
Initial: $\Omega = \{1\}_{I\times O}$, $\Psi = \{0\}_{I\times O}$, $\mathcal{U} = \mathcal{I}$.
while $|\mathcal{U}| > 0$ **do**
  Find the mobile user set $\hat{\mathcal{S}}$ that has the maximum saturability.
  if $\{|\hat{\mathcal{S}}| > 1\}$ **then**
    Choose the mobile use i that has the maximum social degree in $\hat{\mathcal{S}}$.
  end if
  for c_o in $\mathcal{C}$ **do**
    if $\{\ a_{i,o} == 1\}$ **then**
      $b_{i,o} = 1$.
      for j in $\mathcal{I}$ **do**
        if $\{w_{i,j} > 0\}$ **then**
          $a_{j,o} = 1$.
        end if
      end for
      Delete mobile user i in $\mathcal{U}$.
      break;
    end if
  end for
end while
Based on the matrix Ψ, the mobile users are divided into O groups and the mobile users in each group have the same color.
According to the number of candidate mobile users, select proper candidates to form the set $\mathcal{V}_{max}$.

Algorithm 2 Optimal Vaccinated Targets Selection Algorithm

Input: $\mathcal{G}$, $\mathcal{S}$, $\mathcal{F}$, $\mathcal{H}$, $\mathcal{V}_{max}$
Output: The optimal vaccinated targets.
Initial: $\mathcal{F} = [\ ]$, $\mathcal{H} = [\ ]$.
for v_n in $\mathcal{V}_{max}$ **do**
  Calculate the infected possibility of candidate v_n with Eq. (32).
  Calculate the infecting ability of candidate v_n with Eq. (39).
  Calculate the spreading centrality of candidate v_n with Eq. (40).
end for
Sort the candidates based on their spreading centralities.
for v_n in $\mathcal{V}_{max}$ **do**
  if $v_n \notin \mathcal{S}$ **then**
    $\mathcal{F} = \mathcal{F} \bigcup \{v_n\}$.
  end if
end for
for $\mathcal{H} \in \mathcal{F}^H$ **do**
  Calculate the number of unhealthy mobile users at the stable state, by the infectious disease spreading analysis model in Eq. (27), (28), and (29).
end for
Select the group of mobile users that can generate the minimum number of unhealthy mobile users as the optimal vaccinated targets.

a large computation power. As such, in this article, we propose a novel near-optimal vaccinated target selection strategy. The proposed strategy includes three steps. The first step is to select *optional candidates* that are most widely distributed, with which the phenomenon that vaccinated targets are too concentrated is avoided when infectious sources (i.e., patients) are located in different areas. The second step is to choose the *proper candidates* from the set of optional candidates based on the spreading metric calculated by spreading ability and spreading probability. In specific, the candidate with the high spreading ability and large spreading probability is easy to be chosen as the vaccinated target. The third step employs the spreading analysis model to avoid the redundancy effects of the chosen proper candidates, so as to find the *optimal vaccinated targets* that have the maximum prevention performance from the proper candidates. Therefore, the proposed vaccinated target selection scheme adequately takes the location distribution of infectious sources, social contact, and preventing the ability of mobile users into account, whereby the number of infected patients is reduced as much as possible.

Before selecting vaccinated targets, the number of vaccinated targets should be determined based on the resource budget, which is denoted by H. Besides, to avoid the redundant effects of mobile users on containing the infectious disease, we choose excess mobile users as proper candidates, whose amount is

$$F = \lfloor \sigma H \rfloor + S \tag{31}$$

where σ is an adjustment parameter and $\sigma \geq 1$ and $\lfloor \cdot \rfloor$ is the floor function.

