A hybrid model for HIV transmission among men who have sex with men

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A B S T R A C T

AIDS has spread throughout the world for decades. Men who have sex with men (MSM) is the harder-hit sector of sexually transmitted diseases due to their physiological characteristics. However, because homosexuals suffer discrimination and exclusion in many aspects, the relevant data about the spread of HIV in this group are scarce. Therefore, building a network model to study and analyze this problem can provide valuable reference for the prevention of HIV. Complex network can establish fixed edges between vertices, and ignores the spatial characteristics of the network. These two aspects are exactly what cellular automata are good at, but cellular automata are rarely used in the problem of HIV propagation among MSM populations. Therefore, we combined the advantages of these two methods, and got a new hybrid model. It may provide us with some theoretical factors that affect the spread of HIV and provide guidance for the actual prevention work.

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1. Introduction

1.1. HIV transmission among MSM

Since the first case was discovered in 1981, AIDS has gradually developed into a worldwide infectious disease. According to the data from UNAIDS, by the end of 2015, there have been 36.7 million people living with HIV, including 2.1 million people newly infected (UNAIDS, 2016). Studies show that men who have sex with men (MSM) is at 19 times more risk of contracting HIV than normal sexual intercourse (amfAR, 2008). Thus MSM has been the main group faced with the risk of getting infected with HIV. In 2015, the significantly increasing HIV prevalence among MSM has resulted in 25% of the newly infected HIV in China and more than 66% of the newly infected HIV in Shanghai (Shanghai Municipal Commis, 2015). Recent years, a series of new problems such as the openness of sexual concepts, the rapid development of the Internet and the proliferation of new-type drug have brought enormous challenges to the prevention of AIDS among MSM population. Therefore, it is necessary to simulate the contagion of HIV among MSM through academic models. What’s more, we can find out the factors influencing...
this process and predict the transmission of HIV among MSM, providing theoretical bases for the formulation of relevant policies.

1.2. Relevant models

Compartment model such as SIR is the simplest model of the spread of a disease over a network. This model reflects the classification ideology. For example, SIR divides the population into three classes: susceptible (S), infective (I) and recovered (R). It can represent the most fundamental dynamic characteristics of epidemics. However, diseases can only spread between those individuals who have physical contact of one sort or another, and the structure of the contact network is important to the pattern of development of the disease (Bailey, 1975; Sun & Gao, 2007).

At present, the study of infectious diseases includes mathematical model, cellular automata model, complex network and dynamic network model, and dynamic network models are used more and more widely, because the dynamic network model considers the individual autonomous behavior and the individual complex network, it is more in line with the reality social network.

Complex networks are widely used methods in the study of epidemics. They usually refer to network models with topological structure in network theory. Complex networks don’t care about the size, location, shape, function, or way of connection between vertices in the network. Instead, they just pay attention to how many vertices there are and whether there is an edge between two random vertices in the network (Newman; Xia et al., 2008; Lou et al., 2009; Ababou et al., 2011).

Cellular automata are dynamic systems with discrete time and space. Each cell scattered in the regular grid takes a finite discrete state and updates itself synchronously in accordance with the defined local rules per unit time. A large number of cells form the evolution of the system through simple interactions. However, regardless of characteristics, cellular automata ignore the fact that social phenomena emerge from regular and frequent human interaction. In other words, they emphasize epidemic characteristics (e.g., transmission, mortality, and recovery rates) at the expense of population structure, social space, heterogeneity, localization, and interaction (Ahmed & Elgazzar, 2001; Huang et al., 2005; White et al., 2007).

Dynamic network model based on Agent (Li and GuihongZhang, 2012), for example, rules on the network nodes is a two-dimensional motion to the surrounding nodes at a certain probability space, to represent the movement of the individuals in the realistic society, but this model is more suitable for air or more directly contact transmission way of disease. HIV’s transmission mode is a special, it does not spread easily from one infected person to another by moving around, most infections are caused by close contact, therefore the provisions of the individual movement is not suitable.

1.3. Existing researches

In the current field of epidemiology, simulation approaches for sexually transmitted diseases such as HIV are still dominated by complex networks. For example, Vieira IT built a network model that studies different topological structures using the small world network as the basic framework (Vieira et al., 2010). Xie L established a network model based on scale-free networks and added sex role preference into it (Xie & Yao, 2013). After that, Shen ZF took the addition of new vertices and removal of dead vertices into account based on Xie’s model (Shen et al., 2017). Cissé B studied the impact of neighborhood structure on epidemic spreading by means of cellular automata approach (Cissé et al., 2013). López L addressed population heterogeneity and distribution in epidemics models using a cellular automata approach (López et al., 2014). Athithan S created a dynamic cellular automata based on epidemic spread model for population in patches with movement (Athithan et al., 2014).

