Efficient Vaccination Strategies in a Social Network with Individual Mobility

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Abstract: Vaccination is a primary means used to control infectious diseases. Various epidemic models have been developed to find efficient vaccination strategies. However, few models and vaccination strategies have explicitly taken individual mobility into consideration. New models and vaccination strategies are needed for today’s highly mobile society. This paper presents an individual-based epidemic model that allows individuals to travel between communities. Based on such a model, three vaccination strategies are investigated, including the travel-based, contact-based, and random vaccination strategies. The simulation results show that inter-community travel would be a major consideration for designing vaccination strategy. The contact-based vaccination strategy is preferable in a population with a large number of inter-community travelers, for instance the metropolitan areas. The travel-based vaccination strategy is preferable in a population with a small number of inter-community travelers, such as the rural areas. From a spatial perspective, the travel-based vaccination strategy efficiently confines the spatial spread of diseases, thus minimizing affected areas. This research provides useful insights into the community-based planning for infectious disease control.

Keywords: Vaccination, Social Network, Individual Mobility, Epidemic modeling, Infectious Diseases
1 Introduction

Infectious diseases, such as HIV/AIDS, measles, and influenza, are one of the leading causes of death (Lopez and Murray 1998). A fundamental issue in epidemiology is to find efficient strategies to control infectious diseases (Gordis 2000). Vaccination is a primary means to provide individuals with immunity, and to control epidemics of infectious diseases. Strategies of vaccination consider who, when, and where the vaccines should be applied in a population (Dutta 2008). An efficient vaccination strategy aims to minimize the impacts of an epidemic. Recently, the outbreaks of Severe Acute Respiratory Syndrome (SARS) and avian influenza have posed serious threats on public health (Ferguson et al. 2004, Galvani 2004). The vaccine supplies for these emerging infectious diseases are often limited, due to the time of development and production (Longini and Halloran 2005). Thus, looking for efficient vaccination strategies becomes an urgent issue for researchers and health policy makers.

Epidemic models are important tools for exploring vaccination strategies (McKenzie 2004). An epidemic can be modeled by simulating the transmission of an infectious disease from one individual to another through physical contacts. Based on epidemic models, the impacts of vaccination strategies can be predicted and evaluated. In the current literature, few vaccination strategies have explicitly considered individual mobility over space and time. Many vaccination strategies are developed from epidemic models that emphasize social behaviors of individuals. But the spatial behaviors are not always considered (Sattenspiel and Dietz 1995). In these epidemic models, the contacts among individuals are assumed to be constant, spatially and temporally (Keeling and Eames 2005). In today’s society, people move far more frequently than ever before. Their physical contacts form and break over space and time, leading to spatio-temporal heterogeneity in disease transmission (Keeling 1999, Koopman and Lynch 1999). Epidemic models and vaccination strategies that ignore individual mobility may not be appropriate for today’s mobile society (Bian 2004, Reluga et al. 2006). New vaccination strategies are needed to account for mobile individuals.

This paper explores vaccination strategies using a network model that explicitly considers individual mobility. The network model represents individuals and their social contacts. The entire population is spatially distributed within a number of communities. Individuals are allowed to travel between daytime and nighttime. During either time period, individuals may have contact with other individuals if their spatial locations are in the same community. Based upon this model, three vaccination strategies are simulated, including the travel-based, contact-based, and random vaccination strategies. Their efficacy in disease control is evaluated to suggest the optimal strategy. The remainder of this paper is organized as follows. The next section reviews the research on network models and vaccination strategies. Section 3 describes the design of the network model with individual mobility, and three vaccination strategies. Section 4 presents the simulation results. The final section discusses the conclusion and implications.

