An Agent-Based Approach to HIV/AIDS Epidemic Modeling: 
A Case Study of Papua New Guinea

by

Alisa Joy Rhee

Bachelor of Arts
Wellesley College, 2001

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and the Department of Civil and Environmental Engineering
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ABSTRACT

Since AIDS was first discovered, mathematical models of the transmission dynamics of HIV have been developed to determine the drivers of the epidemic. It has become apparent that the most profound factor in the proliferation of this disease is the aggregate effects of individual behavior and perception of risk.

Agent-based models (ABM) allow one to simulate the social and sexual interactions which may describe the societal context in which HIV may spread. Using this framework, I construct a simplified social and sexual network that represents Papua New Guinea. This country is used as a case study because it illustrates extremes in network topology. Papua New Guinea is characterized by geographic isolation of ethnic groups, such that ideas of behavior change, stigma reduction, and safe sex practices may spread very slowly. Furthermore, sexual networks in Papua New Guinea are complex and sexual violence and cultural practices may amplify the rate at which HIV is spread.

Ultimately, the purpose of HIV transmission models is to hypothesize about drivers of the epidemic which will then shed light on appropriate interventions and prevention measures. ABMs facilitate the development of network-based public health interventions. Such interventions, like home-based care programs, may have great promise in Papua New Guinea.

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## Abbreviations

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<tbody>
<tr>
<td>ABM</td>
<td>Agent-Based Model</td>
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<tr>
<td>AIDS</td>
<td>Acquired Immune Deficiency Syndrome</td>
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<td>ANC</td>
<td>Antenatal Clinic</td>
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<td>ARG</td>
<td>AIDS Restriction Gene</td>
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<td>ART</td>
<td>Anti-Retrovirus Therapy</td>
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<td>AUSAID</td>
<td>Australian Agency for International Development</td>
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<td>CDC</td>
<td>The Center for Disease Control and Prevention</td>
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<tr>
<td>DE</td>
<td>Differential Equation</td>
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<tr>
<td>FSW</td>
<td>Female Sex Worker</td>
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<tr>
<td>HAART</td>
<td>Highly Active Anti-Retrovirus Therapy</td>
</tr>
<tr>
<td>HIV</td>
<td>Human Immunodeficiency Virus</td>
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<tr>
<td>HSV-2</td>
<td>Herpes Simplex Virus Type 2</td>
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<tr>
<td>IDU</td>
<td>Intravenous Drug User</td>
</tr>
<tr>
<td>MSM</td>
<td>Men who have Sex with Men</td>
</tr>
<tr>
<td>NAC</td>
<td>National AIDS Council</td>
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<tr>
<td>PLWHA</td>
<td>People Living With HIV/AIDS</td>
</tr>
<tr>
<td>PNG</td>
<td>Papua New Guinea</td>
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<tr>
<td>SIR</td>
<td>Susceptible-Infectious-Retired</td>
</tr>
<tr>
<td>STI</td>
<td>Sexually Transmitted Infection</td>
</tr>
<tr>
<td>UNAIDS</td>
<td>Joint United Nations Program on HIV/AIDS</td>
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<td>UNDP</td>
<td>United Nations Development Program</td>
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<tr>
<td>VCT</td>
<td>Voluntary and Counseling Centers</td>
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<td>WHO</td>
<td>World Health Organization</td>
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1 Introduction

Current HIV/AIDS Situation World Wide

According to the World Health Organization (WHO), since Acquired Immune Deficiency Syndrome (AIDS) was first discovered in 1981, more than 60 million people worldwide have been infected by the Human Immunodeficiency Virus (HIV). The United Nations High Commission on Human Rights recognizes the necessity to protect the rights of People Living With HIV/AIDS (PLWHA) and for countries to be accountable for the protection of these individuals against stigma and discrimination. Peter Piot, director of the Joint United Nations Program on HIV/AIDS (UNAIDS), states that HIV/AIDS is unlike other diseases because it primarily affects young adults at all levels of education and skill—reducing productivity for entire economies. The epidemic diminishes years of investment in human capital (Piot, 2000). UNAIDS estimates that in 2005, there were 4.9 million new cases of HIV, for a total of 40.3 million individuals living with HIV/AIDS (WHO and UNAIDS, 2005). Of new cases in 2005, approximately 50% were 15-24 years old and about 50% were women.

Behavioral Drivers of the HIV Epidemic

Although much of the focus of HIV/AIDS is on the biological mechanisms of transmission and attack on the body, HIV/AIDS is a disease which is spread by risky behavior. Individuals are put in vulnerable situations where they are exposed to the HIV virus. The actual viral exchange which occurs is most often in a social or sexual context. Public health policy usually involves biomechanical preventive measures, such as needle exchange programs and condom distribution; however, ultimately HIV is spread by unsafe practices. Although the
Mathematical Models Offer Insight into Dynamics of Epidemics

Since AIDS was first discovered, mathematical models of the transmission of HIV have been developed to hypothesize the causative factors of the epidemic. Many models focus on the biological aspects of virus transmission; mixing dynamics of low and high risk individuals; and the impact of a core group of virus transmitters within a community. It has become apparent that the most profound factor in the proliferation of this disease is behavior and personal choice. Historically, epidemics have been modeled using a system of differential equations to describe the population dynamics in which disease is spread. In most cases, behavior change, such as stigma reduction and increasing awareness, has been modeled using an exogenous variable to change rates of infectivity within the population.

However, behavior change may not directly affect the rate at which a virus is spread within a population. Using agent-based models (ABM), we can take a closer look at the impact of behavioral feedbacks that may occur during the epidemic. Specifically, ABMs allow one to build theoretical models of social and sexual networks that may describe the societal context in which a disease may spread. Using models defined by Kretzschmar and Morris (Kretzschmar and Morris, 1996) and Axelrod (Axelrod, 1997), I construct a simplified social and sexual network that represents Papua New Guinea (PNG). This country is used as a case study because Papua New Guinea illustrates the extremes in network topology. PNG is characterized by extreme geographic isolation of ethnic groups, such that ideas of behavior change, stigma reduction, and safe sex practices may spread very slowly, as many individuals lack access to information and HIV prevention resources. Furthermore, sexual networks in Papua New Guinea
are complex. Female sex workers (FSW) are found throughout the country and often do not use protective measures against sexually transmitted diseases. Sexual coercion is an accepted practice in Papua New Guinean society, exacerbating the rate at which HIV may spread.

This thesis examines the relevancy of an agent-based approach to the HIV epidemic in Papua New Guinea. Chapter Two describes the etiology and natural history of AIDS to motivate the individualistic aspect of disease spread models. It is expected that HIV prevalence in PNG may reach levels seen in Sub-Saharan Africa. Chapter Three describes the societal context in which HIV is spread in Papua New Guinea and explains why such forecasts are made by policy makers.

Theories which describe the determinants of the HIV epidemic have changed over the years, as the sophistication and complexity of HIV transmission models have been developed. Chapter Four provides an overview of the evolution of HIV transmission models since the etiological agents of HIV were first discovered. The rational for an agent-based approach to HIV epidemic models is introduced in Chapter Five. Chapter Six presents an agent-based model for the HIV epidemic in PNG, which extrapolates from insights of past models that may be appropriate for this country. I present the results of this model in Chapter Seven and discuss policy implications and concluding thoughts in Chapter Eight.
2 Etiology and Risk Factors of AIDS

Etiology of AIDS

In 1981, the first case reports of AIDS related opportunistic infections were published in the Morbidity and Mortality Weekly Report. The Center for Disease Control and Prevention (CDC) reported the deaths of several homosexual men in California and New York City that had rare diseases which occur only in individuals with suppressed or deficient immune systems. Not until 1983 were the causative agents of AIDS linked to HIV. Since then, much research has been invested into understanding the etiology of AIDS, palliative medicines, vaccines, and policy interventions to prevent the spread of HIV. Though more than two decades have past, there is still much uncertainty over the biological mechanisms of HIV and the risk factors which affect the spread of the virus.

Today, transmission of HIV usually occurs through sexual intercourse, the sharing of intravenous needles, or vertical transmission from mother to child. The immune response to the virus is quite variable and is dependant on the host and other health related factors. After the virus has entered the body, individuals experience an acute infection phase. About 70% of individuals experience acute infection 2-6 weeks after initial infection (Dorrucci et al, 1995). Those that are infected may have no symptoms or may experience mild flu like symptoms such as fever, fatigue, headache, and a sore throat. Duration is normally less than 14 days. Those that experience a longer acute phase usually progress much faster to AIDS.

Eventually, the immune system responds to the foreign virus and the CD4+ helper T-lymphocytes and other cells combat the virus. Viral load declines, CD4+ cell counts increase, and the individual enters into what is known as a latent period. The virus is not dormant, but resumes replication within tissue compartments, especially lymphoid tissue. However,
detectable levels of the virus in the blood decrease. Individuals are infectious, though much less than the acute phase, as the efficiency of transmission is most dependant on the viral load of the infected individual (Quinn et al, 2000). For the majority of HIV cases, the immune system eventually fails, CD4+ cell counts decrease, viral load rebounds, and individuals progress to AIDS.

AIDS is clinically defined by a CD4+ count of less than 200 cells/mm³ or an HIV/AIDS-related opportunistic infection (due to the loss of CD4+). Common opportunistic infections are: candidiasis of the bronchi, trachea, lungs or esophagus; herpes zoster; *pneumocystis carinii* pneumonia, and Kaposi's Sarcoma. These opportunistic infections often coincide with different levels of CD4+ count. Kaposi’s Sarcoma tends to come earlier during the AIDS phase, occurring at CD4+ levels of 300-250 cells/mm³ (Ledergerber et al, 1999). *Pneumocystis carinii* pneumonia frequency occurs when CD4+ are at 100 cells mm³.

On average, the progression from initial infection to AIDS is nine years without treatment (Nadler, 2005). Rapid progressors may be diagnosed with AIDS in as short as 1-5 years after infection; long term non-progressors may not be diagnosed with AIDS until 20 years later (O’Brien, 2004). Genetic variation plays a role in the speed of AIDS onset. AIDS restriction genes (ARG) are polymorphic variants in human genes that influence the outcome of HIV exposure or infection. It was found that variants such as CCR5 delay AIDS, while other genetic variants, like CCL5, accelerate progression to AIDS (O’Brien, 2004). Without therapies, most individuals die within 1-3 years of diagnosis with AIDS (Nadler, 2005).

For those individuals on Highly Active Antiretroviral Therapy (HAART), life expectancy may be extended up to 36 years. HAART is a cocktail of various drugs that target certain aspects of the virus life cycle. Reverse transcriptase inhibitors suppress virus replication by
blocking the virus' DNA replication process. Protease inhibitors block the enzyme the virus needs for protein synthesis for replication. Other therapies inhibit the binding of the virus to macrophages (cells that remove pathogens) or CD4⁺ cell receptors. Viral reproduction is suppressed with HAART, but not completely stopped. Because the virus is prone to inaccurate replication, resistant HIV strains eventually emerge.

CD4⁺ lymphocytes and macrophages are the primary targets of the HIV virus. The virus first binds to certain receptors on the host, allowing the virus to penetrate the cell. The virus replicates inside the victim cell, exits the host, then finds another cell to invade. Once the HIV virus enters the host, it is unclear how it is destroyed. In some cases, nearby CD4⁺ cells—physically unharmed by the HIV virus—simply commit suicide, otherwise known as apoptosis. In other cases, the immune system wrongly perceives that a cell is infected with the virus and is destroyed by the immune system (autoimmune destruction). Nearby uninfected cells are also destroyed during the killing process of another CD4⁺ cell (bystander phenomenon). CD4⁺ cells are destroyed faster than new cells are created, thus the immune system is slowly weakened (Nadler, 2005).

Different clades or subtypes of HIV exist in various parts of the world. Clades are distinguished by letter—from A through I. Part of the difficulty in finding a cure for AIDS is that a vaccine for one subtype will not be affective against a different subtype. Subtype C is found most frequently, representing 47% of subtypes found in the world. This subtype is mostly found in Africa, India, and China. Subtype A is found most frequently after Subtype C, and makes up 27% of subtypes. It is found in South-East Asia, Africa, and Russia. Subtype B makes up 12% and is most frequently found in developed countries in North America, Western Europe, and Australia.
Uncertainty in Risk Factors

In Sub-Saharan Africa, there is wide geographic discrepancy in HIV prevalence and researchers and health practitioners question which factors impact the magnitude of the epidemic.

