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Impact of social behaviors on epidemiological models:
A computer simulation on HIV epidemic

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Impact of social behaviors on epidemiological models: A computer simulation on HIV epidemic

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Abstract

The HIV/AIDS epidemic has been a major concern for health department of every government. For no cure has been found yet, the emphasis is on prevention. In order to organize prevention, governments have set up different campaigns that tend to be more or less successful. The way to lead a campaign is strongly related with the cultural background of a population. This difference of background leads to give a model of a social population using different parameters. In this research, we propose to assess the impact of social behaviors on HIV/AIDS epidemic. To do so, we build an agent based computer simulation that implement a model of sexual network and implement also a set of individual social behavior. The objective is to try to reproduce the epidemic curve of HIV/AIDS in the male homosexual community in Taiwan. We want to assess the influence of different policies on the social behavior of each individual and the consequences on the spreading of the epidemic. The purpose of this computer simulation is first to build an artificial social network representative of the high risk homosexual community.

Keywords: Agent model, HIV/AIDS epidemics, MSM, scale free social networks

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1. Introduction

The main motivation to research in the field of transmission of the Human Immunodeficiency Virus (HIV) through populations is probably because of the huge consequences it has on the life of millions human beings. A United Nation report published in November 2004 stated that 39.4 millions of people were living with the HIV and that 4.9 millions of people have contracted the virus in 2004 with more than a 50% increase in East Asia. This report also emphasize the lack of adequate resources and political leadership, especially where the HIV is implanted in stigmatized or marginalized populations like sexual workers, injected drug users and homosexuals.[1]

This paper proposes a computer simulation model based on agents to reproduce an artificial social network having scale free properties. The population studied here is limited to Men who have Sex with Men (MSM) in high risk places like homosexual saunas or bars in Taiwan. The data are provided by the AIDS Prevention and Research Center of National Yang Ming University in Taiwan

Many simulation methods have been developed to address this issue. Most of them are based on statistical research on sexual network properties and follow the general characteristics of the populations without focusing on the individual behavior. Our model is agent based and follows an individual to general approach. Individual agents are able to modify there behavior and create a general tendency which consequences can become relevant in the entire population. Following previous works in sexual networks studies, this model focuses on the links among individual in order to achieve scale free network properties [2] depicting a small world phenomenon.

The article is structured as follow. First of all we are surveying the previous studies in simulation of sexual transmitted diseases. Then we detail the different layers that organize our model. We emphasize on the composition of the social network for it is one of the most important aspect of this research. Afterwards we present the results of the experiments.

2. Previous sexual networks studies

Although different approaches have been implemented for social network simulation, we can classify them into two groups: analytical simulations using a continuous model and network-model based simulations. Analytical simulation tries to provide a model formulated into an integro-differentiable system. Unfortunately the complexity of such a system grows quickly for the analytical representation of multivariable and complex phenomenon of stochastic processes quickly become very difficult to manage in terms of computation and stability of the equations. The second approach, the network-model based simulation, is to see the problem from a different angle and to try to reach a solution step by step by step while affecting the behavior of various objects composing the model. It is not based on an analytical representation, but more on objects representation. This agent based simulation belongs to this category. This type of study is usually split into two parts: the first part deals with the structure and behavior of the population which we are working with; the second part is the intrinsic properties and characteristics of the disease which we are studying.

It is essential to note that in Sexual Transmitted Diseases (STD) simulations, the model of the sexual network is extremely important. The properties and rules that the HIV epidemic follows can be described into a simple model. Therefore we will emphasize on the previous sexual network studies in this section.

Sociologists and statisticians have been studying social networks for more than 50 years. Social Network Analysis bring and important insight on how to conceptualize and model social interactions. The sexual network is one kind of social network. In standard epidemiological models, random interactions among people are often assumed, especially if the medium of transmission is the air. In Sexual Transmitted Diseases, randomness does not stand anymore for sex does not happen by haphazard. Therefore a first approach of in STD simulation was to divide the population into subgroups defined according to various criteria. Those criteria can be age, ethnicity, social economical class, short time or long time partners, heterogenic degrees of sexual activity for instance. [3]

It is easier to deal with a population divided into subgroups, usually referred as core groups, and study the interaction among those groups. Three types of scenario emerge from this model. In the first one, called assortative interaction, most contacts take place inside subgroups; this means that sexually active people have sex with other sexually active people; whereas sexually low active people only have sex with other sexually low active people. In the second scenario, called disassortative interaction, most contacts take place in between the subgroups; this means that sexually active people have sex with sexually low active people. Theoretical studies of these models have demonstrated that assortative interaction generates a faster epidemic with a lower size. Disassortative interaction generates a larger size of epidemic, but the spreading is slower. In a mix scenario where interaction takes place both inside the subgroups and in between the subgroups, also called symmetric interaction, the result of speed and size of spreading of the epidemic is somewhere between the two previous models. Groups have different network patterns depending of the type of individuals belonging to this group. Figure 2.1 and 2.2 illustrate the different network shapes between sexually active and sexually low active people.

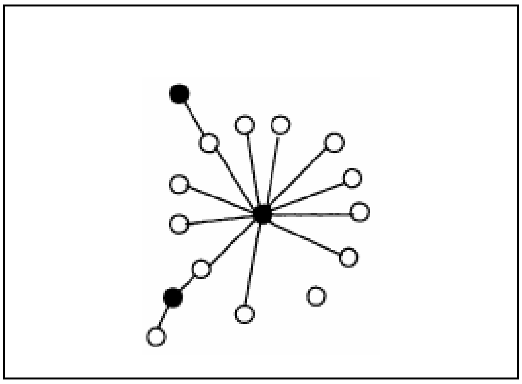

Figure 2.1: *Sexually active people maintain several links with their partners. This structure is a favorable field to induce a fast spreading of the epidemic once the central node is infected.*

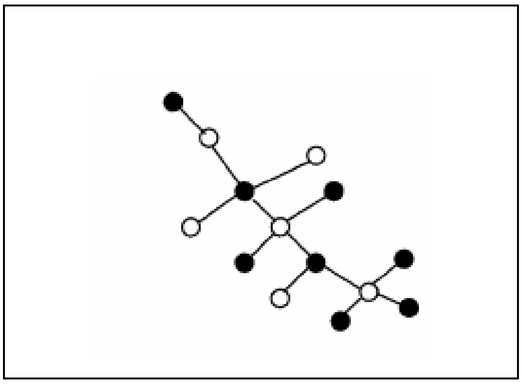

Figure 2.2: *Sexually low active people generate that kind of long structure. They tend to include more nodes that the sexually active people network, which therefore explains why the size of the epidemic is larger.*

Most of empirical studies indicate that assortative interaction is closer to reality. And exception arises from the study of the male homosexual population in Iceland which shows strong disassortative patterns. [4].

It is interesting to take a closer look at the results of empirical studies of sexual networks. A study based on clinical contact tracing and volunteered information associated with contact tracing in Manitoba, Canada, is one of the rare example of reconstructed sexual network. Surveyed subjects are who are confirmed to be positive to a STD (a total of 4544 individuals in this study) are asked to list their sexual partners. Those partners are as many potentially infected subjects. These subjects are in turn, contacted, tested and asked to provide their own sexual partners, and so on until we can reconstruct part of the sexual network. Of course this kind of study relies on volunteered information and data are extremely difficult to obtain. The method is also arguable as the reconstruction of the sexual network relies only on the infected subjects and does not bring insight about the complete picture of the sexual network. Nevertheless, it has revealed that sexual networks are constituted of many relatively small clusters. The interesting point is to find out how those small clusters overlapped each other and foster the spreading of the epidemic. [5]

Sexual Networks are not static. Partnership evolves as time goes by, following different scales for different individuals. It is therefore necessary to consider the concurrent relationships on a network. [6] These studies have been developing new models to represent the nature of relations, involving fidelity among partners and transmission among two non-concurrent relationships that would happen relatively closely in time. Sexually low active populations tend to be more static whereas sexually active populations are much more dynamic. The influence of sexually active population in a network plays a major role in the spreading of sexual infections. Therefore the precision of the model of this subpopulation is of major importance.