2 Network models and vaccination strategies

The epidemics of infectious diseases are intrinsically related to human social networks. The contacts between individuals form a social network that channels the transmission of diseases (Meyers et al. 2005). In epidemic modeling, the social network can be properly modeled by nodes and links (Wasserman and Faust 1994). The nodes represent individuals and the links represent contacts among individuals. Based on this network, diseases can spread throughout a population. Vaccination prevents individuals from infection, and removes them from the network (Madar et al. 2004).
A variety of properties have been revealed to describe how individuals are linked in a society. Three properties have been widely modeled and studied in epidemiology. First, individual contacts are highly localized, that is, an individual is more likely to have contact with people nearby in terms of either social or spatial distance (Harris 1974). These localized contacts can be simply modeled by the lattice networks (Rhodes and Anderson 1996). Individuals are positioned on a regular grid, and only adjacent individuals are linked. Because individuals only contact with their neighbors, the lattice networks predict a wave-like spread of infection, with infection spreading out in a roughly circular manner (Keeling and Eames 2005). This wave-like spread of infection is commonly observed in pandemics over a large geographic area (Grenfell et al. 2001). In lattice networks, people that are socially or spatially close to the infected individuals are suggested to be vaccinated (Kiss et al. 2005, Tildesley et al. 2006).

The second property, observed in many human societies, is called “small-world phenomena”, or “six degrees of separation”. In other words, everyone can be connected to any other individual through at most six social links (Travers and Milgram 1969). A small-world network can be built by adding a few random links into a lattice network. These random links provide shortcuts to connect individuals. Hence, small-world networks are characterized by highly localized contacts, but short length paths (Newman et al. 2006). In the context of disease transmission, highly localized contacts mean that most infection occurs locally. However, short path lengths enable the disease to spread throughout the network much more rapidly than the wave-like spread (Watts and Strogatz 1998). In small-world networks, individuals who are socially active are encouraged to be vaccinated and restricted (Zanette and Kuperman 2002).

The last property is called “scale-free” property. This means a few individuals have significantly larger number of links than the rest of individuals (Newman 2004). A scale-free network can be constructed by linking each new individual preferentially to individuals that already have a large number of links (Albert et al. 2000). The number of links per individual, in the resultant network, takes a power-law distribution. The “scale-free” property has been observed in many networks of disease transmission, such as sexually transmitted diseases and SARS (Liljeros et al. 2001, Riley et al. 2003). Disease spread in a scale-free network shows a hierarchical diffusion pattern. Individuals with large number of links are infected fast, and then they act as hubs to distribute infection to the remaining individuals (Barthelemy et al. 1999). Therefore, individuals who have a large number of links are recommended to be vaccinated (Pastor-Satorras and Vespignani 2002).

These network models play a vital role in shaping our understanding of disease transmission, and providing insights into vaccination strategies (Newman 2002). However, most models and vaccination strategies are developed in a non-spatial context. The mobility of individuals is implicitly considered, or even ignored. Individuals are assumed to stay at a fixed position and their links are kept static over space and time. These assumptions contrast with our common sense that individuals move over space and time, and contact with different groups of individuals at different time and locations (Golledge and Stimson 1998). New network models are needed to incorporate individual mobility, and allow vaccination strategies to consider human contacts varying over space and time. The paper intends to fill this knowledge gap.

3 Methodologies
3.1 The network model with individual mobility
The network model is conceptualized using an individual-based two-tier framework, as proposed by Bian (2004). Each individual is a modeling unit. The two tiers refer to the daytime
population and nighttime population, respectively. Either population is distributed in a number of communities. Four assumptions are made in this model. First, individuals have explicitly spatial locations, with \((x, y)\) coordinates, in the daytime tier (Fig. 1.a) and nighttime tier (Fig. 1.b). Second, at each tier, individuals are grouped into the same community based on their spatial closeness. An individual may have contact with another individual if they are in the same community. Third, individuals travel between two tiers (daytime and nighttime). They may take either inter-community travel or inner-community travel. The travel behaviors are represented by the individual lifelines, following the concepts of time geography (Fig. 1.c) (Hägerstrand 1970, Lenntorp 1977). These lifelines link the communities at two tiers into a global network of human contacts. Fourth, the societal-wide contacts follow a scale-free structure, i.e., a few individuals have much more contacts than the rest of individuals (Fig. 1.d). This model provides a community-structured and spatio-temporally dynamic network of human contacts.

