

# Modeling and Simulating Human Vaccinating Behaviors On a Disease Diffusion Network

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## Abstract

As human is the host of disease infection, its social interactions and vaccinating behaviors influence the dynamics of disease spreading. Previous disease diffusion models are mainly based on the homogeneous mixing assumption, which assumes that individuals in population are identical to each other in terms of disease infection. This assumption ignores inherent heterogeneities in both human contact patterns and individuals' possible behavioral choices. By comparison, we design a disease diffusion model, in which a SIV disease model transmits on a social contact network with scale free topology. We assume that each individual in population will make their self-interest decisions, vaccinating or not, according to the perceived payoff of different choice. Under the AOC modeling framework we incorporate human decision making features, e.g. self-interest choice, following neighbors, panic irrationality, etc, into individual's behavioral sets, and observe how the individual-level decision making behaviors can directly determinate the global-level disease diffusion dynamics and inversely how the disease spreading influence individuals' vaccinating choices.

## 1. Introduction

In recent years, several serious epidemic outbreaks show that disease diffusion is no longer confined within a local region but involved every corner of the world. These epidemic outbreaks share some common complex characteristics, such as quick spreading through continents, intense outbreak in a certain population communities, unexpected lower new infection case or even sudden disappearance [1][2]. How to characterize or even predict these complex disease diffusion patterns is critical important and urgent, for we do not know when and where a new epidemic attack will happen.

However, even armed with the most progressive biochemistry theories and brilliant innovations of modern biotechnology, it is still hard to trace the expansion of disease spreading.

Based on the analysis of epidemic spreading datas, these complexities should be blamed to the combination of disease infections and human social contact behaviors. Human long range travels facilitate the disease spreading cross nations or even continents; individuals' vaccination attitude or self-interest behaviors will greatly influence the potential disease diffusion. Interactions between individuals are both the infection mediums and the information exchange channel. Hence, the problems of epidemic spreading are involved both the macro disease diffusion dynamics and micro human behavioral patterns.

How to understand the relationship between heterogeneities of human social interactions and disease diffusion dynamics is one of the most prominent challenges in epidemic spreading research. The previous analysis of disease diffusion is mainly based on statistical model and differential equations, e.g. homogenous mixing assumption, assuming that individuals in a population have the same probability to contact with each other and thus have the equal chance to be infected by infectious ones [3][4]. These assumptions failed to reveal the complexity in both diffusion dynamics and individual behavioral heterogeneities and thus obscure the veiled correlation between local human individual behaviors and global epidemic spreading dynamics, which we can call it local-global relationship for short.

To analyze the local-global relationship, a methodology called Autonomy-Oriented Computing (AOC) provides a fundamental framework to investigate the emergent complex patterns in epidemic spreading system. AOC emphasize the modeling of autonomy in the entity of a complex system and designing the self-organization mechanism of them to achieve a global level emergent dynamics. In this study, we will build a multi-agent system model following the modeling framework of AOC. In our model, we present the disease infection system as an autonomy agent system which is located on a social contact network with a scale free topology. For the artificial behavior construction, we specify the individuals' vaccinating decision making mechanisms and individual interaction rules. Thus, based on the performance measurement, we can investigate the

relationship between the agents' local behaviors and the global dynamics of disease diffusion process.

The reminder of this paper is organized as follows: section 2 gives a basic formulation structure of our simulation model. Section 3 formulates a social contact network with a scale free topology. In Section 4, we introduce the SIV disease diffusion model to represent close contact disease transmission. Section 5 designs a behavior mechanism for individual decision making. Finally, the paper is concluded in Section 6.

## 2. Basic Formulation Structure

As mentioned above, the goal of this study is to design a simulation model which can examine the relationship between individuals' local behaviors and global disease diffusion dynamics.