In most populations in Africa, there is little contribution of infection spread through intravenous drug use—for the most part, HIV transmission occurs through heterosexual contact. In Sub-Saharan Africa, women tend to be infected at an earlier age than men and also bear a larger portion of the HIV burden, although prevalence between countries varies greatly. In the United States and European Union, the AIDS burden falls most heavily on intravenous drug users (IDU) and men who have sex with men (MSM). HIV/AIDS is considered to be a concentrated epidemic in these countries because HIV persists among relatively isolated social groups of high risk individuals. Other countries are categorized as a generalized epidemic—a term used by WHO to represent an epidemic with a general prevalence of over 1%. In a concentrated
epidemic, risk of acquiring HIV depends on one’s local network of sexual or social contacts. On the other hand, in a generalized epidemic, risk of acquiring HIV/AIDS from unprotected sexual contact may be high because HIV is assumed to have permeated most parts of the country.

Among organizations such as UNAIDS and WHO, there is a consensus that the following factors may exacerbate the HIV/AIDS epidemic within a country (UNAIDS, 1999):

- Gender inequality and tendency for sexual coercion
- Tendency for large age disparity between partners
- High prevalence of other sexually transmitted infections
- Tendency for alcohol and drug consumption before sexual acts
- Frequent movement of people, especially due to migrant labor or political instability
- Topology of sexual partner networks.

Although many policy makers and researchers will agree that the factors given above exacerbate the spread of HIV/AIDS in theory, it is difficult to validate the wide discrepancy between neighboring countries in Sub-Saharan Africa by these risk factors. A study conducted in Zimbabwe found that individuals that delayed the onset of sexual debut and had fewer partners were less likely to have HIV (Gregson, 2006). But other studies have had unexpected findings. Theoretically, the occurrence of other sexual transmitted infections (STIs) should increase the probability that HIV is spread in a sexual act because lesions in the skin create openings that the virus can invade. Using data from the Rakia, Uganda cohort study, Quinn and colleagues calculated the additional risk in the following factors: more than two sexual partners in the past year, genital ulcer disease, syphilis, gonorrhea, Chlamydia, trichomonas and other STIs.¹ However, none of these factors were found to be a statistically significant risk for HIV transmission. Similarly, in the 1990s, HIV prevalence in Zimbabwe increased 12% annually, however overall STI prevalence decreased about 25% over this same period. Although HIV transmission is much less efficient than STIs, it was able to spread more widely than other

¹Quinn et al used multi-variate regression analysis to calculate adjusted relative risk ratio.
sexually transmitted diseases (Brewer et al, 2003). Because HIV prevalence has surpassed STI prevalence in countries such as Zimbabwe, some researchers hypothesize that medical care may actually expose patients to the virus. Individuals may contract HIV during medical treatment, which may cause pregnant women, military personnel, and blood donors to be especially vulnerable (Gisselquist et al, 2002).

In a study comparing the HIV epidemic in four African cities, two with high prevalence—Kisumu, Kenya and Ndola, Zambia—and two with low prevalence—Yaounde, Cameroon and Cotonou, Benin—age at sexual debut, lack of circumcision, genital herpes, and trichomoniasis were correlated with higher HIV prevalence. No other factor thought to be associated with HIV—high rate of partner change, age disparity between spouses, sex with prostitutes, low condom use—were found to have an association (Auvert et al, 2001). This study found only two variables that were consistently independent risk factors for HIV in each city: herpes simplex virus type 2 (HSV-2) and the lack of male circumcision.

However, most of these studies that focus on epidemics in developing countries are prone to bias and inaccurate data. Such studies may not have considered important cultural factors or community-wide behavior change that occurred because of the longevity of the epidemic in that area. Extremely isolated countries and communities, like those in Papua New Guinea, also have unique characteristics that extend beyond traditionally recognized risk factors. The next chapter describes cultural and geographical aspects of Papua New Guinea that may impact the transmission of HIV/AIDS within the country.

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2 These studies often coincide with interventions to promote condom usage, AIDS education, and STI treatment. Participation is voluntary; therefore individuals are self selecting themselves to be in the study. Furthermore, it is difficult to ensure accurate data collection, especially on past partner information, when educators intimate that having multiple partners is risky behavior. Retrospective data collection may not be accurate because of memory biases or shame of disclosure.
3 HIV/AIDS in Papua New Guinea

Introduction and Current Statistics

Papua New Guinea is the first country in the South Pacific to be classified by the World Health Organization (WHO) as undergoing a generalized HIV epidemic. It is estimated that there is an HIV/AIDS prevalence of 1.7% in the population of 5.4 million people—although it is recognized that Papua New Guinea is in the early phases of the epidemic. It is often said by the media and multilateral aid organizations that the epidemic in Papua New Guinea will be similar to Sub-Saharan African countries if a coordinated response does not occur soon. This chapter examines the specific risk factors which cause Papua New Guinea to be susceptible to a large scale epidemic.

HIV and STI Prevalence

The first case of HIV was discovered in Papua New Guinea in 1987. By the end of June 2004, 9,851 cases were reported. Of these reported cases, 61% were reported from Port Moresby, the capital city and only throughway for international travel.
HIV cases are reported from antenatal (ANC) and Sexually Transmitted Infection (STI) clinics, blood drives, military recruitment tests, epidemiology and anthropology studies, and three recently established HIV/AIDS Voluntary and Counseling Centers (VCT). In 2003, the ANC in Port Moresby had 1.35% prevalence among pregnant women and 20% at the STI clinic. It is estimated that only one out of five HIV cases are reported (Moodie and Fry, 2000). At the current rate of incidence, AUSAID estimates that 10% of the population may be infected in fifteen years (Caldwell, 2000).³

The prevalence of other STIs is very high. In one study which compared STI prevalence in two major cities—Port Moresby and Lae—researchers recruited self identified female sex workers (FSW). The study tested women in 1998 and 1999 for HIV, syphilis, Chlamydia, gonorrhea, and trichomoniasis. Prevalence was found to be 10%, 32%, 31%, 36%, and 33%, respectively, in a cohort of 400 women. HIV prevalence in Port Moresby, 17%, was higher than

³ Estimates of prevalence among the generalized population are extrapolated from the available data reported from the sites mentioned. However blood drives usually occur at local schools and thus represent a low risk population, further underestimating the true prevalence (Personal conversation with Dr. Carol Jenkins).
Lae, 3%. Of these women, 78% had at least one STI and 45% had more than one (Mgone et al, 2002). However, high STI prevalence is not limited to commercial sex workers. In a study which randomly selected women in the remote Asaro Valley in the Eastern Highlands, it was found that 58% of women had one or more STDS (Passy, 1996).

However, all statistics on HIV and STI prevalence are reported with much uncertainty. It is acknowledged that the higher incidence of HIV in Port Moresby is due to the better availability of facilities in the capital city and true prevalence in the more remote parts of the country is completely unknown.

WHO estimates that 50% of mortality in Papua New Guinea is due to communicable diseases. AIDS is the leading cause of adult mortality at Port Moresby General Hospital and malaria the leading cause of outpatient visits (WHO, 2005). It is widely acknowledged that there is a need for a sustainable flow of antiretroviral therapies (ART), a greater number of health facilities, better trained professionals, and countrywide coordination in prevention, treatment, and stigma reduction.

Geography and Mobility

Papua New Guinea is one of the most diverse and isolated countries in the world. More than 800 languages are spoken in Papua New Guinea, one-seventh of all languages in the world (Gibson and Rozelle, 2003). The abundance of languages is a result of the physical and social isolation of Papua New Guineans for hundreds of years. Impenetrable bush, high mountains, swamps, and isolated islands keep communities highly fragmented. In fact, before colonization there was limited contact between ethnic groups—outside of trade and warfare (Walsh, 1987).

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4 This could be due to a significant imbalance in the availability of testing facilities. There are 28 laboratories throughout the country that perform HIV testing, although Papua New Guinea National HIV Reference Laboratory is the only laboratory which is authorized to confirm and reports results (Babona et al, 1996).
The road system in Papua New Guinea is completely fragmented—there is no highway which connects the major cities. In Port Moresby, paved roads extend out 20 miles and abruptly end. It is estimated that the average travel time from a village to a government facility is three hours. The average travel time from village to the nearest road is 2.5 hours, (Gibson and Rozelle, 2003) although in the highlands, the average time is about four hours. Many parts of the country are only accessible via airplane or canoe.
Figure 3.3 Map of Roads in Papua New Guinea

Source: United Nations Department Of Peacekeeping Operations

Figure 3.4 Provinces of Papua New Guinea

Source: Walsh 1987
The Highlands of Papua New Guinea (Eastern, Western, and Southern Highlands; Simbu and Enga Province) holds one-third of the population. It is also the least urbanized region and the last to have contact with the outside world—the first foreigners entered this region in the 1930s. It is estimated that 33% of the rural population and 11% of urban population live below poverty line. Poverty is highest in the highlands and north coast region (Gibson and Rozelle, 2003).

Although there are few means of transportation, individuals are relatively mobile—migration occurs mostly by young men in search of work. In 1980, the first country-wide census was taken. It was found that 1 in 10 individuals moved permanently to another province from their place of birth. Migration usually flows from poorer parts of the country to more urban areas: Lae and Madang—port towns; Wau and Bulolo—mining towns; the plantations in the islands region, and Port Moresby. The mobility of individuals has caused some concern for HIV spread. Circular migrations may bring HIV to isolated parts of Papua New Guinea and the disease may persist because of the insular nature of social and sexual groups in remote areas.5

**Government Response is Inadequate**

The National AIDS Surveillance Committee was established within the Department Of Health in 1986 to develop a country wide surveillance program and establish policies for diagnosis, HIV prevention, and care to People Living With HIV/AIDS (PLWHA). The organization functioned sporadically from 1988 to 1994 and efforts for a surveillance program were not successful. By 1995, only passive surveillance programs were instituted in some parts of the country (World Bank, 2004). The National AIDS Council (NAC) was established in 1997

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5 One airport in the island province of East New Britain had a sign which said “Don’t Bring AIDS to Rabaul.”
as a formal government entity to coordinate prevention and education efforts (Malau, 1999). The Medium Term Plan—developed by the Department of Health in conjunction with WHO—outlined new objectives to be reached by 2002. The Medium Term plan called for a multi-sectored approach to AIDS prevention and summarized targets for education programs, laboratory support, program management, and surveillance. This too had limited success in implementation. The national plan was too broad in nature and did not contain enough direction to implement policy. Furthermore, several programs have been administered in Port Moresby, but as many as three-fourths of infected people are in rural areas (World Bank, 2004). Australian Agency for International Development (AUSAID), Australia’s foreign assistance program, is the main aid agency that operates in Papua New Guinea. Other countries, such as Japan, US, and New Zealand, have small aid programs in Papua New Guinea; however AUSAID coordinates HIV programs with the Papua New Guinea government. In general, there is little coordination between AUSAID and religious institutions which provide many health services throughout the country. Unfortunately, because of poor surveillance programs, it is difficult to gain the political momentum to organize a country-wide response to AIDS due to the lack of reliable knowledge of the pervasiveness of HIV/AIDS and the impact it will have on the country.

The Role of Church in HIV/AIDS Prevention

One common factor among Papua New Guineans is an affiliation with a religious institution. Self proclaimed Catholics and Lutherans make up more than half the population (Luker, 2004). Churches in Papua New Guinea are the most effective institutions for influencing societal values, as they serve as locations for social gatherings, information exchange, and moral guidance. Although it is recognized that religious institutions have a strong influence on

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6 Personal communication with Robyn Biti, AUSAID.
influencing cultural norms, religious ideals and local beliefs are often at odds with each other; animism is still practiced in most villages, even among professed Christians.