On the one hand, using complex network models alone to simulate real networks make some problems. First of all, the edges between vertices in complex networks won’t change once established which obviously not agree with reality. A study in 2001 in St Petersburg, Russian Federation, found that 22.7% of MSM reported selling sex (World Bank, 2011). In Paraguay, 29% of MSM indicated that they were currently engaging in selling sex (Chinaglia et al., 2008). It is obvious that causal sexual relationships are quiet general among MSM. Next, the subjects of complex networks tend to be edges instead of nodes, and the rules of evolution are so simple that the characteristics of vertices affecting epidemic propagation can’t be obtained. On the other hand, cellular automata are able to create random edges between vertices during every unit time, but they can’t keep these edges steady. What’s more, cellular automata have difficulty in showing universal laws of epidemic transmission.

Complex networks and cellular automata both have their advantages and drawbacks. In this paper, we create a hybrid model consisting of these two models. We define a node’s influence scope in this model and search for qualified object that can be infected in the scope, therefore, simulation efficiency can be improved.

2. Methods

The overall idea of this model is: matrix of a line array is used to describe each node in the network model, each node is individual for each simulation. Before simulation, the parameter value of each node is set the initial state (in the actual simulation, there is no special requirement that each state is generated according to pseudo-random function rand), the parameter value represents each individual infection status and behavior preference. In this paper, all nodes are divided into two categories: random relation nodes and stable relation nodes. The dynamic simulation of random relation nodes is similar to that of cellular automata, and the simulation of stable relation nodes is based on complex network model.
2.1. Network structure

In our model, each vertex represents an individual. It is described by a matrix in algorithm implementation. The matrix is shown as below:

\[
\begin{bmatrix}
ID & t & x & y & C & P & S \\
\vdots & \vdots & \vdots & \vdots & \vdots & \vdots & \vdots \\
\vdots & \vdots & \vdots & \vdots & \vdots & \vdots & \vdots \\
\end{bmatrix}
\]

The meaning of each variable in the array is shown in Table 1. Individuals who do not have stable relationships tend to have random contacts with others and are determined only by evolution rules of each step. As to vertices with stable relationships, they will contact with the same vertices that have stable relationships with them. These stable relationships are implemented by adjacency matrix as follows in our algorithm:

\[
\begin{bmatrix}
1 & \ldots & i & \ldots & j & \ldots & n \\
0 & \ddots & \vdots & \vdots & \vdots & \ddots & \vdots \\
0 & \ddots & a_{ij} & \ddots & \vdots & \ddots & \vdots \\
\vdots & \ddots & \vdots & \ddots & \ddots & \vdots & \vdots \\
0 & \ddots & \vdots & \ddots & \vdots & a_{ji} & 0 \\
\vdots & \ddots & \vdots & \ddots & \ddots & \vdots & \vdots \\
0 & \ddots & \vdots & \ddots & \ddots & \ddots & 0 \\
\end{bmatrix}
\]

The matrix is \( n \times n \) when there are \( n \) vertices in the network. The value of \( a_{ij} \) is:

\[
a_{ij} = a_{ji} = \begin{cases} 
0 & \text{i and j don’t have a stable relationship} \\
1, 2, \ldots, T_s & \text{i and j have a stable relationship}
\end{cases}
\]  

(1)

When vertex \( i \) and \( j \) have a stable relationship, the value of \( a_{ij} \) means existing time steps of this relationship. Vertex matrix, adjacency matrix and evaluation rules construct the network model of our project.

2.2. Simulation process

Cellular automata and complex networks are both insufficient in some aspects to simulate the propagation of HIV among MSM. Therefore, we divide all the vertices into two categories: vertices with casual relationships and vertices with stable relationships. The former have evaluation rules just as cellular automata while the latter are performed through the method of complex network.

Firstly, all the parameters shown in Table 2 should be set up before simulation. Then we need to set up the initial conditions of all the vertices in the network through random functions or according to specific requirements. When the dynamic loop begins, the two types of vertices with contrary tendency of relationships will abide by different evolution rules.