A modern approach to study social networks is based on the Small World Properties. In sexually transmitted diseases, there is contagion between two nodes if those nodes are linked together. Most of the sexual networks have a very low average number of connections to other nodes but with a very big variance. In other words, most of the people in a sexual network have very few partners, but a small number of them have a lot of sexual partners. This architecture of network is closely related to Small World networks.

In a Small World network, most of the nodes have a close connectivity with their closest neighbors, therefore influencing the network on a local level, but only few nodes have a longer connection, linking randomly other parts of the network, therefore bringing two different regions closer to each other. (Figure 2.3 and 2.4) The interesting property of this kind of network is that the average distance between two random nodes is dramatically decreased due to the presence of these few nodes with longer links.

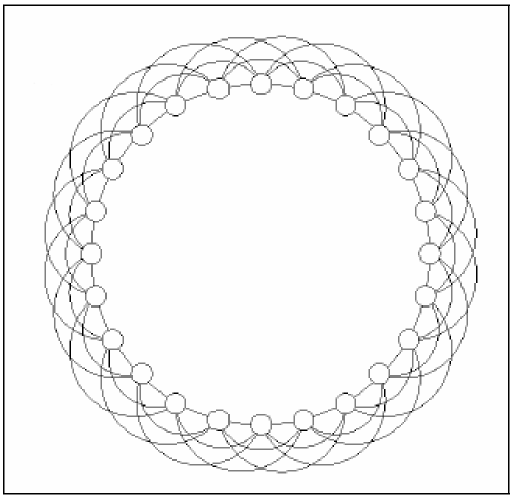

Figure 2.3: *In a regular network, on node on one side of the network need a lot of intermediate nodes before reaching its opposite node on the other side of the ring. They stand at a far distance from each other.*

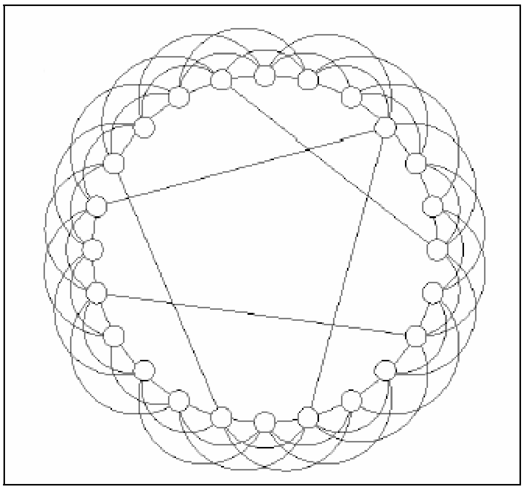

Figure 2.4: *In a Small World, a few nodes connect other parts of the network located far away from them. Therefore, two opposite nodes are now closer to each other thanks to the longer links that exist between two remote regions in the network.*

It is possible to classify Small World networks into different sub-classes of networks. These sub-classes are categorized according to the degree of distribution *P(k)* of a link to a node. Three classes of networks have been identified; single-scale, broad-scale and scale-free networks. The sexual networks belong to the category of scale-free networks. [1][7][8]. In a scale-free network, most of the nodes have a small number of connections to other nodes, whereas a few nodes only actually have an important number of connections. It is possible to represent different categories of scale-free network just by changing the distribution for connectivity between nodes. The following graph (figure 2.5) shows the degree of distribution *P(k)* depending on the number of links *k* if a power law or a Poisson law is applied.

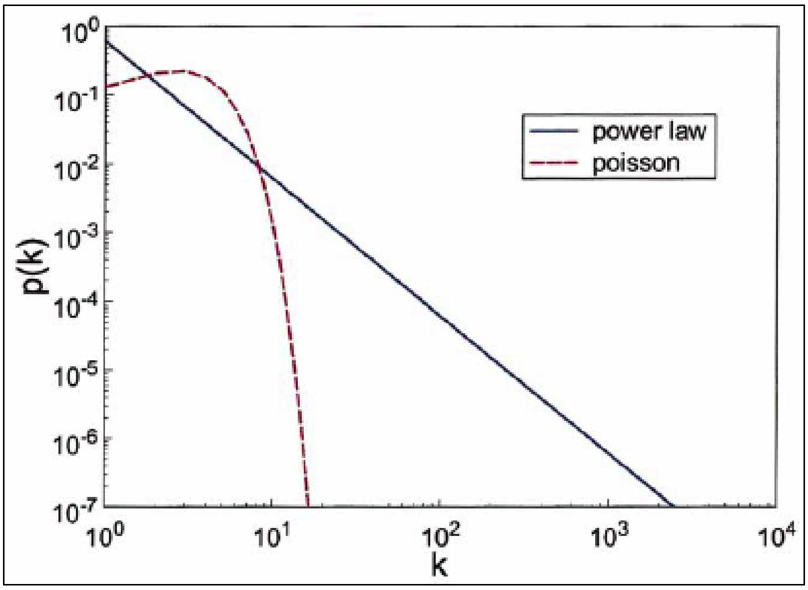

Figure 2.5: *Comparison of the functional form of a Poisson distribution and a power-law distribution for connectivity, k, with logged axes. Studies suggest that the connectivity distribution for sexual contacts might follow a power law, thus indicating a scale-free network structure.*

The sexual network following a scale-free pattern explains how an epidemic can be spread quickly on a large scale. The size and speed of the epidemic being determined by the law used to model the distribution of links. A high number of highly connected nodes will speed up the spreading of the epidemic on a large scale. That is the reason why the distribution of connectivity plays a major role while attempting to build up a social network model.

Therefore the challenges in design and analysis of the HIV/AIDS epidemic relies in the sexual network study, given that data are extremely difficult to obtain.

3. Preliminary study and design of the model

According to the research of [1], the highly active sexual groups in the population play one of the most important roles in the sexual network. Therefore, the understanding of this core population is of major importance. The simulation model is mainly based on a study of statistical data from a survey that was directed by the "AIDS prevention and Research Center of National Yang Ming University - Taiwan" under the supervision of Professor Chen. This survey was conducted in 2003 in Taipei and Taichung, two major cities in Taiwan, and covers about 1000 samples of the homosexual population. This survey was lead in homosexual saunas and bars. The questionnaire covers different aspects in order to provide insight on the structure of this population as well as its behavior. It was used to give a global understanding and build the agents' behavior. Homosexual saunas and bars are referred as high risk places for they stand for locations where it is easy to encounter new sexual partners and are therefore frequented by sexually very active people who belong to the high risk population.

Different aspects need to be covered in the preliminary studies, such as the structure of the population, time scale in the frequentation of high risk places, the frequency of change of sexual partners, behavior regarding the establishment of new partners, the duration of a relationship between partners, usage of condoms, attitude regarding HIV testing, etc.

The data that are available and related to the population's structure is not very important in this study because we do not have explicit relation between age, or marital status or education level and social behavior or impact on the HIV disease. Nevertheless, it is important to shape the size of the high risk population in the entire network. In order to reflect the evolution of the HIV epidemic in the homosexual community in Taiwan, it is not possible to concentrate only on the high risk population for which we have statistical data. It is also necessary to make assumptions on a larger population which may have different behavior. The validity of these assumptions needs afterwards to be verified by simulation. The idea of the model is to have a majority of agents which are not active sexual agents, but more stable with a behavior that potentially represent a low risk for themselves. This category of agent represents the majority of the population and can be seen as a pool or reserve of susceptible agents from which the total number of HIV cases can grow. The high risk population is a minority but because of its important sexual activity acts as en engine to spread the virus inside and outside its population, and to increase the risk for other agent to be infected. Therefore the appellation of core population is justified we want to demonstrate that the behavior of this category of agent plays a major role.

In order to build this structure, we have based the distinction between high risk and low risk subpopulations according to their behavior regarding the number of partner one is willing to have, its condom usage policy, as well as its degree of "faithfulness" regarding its long term partners. Therefore we make a distinction between short term partners that we call *Free Links* because this linkage between two agents moves freely from a partner to another; and the long term partners that we call *Fix Links* because the linkage between two agents is fixed over a long period of time (the order of a few years).

The small world model provides very interesting and powerful properties to a social network. We decide to build the agent network in order to give it small world properties. To reach such a result, it is necessary to distribute the number of links of each agent among the network so that over a long period of time (typically many years) the distribution of the links of all the agents composing the population displays the pattern of a scale-free power-law.