For discussion purposes, a working model is built with a total population of \(N=5000\). The population is assumed to be closed (there are no births, deaths, or migrations during the epidemic). First, the population at each tier is composed of 50 communities. The K-mean clustering algorithm is used to cluster individuals spatially close together into communities. Each cluster of individuals represents a community, and the average size per community is 100 individuals. Second, individuals are linked by the preferential attachment algorithm to generate a
“scale-free” structure (Albert et al. 2000). The average number of links per individual in a day (including daytime and nighttime) is close to eight. Third, the probability of travel between community $i$ and $j$ follows a distance-decay function, $(1/d_{ij}^2) / \sum(1/d_{ij}^2)$, where $d_{ij}$ is the spatial distance between community $i$ and $j$. This assumption is consistent with many empirical studies on travel behaviors between communities (Rushton 1969, Clark and Unwin 1981).

Lastly, a proportion of population ($p$) is randomly selected to take inter-community travel between daytime and nighttime. The remaining individuals are assumed to take inner-community travel between daytime and nighttime. Since inter-community travelers provide connections between communities, the value of $p$ controls the connectivity of a network. In graph theory, the network connectivity can be measured by the maximum connected component (MCC). The MCC is the largest sub-network, within which every pair of nodes can be connected through a number of links (Newman et al. 2002). The number of nodes contained in the MCC is referred to as the size of MCC, and implies the largest number of infection possible during an epidemic (Holme 2004). If the size of MCC is less than the total number of nodes, only a subset of nodes can be connected, and the entire network is “under-connected”. If the size of MCC equals the total number of nodes, and all nodes can be exactly connected by the minimum links, the entire network is “full-connected”. If the size of MCC equals the total number of nodes but the number of links exceeds the minimum, the entire network is called “over-connected” due to redundant links. In reality, the under-connected networks may represent rural areas, where only a few individuals travel between small towns during a day. The over-connected networks may represent metropolitan areas, where much more individuals commute between suburban and urban areas during a day.

In our working model, the network is observed to vary from under-connected, to full-connected, to over-connected, by increasing the value of $p$ from 0% to 20% (Fig. 2). $p=8\%$ is found to be a critical value, at which the size of MCC reaches a plateau and the network becomes full-connected. Below this critical value, the network is under-connected since the size of MCC is smaller than the total population $N$. Above this critical value, the network becomes over-connected, because the size of MCC stops growing but the number of redundant links keeps increasing. For comparison purposes, two network scenarios are designed: an under-connected network given $p=3\%$ and an over-connected network given $p=15\%$.

![Fig. 2](image_url) The size of the maximum connected component as a function of $p$. The delineation between the under-connected and over-connected networks occurs at $p=8\%$. 

4
3.2 Disease transmission and vaccination strategies

The ultimate purpose of modeling social networks is to simulate disease transmission and evaluate vaccination strategies. In the working model, each individual is associated with an infection status. The infection status can be either Susceptible, Infected, or Recovered, following the classic SIR model (Kermack and McKendrick 1927). At each time step, a susceptible individual will be infected with a probability of 10%, once in contact with an infected individual. The disease is assumed to be latent for one day in an infected individual, and afterwards it can be transmitted to other susceptible individuals during the following four days. Then, the infected individual turns to recovered and is immune to infection during the epidemic. The simulation takes a bi-daily time step between daytime and nighttime over 150 days. The Monte-Carlo method is used to simulate the infection between individuals. One infected individual is introduced into the network to initialize the infection.

Vaccination is often applied to only a fraction of population before an infection starts. This is because vaccines are limited and may also have adverse effects (Ferguson et al. 2003). Three vaccination strategies are investigated, including the travel-based, contact-based and random vaccination strategies. The travel-based vaccination strategy aims to vaccinate a fraction of population who travels between communities. The contact-based vaccination strategy aims to vaccinate a fraction of population who has a large number of direct contacts. The random vaccination strategy aims to vaccinate a fraction of population based on a random selection. Each of the three vaccination strategies is simulated under the two pre-defined network scenarios. The vaccination fraction of population \( f \) is varied from 0% to 10% in simulation.