Step 1 (Optional Candidate Selection): We first find the optional vaccinated mobile users (i.e., optional vaccinated candidates) that are most widely distributed in the network. In reality, infection sources are distributed in different places. To slow down the spread of the infectious disease as soon as possible, we should select the candidates that are also distributed in different locations to be vaccinated. Here, we devise a graph coloring algorithm to search the optional candidates. The detailed process is expressed in Algorithm 1. Let $\mathcal{C} = \{c_1, c_2, \ldots, c_O\}$ denote the set of colors used in the network. Then, we denote a color matrix $\Omega = \{a_{i,o} | a_{i,o} \in \{0, 1\}\}$, which represents the restriction of social graph coloring. If $a_{i,o} = 1$, mobile user i can use the color c_o. Otherwise, $a_{i,o} = 0$ means that color c_o has been used by the neighbors of mobile user i who cannot use this color again. As such, if two mobile users have an edge linked with each other in the social graph, they should have different colors. Let $\Psi = \{b_{i,o} | b_{i,o} \in \{0, 1\}\}$ denote the coloring matrix, which represents the mobile users' color usages. If $b_{i,o} = 1$, mobile user i has used the color c_o. Otherwise, $b_{i,o} = 0$ indicates that color c_o has not been used by mobile user i.

From step 22 of Algorithm 1, mobile users are divided into O groups, whose set is denoted by $\mathbf{V} = \{\mathcal{V}_1, \mathcal{V}_2, \ldots, \mathcal{V}_O\}$. In group $\mathcal{V}_o$, mobile users have the same color o. Since two neighboring mobile users cannot have the same color, the mobile users in the same group are located at different places. Then, we select group with the largest number of mobile users as optional candidates, whose set is denoted as $\mathcal{V}_{\max} = \{v_1, v_2, \ldots, v_N\}$ (i.e., step 23).

Step 2 (Proper Candidate Selection): In order to select the optimal targets for vaccination, we should find proper candidates that have the large opportunities and strong abilities to spread the infectious disease from the optional candidates selected in step 1. In other words, we want to find mobile users that are easily infected and fast spread the infectious disease. Here, we first calculate two metrics: 1) infected possibility and 2) infecting ability. The infected possibility is used to measure the possibility that the mobile user is infected. If the

mobile user is closer to infected sources, he/she is more likely to be infected. Here, we use the shortest path to calculate the optional mobile user's infected possibility. The shortest path between an infection source and a candidate can be searched by the Dijkstra algorithm [41]. Since the edge weight indicates the disease spread probability between two mobile users, the larger edge weight has a shorter distance. As such, the distance between mobile user i and mobile user j can be calculated by $d(i,j) = (1/w_{i,j})$. Here, if the distance between two mobile users is larger, the infectious disease is more hardly spread, i.e., the infected possibility is smaller. The weight is calculated from the social contact information of mobile users, which indicates the spread probability. In specific, the larger weight on an edge indicates a higher disease spread probability between two vertices of this edge, i.e., the distance between the corresponding two mobile users is smaller. As such, we utilize the reciprocal of the weight as the metric of distance. Then, the infected possibility of vaccinated candidate v_n, $v_n \in \mathcal{V}_{\max}$ can be calculated by

$$\phi_i = \sum_{s=1}^{S} \sum_{z=1}^{Z_{s,n}} \frac{\varepsilon}{\sum_{(i,j)\in P_{z,s,v_n}} d(i,j)} \tag{32}$$

where $Z_{s,n}$ is the number of shortest path between the infection source s and candidate v_n. P_{z,s,v_n} is the zth shortest path between the infection source s and vaccinated candidate v_n. Here, $P_{z,s,v_n} = \{(s,s_1),(s_1,s_2),\ldots,(i,j),\ldots,(v_{n,1},v_n)\}$. ε is the adjustment parameter.

To calculate the candidate's infecting ability, we jointly consider the local effect and global effect on the spread of the infectious disease. We first calculate the number of infected mobile users who are nearest to the candidate v_n. Namely, the number of mobile users that are infected by candidate v_n and have one hop distance to candidate v_n in social graph, is calculated by

$$\xi_1(v_n) = \sum_{j\in\Xi(1,v_n)} \mathbb{1}_{\{X_j=1\}} \tag{33}$$

where $\Xi(1,v_n)$ is the set of mobile users that have one hop away from the vaccinated candidates v_n. Since $\mathbb{1}_{\{X_j=1\}}$ is a random variable, $\xi_1(v_n)$ is also a random variable. Based on the edge weight, the expectation of $\xi_1(v_i)$ is

$$\mathbb{E}[\xi_1(v_i)] = \sum_{j\in\Xi(1,v_n)} \frac{w_{v_n,j}}{\Pi}. \tag{34}$$