A first approach of the power-law which is to be used can be retrieved from the result of the survey. Data of the cumulative number of sexual partners over the past three month, based on about 500 samples, actually do give a curve that is representative of a power-law with a scaling exponent of 0.77 for a distribution of the number of partners k>1. See figure 3.1

We remind that scale-free networks are characterized by a power-law decay of cumulative distribution of the form:

$$P(k) \approx k^{-\lambda}$$

With:

k: Distribution of the number of partners

λ: Scaling exponent

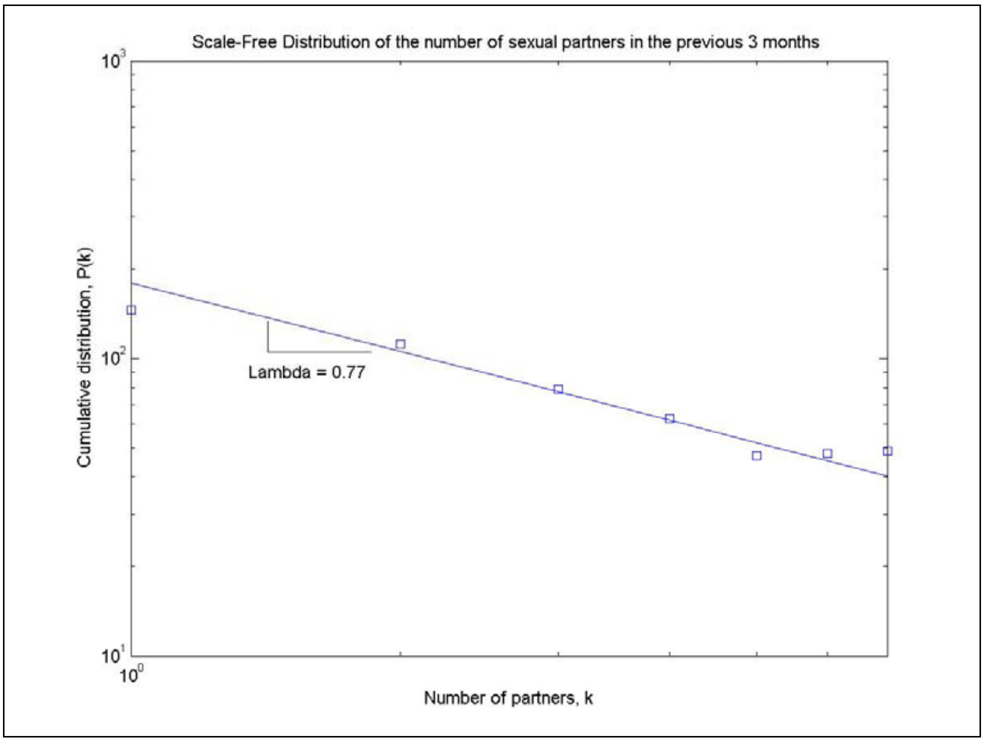

Figure 3.1: *Scale-Free Distribution of the number of sexual partners in the "sexually active" homosexual community of Taiwan on log-log axis. The low value of the scaling exponent λ indicates that people in this population tend to have a lot of sexual partners, especially considering such a short period of time of 3 months.*

As stated before, this survey only covers the high risk population. The majority of the population might bear a similar pattern but with a different scaling exponent and curve shape. As we want to achieve a power-law distribution over a long time among all the agents of the simulation, we suppose that there exist such a function or class of functions *Pf* that represents a correct distribution of links among the agents. Such a function as the following general expression:

$$P(k) \approx ak^{-\lambda} + b$$

And it's the plot of the general expression is as in Figure 3.2:

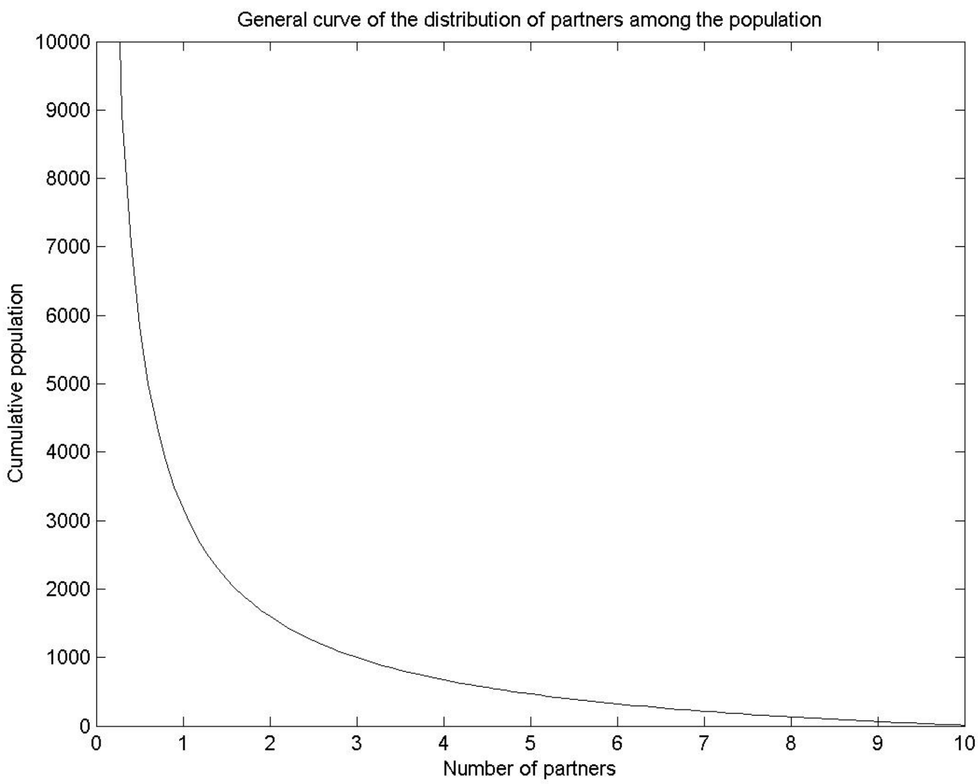

Figure 3.2: *General curve of the distribution of partners among the population*

We need to consider different parts in this graph. People having several sexual partners are more likely to have a different behavior than people with one only stable sexual partner. Therefore it is interesting to approach the problem by dividing the curve into different sections. Each section shall represent a type of subpopulation where each subpopulation may have a different profile. The choice here is to divide the population into 3 clusters. One cluster with a very high number of sexual partners can be correlated with high risk sexual behavior but a low number of individuals (as suggest the power law, see figure 3.3). We call it the alpha population. A second cluster called beta population which is characterized by an active sexuality but with a less extreme behavior as the alpha population and a higher number of agents. Then the gamma population is the third cluster and represents the rest of the population. As suggested by the power law (see figure 3.3) they have a few number of sexual partners, for most of them it is around 1, but they represent a high number of agents in the population.

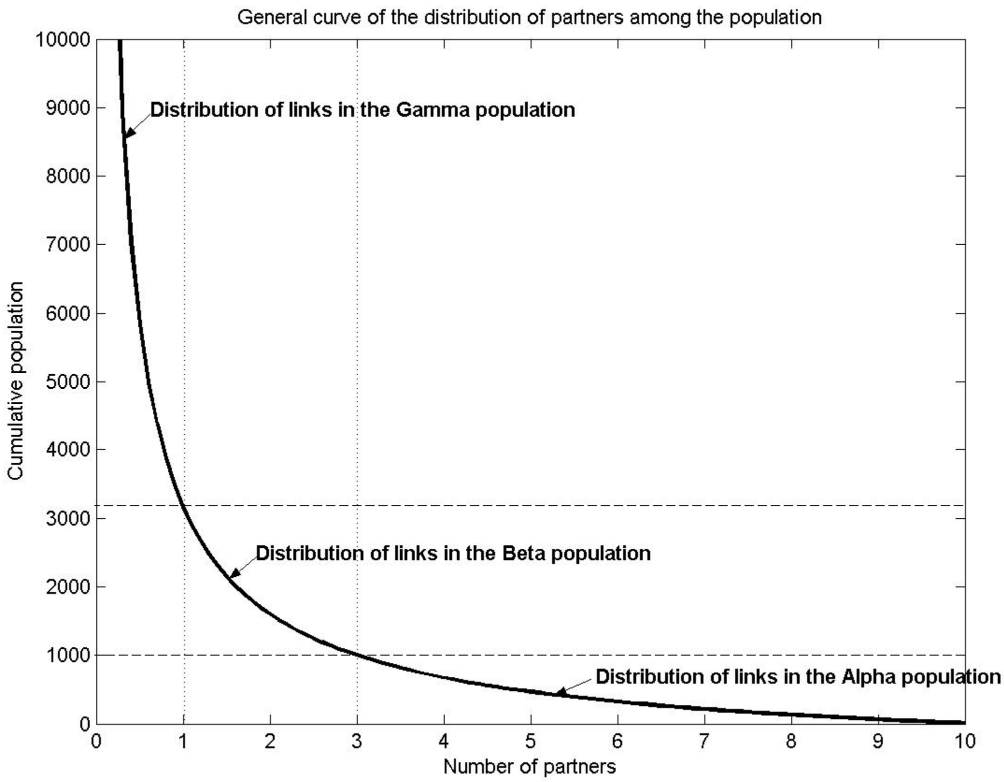

Figure 3.3: *General curve of the distribution of the alpha, beta and gamma populations*

Thus, each part of the previous power law is a representation of the distribution of the links, or partners for each agent in the society. We will discuss in the chapter 4 the main parameters that define the profile and the behavior of each subpopulation.