The basic formulation structure includes the following parts, as shown in Figure 1:

1. Social contact network. This network, in which nodes stand for autonomy agents and edges characterize contact, represents the heterogeneity in individuals' neighborhood interactions.
2. Local decision making mechanism. In each time unit, individual will make a vaccination decision based on three concerns: (1) respective payoff of vaccinating or not, (2) history records of vaccination decisions, (3) environmental evaluations.
3. Disease infection model. Infectious disease can stochastically spread along edges of connected individual pairs in terms of interaction quality and vaccination decisions.
4. Global characteristics of disease diffusion process. These Global features include (1) Population immunization patterns, which characterizes individuals' decisions of vaccination in population level, (2) Epidemics spreading dynamics, which reflect the individuals' infection state on the population communities.

Thus, we can investigate the coupling relationship between local individuals' behaviors and global epidemics spreading dynamics.

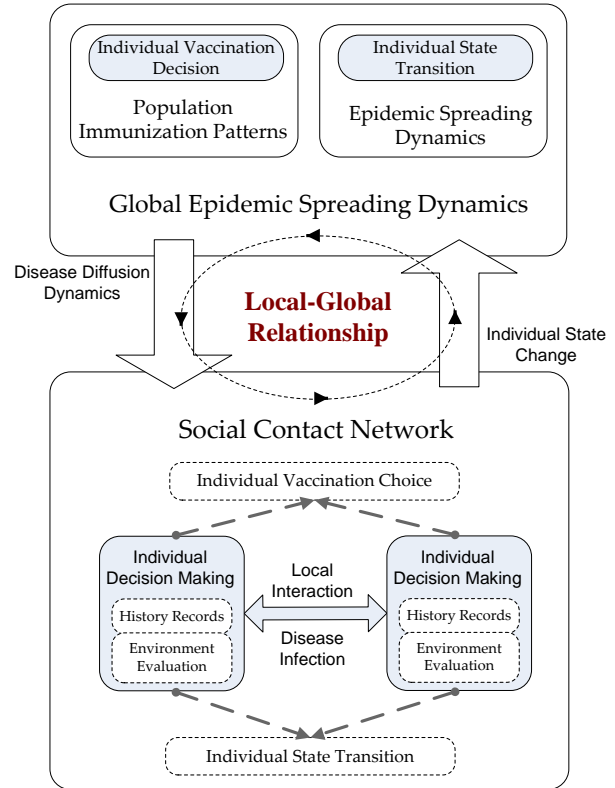


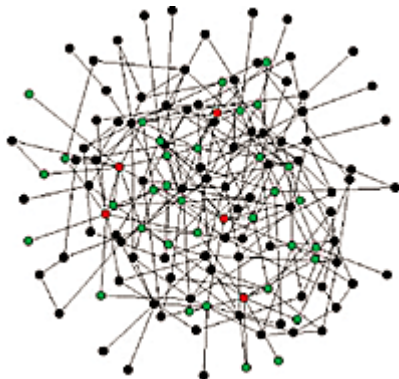
Figure 1, Basic formulation structure of epidemic spreading model

## 3. Social Contact Network

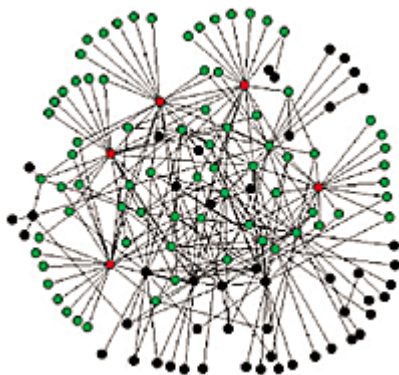
Many epidemics spreading through human populations are mainly based on individuals' physical interactions. These individual level interactions can be thought to form a network with nodes, standing for hosts, and links, representing interactions. During an epidemic outbreak, the spreading of individuals' infection can be viewed as disease diffusion along network links. So the features of human contact pattern can be interpreted as the structural complexity of social contact network.

To build a contact network model, the statistical data are needed to exploit the properties of real human interaction patterns. Many progresses have been achieved, such as tracing all infected individuals and their contacts during or following an outbreak [10], surveying individuals in populations [11] and using census [12], and social characteristic [13] and so on. Among all these properties of real human contact patterns in epidemic spreading process, scale free network draws more and more concerns. Scale-free network is characterized by degree distributions which follow a power law distribution meaning that a small fraction of nodes have highly connected edges [14]

(Figure 2.b). Scale-free properties have been found in many fields, such as information technology (e.g. the Internet, the World Wide Web) [15][16] and biological systems (e.g. metabolic, protein interactions, transcription regulation and protein domain)[17~21].