Then, we consider the mobile users that have two hops away from the candidates v_n. We have

$$\xi_2(v_n) = \sum_{j\in\Xi(2,v_n)} \mathbb{1}_{\{X_j=1\}} \tag{35}$$

where $\Xi(2,v_n)$ is the set of mobile users that have two hops away from the candidates v_n. Similarly, based on the edge weight, the expectation of $\xi_2(v_n)$ is

$$\mathbb{E}[\xi_2(v_n)] = \sum_{j\in\Xi_2(v_n)} \frac{w_{v_n,i_1}}{\Pi} \frac{w_{i_1,j}}{\Pi} \tag{36}$$

where mobile user i_1 is the neighbor of both candidate v_n and mobile user j. Furthermore, let $h_{\max}(v_n)$ denote the largest number of hops for candidate v_n's shortest path in social graph. The expectation of $\xi_{h_{\max}(v_i)}(v_i)$ is

$$\mathbb{E}\big[\xi_{h_{\max}(v_n)}(v_n)\big] = \sum_{j\in\Xi_{h_{\max}(v_n)}(v_n)} \psi(v_n,j) \tag{37}$$

where $\Xi_{h_{\max}(v_i)}(v_i)$ is the set of mobile users that have $h_{\max}(v_n)$ hops away from mobile user v_n. $\psi(v_n,j)$ is the probability that mobile user j is infected when mobile user v_n is the infection source. $\psi(v_n,j)$ can be obtained by

$$\psi(v_n,j) = \frac{w_{v_n,m_1}}{\Pi} \prod_{h=2}^{h_{\max}(v_n)-1} \frac{w_{m_{h-1},m_h}}{\Pi} \cdot \frac{w_{m_{h_{\max}(v_n)-1},j}}{\Pi}. \tag{38}$$

Here, m_1, m_{h-1}, m_h, $m_{h_{\max}(v_n)-1}$ are the intermediate mobile users in the shortest path between candidate v_n and mobile user j. As summary, the infecting ability of candidate v_n can be calculated by

$$\xi(v_n) = \sum_{h=1}^{h_{\max}(v_n)} \xi_{h(v_n)}(v_n). \tag{39}$$

The infection ability evaluates a mobile user's likelihood of infecting others if he or she is infected, while the infected probability assesses the likelihood of the mobile user being infected given the current knowledge of the infected patient set $\mathcal{S}$. When choosing a vaccination node, both infection ability and infected probability should be considered. As such, we define the *spreading centrality* combining them to get candidate v_n's spreading centrality

$$\zeta(v_n) = \frac{\phi(v_n,\mathcal{S})}{\max\limits_{v_n\in V_{max}} \phi(v_n,\mathcal{S})} \cdot \frac{\xi(v_n,\mathcal{S})}{\max\limits_{v_n\in V_{max}} \xi(v_n,\mathcal{S})}. \tag{40}$$

Then, we sort the candidates based on the spreading centrality and choose F [determined in (31)] top candidates as proper targets.

Step 3 (Optimal Vaccinated Target Selection): Finally, we utilize the infectious disease spreading analysis model (analysis in Section IV-B) to calculate the marginal effect of each optional target, and select H targets with the largest marginal effects as the optimal vaccinated targets. Let $\mathcal{F}$ and $\mathcal{H}$ denote the set of proper targets and optimal vaccinated targets, respectively. The selection algorithm is shown in Algorithm 2.

V. Performance Evaluation

In this section, numerous simulations are performed to evaluate the performance of the proposed scheme. The simulation setup is first presented, and then we analyze the simulation results.

A. Simulation Setup

In the simulation, based on [20], [22], and [42], the parameters are set as follows. The number of mobile users is 500. By using the Barabasi–Albert model [43], a synthetic scale-free network is generated. Then, we mine the data on mobile users' contact with 2000 time slots according to the topology of the generated network. At each time slot, a mobile user contacts to each neighbor with a probability of 0.3 [22]. The probability