4. Simulation’s implementation

The simulation’s model is based on multiple layers. Each layer plays a specific role in providing a model to describe and represent of a specific issue or phenomenon. The layers can be physical as well as virtual, but their definition implies a major role to play either for another layer or for the overall simulation directly. The layers then communicate with one another to exchange information of their own computation results. In this study there are a total of 5 layers. These layers are: Agent, Agent Behavior, Links, Contact Frequency and Epidemic Model.

In this section we will go through the details of each layer. As a first approach, these layers can be divided into 2 categories: Social Network Model and Epidemic Model. As we have detailed in the Previous Studies’ section, the Social Network Model has spatial properties, temporal properties, and intrinsic properties that make it change as time passes. The approach of this work is to assess the influence of individuals, i.e. agents, over the entire population. Therefore we have chosen to mix global social network behavior and individual behavior, but to reflect the intrinsic changes in this society through the combination of individual agent’s change in their behavior. The global structure of the society is defined in the Agent layer. The spatial concepts are reflected in the Links layer, whereas the temporal concepts appear in the Contact Frequency layer. The individual intrinsic changes are modeled in the Agent Behavior. Finally, the second category of layer contains only one layer which is the Epidemic Model. Because there is no cure to the HIV/AIDS epidemics, it appears obvious to choose the simple SI Model, where SI stands for Susceptible Infected.

The review of these layers is explored in details in the following sub-sections.

4.1. Agent layer

The Agent layer defines the structure of the population. The pool of agents is defined in this layer, and the characteristics of each agent are defined here as well. Following the Sexual Network studies from [9] it has been demonstrated that a population contain different patterns of individuals. As for Sexual Network, sexually active people are one important pattern. In the Agent layer, we actually define 3 patterns.

The core of this population is the very sexually active agents. Their typical characteristic is to represent a very small minority, but they play an important role in the epidemic simulation because of their behavior and the important risk they represent for the rest of the population.

The second pattern is defined by sexually active agents. More important in term of number than the very sexually active agents, they nevertheless are far from representing a majority in the total population. They have a sexual activity that can be classify as higher as the average, but with a different behavior, “more responsible”, when compared with the very sexually active people.

The third pattern is the low sexually active agents. They are the majority of the population in term of number. They represent the pool of potential infected people with still the lower risk.

The justification for having an intermediate class of population between a very active sexual population and a low active sexual population is that the gap between these 2 patterns is too big in our sense to be close to a realistic model of a society.

4.2. Agent Behavior

The Agent Behavior defines the initial behavior of an agent as well as the adaptation of the agent to its environment. There are two major behaviors that can be implemented. The first one is the usage of condoms as a prevention of STD (Sexual Transmitted Diseases), including HIV. Using condom has become more and more common since people are more aware of the risks of STD. Therefore we can globally assess an increase in using condom along the time of the simulation. Survey from YM University data also show that that the behavior towards condom usage is not the same in the sexually active population when an agent is aware of being HIV positive. Unfortunately it doesn’t show an increase in the frequency of using condoms. It is difficult at this stage of the research on these populations to determine the clear motivations behind this attitude. Nevertheless, this parameter is implemented with a moderation factor.

Another type of agent behavior related to condom usage is with whom are condoms used. For long term patterns, referred in the simulation as "Fix Links", we assume that the probability for that type of couple to use condoms is extremely low. Behind this assumption is the concept of fidelity and the fact that wanting to use a condom in this case might be a confession of unfaithfulness! But, for short terms relationships, referred in the simulation as "Free Links", it is assumed that agents are more careful with this kind of sexual intercourse and might be more willing to convince their partner to use condoms. The data used in this case are taken from the survey published by YM University.

The second important agent behavior implemented in the simulation is the willingness to have HIV tests. It has become more and more frequent today for people who are taking risks to test themselves. It remains a recent change in people habit but nevertheless an important one. It is difficult to track this change in people's behavior along the years for we lack of statistical data over the past 20 years. But actually implementing such a behavior is important for the role of HIV positive agents who are aware of it. This will influence their behavior in term of using condoms and influencing their peers to have HIV tests.

Another possible agent behavior appears to be important to refine the simulation's results; it is the use of drugs by agents before having sex. Some studies show that the drug factor might lead to forget or be less willing to use condom during a sexual intercourse. This behavior has not been implemented and can be the object of further studies.

4.3. Links

The links reflect the spatial aspect of connection between agents. On the epidemic level, it will determine the importance of the size of the epidemic. The ability of creating new links, therefore new sexual contact between agents, is one of the key vectors of the HIV propagation.

Following previous social studies on sexual networks, it shows that 2 kinds of relationships exist: Short Term and Long Term relationships. Statistically a big majority of people are involved in fix relationships or long term relationships. In the simulation, we use the terms “Fix Link” to qualify the type of link that exist between 2 agents involved in a Long Term relationship. We use the term “Free Link” to qualify Short Terms relationships between 2 agents. A short term relationship can last from on sexual intercourse to a few months. But when the time frame of a relationship reaches the scale of years then we talk about “Fix Links”.

This distinction between Free and Fix links is important. Agents act sexually differently with their Free and their Fix links. This distinction is also necessary to reflect the propagation of the epidemic outside the borders of the so called high risk population. Low risk population typically belongs to sexually low active population (This appellation doesn’t mean that they have less sexual intercourse, but a fewer number of sexual partners). This type of population is characterized by strong fix links, but the existence of a few free links are still to be taken into consideration. It is these free links that can be the vector to propagate the HIV virus in this population. From this point of view, the “gamma” population belongs to the category of low sexually active people. It is a domain where the spreading of the epidemic is slower, but because of its size, it can reach a higher volume in term of number of infected people. We show here that the knowledge of the size of this population is not necessary for the assumption is that it is a lot bigger that the “alpha” and “beta” population. Screening these last 2 populations is much more important as they represent the core of higher activity. The “gamma” population is merely at this scale an infinite pool of agents in the susceptible state (with the potential to be infected).

Fix links are distributed within agents belonging to the same population (alpha, beta or gamma population). The number of fix links is by its own “nature” low, and is typically one. Different simulation scenarios of the frequency of distribution of free links have been executed. The details are discussed in the next sub-section Contact Frequency.

Free links are distributed within agents belonging to the same population, and across agents of different population. The number of possible free links for an agent depends on the population it belongs to. Alpha population agents have more free links than Beta population agents. Beta population agents as well have more free links than Gamma population agents. The distribution of the number of free links is done in order to achieve, in the long term (a few years) a power law distribution in the number of partners over the entire population represented in the simulation. Based on [Lilejos] studies, the number of sexual contacts over a lifetime in a population follows a power law curve.

Free links and fix links combine assortative and disassortative patterns in the populations. Statistically, even if the alpha population is small, an agent belonging to the alpha population have more chances to connect free links with other alpha population agents because the important number of free links they can have. Therefore obvious assortative and disassortative patterns appear with the alpha and beta population. The gamma population reflects more assortative patterns, but because of its importance in term of number of agents, even if the probability per agent to have free links is low, there are some disassortative patterns that are reflected here as well. These free links in the gamma population are statistically disassortative, meaning that they will take place with agents from the alpha or beta population, because these agents are able to connect a lot of free links. The existence of free links in the gamma population plays a major role in the bridge between the different types of populations.