In Papua New Guinea, churches provide almost 50% of health and education services, filling gaps where government services do not exist. Churches also run their own radio and television stations (Luker, 2004). Because religious institutions control many education, health, and media services, the voice of the church is very powerful—but the response to HIV/AIDs has been varied. For the most part, churches emphasize monogamy and non-dependence on condoms. There are reported instances of preachers exhorting that condom usage will cause individuals to lose their salvation. It has also been reported in some health facilities that nurses will not give condoms to unmarried men. Some prominent members of the Catholic community denounce the use of condoms claiming that it promotes sex (Luker, 2004). On the other hand, some churches have developed HIV/AIDS prevention programs centered on education and stigma reduction. The Anglican Church has made efforts to improve condom availability through their HIV/AIDS prevention programs and campaigns to reduce AIDS discrimination (Eves, 2003). It is important that a large scale response to HIV prevention involves coordination with religious institutions, as churches have more leverage in promoting awareness and safe practices within these communities.

**Gender Based Violence**

WHO considers gender-based violence an issue of global public health (Heise et al, 1994). Widespread violence against women is a concern for policy makers, not only because of the physical and psychological damage that may be incurred, but also because of the underlying societal norms it suggests—that women cannot fully participate in decision making in society. In many countries, women cannot negotiate condom usage because of the lack of respect for
women’s rights and independence. Not only is it difficult for women in Papua New Guinea to negotiate with their partners, coercive sexual intercourse is culturally accepted. Researchers and anthropologists believe that rape may be higher in Papua New Guinea than in any other country (Borrey, 2000). Rape is a major concern for the spread of HIV; microscopic tears in the mucosal lining of the vagina can occur during normal sexual activity and coercive sexual activity may increase the chance of tears.

Women that demonstrate influences of western culture or modernization in their behavior and dress are often harassed and denounced by the church and community (Zimmer-Tamakoshi, 1993). Fears of rape restrict women from speaking openly about gender rights. In some cases, it prevents girls from attending school (Zimmer-Tamakoshi, 1993). In a survey of domestic violence in rural areas, 67% of women admitted to being beaten by their husband (Zimmer-Tamakoshi, 1993). Coercive sexual relations occur between married partners, acquaintances, and strangers. The high incidence of rape may be due to the perception that mental or physical damage does not occur during intercourse even if it is coercive (Banks, 2000). However, when rape victims were questioned, women admitted to a feeling of shame, as do their families (Zimmer-Tamakoshi, 1993).

Pack rape, known as line-up, is commonplace throughout the country. In Goroka, a major town in the Eastern Highlands, the Public Prosecutor’s Office stated that pack rape may occur more often than traditional rape in that region. The number of reported sexual offences was about 1,200 each year, between 1994 and 1996, although this most likely grossly underestimates the true incidence of rape.

One researcher compiled a survey of women’s views on sexual violence in various provinces. Borrey hypothesized that the criminality of coercive sex is a concept not recognized
in many parts of the country. She found that when asked for examples of what she described as rape, individuals responded with instances of adultery. Women did not describe incidences of rape unless explicitly probed for situations where consent was not given. Borrey believes that illustrations of adultery were often cited because of the societal aversion for extramarital affairs of men (and the normalcy of rape). She also observed that bonds are closer between men than between partners—to the extent that men would share their partners with others that would not otherwise have access to sexual intercourse (Borrey, 2000).

The status of women has serious repercussions on the HIV/AIDS epidemic in Papua New Guinea. Women may be exiled from their villages, without access to food or water, if her HIV positive status is exposed.\(^7\) In one study which compared attitudes of sexuality and HIV in urban, peri-urban, and rural areas, nearly all participants said that they would expect to be banished from the family if they had AIDS (Jenkins and Alpers, 1996).

There is much stigma associated with HIV because of assumptions of adultery and religious discretion towards issues of sexuality. The violence inflicted on individuals that are HIV positive prohibits open discussion of status between partners and discourages individuals from seeking treatment or getting diagnosed.

**Commercial Sex Workers May be Core Group Transmitters**

Female sex workers (FSW) in Papua New Guinea may be a core group of transmitters of HIV/AIDS. Although commercial sex occurs throughout the country, FSWs are especially prevalent in the few urban cities of Papua New Guinea and along the Highlands Highway (the most extensive road in the country). According to one study, the lowest-paid sex workers have between 300-900 clients a year (Jenkins in Ahlburg and Jensen, 1998). In general, FSWs are not

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\(^7\) Personal communication with a member of UNDP Papua New Guinea. Instances have been brought to their attention of where women with HIV are beaten by their husband and abandoned.
rejected by their families as long as earnings are shared (Jenkins, 1997). Sex workers are also frequently raped by police officers and have reported incidences of pack rape by officers. In a study which compared FSWs in two major cities in Papua New Guinea, 85% of participants reported inconsistent condom use with clients. In Port Moresby and Lae, 52% and 34%, respectively, stated that they had regular partners, and 71% of these women stated that they never used condoms with their regular partners. Twenty seven percent reported having been pack raped at least once in their life (Mgone et al, 2002). A study by USAID interviewed FSWs in Port Moresby and Goroka using contact tracing methods. About 65% of participants reported sexual relations with at least one non-paying partner in the previous seven days. Participants reported 62% and 32% consistent condom usage with paying clients, in Port Moresby and Goroka respectively, and 34% and 16% consistent condom usage with non-paying partners. Only 20% and 10% utilized VCT facilities in their respective cities (Maibani-Michie, 2005).

Cultural Practices and Taboos are Independent Risk Factors for HIV/AIDS Transmission

Other sexual behaviors that may spread HIV/AIDS throughout the country are high rates of partnership formation and other cultural practices. Jenkins (in Caldwell, 2000) found that the average number of long-term partners for men was 10 during adolescence, to over 20 by the time men reach 60. Ritual homosexuality among men is commonly practiced in several parts of the country.

8 Because participants were brought into the study by referral from other FSWs, it is difficult to assess if these findings are generalizable to FSWs in Port Moresby, Goroka, and in other parts of the country.
country (Caldwell, 2000), usually in ceremonies for “rights of passage” and “fertility enhancement” (Jenkins, 1994).

In a study which surveyed a population in Lelet, Central New Ireland, it was found that there is very little knowledge about HIV/AIDS and Christianity was a framework often used to understand the disease. The Lelet believe that misdeeds are punished through supernatural means or human agents and that the spread of AIDS—and promiscuity that is associated with the epidemic—indicates that the Last Days are near (Eves, 2003). Even before the influence of western missionaries, the Lelet associated sexuality with shame. Sexual intercourse was referred to as pasin nogut, or bad behavior. Before colonization, sexual relations outside of marriage were punished by death. Even today, adulterers are penalized in some manner—usually the sacrifice of a pig.

In Lelet, there is much taboo regarding the interactions of men and women and sexuality. Women must avoid the physical position of being above men; they are forbidden to climb a tree if a man is around. In the same way, men must not walk underneath a woman’s house nor walk beneath her hanging clothes. Their association of sexuality and shame may inhibit discussions of HIV/AIDS prevention. There is little awareness of the pathways by which HIV/AIDS may be transmitted. Some villagers believe that HIV may be spread by sharing a cigarette or wearing an infected person’s clothes (Eves, 2003).

Unfortunately, religious institutions, which are the only source of education and media information in some regions of the country, do not encourage proper awareness of AIDS. There are stories of AIDS recovery through supernatural intervention; the silence of the church allows individuals to believe that AIDS is caused by sexual misconduct. For example, it was heard that

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9 No cases of HIV/AIDS have been reported from this area.
a man in Ugana, a coastal village in New Ireland, contracted AIDS. He confessed his sins to his village, and was soon cured (Eves, 2003).

Other examples of poor knowledge of sexually transmitted infections abound. One study of STI knowledge in the Eastern Highlands Province found that individuals associated STIs with types of people or occupations. They believed that “loose women” or women with multiple marriages were susceptible to STIs, as were highway drivers. Only one person expressed the view that all sexually active persons are at risk. Many in this province believe that STIs were caused by unhappy spirits in the body, and that the person would heal only after the spirit was appeased by a sacrifice. In the Asaro Valley of the Eastern Highlands, women put mud on their stomachs in the belief that it prevents pregnancy. Women that became infertile, due to STIs or other health related problems, assumed that this practice caused their sterility (Lemeki et al, 1996).

Lemeki et al found that women did not utilize local health facilities, if they existed, because of the lack of privacy and unpleasant treatment from hospital staff or the expectation that symptoms would eventually disappear (Lemeki et al, 1996). In general, utilization of STI services are low because of taboos surrounding sexual activity and little knowledge of STIs (Passy, 1996).

Social Networks – Wantok

A unique aspect of Papua New Guinean culture is the concept of a wantok. Literally, wantok is translated as “one tongue.” Wantok refers to a bond between members of a community which requires a sharing of duties and responsibilities between a group of individuals. The wantok network requires that members share resources—benefits are considered communal and the needs of the wantok come before the needs of the individual (Lea, 1993). Even marriage
partnerships may be formed for strategic benefits of the wantok. Although wantok networks
have weakened in urban areas, it is commonly believed that “wrong” acts are only those which
harm the wantok, regardless of actual legality (Lea, 1993).

The wantok is a source of culture, social activity, and social welfare. It is believed that
there is relatively little poverty because funds are redistributed through the wantok network.
However, if an individual is discovered to have HIV/AIDS, he or she may not be supported by
the wantok, promoting non-disclosure of HIV status.

Risk Factors Unique to Papua New Guinea

There are many cultural indicators in Papua New Guinea that suggest a severe HIV/AIDS
epidemic may occur. The government is overly reliant on AUSAID to develop and coordinate
HIV prevention and treatment programs. The government evades public health responsibilities
by awaiting the actions of international donors. Geographic isolation of the many ethnic groups
makes it logistically and linguistically difficult to promote ideas of safe sexual practices and non-
discrimination of PLWHAs. Rape and domestic violence not only physically perpetuate the
spread of HIV; it also prevents women from disclosing their HIV status and taking advocacy
roles in HIV programs. Commercial sex workers may play a role in facilitating the spread of
HIV, as safe sex practices are not always used. Cultural taboos prevent open discussion of
sexuality and sustain incorrect ideas of HIV transmission and risk. These cultural factors must
be taken into consideration when estimating current and future AIDS prevalence in Papua New
Guinea. Although many HIV transmission models attempt to predict and explain drivers in HIV
epidemics around the world, it is important to capture cultural and country specific dynamics.
The following chapter provides a survey of HIV transmission models and provides a basis for the
model of HIV transmission for Papua New Guinea, presented in Chapter 6.
4 Survey of HIV Transmission Models

HIV Public Health Models

The history of HIV models extend as far back as the discovery of the etiological agent of AIDS in the early 1980s. Public health models range from cost-benefit analyses of policy interventions to pharmacokinetic models of anti-retroviral impact and resistance on the immune system. This chapter presents the evolution of health models which focus on transmission dynamics of HIV/AIDS within heterosexual populations.

Extrapolation Models

HIV transmission models attempt to predict the magnitude of an epidemic within a given population and may also analyze the drivers which facilitate HIV spread. The simplest HIV models are extrapolation or back calculation models that were developed in the mid- to late 1980s. These models focus on projecting the future epidemic curve of a country by extrapolating from current prevalence data on a subset of individuals in the population. These models were frequently used by organizations such as UNAIDS and WHO to estimate the number of people infected with HIV. Although simplistic, these models served to draw the attention of the international community for a policy response.

Epimodel, an extrapolation tool, was first developed for the United Nations. This model uses the prevalence measured at a point in time and a reproduction (or infectiousness) rate, and predicts the date the outbreak began and future prevalence. Because of the overgeneralization of this model, it was replaced in 2003 with the UNAIDS Estimation and Projection Package. Four parameters are used in this model: a prediction of the year the epidemic began, the size of the initial population at risk, the force of infection (or the rate of transmission normalized by the proportion of the population already infected), and the rate in which individuals enter a high risk
category (UNAIDS and WHO, 2003). Because of the paucity of data in developing countries, these models are often the best tools for policy makers.