On the one hand, vertices with tendencies of causal relationships evolve under rules like cellular automata. In a certain step, the infected individuals are screened out and delineated within a predetermined vicinity of them. Within this range, these infected individuals will temporarily contact with other individuals meeting the requirements listed as below:

1. Equally with tendencies of causal relationships;
2. Susceptible and uninfected;
3. Having suitable sex role preference (refer to Table 3).

Table 1

| Attribute | Description                               | Value          |
|-----------|-------------------------------------------|----------------|
| ID        | Unique serial number of each vertex       | \( 1 - N_0 \)  |
| \( t \)   | Times steps after a vertex gets infected  | \( 1 - T_0 \)  |
| \( x \)   | The ordinate of a vertex in the grid      | \( 0 - L \)    |
| \( y \)   | Epidemiological condition of each vertex  | 0(susceptible), 1(infective), \(-1\)(dead) |
| \( C \)   | Sex role preference for MSM               | 0(bottom), 1(versatile), \(-1\)(top) |
| \( S \)   | The tendency of nodes to keep stable relationships | 0(no), 1(yes) |
On the other hand, vertices with tendencies of stable relationships evolve under rules of complex networks. In a certain step, the first thing is to screen out infected vertices. Then examine the relation conditions of them. If an infected vertex has not built a relationship with any other vertex, then search out a nearest vertex meeting the requirements listed as below:

1. Equally with a tendency of stable relationship;
2. Susceptible and uninfected;
3. Having suitable sex role preference (refer to Table 3).

When two vertices have a stable relationship with one another, as long as this relationship exists, they will always contact with the same object in each subsequent cycle.

After contact, the infected vertices will pass HIV to their partners with time-dependent probability shown in Table 3.

The variable \( t \) means time. \( p_A \) is the possibility that infected individuals at top positions transmit HIV to uninfected ones at bottom positions. \( p_B \) is the possibility that infected individuals at bottom positions transmit HIV to uninfected ones at top positions.

At the end of every step, the number of infected vertices will be counted and the length of their infection will be added with a unit time. If an individual’s infection time reaches the death time \( T_d \), it will be removed from the network and new vertices will be added to the network at the same time. As to vertices with stable relationships, the length of their relationships’ existence will also be added with a unit time. When these relationships’ existing time run up to preinstalled time \( T_s \), they will be deleted. In particular, if one side of a stable relationship is removed from the network, this relationship will also be removed and the other one will look for connection again in the next step.

A more vivid depiction of this process is shown in Fig. 1. In view of conciseness, the removal of dead vertices, the addition of new vertices and the deletion of stable relationships are not shown in the figure. Fig. 3 magnifies the relationships between vertices in Fig. 1 at a particular time in a simulation process. Fig. 2 depicts the social relationship development principle of an infected person in the model.

3. Results

All the parameters in Table 2 have their corresponding realistic meaning. How their effect on the simulation results of the model is the main problem that we will solve by this model. In particular, how the stability of relationships between individuals and the spatial distribution characteristics influence the simulation results is the focus of this study, what is previous searches have ignored. Fig. 4 shows the flow chart of HIV transmission among MSM. We use variable-controlling approach to keep the other parameters constant while give different values to the target parameters. Then display the

### Table 2
Parameters of the network.

| Parameters | Description | Value |
|------------|-------------|-------|
| \( N_0 \) | The total of vertices in the network | user-defined |
| \( L \) | The length of the square mesh region | user-defined |
| \( R \) | The maximum distance between two vertices that have relationship with each other | user-defined |
| \( T_0 \) | The total duration of the simulation | user-defined |
| \( T_d \) | The number of steps for the death of an infective vertex | estimate |
| \( T_s \) | The average steps for the stable relationships between individuals | user-defined |
| \( P_0 \) | The percentage of infected individuals at the initial stage | \( 4.9\% \) (Zhu et al., 2004) |
| \( P_t \) | The percentage of top preference in the network | \( 34\% \) (Yee, 2002) |
| \( P_b \) | The percentage of bottom preference in the network | \( 37\% \) (Yee, 2002) |
| \( P_v \) | The percentage of versatile preference in the network | \( 29\% \) (Yee, 2002) |
| \( P_s \) | The percentage of individuals preferring to build stable relationships with others | user-defined |

### Table 3
Different types of the HIV transmission among MSM.

\[
\begin{align*}
p_A &= 1.017 \times 10^{0.0094t - 2} \\
p_B &= 5.3702 \times 10^{0.009t - 3} \\
p_C &= \frac{p_A + p_B}{2} 
\end{align*}
\]

| Types | Inclusions | Possibility |
|-------|------------|-------------|
| A     | T → B, T → V, V → B | \( p_A \) |
| B     | B → T, B → V, V → T  | \( p_B \) |
| C     | V → V       | \( p_C \) |

T: top preference, B: bottom preference, V: versatile preference.
results in the same picture so that we can observe the relevant laws intuitively. All the figures shown below use average values of ten times’ simulations.