4.4. Contact Frequency

The contact frequency reflects the temporal aspect of the links that can bind 2 agents. The sexual network is a dynamic network. It is dynamic in 2 ways. The first way is with the number of new contact that an agent will establish. New links appear while existing links are broken up. The underlying mechanism is important to understand because connecting a link to a new agent might open a whole new portion of the sexual network to the spreading of the epidemic. Alpha and beta population are more incline in developing new link that can be the gamma population. Another characteristic of the so called high risk population is the fact that they tend to establish a relatively high number of new links, whereas the gamma population will have a low tendency to establish new links.

The other aspect in which the sexual network is dynamic is within the activity of the existing links. Some links are more active than others, meaning that the number of contact is predominant with certain agents over other agents. For example, a fix link within agents belonging to the gamma population will show more frequent contact than a free link in this same population. A free link in the alpha population might just provoke contact for one or two times, thus showing a low contact frequency.

There exist somehow a trade off between the number of links that an agent can maintain and the duration of this link in time. The more links an agent has, the weaker they will be and therefore the shorter they might exist. On the contrary, maintaining fix links in the long terms might prevent from actively building new links in the sexual network.

4.5 Epidemic Model

This research focuses only on providing an estimation of the number of HIV cases based on the study of the homosexual sexual network. The change from HIV to AIDS is not taken into consideration. Therefore the S.I. Model (Susceptible / Infected) appears as a natural choice. This layer deals with the status of each agent and the transmission parameters that lead an agent from the susceptible status to the infected status. In order to refine the behavior of agents, we actually distinguish two subdivisions in the infected status. The first subdivision bears the same name and is called infected status, the second one is HIV status. The subdivision infected status is corresponding to the state of an agent, the first few weeks after his contamination and before he develops the antibodies that would allow a detection of the HIV virus. During this infected period, the agent cannot know if he is contaminated or not by the virus, and this status might influence his behavior in terms of number of sexual contacts or usage of condoms. The second subdivision is the HIV status. An infected agent automatically turns to HIV status after a period ranging between 6 to 12 weeks. According to recent medical results, the fastest test results can be achieved now after 2 weeks following the contamination. However, we do not have any statistic data regarding the reliability of this test, and as a matter of fact, we have no evidence that the population we are studying has access to such tests. The second period of incubation before the AIDS symptoms appears is in average of 10 years. In order to provide a model for the transition of the HIV status to the AIDS status, it is fundamental to study the evolution of the medical treatments along the past 20 years. This is outside the scope of our research and such implementation has not been done.

All agents that are not contaminated are in the susceptible status, because they all are potential targets of the epidemic. For an agent to change its status to infected, he needs to be exposed to the HIV virus. In this simulation we consider only the subpopulation of homosexual people that are infected only by sexual contact. The influence of male or female sexual workers and needle sharing which are also important causes in the spreading of the HIV epidemic are not discussed in this work. They can be recommended as topics of a future research in order to enhance the current results. Therefore the only possible transmission factor which is modeled is via sexual intercourse with infected agents.

Sexual contacts between two agents in the susceptible state, with or without using condoms, do not change the state of any of the two agents.

Sexual contacts between two agents in the infected or HIV state, with or without using condoms, do not change the state of any of the two agents either.

Sexual contacts between two agents, one being in the infected or HIV state and the other one being in the susceptible state might lead to the infection of the susceptible agent. In the case that the agent being infected by the virus uses condoms, it will reduce the probability for the susceptible agent to be contaminated. Although we do not allow 100% of non-transmission probability because using condoms (often referred as “safe sex”) is only considered as a way *to reduce* the risk of transmitting sexual diseases. Therefore a susceptible agent having safe sex with a contaminated agent only has 0.01% of probability to be infected. On the other hand, not having safe sex between a susceptible agent and an infected agent do not automatically lead to the infection of the susceptible agent. There are no proofs that oral sex is a vector of transmission of HIV. Furthermore the practice of anal sex in the homosexual communities shows that the transmission factor of the disease is not as important as the practice of heterosexuals. Therefore we grant a percentage of 99.9% of probability for a susceptible agent to be contaminated by an infected agent in the case of non protected intercourse.

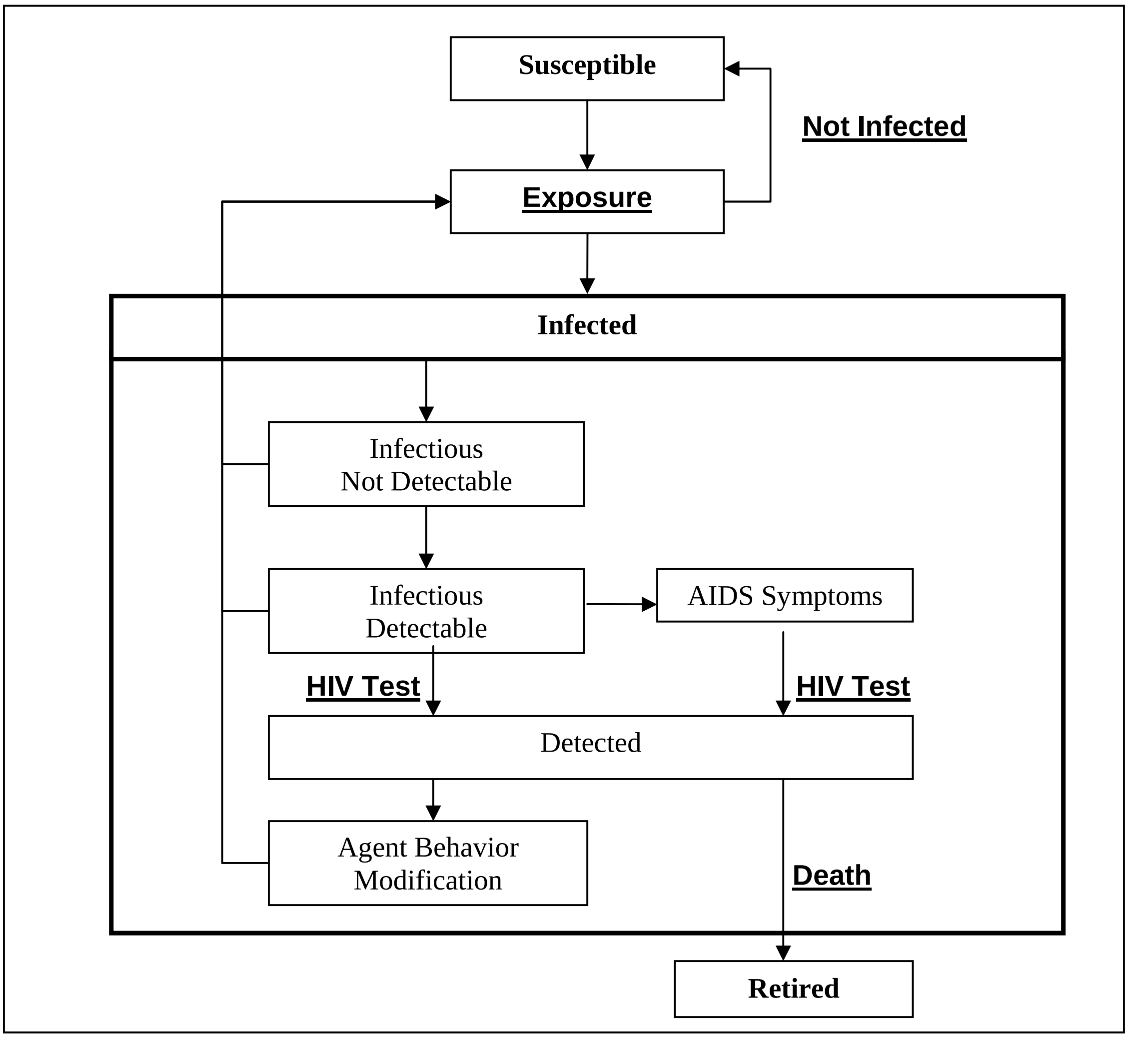

Figure 4.1: *Block diagram of the complete contamination process for HIV and AIDS. Nota: The current simulation covers only the HIV part; the AIDS Symptoms, Death state and Retired are not implemented.*

4.6. Block diagram

The model of the simulation is decayed into five layers, but the actual implementation is composed of objects or blocks which communicate with one another in order to effectively describe the function of the layers described below. The block diagram detailing the flow of the simulation is described below in the figure 4.2. The explanations regarding each element are grouped in the table 4.1. The Agent and the Agent Behavior are two stand alone blocks. The layers Links, Contact Frequency and Epidemic model are managed by the block Rule because they are all set under the form of rules. The shape of the power-law is one of the rules for the distribution of links.