**Differential Equation Models**

Differential Equations (DE) are frequently used to simulate epidemics. Equations define the number of infected individuals within a population and the rate at which individuals become infected. Susceptible-Infected-Retired/Recovered (SIR) models served as the basis for most DE models of epidemics. The following diagram describes the system of most DE HIV transmission models:

![SIR Compartments Diagram]

Let $X$ be the number of Susceptible individuals in Population $N$, $Y$ the number of individuals infected with HIV, and $A$ the number of individuals that have progressed to AIDS. Then a simple compartmental model of the HIV epidemic may be described by the following system:

$$\lambda = \beta c \frac{Y}{N}$$  
\text{Equation 4.1}

$$\frac{dX}{dt} = -\lambda X$$  
\text{Equation 4.2}

$$\frac{dY}{dt} = \lambda X - \nu Y$$  
\text{Equation 4.3}
\[ \frac{dA}{dt} = vY - dA \]

Equation 4.4

\[ \frac{dN}{dt} = -dA \]

Equation 4.5

\[ R_0 = \beta c \]

Equation 4.6

The force of infection, \( \lambda \), is the rate at which susceptibles as an aggregate become infected. Let \( \beta \) be probability of HIV infection within a partnership involving one uninfected and one infected partner, \( c \) be the rate at which partnerships are formed, \( v \) the progression rate from HIV to AIDS, and \( d \) be the mortality rate of those with AIDS (i.e. the likelihood of mortality per time unit). In Equation 4.3 it is assumed that those in the AIDS phase do not contribute to HIV spread because of the weakness in health of individuals that have progressed to AIDS. \( R_0 \) refers to the reproduction rate. Mathematically, the reproduction rate is the product of the per-partnership probability \( \beta \) of the transmission of the virus, the number of partnerships per time period that could result in transmission \( c \), and the duration of infectious period \( D \). Reproduction rate refers to the number of secondary infections which result from an infected individual. If the reproduction rate is above 1, the epidemic will persist, if it is below 1, it will eventually die out.

In this system, all individuals within each compartment are homogenous and have equal probability of interacting with others. Such models allow the user to experiment with different levers to solve the system. In other words, the rates of \( \beta \) and \( c \) can be modified to obtain a reproduction rate of less than 1. Policy interventions are represented in this SIR model by decreasing contact rate and transmission probability or increasing duration. For example, the

\(^{10}\) \( \beta \) refers to the biological efficiency of the virus. This variable is derived from epidemiology studies of discordant partners, where the probability of transmission from the infected partner to the uninfected partner is measured over a period of time or per sexual act.
impact of an education program that results in an increase in condom usage would be represented by lowering the $\beta$ term in the system. Uptake of HAART is represented by the increase in duration of infectious period $D$.

**Development of Transmission Models within the Biomathematics Community**

Advances were made within the Biomathematics community with the development of more complex and realistic models which incorporated possible risk factors in HIV transmission. Anderson et al pioneered HIV transmission models, using differential equations to simulate the epidemic in developed countries, specifically among groups that tend to be homogenous, such as the homosexual population in San Francisco and New York City (Anderson et al, 1986). Anderson et al extended from other STD models (Hethcote and Yorke, 1984) the idea of a core group of HIV transmitters in which the disease spreads rapidly and persists. This may occur in situations that attract large numbers of people, such as urban areas, military bases, and large scale infrastructure projects. Core groups are individuals that are highly connected to each other and have circular social patterns—individuals tend to move about the same group of individuals. In terms of the heterosexual spread of HIV, core group usually refers to commercial sex workers and their regular clients.

Anderson et al divided the population $N$ into groups, indexed by sexual activity group $i$. Sexual activity groups are characterized by rates of partner change per unit time. The rate of change in the susceptible population—for each activity group—is defined as:

$$\frac{dX_i}{dt} = -\lambda X_i$$

Equation 4.7

The force of infection, $\lambda$, is given as:
The rate of infection is dependent on $\beta$ and the probability that a randomly chosen partner is infected. The $\lambda$ function is weighted by the total infected contacts within the population, per activity group. This is referred to as proportionate mixing, where the probability of choosing an infected partner is weighted by the increasing risk (higher $c_i$ and $Y_i$) of different activity groups in the population.

Anderson et al. also extended the SIR model to describe unique aspects of HIV. In 1986, when the model was published, it was hypothesized that the relationship between incubation time and likelihood of the onset of AIDS may be a linear function of time. Thus variable incubation periods were added into the model:

$$\nu(\tau) = \alpha \tau$$

Equation 4.9

and the rate that individuals become infected is expressed in partial differential equation form as:

$$\frac{\partial Y}{\partial t} + \frac{\partial Y}{\partial \tau} = -\nu(\tau)Y$$

Equation 4.10

This model provided the groundwork for future deterministic HIV models.

**Incorporating more Realism to Analyze Transmission Risk Factors**

As the epidemics in countries around the world matured, the speed and peak of the HIV epidemic had different characteristics between and within countries, especially in Sub-Saharan Africa. Models began to incorporate factors that could be responsible for these differences. It was apparent that sexual behavior varied from country to country. Customary time of sexual
debut, intravenous drug use, circumcision, and urban migration all seemed to be possible risk factors for HIV transmission within a population. Furthermore, the heterosexual spread of HIV has a significant social aspect in transmission. Sociology studies in other disciplines showed that individuals exhibited homophily or preferential mixing—the predilection to interact with individuals with similar characteristics (Bearman et al, 2004).

Garnett and Anderson explored the effect of intermixing high and low risk groups in the heterosexual spread of HIV—specifically in developing countries (Garnett and Anderson, 1993). The Anderson et al model was extended to incorporate probabilities of mixing between groups. Garnett and Anderson further segment the population by sex $k$, sexual activity group $l$, and stage of infection ($s = 1, 2, 3$ to denote variable infectivity in 3 stages before AIDS onset) dependent on time $t$ and age $a$. Therefore, the susceptible and infectious population is defined in partial differential form as:

$$\frac{\partial X_{kl}(a,t)}{\partial a} + \frac{\partial X_{kl}(a,t)}{\partial t} = -\lambda_{kl}(a,t)X_{kl}(a,t)$$

Equation 4.11

$$\frac{\partial Y_{kl}(a,t)}{\partial a} + \frac{\partial Y_{kl}(a,t)}{\partial t} = \lambda_{kl}(a,t)X_{kl}(a,t) - \gamma_{s}(a)Y_{skl}(a,t)$$

Equation 4.12

$$\frac{\partial Y_{skl}(a,t)}{\partial a} + \frac{\partial Y_{skl}(a,t)}{\partial t} = \gamma_{s-1}(a)Y_{(s-1)kl} - \gamma_{s}(a)Y_{skl}(a,t)$$

Equation 4.13

Garnett and Anderson extend the force of infection $\lambda = \beta c \frac{Y}{N}$ to include more heterogeneity. Contact rate is defined by the rate an individual of sex $k$, sexual activity group $l$, and age $a$ acquires a new partner of group $m$ of age $a'$ at time $t$. Therefore:

$$c = c_{klm}(a,a',t)$$

Equation 4.14
In the previous Anderson et al model, the probability of choosing an infected partner was weighted by sexual activity groups. Garnett and Anderson explicitly define mixing between groups by $\rho$, which is the probability that an individual of sex $k$, sexual activity $l$, age $a$ will have a partner of the opposite sex in the sexual activity group $m$ of age $a'$.

$$\rho = \rho_{km}(a,a')$$

Equation 4.15

Therefore the force of infection becomes:

$$\lambda_{kl}(a,t) = \sum_{m=1}^{n} \left[ c_{km}(a,a',t) \rho_{km}(a,a') \frac{\sum_{s=1}^{r} \left( \beta_{sh} Y_{skm}(a',t) \right)}{N_{km}(a',t)} \right] da'$$

Equation 4.16

The integral is evaluated between the age that sexual activity begins $\tau$, and the age that sexual activity stops, $\psi$, for all $n$ activity classes. Mixing depends on explicitly defining a matrix of probability contacts between each sexual activity group.

Instead of specifying probabilities of mixing for each group, Jacquez et al extended the research of Garnett and Anderson by assuming that there could be several high risk groups within a low risk population. Jacquez et al assumed that these groups would exhibit preferred mixing (sexual contacts primarily within one's social network), and examined the impact of varying the proportion of intra- and inter-group mixing between the high and low risk groups.

Jacquez et al define preferred mixing by:

$$\rho_{ii} = \rho_i + (1 - \rho_i) \frac{c_i(1 - \rho_i)(X_i + Y_i)}{\sum_k c_k(1 - \rho_k)(X_k + Y_k)}$$

Equation 4.17
\[ \rho_j = (1 - \rho_i) \frac{c_j (1 - \rho_i)(X_j + Y_j)}{\sum_k c_k (1 - \rho_k)(X_k + Y_k)}, \quad j \neq i \]

Equation 4.18

where \( \rho_i \) is the proportion of contacts in group \( i \) that are reserved for its own group. If \( \rho_i \) is 0, it is proportional mixing, if \( \rho_i \) is 1, there is no mixing between groups.

They found that for high activity risk groups a greater proportion of inter-group mixing decelerates the epidemic within this group. However, the rate of infection in the low activity group is highly sensitive to the increased mixing with high risk groups. The rate of infection increased with the greater proportion of mixing with the high risk groups, although the number of contacts and transmission probabilities did not change.

**Development of Partner-Based Models**

In the models described above, all individuals are susceptible to infection throughout the entire simulation of the model. However, in a sexually spread HIV epidemic, the possibility of transmission only occurs within a partnership. Dietz and Hadeler pointed out that if a partnership is formed between two uninfected individuals, they are immune from infection during the duration of the partnership (Dietz and Hadeler, 1988). Therefore, the rate of partner change may be considered an independent risk factor, as the formation of a new partnership results in another opportunity for transmission to occur.

The models presented thus far define the contact rate \( c \) as the rate of partnership formation and \( \beta \) as the probability of transmission per partnership. Dietz and Hadeler consider the case of heterosexual partnerships, and define the contact rate as the number of sexual acts
within a partnership that may result in infection. The probability of transmission is defined per sexual act.

Pairs are formed at rate $p_{ij}$ and separated with rate $\sigma_{ij}$. Let $c$ be the rate of sexual acts within a partnership and $\beta$ the probability that an infection occurs during a sexual act. Single individuals (i.e. individuals outside of partnerships) are defined as follows:

- $x_0$: female single, uninfected
- $y_0$: male single, uninfected
- $x_1$: female single, infected
- $y_1$: male single, infected

And heterosexual partnerships using the following classification:

- $p_{00}$: partnership, both partners uninfected
- $p_{01}$: partnership, female infected
- $p_{10}$: partnership, male infected
- $p_{11}$: partnership, both partners infected

The system is defined as:

\[
\begin{align*}
x_0 &= -\left(\phi_{00} + \phi_{01}\right) + \sigma_{00}p_{00} + \sigma_{01}p_{01} \\
y_0 &= -\left(\phi_{00} + \phi_{10}\right) + \sigma_{00}p_{00} + \sigma_{10}p_{10} \\
x_1 &= -\left(\phi_{10} + \phi_{11}\right) + \sigma_{10}p_{10} + \sigma_{11}p_{11} \\
y_1 &= -\left(\phi_{01} + \phi_{11}\right) + \sigma_{01}p_{01} + \sigma_{11}p_{11} \\
p_{00} &= -\sigma_{00}p_{00} + p_{01} + p_{01} + \phi_{00} \\
p_{01} &= -\left(\sigma_{01} + \beta c\right)p_{01} + p_{11} + (1 - \beta)\phi_{01} \\
p_{10} &= -\left(\sigma_{10} + \beta c\right)p_{10} + p_{11} + (1 - \beta)\phi_{10} \\
p_{11} &= -\sigma_{11}p_{11} + \beta cp_{01} + \beta cp_{10} + \beta \phi_{01} + \beta \phi_{10} + \phi_{11}
\end{align*}
\]

Equation 4.19

Pair formation is modeled by the function $\phi(x, y)$ and describes the probability that individual $x$ will form a partnership with individual $y$. The function $\phi(x, y)$ essentially computes a compatibility formula where partnership formation is dependent on attributes of the two individuals.
The Dietz and Hadeler model catalyzed a new way of thinking about the structure of sexual networks that may influence the spread of disease. Modelers began to think more about partnerships and sexual network topology as an independent risk factor for HIV transmission. Specifically, if individuals engage in sexual activity over some period of time with more than one partner, the epidemic may spread much faster—which is not unusual for commercial sex workers. In a paper published by Kretzschmar and Morris, they demonstrate that the structure of the network is important, since infection is passed from individual to individual (Kretzschmar and Morris, 1996). Because infectivity is variable and has relatively low efficiency, the spread through a concurrent network may be dramatically faster than infection spread through a network of serially monogamous individuals. Kretzschmar and Morris use contact graphs to demonstrate this relationship. In the graphs below, nodes represent individuals and edges represent a partnership.

