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Vaccination strategies of an SIR pair approximation model with demographics on complex networks

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ABSTRACT

Pair approximation model is an effective tool to study epidemic spread on complex networks. It can more accurately capture the effects of network structure on the spreading process. That then helps us grasp the spreading laws of epidemics on networks and further make effective prevention and control measures. Vaccination, an important measure for prevention and control of infectious disease, has made great achievements in public health. In this paper we study vaccination strategies with the help of pair approximation epidemic model with demographics. We firstly introduce constant vaccination into SIR pair approximation model. The reproduction number and endemic prevalence of disease are investigated, the critical vaccination rate which can help to control disease transmission is also given. Considering the restriction of financial resources, it is necessary to control disease transmission simultaneously to reduce vaccination cost. To this end, we further investigate optimal vaccination of SIR pair approximation model by use of optimal control theory. The existence of optimal solution is established and optimality system is derived. Finally, a series of stochastic simulations on different initial networks are performed to demonstrate our theoretical models and some numerical simulations are provided to observe and analyze different vaccination strategies.

1. Introduction

As indicated by epidemic history, the spread of infectious disease—a major threat to the health of human being—has taken the lives of millions of people [4]. Therefore, it is crucial to understand infectious diseases and to develop appropriate control strategies. In the paper [17] Kermack and McKendirck established the susceptible-infected-recovered (SIR) framework which forms the basis of mathematical models. After their pioneering work, the use of mathematical tools to study and understand the spread of infectious disease is an established and fruitful area of research (see, e.g., [16]). However, the early models do not consider realistic human behaviors and interactions. It has long been acknowledged that the connectivity pattern between individuals in human beings is an important factor in determining the properties of a disease spreading process. Using networks to model disease transmission, where individuals are represented as nodes in a network and the connectivity between individuals is represented by links between the nodes, allow us to capture a high level of detail of many realistic processes and lead to more accurate models, especially when compare to classical compartmental models which usually operate on the assumption of homogeneous random mixing. The works [15,28–30] done by Pastor–Satorras, Vespignani and Newman et al. are the famous representative researches in this area, and they present detailed analytical and numerical studies on some epidemic models in the framework of complex networks.

Pair approximation model, one of the network-based epidemic models, offers an explicit treatment of the epidemic process both at node and link level and hence has led to a much better understanding of the role of contact heterogeneity, assortativity and clustering of contacts. Up to now extensive investigations on pair approximation model have been performed. Keeling [14] built pair approximation model of susceptible-infected-recovered (SIR) epidemic with cluster and discussed the basic reproduction number of the model. Bauch [3] established pair approximation model of susceptible-infected-susceptible (SIS) epidemic and analyzed its basic reproduction number, analysis of global dynamic for this model was provided in [25]. Furthermore, to reveal the influ-

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ences of birth and death of individuals on disease spread and the topological evolution of the underlying networks, we studied an SIS pair approximation model with demographics [26] based on Markov chain. Recently, being different from the previous pair approximation models based on Markovian epidemics, a series of pair approximation models are extended to non-Markovian epidemics (see, e.g., [18,36,37]).

Understanding the spread of infectious disease is one of the motivations to explore mathematical models. The other and perhaps more important purpose is to develop effective strategies for disease prevention and control. Measures for prevention and control of infectious disease include vaccination, treatment, quarantine, isolation, and prophylaxis (see [27]). Vaccination is one of the greatest achievements of public health. Research and practice results show that if a large majority of people are vaccinated, it is much more difficult for an outbreak of disease to occur, this is so-called herd immunity. Typical cases are that vaccination has led to the complete eradication of smallpox worldwide, and a near eradication of polio.

Mathematical models including vaccination aid in deciding on a vaccination strategy and in determining changes in qualitative behavior that could result from such a control measure. There are two points in which vaccination models can differ from one another. The first is that some models assume that vaccination is equivalent to going through the disease and treat vaccinated individuals as recovered individuals (see, e.g., [21,38]). Thus a recovered compartment model can include vaccinated individuals without an additional class. Other models assume that vaccinated individuals have to be separated into a vaccinated compartment (see, e.g., [2,8,11]). In addition, epidemic models with vaccination on complex networks also have been extensively studied, one may refer to [7,9,31–33,40,41] for more details.