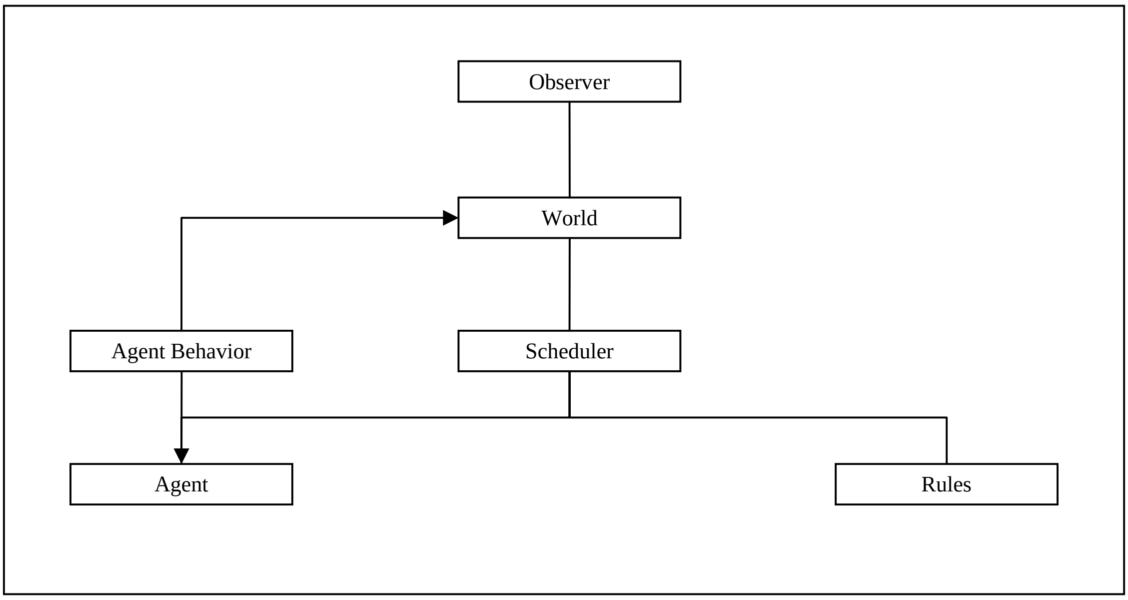

Figure 4.2: *Block diagram of the HIV computer simulation. The epidemic model is included in the rules that follow the environment.*

Objects	**Properties**	**Methods**
Observer	Higher Class in the Hierarchy	Receive information from lower classes and create the screen display
World	2D lattice containing agents	Define the structure of the social network. Can be influenced by ***Agent Behavior***
Scheduler	Define the time into rounds of 1 month	Define events to happen to each *Agent* during a round, Make sure the ***Rules*** *are respected.*
Rules	Set of Rules applied in the simulation (related to the contamination, evolution of the HIV, epidemiological model, etc…)	Communicate the rules to the ***Scheduler*** and the ***Agent***
Agent	Represent a human	Can change to different states (following the epidemic model) and interact with other agents
Agent Behavior	Set of behavior rules based on statistical surveys	Control the behavior of the agent (how many contacts, use protection or not, etc…)

Table 4.1: *Details of the properties and methods of each block component of the simulation.*

5. Experimental results

5.1. Foreword

The experiments focus on different models and policies, in order to try to fit the reported cases in the best way. It is important to note that the reported cases underestimate the reality of the epidemic because of screening limitation. Therefore the shape of the reported curve might not reflect the reality of the evolution of the epidemic along the years. The recent explosion in the number of HIV reported cases might be a side effect of people being aware of this epidemic and willing today to be HIV tested! Following this hypothesis, we suppose that a large number of the population infected in the past might come out in recent statistics. It also means that more people are willing to be HIV tested and that it becomes a common behavior among people.

We are here pointing out a contradiction between the simulation and the reality in term of reported cases. In the reality, the hypothesis that a greater percentage of the population is willing to be tested will result in an increase of the HIV reported cases in the statistics, because this behavior facilitates the screening of infected people. On the other hand, in the simulation, when an agent is being tested positive to HIV, this agent is willing to be more cautious in his sexual relations, and therefore this policy shall prevent the number of simulated HIV cases to grow too fast, resulting in a lower number of reported cases.

Therefore, comparisons between the reported cases and simulated cases shall be carried out while taking in consideration such kind of parameters.

In this section we propose to report the results of a few important parameters. Parameters such as the number of links and the contact frequency, usage of condoms or drug have been fixed for the alpha and beta population according to the survey's statistics. The gamma population plays the role of pool of potentially infected people. We have implemented a more traditional behavior in this population in order to balance the effect of the important number of gamma agents against their low sexual activity. This traditional behavior is a conservative approach for it tends to underestimate the effects in spreading the epidemic in the population.

Parameters presented in this section are related to the evolution of social behavior among the past 20 years. Based on today’s surveys it is difficult to estimate the behavior and habits of this population 20 years ago. Therefore, it is necessary to approach a rough estimation of the evolution in the homosexual population by simulation. Because HIV was not a topic of active research 20 years ago, there was very few data collected at this time. In order to complete this picture, I tried to model a plausible change in agent’s behavior based on a feed-back from the older generation of homosexual people. One of the most important feed-back is the increase of young men “coming-out”, which motivates here a change in the cardinal of the alpha and beta population within the time. The second important parameter is a great increase of usage of drugs within young adults (Between 20 and 30 years old). This suggests that drug has become an important parameter, and that it does affect people’s behavior towards protection of MST. It also suggest that using drug today may be more popular than 10 years ago.

We propose to review two policies in the expansion of the alpha and beta population within the time, as well as the influence of drug and the increase of drug usage within the recent years. The review of different models to estimate these parameters are presented in the following subsections.

5.2. Dynamic change in the population

Social Networks are dynamic, they change within the time and their size changes as well. The model of this simulation separates the whole population into alpha, beta and gamma populations. Motivated by the fact that more men tend to publicly assume their homosexuality, the size of the homosexual population have change during the past 20 years, and the size of the different clusters alpha and beta have change as well. Unfortunately, the lack of information related to this dynamic in these sub-populations makes it difficult to estimate. Our model being based on today’s information strongly suggest that it is impossible to fit the actually HIV cases reported by surveys if we do not consider such a dynamic in the populations.

In figure 5.1, we compare 3 models. The curve labeled as “No Increase” shows the number of simulated HIV cases if we do not consider any increase in the alpha and beta populations. This curve obviously underestimates the reality, and the slope tends to flatten in the long term. This shape is due to a saturation of the number of infected agents in the sexually active populations. One way to stimulate the number of infected cases would be increase the exchange between the alpha/beta populations with the gamma population as the latest constitute an important pool of potentially infected agents. But doing so would contradict the hypothesis that the gamma population has a low level of sexual activity outside the fix partners. Therefore the second possibility is to increase the number of agents in the alpha and beta populations.

Two models are implemented and the results are labeled, in Figure 5.1, as “Model 1” and “Model 2”. The model 1 is design in order to reflect major possible changes in the increase of these populations. These major changes do not occur on a regular basis but could have a great influence in shifting people’s habits. These changes are sexual revolutions like we have experimented in the 70’s in Europe for instance. Similar phenomenons have appeared in the homosexual community and have lead to concepts like “Gay Pride”. In the model 1, we assume that these events took place 3 times during the past 20 years and have had a major role to play in increasing the alpha and beta populations. The result is an increase in the number of simulated HIV cases, separated into distinct phases.

The second model for population increase is labeled as “Model 2” in Figure5.1 and assumes that the growth of these populations is the result of a linear increase among years. The function represented in model 2 is linear. It is unlikely that the real increase of the homosexual population follows such a law, but it emphasizes on the fact that such a growth is not directly marked by events but is much of a smoother process. It reflects a different point of view from the model 1. It is outside the scope of this study to choose between these 2 points of view, but the possibility of implementing different social theories remains possible.