![Figure 4.2 Contact Graphs](image)

In the first graph from Figure 4.2, all individuals may be infected with HIV if the middle individual is infected. In the second graph, the virus has to travel through each of the individuals to infect all connected individuals. Because of varying infectiousness in the duration of the disease, the transmission may not spread through the entire network.
The Kretzschmar and Morris model also advanced the field of HIV modeling by using an agent-based approach to disease simulation. While the mathematical models formulated above reasoned about the aggregate counts of individuals with different characteristics, in agent-based models, objects (or "agents"), are explicitly defined and represented in the model. Each agent has characteristics and rules of behavior. Partnerships are formed between discrete individuals and a dynamic sexual network is explicitly defined. Kretzschmar and Morris used the equations defined by Dietz and Hadeler to develop rules of agent behavior at the individual level.

The following algorithm is used to simulate a sexual network and HIV transmission (Kretzschmar and Morris 1996):

- Partnerships are formed at each time step with probability $\rho$.
- Two individuals are randomly chosen until a partnership is formed according to a mixing function $\varphi$.
- In pairs with an infected individual, disease is transmitted with probability $\lambda$ at each time step.
- At every time step, partnerships are separated with probability $\sigma$.

Kretzschmar and Morris analyze the impact of concurrency over four theoretical networks. They compare networks of serial monogamy, random, disassortive, and preferred mixing. They found that in a disassortive sexual network (where individuals are more likely to join in a partnership based on the difference in the number of partners they currently have) the odds ratio of a large epidemic is 4.7.\(^{11}\) In a network where individuals are randomly paired, odds were 1.14, with preferred mixing odds were 1.29, and in a network where monogamy was practiced, the odds were 0 (Kretzschmar and Morris, 1995).

\(^{11}\) A large epidemic was defined as an HIV/AIDS prevalence greater than 1%.
Incorporating Behavioral Feedback: System Dynamics Approach to HIV modeling

While the differential equation models as described above offer a detailed dynamic characterization of the spread of HIV within a population, they typically assume that an individual’s sexual behavior does not change in response to the spread of that disease. In other words, classic compartment models of HIV generally do not define explicit behavioral feedbacks into the system. Behavioral feedbacks—such as increased awareness of HIV risk or consistent usage of condoms—is incorporated into models not by explicit equations, but by manual increases or decreases to the contact rate or transmission efficiency. Perhaps a System Dynamics approach is particularly relevant to HIV modeling because of its emphasis on identifying reinforcing mechanisms that sustain particular dynamics within the system. Although HIV is a viral disease, heterosexual epidemics are ultimately driven by behavior patterns of sexual practices.

In System Dynamics, aggregate characteristics, variables, and feedback mechanisms are the main components of the system. Relations between stocks or compartments and other variables are defined to form a series of differential equations. Variables are continuous and are dependent on time and impacted by feedback mechanisms that may be dependent on stocks in the system and time delays. System Dynamics models are not necessarily mathematically different in its characterization of a system from DE models. However, incorporating behavioral feedback would allow parameters, such as infectivity $\beta$ and contact rate $c$, to change over time by making explicit the linkages between such parameters and other dynamic variables.

The drag-and-drop development environment in most System Dynamic modeling applications allow for visualization and incorporation of underlying variables that are important
to identify within the system. For example, propensity to disclose HIV status and perception of HIV prevalence are factors which impact the rate of HIV infection, although may be difficult to define using differential equations. The figure below (Sterman, 2001) uses the stock-and-flow diagramming techniques common in System Dynamics to depict the impact these variables have on infectivity and contact rate.

Figure 4.3 Impact of Perceived Prevalence and Disclosure on Infectivity

Figure 4.4 Impact of Behavioral Feedbacks on Infection Rate
Although no other dimension or state is added into the model, the explicit recognition of behavioral feedbacks in System Dynamics—such as AIDS disclosure—is an important variable when modeling intervention and defining the boundaries in the social systems in which the HIV epidemic occurs.

**Further Analysis of Structured Networks**

A cohort study undertaken on HIV spread in Colorado Springs resulted in a number of papers that examined the cohesiveness of groups within a sexual network. In one study which recreated the network of this cohort, it was found that within this community, the average distance to an individual with HIV was two connections away (Klovdahl et al, 1993). The network was created by a contact tracing method aimed at identifying potential transmission contacts from a source individual (Keeling and Eames, 2005). Although contact tracing does not capture the entire network, the areas of the network with the highest burden should have the most detail (Keeling and Eames, 2005). Potterat et al compared the network dynamics of HIV in Colorado Springs and the spread of syphilis in a small community in Atlanta, using contact tracing to analyze the changes in the sexual network over time (Potterat et al, 1999). In a prospective look at the Colorado Springs population from 1988-1992, it was found that the size of the average component (i.e. group of individuals in which the path length is equal between all members) of the network decreased during this time of increasing awareness of HIV risk. In other words, the density or connectivity of the network grew smaller during this period. At the same time, HIV incidence decreased, intimating that the structure of transmission networks, particularly the density of sections of the network, may play a role in the spread of STDs. This hypothesis was further affirmed by the data from Atlanta. The sexual network, which was analyzed for the time period 1996-1998, exhibited increasing cohesion. In an 18 month period,
the number of components decreased from a dozen small groups to one large component of 95 people. This study suggests that the structure of networks both influences and is influenced by the spread of HIV.

**Complexity in HIV Models**

Many transmission models have been developed in the past two decades. Recent models analyze variables such as the cumulative lifetime risk of HIV infection or incorporation of high risk areas—such as main highway fares or military bases—into a social space in the model (Koopman and Chick, 2000). However, it is difficult to validate models that are highly complex and have many dynamic components. Furthermore, models which have greater detail also require more processor time to execute.\(^\text{12}\) It is unrealistic for policy makers to estimate the parameters necessary to run some of the models presented in this chapter. Although mathematical models have challenged the ideas of epidemiologists, modelers, and policy makers, simpler models such as the UNAIDS Estimation and Projection Package have been most useful for health practitioners and aid organizations. It is important to identify and balance major drivers and supplemental details of an epidemic when modeling disease transmission in a given population. Just as health interventions may not be uniformly applied to different countries, HIV transmission models may also need to be developed specifically for unique cultures or regions of the world.

\(^{12}\) The Koopman and Chick model takes approximately four hours to run. Because it is a stochastic model, it requires execution in a large ensemble of realizations to get a clear idea of the behavior of the system and the variables to which it is more or less sensitive.
5 Using an Agent-Based Approach for an AIDS Epidemic Model for Papua New Guinea

Relevancy of Agent-Based Modeling for Papua New Guinea

The unique ethnic heterogeneity and social network structure in Papua New Guinea provides a good case study for which an agent-based approach to HIV epidemic modeling is especially suitable. Defining agents in a system allows the modeler to create rules for individual level decision making, interaction protocols in a structured population, and a focus on the impact of various types of relationships.

In PNG, there are several environmental and cultural factors which may impact the spread of HIV. In particular, the geographic isolation of ethnic groups makes it difficult for new ideas to penetrate their social system. Furthermore, the structure of the sexual network in PNG may exhibit characteristics fostering persistence of diseases with very low transmission probabilities such that diseases with very low transmission probabilities will not die out (Schneeberger, 2001). This chapter presents aspects of the agent-based framework that is particularly relevant to HIV in PNG, where little surveillance occurs, but the impact of social and sexual dynamics on HIV transmission may be speculated.

Defining Agent-Based Modeling

Agent Based-Modeling is a method of computer simulation that defines the behavior of a population of agents within an environment in which global characteristics of the system are the sum of the interactions of the agents. In differential equation models (DE), the model system is defined by a set of equations and the evolution of the system is dictated by the evaluation (numerical integration) of these equations. DE models often use aggregate variables for
populations which have been observed or assumed for the real world, while ABM defines activity at the individual or agent level.

As seen in Chapter 4, DE models usually describe disease spread as an SIR process with rates of infection and transmission defining the epidemic. A typical agent based model has the following characteristics:

- Environment Variables
- Agent attributes
- Rules of behavior

![Figure 5.1 Typical Agent-Based System](image)

Agents are autonomous entities in the model which are defined by certain characteristics or attributes. In disease modeling, the populations of greatest interest are generally those composed of individual persons, and the most appropriate attributes may be age, sex, risk group (high, low, intravenous drug user, commercial sex worker), and geographical location. The properties of the environment are defined for the system. For a disease model, these properties might include population size, geographic distribution of agents, and structure of sexual network. The behavior of agents is defined by rules in this environment. The following are examples of rules which may define an HIV epidemic:
• Agents form partnerships with other agents based on their risk group
• In a sero-discordant partnership, the probability of HIV transmission is .001 per contact
• Progression time from initial infection to AIDS is 9 years without treatment.

Once system and individual variables are defined, observations are made on the aggregate behavior of these agents. Various hypotheses may be tested by changing environment variables or behavior rules.

Relevance of ABM Because of Individualistic Risk Factors

Given the biological and individual determinants of HIV infection and the set of policy interventions under consideration by public health officials, ABM may be a more natural way to model the AIDS epidemic. Probability of transmission from an infected individual to susceptible is dependant primarily on the viral load of the infected person and also other factors such as co-infection of STIs of the susceptible individual and type of sexual union. Because sexual transmission of HIV is an activity—rather than a process—it may be more natural to define HIV transmission as a probability between individuals—as opposed to a specific rate of infection—as is often defined in DE models. Epidemiology studies have attempted to calculate the per contact transmission probability for HIV. Although methods to find this probability are prone to recall bias and inaccuracy, published estimates for male-to-female per-sex-act transmission probability ranges from 0.0005-0.0026 (Chakraborty et al, 2001).13

Many health policy interventions are directed at cohorts which have certain risk factors—which may require an agent-based approach to model such interventions. For example, individuals with HIV are not uniformly infectious throughout disease progression because of

---

13 This probability has been determined through cohort studies of sero-discordant couples. These studies usually control for viral load variability and STIs. Upon sero-conversion of the previously negative individual, sexual contacts are averaged for the duration of the partnership and a probability is assigned for the occurrence of transmission.
variable viral load. Likewise, the likelihood of infecting another individual is not constant because of the asymptomatic phase of the acute infection period and the appearance of HIV/AIDS related opportunistic infections in the latter phases. Agent-based models can simulate changing infectivity by approximating the rise and fall of viral load in agents—thus better representing the transmission probability between two individuals.\textsuperscript{14}

Another intervention that is possible to simulate in an agent-based model is the impact of screening programs in the population. Most screening programs require or recommend individuals to be tested regularly for diseases which are chronic, life threatening, and benefit from early diagnosis. These programs target individuals who would otherwise not seek treatment at an early phase of disease progression. The goal of HIV screening programs is to discover HIV positive individuals who are asymptomatic and reduce HIV spread by encouraging safe sex practices during this period of high infectivity. This intervention could be modeled by eliminating "screened agents" from the infectious pool of individuals from the population. The necessary screening sensitivity and specificity to slow the epidemic may be tested through probabilistic simulations.\textsuperscript{15}

**Behavior Protocols Relevant in HIV Epidemics**

It is apparent that behavior norms and perception of risk is an important aspect of the spread of HIV around the world. Much of the literature on AIDS prevention policy focuses on societal and psychological factors which impact the ways in which individuals make decisions.

\textsuperscript{14} One study which used the Rakai cohort in Uganda found the correlation between transmission probability and other risk factors to be:

\[ P(\log (- \log [1 - f])) = -97.5 + 61.1[\log_{10} v] - 13.7[\log_{10} v]F + 1.02[\log_{10} v]f + 0.35[I(\text{age 25 - 29})] + 0.59[I(\text{age 30 - 34})] \\
- 0.65[I(\text{age 35 - 59})] + 0.56[I(\text{female})] \]

where \( v \) refers to viral load and \( I \) is indicator variable for age of infected individual and sex (Gray et al, 2003). Equation presented as published.