(a) Random Network



(b) Scale Free Network

Figure 2, In the random network, the five nodes with the most links (red) are connected to only 27% of all nodes (green). In the scale-free network, the five most connected nodes (red) are connected to 60% of all nodes (green). (Source Link: [Scale-Free Networks](#))

In this study, a social contact network explicitly represents individual host interactions which are the medium for epidemic spreading. In this network, a node represents an individual host which might be infected by neighbors or infect its neighbors; an edge between two nodes represents an interaction relationship that is a disease transmission path; the weight value of an edge can be interpreted as the quality of individual interaction. A node's degree is the number of edges attached to it and the degree distribution of a network is the frequency distribution of degrees throughout the entire population, which is a reflection of the heterogeneity of individuals contact patterns.

This social contact network is medium for disease diffusion and with a scale free topology to characterize the individuals' contact pattern. It will focus exclusively on the epidemiological impact of the heterogeneity of contact pattern, although other structural characteristics of network, such as node clustering, community structure, or degree correlation, are also important factors to influence the disease diffusion process. For another aspect, the network model is also assumed to be a static network, which means the contact pattern is supposed to be fixed in the epidemic spreading process.

## 4. SIV Disease Infection Model

In the research of epidemic spreading process, many sophisticated models are proposed to simulate the disease diffusion mechanism, such as SIS/SIR model [22], spatial metapopulation models [23][24]. However these traditional models are mainly based on mixing assumption and differential equations, which characterize the statistical features of disease infection.

In this section, we will describe a SIV disease infection model on the social contact network. A scale free social contact network with  $N$  nodes and average neighbor size  $v$  can be generated under the preferential attachment rule [14]. We assume that individual nodes have three possible states in disease infection process, susceptible state (S), infected state (I) and vaccinated state (V) (Figure 3). The disease infections are only transmitted through neighborhood links that the susceptible individual can be infected by its direct infectious neighbors and infected nodes can transmit infection to its direct neighbors. If the individual is vaccinated, so it is safe from disease infection until expiration of vaccination efficacy.

### 4.1. Disease Percolation

In this study, we suppose the disease transmission is a percolation process through the contact network. In each time unit, the infected node will randomly select a direct neighbor to spread disease infection. The probability of a neighbor node being selected  $P_{Trans}$  is proportional to its edge weight value in terms of that of the whole neighbors.

$$P_{Trans(i,j)} = \frac{w_{ij}}{\sum_{k \in neighbor} w_{ik}} \quad (1)$$

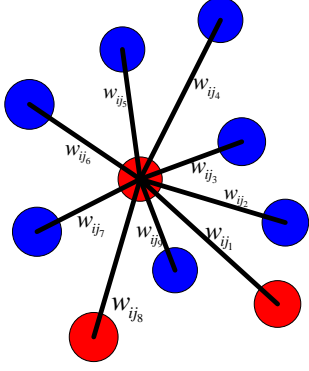


Figure 3, SIV Disease Model

In each time units, if the selected neighbor is in susceptible state, disease infection is successful and the state of the selected one will be changed into infected state; if the selected neighbor is in infected state or vaccinated state, disease infection is failed.

#### 4.2. Individual Infection

If a susceptible node is not vaccinated, it will face the risk of being infected by its infectious neighbors. As we have mentioned the probability of infectious individual  $e_i$  to infect its susceptible neighbor  $e_j$  is  $P_{Trans(i,j)}$ . Thus, a susceptible node  $e_j$  with  $n_{inf}$  infectious neighbors will have a total probability  $\lambda_{inf}$  that node  $e_j$  becomes infected in the current time unit.

$$\lambda_{inf} = 1 - \prod_{i=n_{inf}} (1 - P_{Trans(i,j)}) \quad (2)$$

If a node is infected, the duration of infection can be drawn from a gamma probability distribution function with a mean of  $1/\gamma$  and a variance of  $V_\gamma$  time units, which simulate the difference among population on the demography characteristics. After this infection duration, the infected node can be either died with a probability  $d_{inf}$  as a cost of disease infection, or recovered with a probability  $1-d_{inf}$  to susceptible state without any residual immunity.