It appears that simulations of a dynamic increase of the alpha and beta population leads to more accurate results than static sub-populations. Modeling this dynamic is most likely to be cultural and space dependant, meaning that a model could be meaningful for Taiwan but might not be for countries in Europe for instance.

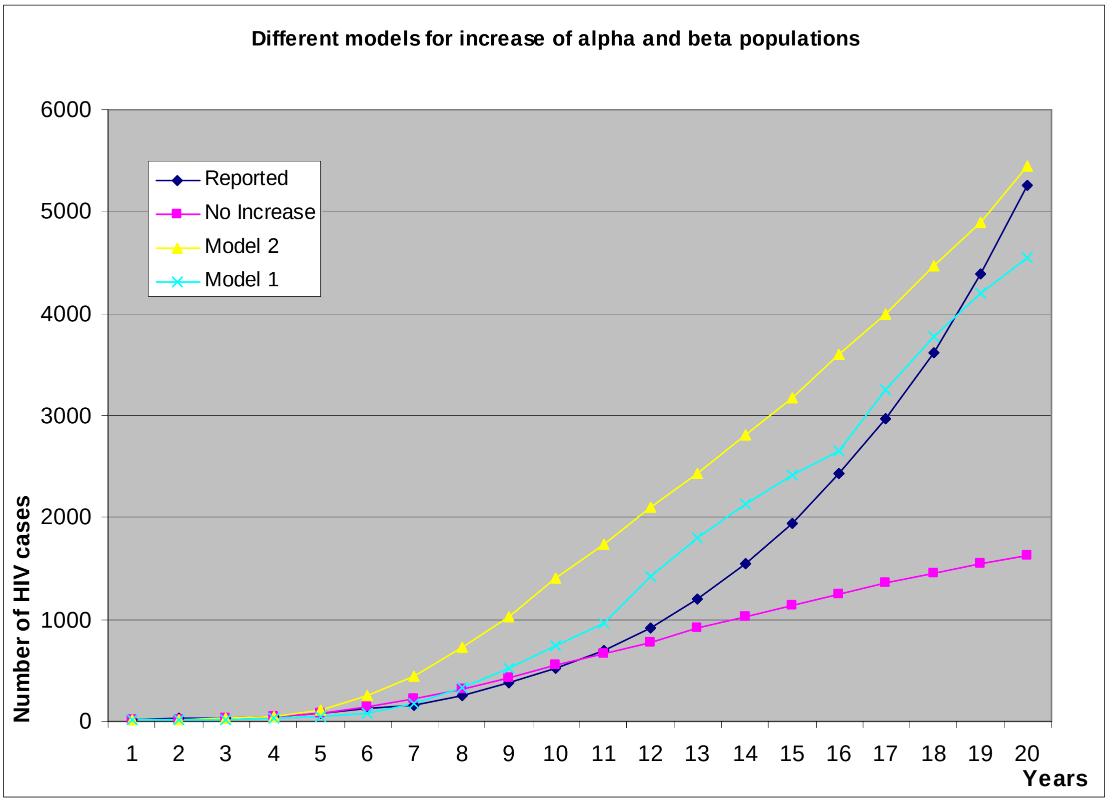

Figure 5.1: *Different models for increase of alpha and beta populations*

5.3. Impact of drugs

According to Tsai Shu-fen of Taiwan's Centers for Disease Control, using drugs has a major impact in the spread of HIV. This occurs in two ways; the first one is while sharing infected needles, but this behavior belongs to heterosexuals as well as homosexuals and is not reflected in this study. The second way is while people takes drug during parties, and forget to protect themselves while they are on drugs. The young generation tends to be more eager to use drugs during parties. This is not a new phenomenon but in recent years, the number of people taking drugs occasionally has increased. It is difficult to assess the impact of such a change in society but it does affect the way the HIV is spread among people. Figure 5.2 shows the result of the simulated HIV cases while considering the usage of drug (labeled as “With Drugs”) and while omitting the usage of drugs (“No Drugs”) with a dynamic increase of the alpha and beta populations following the model 1. The curve labeled “Reported” is always used as a reference. It appears that in the model implemented, the usage of drugs definitely plays role. The gamma population being more conservative, they are not likely to use drugs. Therefore the major population affected by this parameter is the alpha and to a certain extend the beta populations.

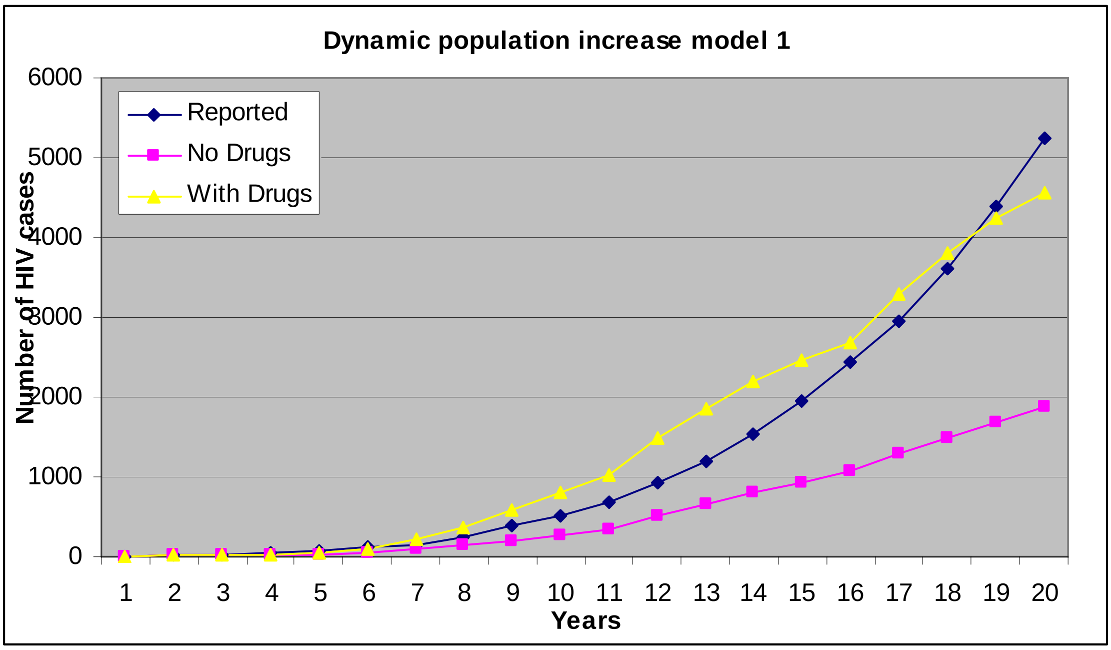

Figure 5.2: *Dynamic population increase using model 1 – comparing the model with and without drugs usage.*

5.4. Discussion on the simulation results

The HIV simulation is agent based and some parameters such as the distribution of link among agents are implemented as random variables. This section discusses the results of the simulation in order to validate and justify the credibility of the model, and show that all simulation’s results converge. Each curve produced in this report is the result of 100 runs of the simulation with the same parameters or policies. The unit of time in the simulation is the month, but results are reported for every year. For each year, the value represented is the average over the 100 runs. At the same time we compute the standard deviation of each point.

The result of the simulation with a dynamic increase of alpha and beta population following the model 1, plus including the usage of drugs and HIV testing is presented in figure 5.3. The curve labeled “Simulated” include for each point the deviation over 100 runs. The upper and lower value for each point is represented by error bars. In order to justify that the deviation on each point is acceptable, the curve labeled “Deviation (%)” represents the deviation over the 100 runs for each point stacked to 100% of the value of the current point. This curve represents the relative error in percentage at a specific point and is related to the axis on the right side of the graph. The relative deviation is taken between the upper and lower values obtained through the 100 runs. It is higher for lower values of the number of infected people but do not exceed 37% of the value of the current point. In term of number of cases, the deviation between the upper and lower value do not exceed 147 cases over an average of 1421 cases for the year 12 which is about 10% of deviation, meaning that the higher value of infected cases would be about 1495 cases and the lower value about 1347.