\textsuperscript{15} Sensitivity refers to the proportion of those with the disease who test positive in the screened group. This includes false negatives. Specificity refers to the proportion of those without disease who test negative in the screened group, which includes false positives.
and evaluate risk. In the previous chapter, it was seen that System Dynamics provides a way to conceptualize behavioral feedbacks and the impact of societal factors that may influence behavior. In most cases, behavioral feedbacks—such as stigma reduction and increasing awareness—have been modeled using a parameter which affects the rate of infection in the population. Because of the emphasis on biological risk factors, HIV transmission models usually do not explicitly define behavior change mechanisms. A decentralized agent-based approach to modeling the HIV epidemic allows one to take a closer look at the interaction of the individual, or local features, with global components that impact the epidemic.

ABM is especially useful when agent behavior is dependent on that of other agents with which they are in social or sexual contact, if behavior is dependant on an individual’s perception of their environment. For example, in rural Zimbabwe, the substantial age difference between females and males in sexual unions is a major behavioral determinant of HIV persistence. It is felt that having sexual relations with younger women will decrease the chance of the male partner acquiring HIV. Females begin to have earlier sexual debuts and larger segments of successive cohorts become infected. Therefore, HIV/AIDS is spreading through cohorts and affecting those that were traditionally thought to be at low risk. (Gregson et al, 2002).

Such behavior patterns may be easier to conceptualize at the level of the agent, where partnership formation protocols may be defined for the individual, instead of calculating cohort sizes and mixing probabilities as utilized in the Garnett and Anderson model (see Chapter 4). Kretzschmar and Morris used an ABM to test the impact of concurrent partnerships on the spread of HIV in their model. By defining various protocols of partner formation, Kretzschmar and Morris tested the difference between serial monogamy, random partnerships, and concurrent partnerships on sexually transmitted diseases. They found that concurrency greatly amplifies the
epidemic, when compared with sequential monogamy, and hypothesized that this factor could partially explain higher prevalence of HIV in regions of the world.

**Diffusion of Ideas Along Social Networks**

Diffusion of ideas is an important factor influencing the effectiveness of behavior change interventions. In other disciplines, such as technology adoption, the spread of ideas is usually characterized at an aggregate level through the Bass model of diffusion of innovation (Bass, 1969). However, an agent-based approach permits closer examination of idea acceptance and the concept of human choice, evaluation of utility, and the impact of group dynamics. In fact, UNAIDs identifies “diffusion of innovation theory” as a basis for HIV intervention which involves: innovation, communication, social systems, and time. This type of intervention considers that individuals are exposed to new ideas within a social network. The context and amount of exposure will determine the rate at which new ideas are accepted. Under this theory, behavior change occurs when key opinion leaders or prominent members of society adopt and endorse behavior change. When prevention beliefs are instilled and widely held within one’s immediate social network, individual behavior is more likely to be consistent with the perceived social norm (UNAIDS, 1999).

Simulation of social networks in an agent-based framework allows the model to incorporate the influence of local social norms and the impact of early adopters in one’s community. Social network theory states that an actor is influenced by his network partners if these individuals are visible and important to him. Visibility is determined by the cohesiveness (or intimacy of the relationship) or social equivalence—an individual is able to relate to the actions of another because of similar backgrounds or social position. It has been found in several studies that one’s perception of risk may be dependant on the norms and views of one’s social
network and not necessarily based on reality. In one study which surveyed over 300 students at one university in the United States, researchers found that consistent condom usage was related to the perception of condom usage among peers in one’s social network (Wulfert and Wan, 1993). In another study performed in Kenya, it was found that there is a high correlation between the beliefs of an individual and the number of individuals in their social network which shared this belief. Specifically, researchers examined the tendency to use condoms and the belief that sexual relations is a source for HIV transmission. For women, there is a tendency to have shared beliefs with individuals in their social network, especially with those that are similar in age and have been in relation for a long period of time. For men, an individual’s belief was influenced by the number of other men in his social network that held a certain belief (Buhler and Kohler, 2002). Thus an individual’s perception of risk or behavioral habits may be dependent on the perceived norm of an individual’s social circle. Because of this, new ideas may be difficult to permeate into cohesive groups because of the tendency for herd behavior, where a threshold of early adopters is necessary to diffuse an idea among a homogenous community.

If a capacity of early adoption is necessary to bring a new idea to a group of individuals, the characteristics and expanse of relationships may be important within a community. In a simple social network, relationships can be classified as acquaintances (or weak ties) and close associates (or strong ties). Relationships characterized by weak ties are less likely to be socially involved with one another than relationships characterized by strong ties. Individuals have a collection of acquaintances, few of whom associate with each other. Therefore, acquaintances comprise of a sparsely connected social network, while a network of close friends exhibit a dense cluster of connections. In dense social clusters with strong ties, individuals tend to share the same beliefs and circulate the similar information, as seen in the Rakai cohort study. On the
other hand, new information may be brought into the group by the weak ties of individuals within a group. This means that individuals with few weak ties may not have access to information from distant parts of the social system and may be confined to local beliefs and views of their close friends. Mark Granovetter, who studies the social construction of economic and political institutions, states that weak ties are important to maintain or else an individual is in danger of alienation from the rest of society (Granovetter, 1983). He argues that cultural diffusion occurs when small groups of individuals who share a culture are not so cohesive that they are entirely closed off from the rest of the system, such that ideas may penetrate from other groups via the weak ties. Granovetter describes the strength of weak ties as the ability to reach out to other groups and receive ideas and information different from one’s own. Therefore, homogeneous cultures do not arise by chance, but are endpoints of a cultural diffusion process (Granovetter, 1983). Thus the distribution of weak and strong ties may be an important factor in PNG to encourage proper awareness of HIV modes of transmission, safe sexual practices, and acceptance of people living with AIDS.

**Modeling Preferential Attachment in Sexual Networks**

Real world networks in which agents exhibit preferential attachment may have important characteristics that would be difficult to capture in a system defined by differential equations. Preferential attachment refers to the phenomenon in a dynamic system in which objects with many connections have a higher probability of forming new connections. Networks whose creation exhibits preferential attachment have a distribution of connectivity such that most objects will have one or two connections, but a few will have a large number of connections that ensure that the entire system is linked together (Albert et al, 2000).
Barabasi and Albert discovered that many networks, such as the World Wide Web, collaborations of scientists, and networks of human sexual contacts, often exhibit preferential attachment. The result of this dynamic creates a *scale-free network*, such that the distribution of edges formally accords with the power law:

\[
P(k) = \alpha k^{-\gamma}
\]

Equation 5.1

\(P(k)\) is the probability that a randomly selected node in the network has \(k\) connections (Albert et al, 2002). It has been shown analytically that if \(\gamma\) is between 2 and 3, the efficiency of the virus can be near zero and still persist within a community (Schneeberger et al, 2004)(Pastor-Satorras and Vespignani, 2001). In one study which aimed to validate if sexual networks are scale-free, it was found that in a sampling of heterosexuals in the United Kingdom, \(\gamma\) varied from 2.48 for males and 3.1 for females. In the same study using a population sample from Zimbabwe, researcher found \(\gamma\) to be 3.07 for males and 2.51 for females (Schneeberger et al, 2004). Therefore, it may be possible for HIV to persist in a scale-free sexual network with very low transmission efficiency—which may explain the robustness of the virus even though it has been found to have just a 1 of 1000 probability of virus transmission (Gray et al, 2001).
Implications for Papua New Guinea

Especially in the case of Papua New Guinea, an agent-based model allows for exploration of the mechanics of disease and idea diffusion. Although different ethnic groups on the island are extremely isolated from one another, the existence of a commercial sex network and mobility of upper class individuals opens the possibility that a scale-free sexual network may also exist in this country. Furthermore, lack of roads and the multitude of languages cause social and geographic isolation of different groups, leading to slow diffusion of new ideas. Inaccurate conceptions of HIV transmission paths must compete with correct knowledge of AIDS prevention and spread. Stories of beating and village eviction upon disclosure of one’s status must be countered with acceptance of people living with AIDS. What may be most prominent in the HIV epidemic in PNG is the slow population response in the form of safer sexual behavior because of extreme heterogeneity between groups and isolation and homogeneity among groups. In other words, most individuals will have very few weak ties, and thus less access to new information. These characteristics may form the most prominent aspects of the HIV epidemic in Papua New Guinea and thus form the basis of the model presented in the next chapter.
6 Methodology

Purpose of Model

Global and local perceptions of HIV risk, societal norms regarding safe sex practices, and individual freedom to modify behavior are particularly important factors in the proliferation of HIV/AIDS around the world. However, many transmission models, like those presented in Chapter Four, focus on epidemiological determinants, mixing functions, and core group dynamics. For the specific case of Papua New Guinea, there is a danger that there are too few weak ties in which individuals can access information in the global social network to increase their awareness of HIV/AIDS risk factors.

I construct a model of HIV transmission and diffusion of HIV/AIDS awareness by the adaptation of two well known models. I use the Kretzschmar and Morris model presented in Chapter Four to develop a theoretical sexual network in which individuals exhibit preferential attachment (Kretzschmar and Morris, 1996). The spread of HIV/AIDS risk awareness is simulated using a cultural diffusion model developed by Axelrod (Axelrod, 1997).

This model examines the impact of social and sexual networks on HIV transmission in a static population. The topologies of these networks represent a theoretical relationship structure that may characterize the HIV/AIDS epidemic in Papua New Guinea.

Model Framework

Within the model, individuals are grouped into isolated communities with random individuals linked to other communities. Incorrect ideas of HIV transmission and propensity for non-disclosure circulate within communities which result in HIV susceptibility. An AIDS awareness intervention program is simulated through an idea diffusion process. Advocates
infuse communities with ideas of safe-sex practices and promotion of disclosure of status and acceptance of people with HIV. Those that are reached by the intervention will practice safe sex, will not contribute to HIV spread, and are considered non-transmitters. Those that are not reached or are influenced to continue unsafe practices are at risk of infection and are considered vulnerable. In other words, if an agent is marked as a non-transmitter, the agent will not pass on HIV if it is already infected, or will not receive it if in a partnership with an infected agent. If an agent is marked as vulnerable, the agent may infect or be infected by another agent. Agents may also be influenced by their peers in their social network and revert to risky practices or be convinced to use safe sex practices. These agents are considered to have relapsed into unsafe practices.

The sexual network is a scale-free network in which most individuals have one or two partners, and a few individuals have many partners. Concurrent partnerships are meant to represent the various circumstances where individuals may have multiple partners. In Chapter Three, such situations were described for Papua New Guinea, such as concurrent partners for commercial sex workers and the frequent occurrence of rape. Because it is difficult to estimate the increase in transmission risk for coerced sexual contact, all concurrent partnerships are treated equally—partner change rate and per-contact transmission probability is kept constant throughout the model.

Two types of dynamic sexual networks and two types of social networks are compared to evaluate the impact of network topology on HIV spread within a population. Scenarios consist of various combinations of these networks and model parameters relevant to the respective network.
Description of Algorithms

Creating Sexual Networks

The spread of HIV is compared between a dynamic sexual network of randomly connected individuals and a sexual network in which individuals exhibit preferential attachment (scale-free). The population size and maximum number of partnerships available are kept constant in all scenarios. One-half of the population is used as the total available partnerships to keep consistent with the Kretzschmar and Morris model. Therefore the randomly connected network and the scale-free network differ in the distribution of concurrent partnerships.

Both networks maintain a steady state of partnerships during the execution of the model. This steady state is reached before HIV is seeded within the population. The expected number of partnerships at the steady state for both networks is:

$$\frac{\rho N}{2(\rho + \sigma)}$$

- $N$ Total population size
- $\rho$ Pair formation probability
- $\sigma$ Pair separation probability
- $\frac{N}{2}$ Available partnerships

The distribution of partnerships is used to measure concurrency in the network. The number of available partnerships is kept constant at $\frac{1}{2}$ of the population, but the distribution of concurrency differs by the proportion of individuals that have multiple concurrent relationships.