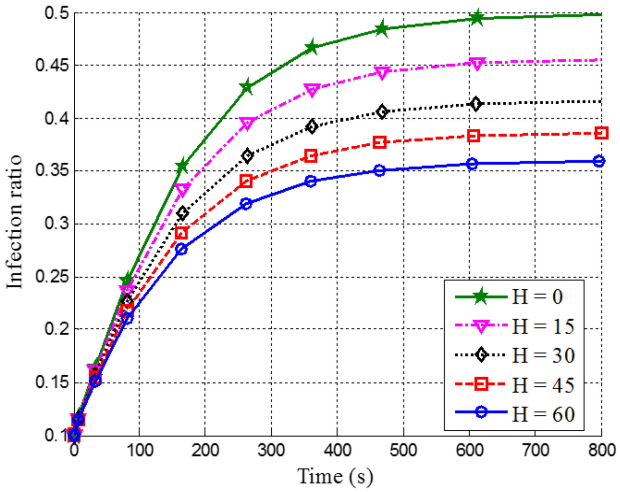

Fig. 4. Evolution of the infection ratio over time, when the number of vaccinated mobile users H changes from 0 to 60. The infection ratio first increases over time and gradually reaches to be stable. Besides, the larger number of vaccinated mobile users induces the lower infection ratio.

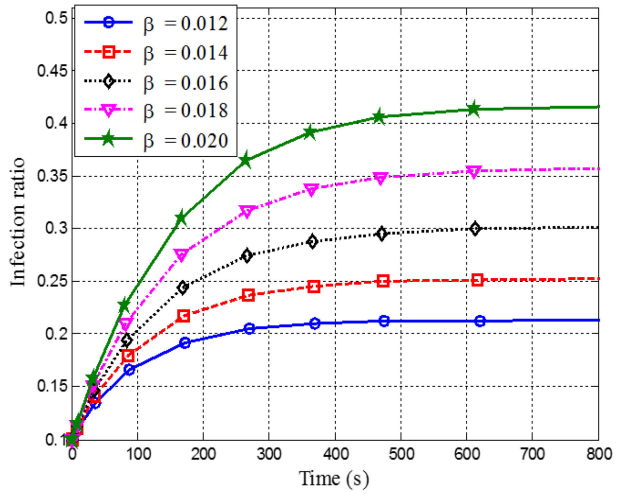

Fig. 5. Evolution of the infection ratio over time, when the disease spreading rate β changes from 0.012 to 0.020. The infection ratio increases faster when the disease spreading rate is larger.

that two mobile users contact indoor is 0.7. To construct the social relationships among mobile users, the probability that two mobile users are strangers is 0.4. When two mobile users are not strangers, the probability that they have one type of relationships is 0.5. Based on the synthetic contact trace, we initiate the infectious process. Initially, we randomly choose 10% of mobile users as the seed set of infection sources to initiate the infectious process. The disease spreading rate is 0.025 and the disease recovery rate is 0.02. The parameter is equal to 0.5 [22]. The infection process is conducted with 800 time slots. We utilize the infection ratio as the metric to show the simulation results. The infection ratio is the ratio of the number of unhealthy mobile users to total mobile users.

B. Simulation Results

Fig. 4 shows the evolution of the infection ratio over time. In the simulation, the number of vaccinated targets changes from 0 to 60. From Fig. 4, the infection ratio increases to be stable at last, where there are no infected mobile users in the network and the infection ratio cannot increase finally. Besides, if the number of vaccinated targets is larger, the infection ratio increases slower and the stable infection ratio is smaller. For example, the maximum of infection ratio with $H = 0$ is 0.5, while that with $H = 60$ is 0.356. In particular, the stable infection ratio decreases more and more slowly with the growth of vaccinated targets. For example, when the number of vaccinated targets increases from 0 to 15, the stable infection ratio decreases by 9%. But the maximum infection decreases by 5%, when the number of vaccinated targets increases from 45 to 60.

Fig. 5 is the evolution of the infection ratio over time, when the disease spreading rate changes from 0.012 to 0.020. From Fig. 5, we can observe that the infection ratio increases faster when the disease spreading rate is larger. A large disease spreading rate makes the disease spread easily. Besides, the stable infection ratio is larger and larger, when the disease spreading rate increases. The reason is that a large number of mobile users can be infected and these mobile users also infect other healthy mobile users. Thereby, if the disease spreading rate is larger, more mobile users should be vaccinated to slow down the disease transmission.