On the other hand we notice that the more the number of infected cases, the less the dispersion in the results. The results are therefore valid in term of reproducibility because their dispersion is limited and also in term of credibility since the deviation within multiple runs do not affect the global trend of the different policies.

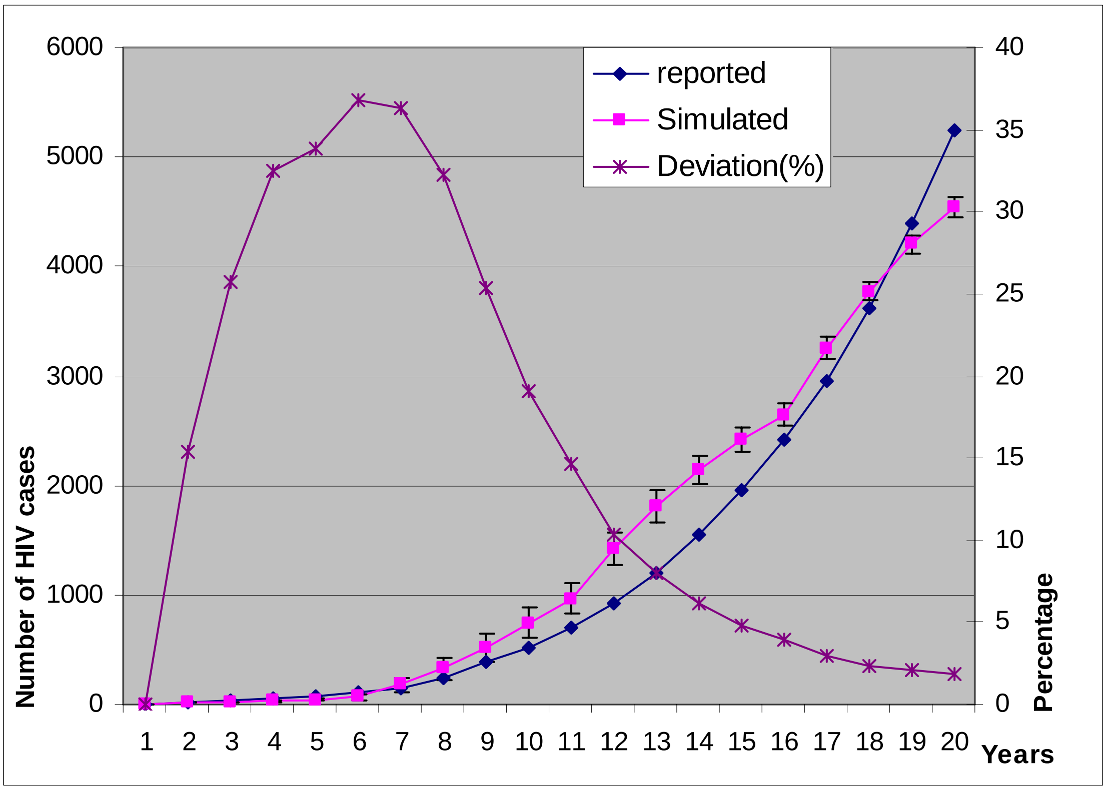

Figure 5.3: *Simulation of the number of HIV cases over 100 runs, including the deviation at each point (labeled "Simulated" - refer to the left axis) as well as the deviation relative to the value of each point (labeled "Deviation(%") – refer to the right axis)*

Figure 5.4 show the same representation of the simulation results and deviation for different policies with a dynamic increase of alpha and beta population following the model 1. The shape of the deviation curves as well as the values all follows a similar pattern. Hence it is possible to provide a good estimation of the range for the accuracy of the simulation results.

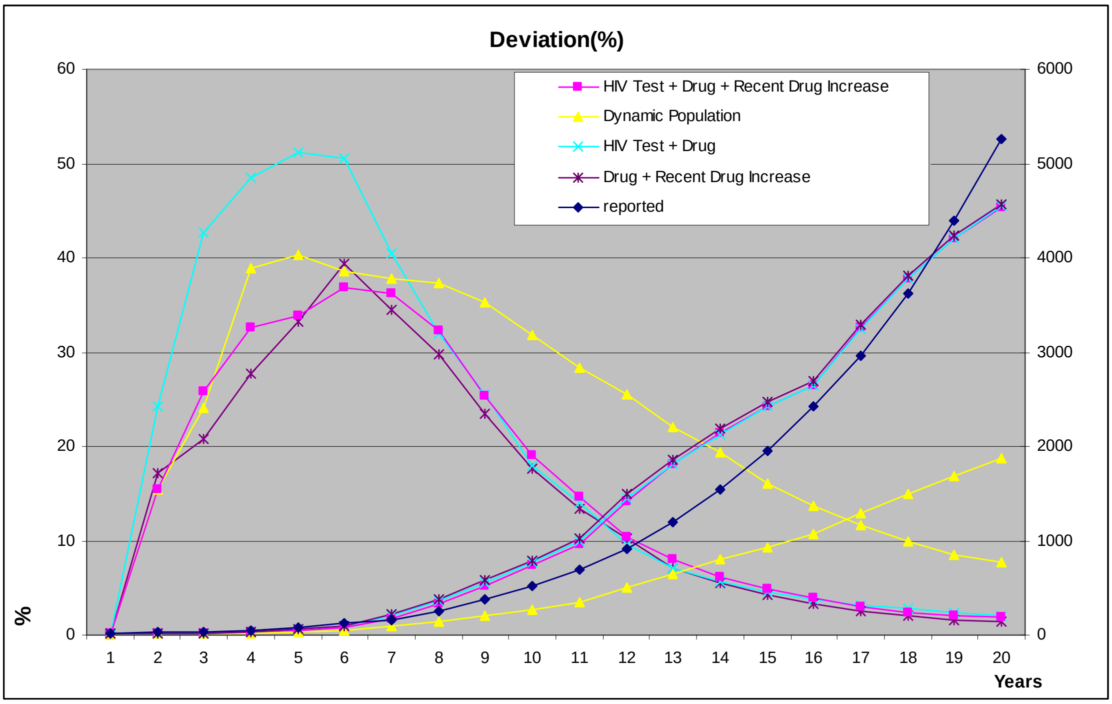

Figure 5.4: *Simulation results (right axis) and their relative deviation in percentage (left axis) for different policies, with the dynamic increase of the population following the model 1*

6. Conclusion

This study tries to establish the foundations in order to build a model that would be able to predict the spreading of the HIV and AIDS epidemics in the homosexual population in northern Taiwan. However it has now been limited to provide a reliable model of the sexual network based on agents' simulation. We believe that establishing a good model of this network is of high importance, and also that an approach based on individual agent behavior offers new path to explore in simulation of sexual transmitted diseases.

We have proven in this study that implementing rules and behavior from statistics based on social studies at the agent level can lead with some adjustment to reflect global population behaviors that are observable in reality. We demonstrate this way that implementing specific behaviors on an individual level can reflect global observations, without the need to introduce a great set of rules on the society's level. This result is in part possible because of the small world properties that are inherent to a scale free network.

In this model, the only rules applied at the society's level are the increase of alpha and beta population, as well as the increase of drug usage in the recent years. To summarize, society's level rules are minimized to reflect only the "global trends". These trends can be cultural or related to people's inclinations or tendencies. It is in our sense not possible to implement this kind of behavior on an agent level when the population considered for the study is as specific and limited as the male homosexual in northern Taiwan.

The simulated curve of the number of infected people that we obtain reflects the general picture of the infected cases reported by medical surveys. Although the shape is different, the scale in the results is maintained on a time scale that ranges of 5 years. Moreover the possibility to apply different social theories might be a way to improve the accuracy of the results.

It would be possible to enhance the current model with more data coming from field studies. It would especially be interesting to keep track of the evolution of such a society within the time. Clustering the results by generations might provide more insight about new trends and new behaviors in today’s and tomorrow’s society. Sorting out parameters like drug usage or condom usage which plays a major role in the spreading of the HIV is definitely an important part of this study. Keeping track of major changes in the sexual habits of people should be considered as important in order to build a more accurate sexual network model, but unfortunately the time frame stretches to decades and the report of such results present field challenges.

AIDS simulation requires additional studies and information such as physiological response to the virus depending on people’s condition, medical treatment, availability and cost of these treatments. Such a work could be supported by the current social network model while completing the layer dealing with the epidemic model.

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