The algorithms for creating the two types of networks are specified informally below:

- **Random**: A sexual network in which individuals are randomly connected to a member of the opposite sex. This network simulates homogenous mixing such that an agent has equal probability of developing a partnership with each agent.
Generative algorithm:
At each time step, for each available partnership, a pair is formed with probability \( \rho \).
To form a partnership, randomly choose one male and one female. If not already paired with each other, a new partnership is formed. Otherwise, repeat random selection of male and female until a partnership is formed.

If either agent has one or more partners, this partnership is formed with probability \( \xi \).
This parameter determines the distribution of concurrency in a randomly connected network.

All existing partnerships have \( \sigma \) probability of separation at each time step.\(^{16}\)

- **Scale-Free**: A sexual network in which individuals exhibit preferential attachment.
  Preference is dependent on the number of partners both agents currently have and also the provinces in which they reside.

Generative algorithm:
For each available partnership, a pair is formed with probability \( \rho \).
To form a partnership, randomly choose one male and one female until a compatible couple is found. For a given candidate pair \( x, y \), probability of pair compatibility is calculated by:

\[
p = 0.1 + 0.9 \cdot \left( \frac{\text{partners}(x) \cdot \text{partners}(y)}{d^2} \right) \cdot \left( 1 - 0.99 I_{\text{[true]} \left( \text{province}(x) \neq \text{province}(y) \right)} \right)
\]

Where \( I_{\text{[true]}} : \text{Boolean} \rightarrow \{0, 1\} \) is the indicator function where \( I_{\text{[true]}} \) is 1 if its argument is true (in this case, if \( x \) and \( y \) are from different provinces), and 0 if it is false.\(^{17}\)

\( d \) maximum number of partners observed in the network.
\( \text{partners}(x) \) degree of individual \( x \)
\( \text{province}(x) \) province in which \( x \) resides

All existing partnerships have \( \sigma \) probability of separation at each time step. The average duration of partnerships is 157.3 time steps. In a simulation of 3 years or 1100 time steps, agents have on average 4.3 partners.

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\(^{16}\) This algorithm is generalized in Kretzschmar and Morris paper. Details of random network creation are adapted from the AnyLogic model created by Hazhir Rahmandad and John Sterman at the MIT Sloan School of Management (Rahmandad and Sterman, 2005).

\(^{17}\) Since there are 100 provinces, the probability that provinces are equal is 1%. Therefore, partnership formation is normalized by this probability.
Creating Social Networks

In addition to the two types of sexual networks described above, two social network structures are analyzed in this model. Agents are linked to each other via social connections. Agents interact only with those in their social network and these networks do not change during the execution of the model. Each agent on average has \( f \) connections. Descriptions of the two social network types and an informal description of their generative algorithms are given below:

**Random:** A social network in which each agent is randomly connected to approximately \( f \) number of agents. Each agent has equal probability of developing a friendship with each agent.

Generative algorithm:
Iterate through each agent in the population. For the selected agent, loop through the remainder of the population. Create a connection with each agent with probability \( \frac{f}{N-1} \).

![Figure 6.1 Random Graph](Image)

**Caveman:** A social network of highly clustered social groups with few connections between any cluster. Each agent has a network of \( f \) agents almost fully connected to each other.

Generative algorithm:
Create \( \frac{f}{N} \) sub-networks fully connected to each other:
- Iterate through each agent in the population and connect every \( f \) agent to each other so as to form a sub-network fully connected to each other.
Create weak ties between sub-networks.

- Iterate through each agent in the population. For the selected agent $a$, loop through the remainder of the population. Create a connection with each agent with probability $\frac{\text{weaktieprob} \times f}{N - f - 1}$. For each such distant connection, randomly disconnect an existing social contact from agent $a$ so that the number of connections in the entire network remain the same.

The concept of caveman social networks originated from *Small Worlds* by Duncan Watts (Watts, 1999).
Spreading Ideas

Ideas are spread along social networks based on compatibility of agents and the number of agents acting as advocates of HIV awareness and transmitters of good ideas. Good and negative ideas are spread depending on the number of attributes that agents share in common. Compatibility is calculated by similarity in belief system, age, sex, education level, and residence type.

- **Idea Spread**
  Randomly choose an agent $a$. Randomly choose an agent $b$ from $a$’s social network. The per-time-step probability that an idea will be transmitted from $b$ to $a$ is equal to the fraction of attributes in common. If the idea is determined to be transmitted, the first agent copies the idea value of the second agent.

- **Idea Advocate**
  Randomly choose an agent in the advocate(s)' social network. Randomly choose an agent $b$ from advocate(s)' social network. The per-time-step probability that an idea will be transmitted from $b$ to $a$ is equal to the fraction of attributes in common. If the idea is determined to be transmitted, the agent $b$ copies the good idea.

This algorithm is inspired by a study which uses Axelrod’s algorithm for cultural diffusion along different types of social networks (Haggith et al, 2003).

Time Step Events

As the model evolves, the processes described above take place in each successive time step. The process can be described at a high level as follows.

At each time step:

- **Partnership algorithms**
  - Choose two individuals. Form a partnership with probability $\rho$. Repeat for each available partnership.
  - Every pair separates with probability $\sigma$.

- **Disease Spread**
  - For every partnership between an uninfected and an infected person, the disease is transmitted with probability $\lambda$. 

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Idea Spread

- An agent is chosen randomly. Another agent is randomly chosen from the first agent’s social network. The good or negative idea is copied from one agent to the other depending on the cultural similarities between the two.
- An agent is chosen randomly from the advocate(s)’ social network. This agent receives the good idea from the advocate depending on the cultural similarities between the two.

HIV Parameters

The parameters related to HIV and transmission spread are gathered from published epidemiology studies. The studies used are listed below.

<table>
<thead>
<tr>
<th>Parameter</th>
<th>Value</th>
</tr>
</thead>
<tbody>
<tr>
<td>Heterosexual per-contact HIV Transmission Probability</td>
<td>0.001 (Gray et al, 2001)\textsuperscript{18}</td>
</tr>
<tr>
<td>Incubation Period for Acute HIV</td>
<td>26 Days (Vanhem et al, 2000)</td>
</tr>
<tr>
<td>Duration Period for Acute HIV</td>
<td>17 Days (Vanhem et al, 2000)</td>
</tr>
<tr>
<td>Duration Latent HIV</td>
<td>9 Years (Nadler, 2005)</td>
</tr>
<tr>
<td>AIDS diagnosis to death</td>
<td>1-3 Years (Nadler, 2005)</td>
</tr>
</tbody>
</table>

Environment Variables and Agent Attributes

The model is defined by rules of partnership formation and separation; the distribution of demographic details; the idea spread algorithm; HIV transmission probability and progress of disease, and data collection parameters. The following table lists the variables used in the model.

\textsuperscript{18} Transmission probability is difficult to approximate, as it depends on the type of sexual contact, co-infections, viral load of infected individual. The probability 1 in 1000 sex acts is commonly used for HIV transmission models in developing countries based on the Gray study on the Rakai cohort in Uganda.
<table>
<thead>
<tr>
<th>Name</th>
<th>Type</th>
<th>Values</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td><strong>Partnerships</strong></td>
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<td></td>
<td></td>
</tr>
<tr>
<td><strong>mixingType</strong></td>
<td>Integer</td>
<td>1,2</td>
<td>Corresponds to sexual network types: Random or Scale-Free</td>
</tr>
<tr>
<td><strong>pairform_prob</strong></td>
<td>Double</td>
<td>0.01</td>
<td>Probability that partnership is formed</td>
</tr>
<tr>
<td><strong>pairsep_prob</strong></td>
<td>Double</td>
<td>0.005</td>
<td>Probability of partnership separation</td>
</tr>
<tr>
<td><strong>xi</strong></td>
<td>Double</td>
<td>varies</td>
<td>Probability that partnership is formed, given either agents have 1 or more partners</td>
</tr>
<tr>
<td><strong>maxPartnrsobserved</strong></td>
<td>Integer</td>
<td>varies</td>
<td>Maximum number of concurrent partnerships seen during model execution</td>
</tr>
<tr>
<td><strong>availPartnerships</strong></td>
<td>Integer</td>
<td>0-1000</td>
<td>Number of available partnerships, given that only 1/2 population number of partnerships are allowed</td>
</tr>
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<td><strong>Demographics</strong></td>
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<td></td>
<td></td>
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<tr>
<td><strong>population</strong></td>
<td>Integer</td>
<td>2000</td>
<td>Number of agents</td>
</tr>
<tr>
<td><strong>numFemales</strong></td>
<td>Integer</td>
<td>1000</td>
<td>Number of agents that are female</td>
</tr>
<tr>
<td><strong>numMales</strong></td>
<td>Integer</td>
<td>1000</td>
<td>Number of agents that are male</td>
</tr>
<tr>
<td><strong>Idea Spread</strong></td>
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<td></td>
<td></td>
</tr>
<tr>
<td><strong>networkType</strong></td>
<td>Integer</td>
<td>3,4</td>
<td>Corresponds to social network types: Random or Caveman</td>
</tr>
<tr>
<td><strong>numFriends</strong></td>
<td>Integer</td>
<td>20</td>
<td>Average number of friends for each agent</td>
</tr>
<tr>
<td><strong>numIdeaBearers</strong></td>
<td>Integer</td>
<td>20,40,80</td>
<td>Number of advocates in the population</td>
</tr>
<tr>
<td><strong>weakTieProb</strong></td>
<td>Double</td>
<td>.1-.5</td>
<td>Probability that an agent in the caveman network is linked to an agent from another province</td>
</tr>
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<td><strong>HIV</strong></td>
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<td></td>
<td></td>
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<td><strong>numHiv</strong></td>
<td>Integer</td>
<td>20</td>
<td>Number of agents infected with HIV at model start</td>
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<td><strong>primaryInfection</strong></td>
<td>Time Steps</td>
<td>26</td>
<td>Incubation period for acute HIV</td>
</tr>
<tr>
<td><strong>acuteHIV</strong></td>
<td>Time Steps</td>
<td>14</td>
<td>Duration of acute HIV phase</td>
</tr>
<tr>
<td><strong>latentHIV</strong></td>
<td>Time Steps</td>
<td>3285</td>
<td>Duration of latent HIV phase</td>
</tr>
<tr>
<td><strong>AIDS</strong></td>
<td>Time Steps</td>
<td>365</td>
<td>Duration from AIDS diagnosis to death</td>
</tr>
<tr>
<td><strong>Database Parameters</strong></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td><strong>dataTimeInterval</strong></td>
<td>Integer</td>
<td>50</td>
<td>Number of time steps for prevalence data to be tracked</td>
</tr>
<tr>
<td><strong>intervalCounter</strong></td>
<td>Integer</td>
<td>varies</td>
<td>Index of time interval during model execution</td>
</tr>
</tbody>
</table>

Table 6.1 Environment Parameters
Agents interact with each other based on the parameters defined in the environment and its own characteristics. Each agent has the following attributes:

**Table 6.2 Agent Attributes**

<table>
<thead>
<tr>
<th>Name</th>
<th>Type</th>
<th>Values</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td><strong>Networks</strong></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Partners</td>
<td>Vector</td>
<td>Agent</td>
<td>Vector which maintains current partnerships</td>
</tr>
<tr>
<td>Friends</td>
<td>Vector</td>
<td>Agent</td>
<td>Vector which maintains current friendships</td>
</tr>
<tr>
<td><strong>Partner Data</strong></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>totalPartners</td>
<td>Integer</td>
<td>varies</td>
<td>Counts total partners for the execution of the model</td>
</tr>
<tr>
<td>partnersDuration</td>
<td>Vector</td>
<td>steps</td>
<td>Vector which maintains the length of current partnerships</td>
</tr>
<tr>
<td><strong>Demographics</strong></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>province</td>
<td>Integer</td>
<td>1-100</td>
<td>Represents region in which agent resides</td>
</tr>
<tr>
<td>beliefGroup</td>
<td>Integer</td>
<td>1,2</td>
<td>Type of belief system of the agent: Christian, Animist</td>
</tr>
<tr>
<td>educLevel</td>
<td>Integer</td>
<td>1,2</td>
<td>Level of Education received: primary, secondary</td>
</tr>
<tr>
<td>dwelling</td>
<td>Integer</td>
<td>1,2</td>
<td>Urban/rural</td>
</tr>
<tr>
<td>age</td>
<td>Integer</td>
<td>1,2</td>
<td>Age group: 20-30, 30-40</td>
</tr>
<tr>
<td>sex</td>
<td>Integer</td>
<td>1,2</td>
<td>Female/Male</td>
</tr>
<tr>
<td><strong>Idea Spread</strong></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>idea</td>
<td>Integer</td>
<td>0,1</td>
<td>Determines whether agent is a non-transmitter or vulnerable</td>
</tr>
<tr>
<td>isAdvocate</td>
<td>Boolean</td>
<td>false,true</td>
<td>True if agent is an advocate</td>
</tr>
<tr>
<td>isIdeaFromAdvocate</td>
<td>Boolean</td>
<td>false,true</td>
<td>True if agent received idea directly from advocate</td>
</tr>
<tr>
<td>goodIdeaReceived</td>
<td>Boolean</td>
<td>false,true</td>
<td>True if agent has ever received idea</td>
</tr>
</tbody>
</table>

Belief group, education level, dwelling, age, and sex are randomly distributed among agents. Agents have an equal probability of receiving one of two values for each of these attributes.\(^{19}\)

Province number is randomly distributed in the Random social network, but is allocated for each agent in the Caveman social network.