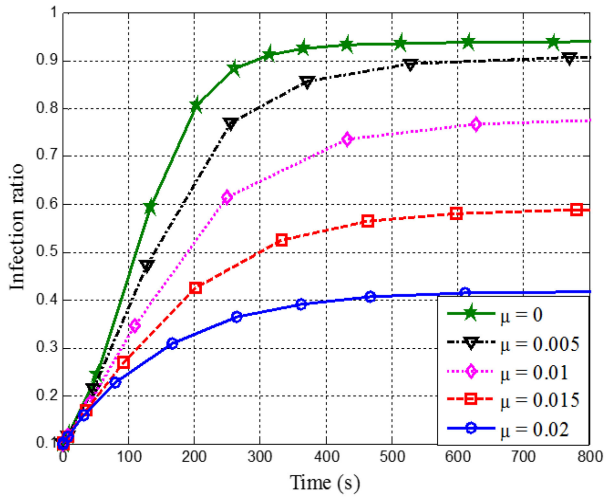

Fig. 6. Evolution of the infection ratio over time, when the recovery rate μ changes from 0 to 0.02. The infection ratio increases faster and the stable infection ratio is large, if the recovery rate is small.

Fig. 6 shows the evolution of the infection ratio over time when the recovery rate changes from 0 to 0.02. Here, the disease spreading rate is 0.02. Thirty mobile users are chosen to be vaccinated. Other settings are unchanged. From Fig. 6, it can be seen that the infection ratio increases faster, when the recovery rate is smaller. Besides, the stable infection ratio is large, if the recovery rate is small. In addition, the difference between two stable infection ratios with different recovery rates is larger and larger. For instance, as the recovery rate increases from 0 to 0.005, the stable infection rate decreases by 2%. The stable infection rate decreases by 30% with an increase of the recovery rate from 0.015 to 0.02. As a summary, if the recovery rate is larger, the number of vaccinated targets can be smaller.

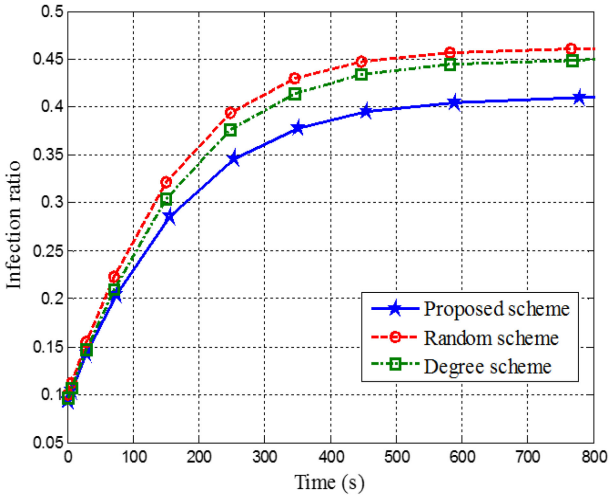

Fig. 7. Comparison of the proposed scheme with two existing schemes, when the simulation time increases. Fixing the time, the proposed scheme has the largest infection ratio among three schemes.

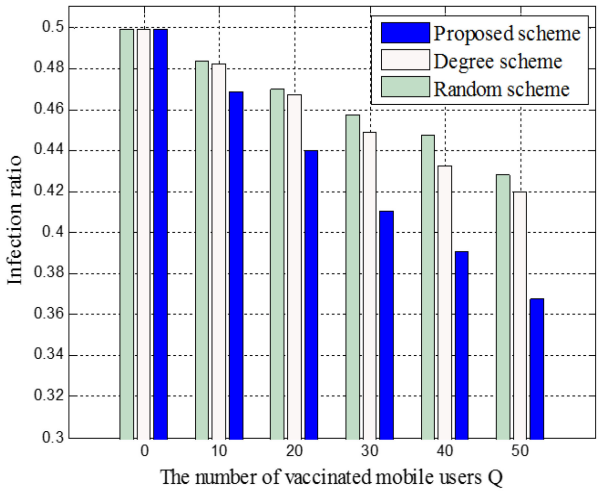

Fig. 8. Comparison of the proposed scheme with two existing schemes, when the number of vaccinated mobile users changes. All infection ratios of three schemes decrease with the growth of the vaccinated targets. Besides, the proposed scheme has a lower infection ratio than the other two schemes over each vaccinated mobile user number.