3.1. The overall simulation results

Fig. 5 is an overall simulation result of the model. It is obvious that the total number descends at the time of 100 months which equal to \( T_d \)’s value. It proves \( T_d \)’s influence on the network model. There are two main factors determining the value of \( T_d \): death time and isolation time. We need reduce the value of \( T_d \) if we want to constrain HIV epidemic among MSM, but that is inhuman. Therefore, the government should introduce relevant policies to make HIV examination universal so that the infected individuals can be isolated from other MSM in sex earlier.

Another thing we can see from Fig. 5 is that the number of individuals with bottom preference has the same trend with the total. It is because transmitting HIV from top to bottom is much easier than that of the opposite, as shown in Fig. 6. It reminds us that individuals with bottom preference need more attention in the prevention of AIDS.

3.2. Influence of the stability of relationships on the network model

There are two parameters that represent the stability of the relationships between individuals, namely, the ratio of individuals with preference of stable relationships \( P_s \) and the average duration of stable relationships \( T_s \).

As shown in Fig. 7, the number of infected MSM tends to descend with the increase of \( P_s \). Fig. 8 shows that \( T_s \) has little effect on the simulation results. Therefore, we speculate that only \( P_s \) represents the stability of the relationships between individuals and it has great influence on the network model.

In reality, an individual has a stable relationship means that he has found a sexual partner and won’t look for other mates in the short term. However, social hostility to homosexuals makes it difficult for them to have open relationships and remain stable for a long time like heterosexual couples. So many homosexuals often keep in touch with multiple sexual partners. What’s more serious, many people in this group choose male sex workers, the high-risk population of AIDS, to meet their physiological demands. Many studies have shown that the widespread prevalence of HIV among MSM is largely due to social
discrimination and cultural hostility to homosexuals. Therefore, it is difficult to control the spread of HIV among MSM before this problem is taken into account and improved, which is shown by simulation results of the model.

Fig. 2. The graph of relationships between infected and uninfected. Infected nodes without the tendency of stable relationship: a range is demarcated near them, and within this range, eligible nodes are screened out for contact; Infected nodes with the tendency of stable relationship: check the connection status of these nodes, if no stable relationship has been established with any uninfected nodes, then find eligible nodes close to this node, and establish stable relationship. For nodes that have established a stable relationship in pairs, they will remain in contact with the same object for as long as the relationship exists in each subsequent loop.
3.3. Influence of spatial distribution characteristics

3.3.1. Global distribution characteristics

The parameter that presents the global distribution characteristics is the side length of mesh region $L$. As depicted in Fig. 9, the number of infected MSM tends to descend with the increase of $L$. We should recognize that the increase of $L$ reduces the density of vertices in the network. In other words, under the same other conditions, the situation of HIV epidemic is more serious in the regions with larger population density. Therefore, these areas need more attention in the formulation of AIDS prevention policies. What’s more, the government had better concern the need of these regions when it comes to allocation of HIV-relevant budget.

3.3.2. Initially infected individuals’ distribution characteristics

In our model, the initially infected individuals account for only a small part of the whole. However, because the dynamic transmission of HIV completely started from this part, the initial distribution of infected individuals also has important influence on simulation results of the model.

In order to show the initially infected individuals’ distribution, we introduce a new parameter $L_d$. As shown in Fig. 10, $L_d$ is the side length of mesh region where the initially infected vertices locate. We can find ‘agglomeration effect’ from both Figs. 10 and 11.

That means if individuals infected or with risks of infection consciously gathered together, the HIV epidemic will be controlled to a certain extent. Therefore, the government should establish more formal centers of activity or online communities. It will benefit not only the HIV patients and carriers of MSM but also the prevention of HIV epidemic on the social level.

3.4. Influence of the sphere of every vertex

We use parameter $R$ to depict the sphere of every vertex. Fig. 12 shows how $R$ influences the transmission of HIV among MSM. We can obviously see that the increase of $R$ facilitates this epidemic.