Here must points out that the dead infected individual does not means to erase the node from the network. It just represents a possible severe punishment for individual's infection, which is an important factor for individuals' decision making.

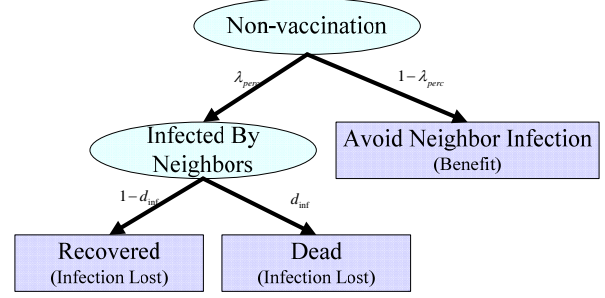


Figure 4, Individual state transition without vaccination

#### 4.3. Individual Vaccination

If the node adopts vaccination choice, it will face death risk caused by the side effect of vaccination. We assume that the death possibility caused by vaccination is  $d_{vac}$ , and the efficacy of the vaccine to provide successful protection from disease infection is  $\varepsilon$ . If the vaccination do not have any side-effects but still fail to immunize the node, the current node will keep in the susceptible state faced with the risk of disease infection.

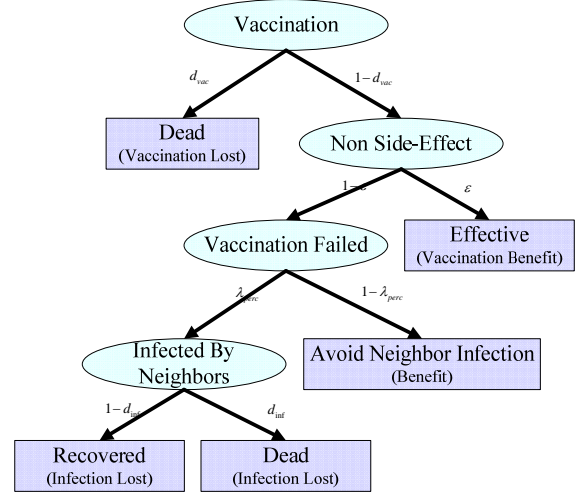


Figure 5, Individual state transition with vaccination

### 5. Individual Vaccinating Decision Making

In the disease infection and vaccination model, each individual face with two kinds of risk, risk of disease infection, and risk of vaccination's side-effect or failure. As the vaccination coverage increase, the infection risk is decreased relatively due to the herd immunity. Hence, the incentive for individual to vaccination is also reduced, which in turn will accelerate the disease transmission. This effect of individuals' behavior on disease diffusion

dynamics can be treated in game theoretical analyses of infection dynamics and vaccination choice.

In this section, we will incorporate individuals' vaccinating behaviors into disease infection model. And the following four aspects will influence individuals' decision making:

1. Perceived payoff value of vaccination and non-vaccination on current status.
2. Individuals' history decision making experience.
3. Environment Evaluation for global disease diffusion dynamics and local neighbors' statuses.
4. Individuals' biased preferential choice based on the above three criteria.

By incorporating individual behaviors into disease infection model, we can observe the correlation between local individual actions to the global epidemic dynamics.

### 5.1. Perceived Payoff Functions

In a given time unit, a susceptible individual can choose either vaccination or non-vaccination based on payoff value  $P_v$  (vaccination) and  $P_N$  (non-vaccination) relatively. Individuals will weigh the benefits of vaccinating, such as immunization protection from neighborhood infection but with small vaccine death risks and some probability vaccine failure, against the benefits of non-vaccinating, such as eliminating risk of vaccine but with possibly infection risk.