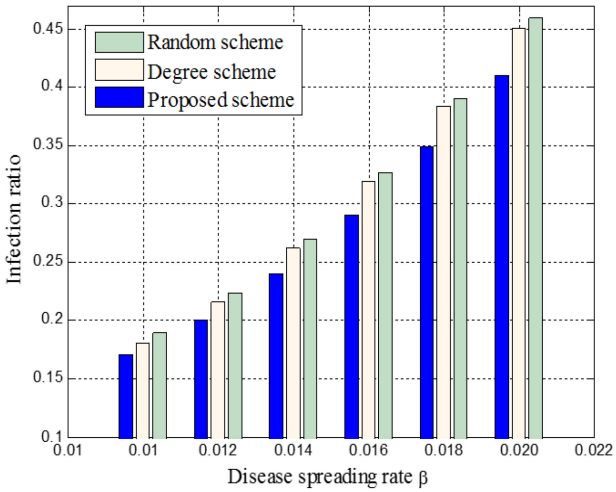

Fig. 9. Comparison of the proposed scheme with two existing schemes, when the disease spreading rates change. All infection ratios of three schemes increase with the growth of the disease spreading rate. Besides, the proposed scheme has the lowest infection ratio among three schemes over each disease spreading rate.

Fig. 7 presents a comparison of the proposed scheme with two conventional schemes (i.e., the random scheme [44] and the degree scheme [45]). The random scheme selects a certain number of mobile users randomly for vaccination. The degree scheme selects vaccination targets by using the node degree. From Fig. 7, we can observe that all infection ratios of three schemes increase over time and reach to be stable at the end. In particular, the proposed scheme has the smaller increase rate than the other two schemes. In the random scheme, since the vaccinated targets are randomly chosen, these vaccinated targets may be isolated mobile users that cannot hinder the spread of the infectious disease. In the degree scheme, mobile users with the large node degrees may be far away from the infection source and have limited abilities to hinder infections spreading. In the proposed scheme, vaccinated targets have the maximum spreading centralities, and these users are widely distributed to independently prevent infectious disease in the respective area.

Fig. 8 compares the proposed scheme with the other two schemes when the number of vaccinated targets changes from 0 to 50. From Fig. 8, we can see that all infection ratios of three schemes decrease with the growth of the vaccinated targets. In addition, the proposed scheme has a lower infection ratio than the other two schemes with each vaccinated mobile user number. In the random scheme, the selected vaccinated targets may be the irrelevant mobile users who cannot significantly hinder the infectious disease spreading. In the degree scheme, although the selected vaccinated targets have the maximal node degree, these mobile users are not the most influential mobile users. But in the proposed scheme, the selected vaccinated targets are the most influential mobile users that have the highest spreading centralities.

Fig. 9 presents a comparison of the proposed scenario with the other two scenarios in terms of the change on the disease transmission rate. The disease spreading rate here increases from 0.01 to 0.02. From Fig. 9, we can observe that all infection ratios of three schemes increase with the disease spreading rate. Besides, the proposed scheme has the lowest infection ratio among the three schemes. In the random scheme, since the selected vaccinated targets have few influences on the disease spreading, the infection ratio increases fastest. In the degree scheme, the selected vaccinated targets have weak abilities to hinder infectious spreading. In the proposed scheme, since the vaccinated targets are selected with the graph coloring, the vaccinated targets are distributed in different areas. Additionally, the vaccinated targets have the maximum spreading centralities, who prevent infectious disease as soon as possible.

VI. Conclusion

We have proposed a novel e-healthcare MSIoTs-based targeted vaccination scheme to control the spread of the infectious disease. The architecture of e-healthcare MSIoTs

has been developed by integrating the e-healthcare system and MSIoTs, whereby the health data and social data are jointly collected. With the health data and the social data, the infectious disease spreading analysis model has been devised to observe the spreading process of the infectious disease. Furthermore, we have designed a graph coloring and spreading centrality-based vaccinated candidate searching algorithm to find the most widely distributed and influential candidates. To reduce the vaccination cost, we have devised a vaccinated target selection algorithm to choose the optimal ones for preventing infectious disease. The simulation results show that the proposed scheme is superior to other conventional schemes. On future work, we will study the privacy preservation mechanism during the exchange of both health data and the construction on the e-healthcare fog of social IoTs.

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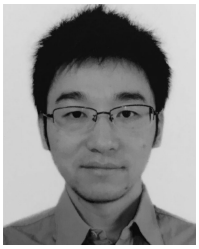

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