Nowadays, rapid development of traffic and network socialization allow us to contact with people far away from us. Simulation results of the network model represent that this trend accelerates the transmission of HIV among MSM. The impact on young MSM is especially obvious because they are dependent on Internet very much. Young people aged 10–24...
years constitute one-quarter of the world's population (Population Division of th, 2012). While in 2013, young people aged 15–24 years accounted for an estimated 35% of all new infections worldwide in people over 15 years of age (UNAIDS, 2012). MSM often acquire HIV while quite young—according to studies primarily in countries where the epidemic among gay men...
and other men who have sex with men is significantly higher than among the general population (HIV and aging, 2013). Therefore, it is really necessary to pay more attention to young MSM in the prevention of AIDS.

Fig. 5. The infected numbers of MSM and subpopulations change over time. $N_0 = 10000$; $L = 100$; $R = 2$; $T_0 = 150$; $T_d = 100$; $P_s = 0.5$; $T_s = 72$.

Fig. 6. The possibilities of three types of transmission change overtime. T: top preference, B: bottom preference, V: versatile preference.
Fig. 7. Influence of the ratio of individuals with preference of stable relationships $P_s$. $N_0 = 10000; L = 100; R = 2; T_0 = 150; T_d = 100; T_s = 72$.

Fig. 8. Influence of duration of stable relationships $T_s$. $N_0 = 10000; L = 100; R = 2; T_0 = 150; T_d = 100; P_s = 0.5$.

Fig. 9. Influence of side length of mesh region $L$. $N_0 = 10000; R = 2; T_0 = 150; T_d = 100; P_s = 0.5; T_s = 72$. 
4. Discussion

Complex networks and cellular automata are both important methods to study social problems, and we combine them to construct a hybrid model that simulates the propagation of HIV among MSM. This model has advantages of the above two methods. It considers both random contacts and stable relationships between individuals. The model can also analyze the spatial distribution characteristics of vertices and other network characteristics. What’s more, it is able to respond to HIV-relevant policies so that we can study their influence on HIV epidemic among MSM.

After plenty of simulation, we find that the stability of relationships between individuals, the spatial distribution of vertices and the activity sphere of individuals all have important influence on HIV transmission among MSM. We believe that the individual proportion of MSM population tending to stable relationship $P_s$ is the most important parameter to measure the stability of inter-individual relationship in the model, which greatly affects the simulation results of the network model. And this parameter also has important practical implications. With the decrease of $L$ value, the final number of infections will increase. With the increase of $R$, the number of final infections increases, and the change curve becomes steeper and steeper. The smaller $L_d$, which means the more concentrated the distribution is, the smaller the final number of infected people will be and the flatter the growth curve will be.

Fig. 10. Distribution of infected vertices under different $L_d$. Uninfected vertices are not shown in the picture. The abscissa and ordinate indicate spatial positions of vertices.
The model still has space for improvement. First of all, the actual population of MSM is not an independent and closed network as we have dealt with. Quiet a number of gay men have sexual intercourse or even get married with women according to the survey. In this case, it is not precise to consider the spread of HIV only within MSM. Next, with the deepening of globalization, the population flow between regions is also one of the problems that must be considered. Last but not least, we assume that the total number of vertices in the model remains constant in consideration of computing efficiency. In reality, the Middle East has a large population growth rate while many countries in the Central Europe have negative population growth. It does make sense to improve the model for study of how population growth rate affects HIV epidemic among MSM.

Declaration of competing interest

The authors declare that they have no conflict of interest.

Enclosed is our manuscript ‘A hybrid model for HIV transmission among men who have sex with men’, for consideration by ‘Infectious Disease Modelling’. Complex networks and cellular automata are both important methods to study social problems. However, they both have defects in simulating the transmission of HIV among MSM. We combine them to construct a hybrid model that has advantages of the above two methods and avoids shortcomings of them. It considers both random contacts and stable relationships between individuals. The model can also analyze the spatial distribution characteristics of vertices and other network characteristics. After plenty of simulation, we find that the stability of relationships between individuals, the spatial distribution of vertices and the activity sphere of individuals all have important influence on HIV transmission among MSM.

It is our intention that this mathematical model will provide a new method to study HIV transmission among people and predict epidemic trend with different interference. We hope these results may provide recommendations for the government’s HIV prevention policies.
Human and animal rights: This article does not contain any studies with human participants or animals performed by any of the authors.

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