What vaccination models in previous literatures have in common is that individuals access to vaccines with a fixed rate, that is to say, control strategies are considered to be constant in time. But in reality, control strategies are variable in time. On the other hand, these models focused on identifying the mechanisms responsible for epidemics but had taken little into account economic constraints in analyzing control strategies. Actually, there is a pressing need to optimize investments for vaccination cost as financial resources are limited. An ideal control strategies should strike a balance between epidemiological factor and economic factor. To this end, optimal control method has been used to describe the optimal vaccination policy as function of the vaccination cost and epidemic dynamics and severity. So far a number of studies in the literature have been made to study the role of vaccination on the spread of infectious disease and economic cost by using optimal control theory (see for example [10,13,20,22,23,42], and monographs [1,24,39] and the references therein for detailed description). In these studies the application of optimal control method is restricted to traditional epidemic models, while connectivity patterns between individuals are ignored. In order to make up for the lack of theoretical research area and develop better vaccination strategy in conformity with practical situation, it is necessary to combine optimal control method with network-based epidemic models. However, until now, only a few literatures contribute to this area. For example, Preciado et al. [34,35] analyzed optimal vaccine allocation for control of SIS, SEIV networked epidemic models. Chen and Sun [5,6] investigated optimal vaccination and treatment of an SIRS epidemic model on heterogeneous networks.

To control the spread of disease as well as reduce vaccination cost, in this paper we concern vaccination strategies including constant vaccination and optimal vaccination of an SIR pair approximation model with demographics on complex networks. Pair approximation model with demographics will bring some advantages for this research. Firstly, pair approximation model is succinct and intuitive, meanwhile can better embody some features of complex networks. Secondly, pair approximation model involves differential equation about the number of susceptible-infected pairs, it is the links between the susceptible and infected that determine the spread of disease on networks, thus more efficiently control strategies may be proposed via reduce the number of susceptible-infected tuples. Finally, the demographics, or rather the birth and death of individuals, greatly affects the network structure, thereby, influences the spread of disease. Coupling the demographics to a pair approximation model is more accordant with social network.

The rest of the paper is organized as follows. In Section 2 we introduce constant vaccination in SIR pair approximation model with demographics. Based on that, the basic reproduction number and endemic prevalence of disease are investigated. Furthermore, the critical vaccination level is also presented to prevent infectious disease. In Section 3 optimal control theory is applied to determine the “best” vaccination regime that will minimize the prevalence and the cost of applying vaccination. We discuss the existence of solution for optimal control problem and give optimality system with the help of Pontryagin minimum principle. Simulations are provided in Section 4. For constant vaccination case, we carry out numerical simulations and stochastic simulations starting with Erdös-Rényi (ER) random network and Barabási–Albert (BA) scale-free network. For optimal vaccination case, numerical simulations are implemented and the influences of vaccination cost on optimal control are investigated. A brief conclusion and some discussions on future research are given in Section 5.

2. Model with constant vaccination

Consider a network representing a population with an average degree n and a constant number of nodes N, i.e., the birth rate is equal to the death rate. Each node on networks may be in one of three possible states: susceptible (S), infected (I), and recovered (R). The number of nodes in state S, I and R at time t are represented by $[S](t)$, $[I](t)$ and $[R](t)$ respectively, with $N=[S](t)+[I](t)+[R](t)$. In addition, the pair $[XY](t)$ stands for the number of ordered $X-Y$ edges (pairs) linking a node in state X with a node in state Y on networks at time t, where $X, Y \in \{S, I, R\}$. Note that $[XX](t)$ or $[YY](t)$ counts twice the number of real pairs at time t. It therefore follows that $[SS]+[II]+[RR]+2[SI]+2[SR]+2[IR]=nN$. Analogously, the triple $[XYZ](t)$ represents the number of triple $X-Y-Z$ at time t and $[XYX](t)$ counts twice the number of real triples, where $X, Y, Z \in \{S, I, R\}$.

About spreading mechanism of SIR epidemics with demographics on networks, there are the following events occurring concurrently at each time step Δt (see [26]). (i) Birth event: each old node with the birth rate τ bears a new node which is susceptible and emits n_0 edges. Each of the n_0 edges is randomly connected to an old infectious node with probability $[I]/N$, old susceptible node with probability $[S]/N$ and old recovered node with probability $[R]/N$. (ii) Death event: each node, irrespective of its state, will die at the death rate τ and all of the edges attached to it are removed. (iii) Transmission event: each susceptible node is infected with the transmission rate β per $S-I$ link. (iv) Recovery event: each infected node recovers with rate γ.

With regard to vaccination, we assume that (i) the vaccination is perfect, namely there is no immune failure individual, (ii) vaccination is available and equiprobable for susceptible individuals, those who have vaccinated will be treated as recovered individuals, (iii) the vaccine confers life-long protection on susceptible individuals.

Based on the above notations and assumptions, we can get a system governed by differential equations for the evolution of the