Each vaccination strategy is evaluated by the prevalence of disease. The prevalence is defined as the proportion of susceptible population that is infected during an epidemic (Gordis 2000). A low prevalence indicates that a small number of individuals are infected, and the vaccination strategy is efficient. In addition, two network parameters are also measured to reflect how the vaccination strategy changes the structure of network. One is the size of MCC, and the other is the average number of direct contacts per individual. The former determines how many individuals are possible to be infected. The latter implies how fast the disease can be transmitted among individuals. An efficient vaccination strategy is expected to minimize both network parameters by removing a fraction of population from the network. For a given vaccination fraction \( f \), the disease prevalence, size of MCC, and average number of direct contacts per individual, are estimated by averaging 100 realizations of each vaccination strategy. The network structure is constructed anew for every 10 realizations.

4. Simulation results

4.1 Epidemics on the network

An epidemic can be described by a curve that indicates the number of daily infections through the course of the epidemic, i.e. epidemic curve. Three descriptive terms can be used to characterize this curve. These include the peak time of an epidemic, the number of infections at peak time, and the total number of infections.

Fig. 3 shows the epidemic curves under a range of network connectivity, by varying the value of \( p \) (the proportion of inter-community travelers in a population). A greater value of \( p \) produces an earlier peak time, a higher peak, and a greater number of infections. The reason is that the increasing number of inter-community travelers connects more and more isolated communities, resulting in a rapid growth in the size of MCC (Fig. 2). The disease can, then, spread from one community to another and infect more individuals. These inter-community travelers also provide
shortcuts for the disease to spread between communities, leading to a faster transmission and earlier peak time. Only a few inter-community travelers (approximately 10% of the population) are sufficient to support a large-scale epidemic. This is because of the low critical value of $p$ to form a full-connected network. In such network, all nodes are connected by the minimum links, and thus all individuals are exposed to the infection.

![Graph showing daily new infections and cumulative number of infections under different values of $p$.](image)

**Fig. 3 (a) The daily new infections and (b) cumulative number of infections under a range of values of $p$ during a 150 day simulation.**

### 4.2 The efficacy of vaccination strategies

For each of the two pre-defined network scenarios, three vaccination strategies are simulated. The results are discussed respectively in the following two sub-sections. The third sub-section investigates vaccination strategies from a spatial perspective. The spatial patterns of infection produced by each vaccination strategy are discussed.

**Vaccinations in the under-connected network scenario**

For each of the three vaccination strategies, the resultant prevalence of disease as a function of vaccination fraction $f$ is shown in Fig. 4.

![Graph showing the simulation results of three vaccination strategies in the under-connected network scenario ($p=3\%$).](image)

**Fig 4.** The simulation results of three vaccination strategies in the under-connected network scenario ($p=3\%$). The $Y$ axis is the prevalence, and the $X$ axis is vaccination fraction $f$. 

Given a fixed value of $f$, the travel-based vaccination strategy produces the lowest prevalence, followed by the contact-based vaccination strategy and random vaccination strategy. Thus, the travel-based vaccination strategy outperforms the other two strategies. The random vaccination strategy is the least efficient strategy, because of the highest disease prevalence. It is also worthwhile to mention that if the value of $f$ exceeds 7%, the travel-based and contact-based vaccination strategies show similar performance. Both strategies reduce the prevalence to near zero, and successfully suppress the epidemic.