*Payoff value  $P_N$  for non-vaccinating*

If the individual does not vaccinate, it can be either infected with perceived infection probability  $\lambda_{inf}$  or not with probability  $1-\lambda_{inf}$ . If the susceptible individual escapes the neighbor infections the payoff value will be  $L_{sus}$ . If the current susceptible individual is infected, and after its infection duration it is died with probability  $d_{inf}$ , leaving the payoff value in this step zero. If the individual survives from infection with probability  $1-d_{inf}$ , the payoff value for this circumstance is  $L_{inf}$ . Hence, the overall payoff value of non-vaccinating individual choice is

$$P_N = (1-\lambda_{inf}) \cdot L_{sus} + \lambda_{inf} \cdot [(1-d_{inf}) \cdot L_{inf}] \quad (3)$$

*Payoff value  $P_v$  for vaccinating*

If a person chooses to vaccinate, then either the vaccine has vital side-effect with probability  $d_{vac}$ , or not with the relative probability  $1-d_{vac}$ . We also suppose that the vaccine without side-effect will be truly efficacious to

provide immunization with probability  $\varepsilon$ , or fail to protect individuals just leaving it still in the susceptible state. If the individual successful vaccinate itself, the payoff value in this step is  $L_{vac}$ . If the individual choose vaccination but the vaccine has neither side-effect to death nor efficacy to immunization, the relative payoff in this circumstance is the same the non-vaccinating individuals. Thus, the overall payoff value for vaccinating individuals is

$$P_V = (1-d_{vac}) \{ \varepsilon L_{vac} + (1-\varepsilon) \cdot [(1-\lambda_{inf}) \cdot L_{sus} + \lambda_{inf} \cdot [(1-d_{inf}) \cdot L_{inf}]] \} \quad (4)$$

In summary, there are four payoffs for individuals' decision.

1. If individual is died either for the disease infection or for side-effect of vaccination, the payoff is zero.
2. If the susceptible individual escapes from disease infection, the payoff is  $L_{sus}$ ,
3. If the infected individual recovers from disease infection, the payoff is  $L_{inf}$ ,
4. If the susceptible individual is successful vaccinated, the payoff is  $L_{vac}$ .

Based on the common sense, it is reasonable to expect that  $L_{inf} < L_{sus} < L_{vac}$ , for individual benefit of successful vaccination is the biggest, and that of recovered individual is the least, the benefit of susceptible individual is in the middle.

### 5.2. History Experience

Each individual in the social contact network has a record of its past experience of vaccination decision making. Individual will evaluate the necessary of vaccination based on the real efficacy of past vaccination memory.

There are four kinds of records for each individual's to vaccination adoption.

1. Individual is vaccinated, and successfully defend infection attacks at least once.
2. Individual is vaccinated, but no infection attack happens in the duration of vaccine.
3. Individual is non-vaccinating, and successfully escapes from infection attacks.
4. Individual is non-vaccinating, but infected by its infectious neighbors.

We assume each of the records above have a payoff value  $h_{vac}^+$ ,  $h_{vac}^-$ ,  $h_{non}^+$ ,  $h_{non}^-$  respectively. We also suppose that  $h_{vac}^+ = -h_{vac}^-$ ,  $h_{non}^+ = -h_{non}^-$ , which are the decision judgment based on the disease diffusion result. Hence, in

time unit  $k$  the historical evaluation of vaccinating behaviors  $H_{vac}(k)$  (vaccination history) and  $H_{non}(k)$  (non vaccination history) can be updated as following:

$$H_{vac}(k) = \lambda_{decay} \cdot H_{vac}(k-1) + h_{vac}(k) \quad (5)$$

$$H_{non}(k) = \lambda_{decay} \cdot H_{non}(k-1) + h_{non}(k) \quad (6)$$

$\lambda_{decay}$  is decay ratio, meaning that the most recent records have a bigger influence on individuals' decision making.