With respect to the network structure, the travel-based vaccination strategy can significantly reduce the size of MCC by a very low vaccination fraction (Fig. 5.a). But it has little effect on the number of direct contacts of individuals (Fig. 5.b). The results imply that by removing a few inter-community travelers, the under-connected network collapses quickly into small isolated communities, although individuals still have a large number of direct contacts. The disease can spread easily within a community, but cannot spread out of the community. This explains why the travel-based vaccination strategy performs best. The contact-based vaccination strategy gradually decreases the number of direct contacts (Fig. 5.b). But the size of MCC still remains large, even at a high vaccination fraction (Fig. 5.a). This means that most individuals remain connected, despite that they have a few direct contacts. The disease can spread throughout a large-size MCC as long as the time is sufficient. The random vaccination strategy slightly reduces both network parameters. Therefore, it results in the highest prevalence and is the least efficient strategy.

![Fig 5. Two network parameters as a function of $f$ for three vaccination strategies in an under-connected network](image)

**Vaccinations in the over-connected network scenario**

Fig. 6 shows the resultant prevalence of three vaccination strategies in the pre-defined scenario of an over-connected network. The contact-based vaccination strategy performs best, because it produces the lowest prevalence given any vaccination fraction $f$. The travel-based vaccination strategy performs better than the random vaccination strategy, only when vaccination fraction reaches a high level (close to 10%). The random vaccination strategy is still the least efficient strategy. The disease prevalence remains high even after 10% of population has been vaccinated.
Fig. 6 The simulation results of three vaccination strategies in the over-connected network scenario ($p=15\%$).
The $Y$ axis is the prevalence, while the $X$ axis is vaccination fraction $f$.

The effects of three vaccination strategies on the over-connected network are shown in Fig. 7. In the travel-based vaccination strategy, removing a few inter-community travelers is not able to significantly reduce the size of MCC (Fig. 7.a). However, individuals still have a large number of direct contacts (Fig. 7.b). The results imply that removing only a few inter-community travelers fails to break the network into small isolated components. The reason is that most nodes in the over-connected network are robustly connected by redundant links. Disease can still be transmitted freely in a large-size MCC and spread fast through redundant links. Conversely, the contact-based vaccination strategy greatly reduces the number of direct contacts by a very low vaccination fraction (Fig. 7.b), although it has little effect on the size of MCC (Fig. 7.a). The results imply that most individuals remain connected, but more links are needed to connect a pair of individuals (a long path length). Since individuals only have a few direct contacts, the likelihood of infection is largely reduced, and disease transmission is slowed down. Therefore, the contact-based vaccination strategy outperforms the other two in the over-connected network.

![Graphs showing the simulation results for three vaccination strategies.](image)

Fig. 7 Two network parameters as a function of $f$ for three vaccination strategies in an over-connected network

The spatial patterns of infection
The spatial patterns of infection produced by the three vaccination strategies are also investigated under the two network scenarios. To make the illustration legible, 2500 individuals are simulated. In the under-connected network, the random vaccination strategy results in a great number of infected individuals (Fig. 8.a). These infected individuals are widely distributed over space. The contact-based vaccination strategy causes fewer infected individuals, but the infections are still widely spread (Fig. 8.b). Compared to the previous two, the travel-based vaccination strategy not only minimizes the total number of infected individuals, but also confines disease transmission within a small geographical area (Fig. 8.c).

![Spatial patterns of infection](image)

(a) Random  (b) Contact-based  (c) Travel-based

Fig 8 illustrates the spatial patterns of infection in the under-connected network produced by three vaccination strategies, given \(N=2500, p=8\%\) and \(f=5\%.\) The “blue-to-red” colored circles represents the time, at which a new infection occurs, with blue indicating the first day of an epidemic and red indicating the last day of the epidemic.

In the case of the over-connected network, the random vaccination strategy fails to control the total number of infected individuals and prevent the widespread of disease (Fig. 9.a). The contact-based vaccination strategy minimizes the number of infected individuals, but the infections are still widely distributed over space (Fig. 9.b). The travel-based vaccination strategy causes more infected individuals than the contact-based vaccination strategy. However, the infections are highly clustered, and disease transmission is limited in space (Fig. 9.c).

![Spatial patterns of infection](image)

(a) Random  (b) Contact-based  (c) Travel-based

Fig. 9 illustrates the spatial patterns of infection in the over-connected network produced by three vaccination strategies, given \(N=2500, p=16\%\) and \(f=10\%.\) The “blue-to-red” colored circles represents the time, at which a new infection occurs, with blue indicating the first day of an epidemic and red indicating the last day of the epidemic.

5 Conclusion and implications
This paper focuses on the issue of individual mobility in disease transmission and control, which has not been well addressed. The presented epidemic model combines the local infection among individuals in a community with long-range infections by inter-community travel. The
SIR epidemics on the network demonstrate the profound effect of individual mobility on disease spread. Since contacts among individuals are highly localized, inter-community travelers are the key to bridging the disease transmission from one community to another. Only a few inter-community travelers are needed to support a large-scale epidemic. The simulation results suggest that individuals’ travel behaviors should be taken into consideration in vaccination.

Three vaccination strategies are simulated based on this network. The random vaccination strategy is the least efficient strategy, because it cannot significantly reduce both the network connectivity and the average number of direct contacts. This is consistent with the established results that the random vaccination strategy only works when the vaccination fraction is above 80% (Pastor-Satorras and Vespignani 2001, Cohen et al. 2003). The contact-based vaccination strategy fails to reduce the connectivity of a network. But it significantly cuts down the direct contacts of individuals. On the contrary, the travel-based vaccination strategy produces little effect on the direct contacts of individuals. But it effectively breaks the entire network into isolates communities. Given limited vaccine supplies, both travel-based and contact-based vaccination strategies perform better than the random vaccination strategy. The travel-based vaccination strategy exhibits the highest efficacy in an under-connected network. This strategy would be preferable in the rural areas, where only a few individuals travel between small towns on a daily basis. On the other hand, the contact-based vaccination strategy is the most efficient strategy in an over-connected network. This strategy would be preferable in controlling disease spread in metropolitan areas, where frequent travels happen every day between suburban and urban areas.

In practice, an optimal vaccination strategy should consider trade-offs between the efficacy and implementation (Gomez-Gardenes et al. 2006). The random vaccination strategy is much easier to implement, because no information is required about the population. But it produces the lowest efficacy in disease control. The contact-based vaccination strategy could achieve higher efficacy, but it is difficult to implement because of two reasons. First, identifying the highly connected individuals requires the information about every individual in a social network, which is often impossible (Holme 2004). Second, the direct contacts of an individual are hard to be well-defined, since this information is highly dependent on subjective judging (Cohen et al. 2003). Compared to previous two strategies, the travel-based vaccination strategy is much more practical because of four reasons. First, if the vaccine supplies are sufficient, the travel-based vaccination strategy could achieve similar efficacy to the contact-based vaccination strategy. Second, the travel-based vaccination strategy can confine the spatial spread of the disease, and minimize the affected areas. Third, in health surveillance, the travel distance and frequency of an individual would be more straightforward to be defined than the number of direct contacts. Lastly, the travel-based vaccination strategy would be easier to implement, because vaccination stations can be set up at inter-community transport hubs, such as the bus terminals and subway stations.

This research is a pilot study of disease spread and control in a hypothetical society with mobile individuals. The preliminary results suggest that the addition of non-traditional data sources, such as the regional travel volumes and patterns, may provide useful information for public health decision making. This research also has three limitations. First, infection status does not affect individual mobility. In other words, individuals keep traveling even if they are infected. In reality, an individual may change travel behavior patterns if they are sick, for example, staying at home. The behavioral responses of an individual to an epidemic need to be
modeled. Second, the probability of inter-community travel only depends on the geographical distance. Other factors, such as the population of a community and characters of regional transportation networks, may also affect the travel between communities. More environmental factors should be considered. Third, the multi-destination travel of an individual is not modeled in this research. An individual who travels to a community must return directly to the home community. A multi-tier model is needed to account for individual’s travel between several locations. In the future research, these limitations will be accounted for in a more sophisticated model that employs census data, workplace data, land use data, and behavior survey data, etc. This future model would reflect human behaviors and contacts within a real society, and thus provide more realistic predictions and suggestions for public health.

References