### 5.3. Environment Evaluation

We assume that each individual has a full ability to communicate with its direct neighbors, but a confined global information achievement. For local interaction, the individual can detect its neighbor's state and vaccination choice of last time. For global information, we suppose that individuals can get the global infection rate as a severity estimation criterion. Thus these environment evaluation parameters will influence individuals' vaccination decision making process.

$r_{vac}$  is the proportion of the vaccinated neighbors to all neighbors.

$$r_{vac} = \frac{n_{vac}}{n_{neighb}} \quad (7)$$

$r_{inf}$  is the proportion of the infected neighbors to all neighbors.

$$r_{inf} = \frac{i_{vac}}{n_{neighb}} \quad (8)$$

$R_{inf}$  is the infection rate in the global network.

$$R_{inf} = \frac{I}{N} \quad (9)$$

### 5.4. Individual Biased Preference Rules

In each time unit, individuals' vaccination decision making is based on three parts (Figure 5):

- (1) Payoff function  $P_V$  and  $P_N$ ;
- (2) History records  $H_{vac}$  and  $H_{non}$ ;
- (3) Environment estimation  $r_{vac}$ ,  $r_{inf}$  and  $R_{inf}$ .

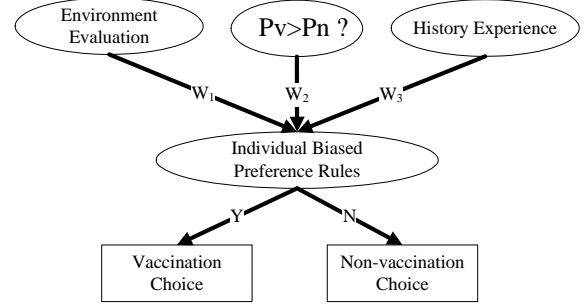


Figure 6, Individual Biased Preference Rules

We assume some biased preference rules to simulate human's irrational decision making behaviors.

- Individuals are more inclined to rely on their history experience.
- Individuals are likely to simulate its neighbor's behaviors.
- Pandemic scare is based on individuals' irrational estimation.

Thus, based on the above biased preference assumptions, we can design the decision making functions as following:

$$E_{vac}(k) = P_V(k) + \xi_i^1 \cdot H_{vac}(k) + \xi_i^2 \cdot [tg(\frac{\pi}{2} \cdot r_{vac}) + tg(\frac{\pi}{2} \cdot R_{inf})] \quad (10)$$

$$E_{non}(k) = P_N(k) + \zeta_i^1 \cdot H_{non}(k) + \zeta_i^2 \cdot [tg(\frac{\pi}{2} \cdot (1 - r_{vac})) + tg(\frac{\pi}{2} \cdot (1 - R_{inf}))] \quad (11)$$

If  $E_{vac}(k) > E_{non}(k)$ , the current individual will adopt the vaccination choice, or vice versa.  $\xi_i^1$   $\zeta_i^1$  are parameters to modify the influence of history experience for vaccination and non-vaccination.  $\xi_i^2$   $\zeta_i^2$  are variables to control the impact of environment estimations.

Function  $tg(\frac{\pi}{2} \cdot r_{vac})$  is designed to simulate individual's neighbor following feature. If the proportion of vaccinated neighbors is increased the current will more inclined to adopt vaccination. Function  $tg(\frac{\pi}{2} \cdot R_{inf})$  tries to describe the potential epidemic scare. If the global infection rate is near 100%, each individual will irrationally adopt vaccination instead of balancing payoff gains.

## 6. Conclusions

It is now well recognized notion that human's behaviors will influence the epidemic spreading. What kinds of relationship coupling the local individual behavioral patterns to the global disease diffusion dynamics is still obscure. Aimed to investigate this core problem in epidemic control, we design a SIV infection model incorporated with complex human behaviors under AOC modeling framework. In this model, we try to investigate what kinds of impact the human behavior will impose on the disease diffusion process, such as self-interest choice, following neighbors, panic irrationality, etc, and inversely what kind of influence will the epidemic dynamics have on individuals' decision making, e.g. mass infection case or scare infection rate. Based on this model, we expect a clear picture to portray the skeleton about the local global relationship in epidemic spreading process.

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