\(^{19}\) The speed of idea spread is sensitive to the number of possible values for each attribute, thus only two values are used for each attribute.
The environment is presented as follows:

Timers
- startEpidemic
- pairFormation
- pairSeparation
- ideaSpread
- copyIdeaCarrier
- gatherStats
- enterDB

Variables related to Idea Spread
- advocateEffectiveness
- goodIdeaSpread
- maxAgentsReached
- countGoodtoBad
- countBadIdea
- countBadtoGood
- countProvinceNoGoodIdeaBearers

Variables related to HIV/AIDS prevalence
- nSusceptible
- nPrimaryInfected
- nAcuteHIV
- nLatentHIV
- nAIDS
- totalPrevalence

Figure 6.4 Presentation of Environment

Timers are used to activate activities in the model. Partnership formation, separation, and idea spread is implemented by timers, which execute methods at a specific time step. The timers gatherStatus and enterDB are used to process and input data into a Microsoft Access database. Other components of the environment are used to collect data as the model is being executed.
The following table describes the variables.

<table>
<thead>
<tr>
<th>Name</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td><strong>Idea Spread</strong></td>
<td></td>
</tr>
<tr>
<td>advocateEffectiveness</td>
<td>Number of agents that currently have good idea, having received idea from advocate</td>
</tr>
<tr>
<td>goodIdeaSpread</td>
<td>Number of agents that currently have good idea, having received idea from social network</td>
</tr>
<tr>
<td>maxAgentsReached</td>
<td>Maximum number of agents that have received good idea at some point during model execution</td>
</tr>
<tr>
<td>countGoodtoBad</td>
<td>Number of agents that reverted to bad idea</td>
</tr>
<tr>
<td>countBadtoGood</td>
<td>Number of agents that never received good idea</td>
</tr>
<tr>
<td>countProvineceNoGoodIdeaBearers</td>
<td>Percentage of provinces that have no agents with good idea, but may at one point have had, but lost</td>
</tr>
<tr>
<td><strong>HIV/AIDS Prevalence</strong></td>
<td></td>
</tr>
<tr>
<td>nSusceptible</td>
<td>Number of agents that do not have HIV or AIDS</td>
</tr>
<tr>
<td>nPrimaryInfected</td>
<td>Number of agents in first phase of HIV, incubation for Acute HIV</td>
</tr>
<tr>
<td>nAcuteHIV</td>
<td>Number of agents in Acute phase of HIV</td>
</tr>
<tr>
<td>nLatentHIV</td>
<td>Number of agents in Latent phase of HIV</td>
</tr>
<tr>
<td>nAIDS</td>
<td>Number of agents with AIDS. If model simulation time is less than 3718 time steps will have no agents that have progressed to AIDS</td>
</tr>
<tr>
<td>totalPrevalence</td>
<td>Total prevalence of HIV and AIDS together</td>
</tr>
</tbody>
</table>

Table 6.3 Environment Variables

The agent object is presented as follows:

![Figure 6.5 Presentation of Agent Object](image)

The agent progresses from susceptible to death through states or phases.

72
Once an agent is marked to be infected with HIV, the agent automatically progresses through the stages as defined in Table 6.1.

The software used to develop the model is AnyLogic by XJ Technologies. See the Appendix for the full implementation of the model. Code is automatically created by the framework or manually written into the AnyLogic development environment in the Java programming language.
7 Results

HIV Spread in Dynamic Sexual Networks

As a reference point, the first three scenarios measure HIV spread among a population assuming no change in behavior of agents for the duration of the model execution. All model parameters remain the same for Scenarios 1-3, with the exception of greater concurrency among fewer agents with each scenario.

In Scenarios 1 and 2, a randomly connected sexual network defines the sexual interactions of the agents, as described in Chapter Six. Concurrent partnerships are distributed by the $\xi$ variable: in Scenario 1, $\xi = 0.1$, in Scenario 2, $\xi = 0.3$, such that the probability of a partnership between a man and female with one or more partners is 10% or 30%, respectively. A Scale-Free sexual network is used in Scenario 3, so that agents with a higher number of partnerships have a greater probability of partnership formation. One hundred 9000 time step Monte Carlo realizations were executed for each scenario with one time step representing one day.

Parameters from the Kretzschmar and Morris model serve as the environment variables for all scenarios.

<table>
<thead>
<tr>
<th>Model Parameters</th>
</tr>
</thead>
<tbody>
<tr>
<td>Population Size</td>
</tr>
<tr>
<td>Pair Formation Probability</td>
</tr>
<tr>
<td>Pair Separation Probability</td>
</tr>
</tbody>
</table>

Table 7.1 Model Parameters from Kretzschmar and Morris

The progression from HIV to AIDS is same for all agents. Initial infection occurs within a partnership between an pre-AIDS infected individual and a susceptible individual.
An index for concurrency, $k_3$, is described by Kretzschmar and Morris to quantify the amount of concurrent partnerships in a network (see Kretzschmar and Morris 1996 for further details). It is mathematically approximated by:

$$\frac{\sigma^2}{\mu} + \mu - 1$$

Equation 7.1

Where $\sigma^2$ and $\mu$ are the variance and mean of the number of partnerships per person observed in the network. Therefore, the greater the proportion of partnerships that are held by fewer individuals, the larger the corresponding value of $k_3$. Partnership distribution and $k_3$ for Scenarios 1-3 is given below.

<table>
<thead>
<tr>
<th>#</th>
<th>Network Type</th>
<th>$k_3$</th>
<th>No Partners</th>
<th>One Partner</th>
<th>Two Partners</th>
<th>Three Partners</th>
<th>Four Partners</th>
<th>Over Five Partners</th>
</tr>
</thead>
<tbody>
<tr>
<td>1</td>
<td>Random</td>
<td>0.263</td>
<td>0.41</td>
<td>0.51</td>
<td>0.0681</td>
<td>0.0058</td>
<td>0.0004</td>
<td>0</td>
</tr>
<tr>
<td>2</td>
<td>Random</td>
<td>0.442</td>
<td>0.46</td>
<td>0.43</td>
<td>0.0951</td>
<td>0.0142</td>
<td>0.0015</td>
<td>0.0002</td>
</tr>
<tr>
<td>3</td>
<td>Scale-Free</td>
<td>0.672</td>
<td>0.51</td>
<td>0.34</td>
<td>0.1156</td>
<td>0.0257</td>
<td>0.0041</td>
<td>0.0006</td>
</tr>
</tbody>
</table>

Table 7.3 Distribution of Concurrency for Scenarios 1-3

Scenarios 1-3 are ordered by degree of concurrency: Scenario 1 has the greatest proportion of agents in monogamous partnerships, and the lowest proportion of multiple concurrent partnerships; Scenario 3 has the greatest amount of concurrency, with a greater proportion of
individuals in multiple concurrent partnerships. Because of preferential attachment, the proportion of concurrent partnerships shifts to fewer numbers of agents.

The epidemic curves of the three scenarios are plotted below.

As demonstrated by Kretzschmar and Morris, the amount and distribution of concurrency in a sexual network affects the speed at which HIV spreads in a population. The epidemic begins the slowest in Scenario 3 (because the scale-free network also has the highest proportion of singles of all three scenarios), the epidemic is slow to spread immediately after HIV is seeded in the population. In Figure 7.1, HIV prevalence begins to increase more rapidly in Scenario 3 than the other two scenarios at the end of 30 months.
As seen in Figure 7.2, after one year, the prevalence in Scenario 3 increases faster than Scenarios 1 and 2, which have fewer concurrent partnerships. By the end of the simulation, prevalence is growing fastest in Scenario 3 and slowest for Scenario 1. The time steps taken to reach one-third HIV/AIDS prevalence in the population is chosen to represent the speed of HIV transmission in these sexual networks.

<table>
<thead>
<tr>
<th>HIV Prevalence Scenarios 1-3</th>
</tr>
</thead>
<tbody>
<tr>
<td><strong>#</strong></td>
</tr>
<tr>
<td>------</td>
</tr>
<tr>
<td>1</td>
</tr>
<tr>
<td>2</td>
</tr>
<tr>
<td>3</td>
</tr>
</tbody>
</table>

Table 7.4 HIV Prevalence Scenarios 1-3
In Scenario 1, the sexual network with the least concurrency, it takes approximately 20.82 years for HIV prevalence to reach 30%. Scenario 2 with proportionally less concurrency, it takes 19.18 years to reach the same prevalence. The scale-free sexual network reaches 30% prevalence in about 18.36 years, the fastest of the three sexual networks. Prevalence after three years is roughly the same in all three scenarios.

**Idea Spread in Social Networks**

The impact of social network topology is compared for two types of social networks: randomly connected agents and *connected caveman* (isolated, clustered networks as described in Chapter 6). A series of scenarios are performed to compare the influence of mixing in the social network. The proportion of friendships that involve two agents in different provinces is used as an index for social isolation of sub-networks. This is noted as *Fraction of out of Province Friendships*. One hundred iterations of each scenario were executed for 1100 time steps (approximately three years). The following parameters are environment variables for Scenarios 4-8.

<table>
<thead>
<tr>
<th>Social Network Parameters</th>
</tr>
</thead>
<tbody>
<tr>
<td>Average number of friendships</td>
</tr>
<tr>
<td>Number of Advocates</td>
</tr>
<tr>
<td>Simulation Time</td>
</tr>
</tbody>
</table>

*Table 7.5 Social Network Parameters*

Scenario 4 is the base case of idea spread in a Randomly connected social network.

<table>
<thead>
<tr>
<th>#</th>
<th>Fraction of out of Province Friendships</th>
</tr>
</thead>
<tbody>
<tr>
<td>4</td>
<td>0.99</td>
</tr>
</tbody>
</table>

*Table 7.6 Scenario 4 Parameters*
On average, the maximum number of agents reached by the intervention is 432. Ninety-nine percent of friendships are between agents from different provinces. The number of agents that were directly influenced by the advocates is about 346. The number of agents that were influenced through their social network is about 78. Approximately seven agents changed their behavior after accepting the good idea. Overall, 424 agents are non-transmitters at the end of the simulation and 1567 did not accept positive ideas through their social network.

Scenarios 5-8 represent a range of social networks varied by sub-network isolation, with Scenario 5 having the most isolation and Scenario 7 the least isolation. The probability of weak ties is incremented for each scenario, as shown by the Fraction of out of Province Friendships.

<table>
<thead>
<tr>
<th>#</th>
<th>Max Agents reached</th>
<th>Advocate to Peer Spread</th>
<th>Peer to Peer Spread</th>
<th>Relapsed</th>
<th>Vulnerable</th>
<th>Non-Transmitter</th>
<th>HIV Prevalence</th>
<th>Fraction of Provinces not Reached</th>
</tr>
</thead>
<tbody>
<tr>
<td>4</td>
<td>432.02</td>
<td>346.85</td>
<td>77.80</td>
<td>7.37</td>
<td>1567.98</td>
<td>424.65</td>
<td>30.06</td>
<td>0.014</td>
</tr>
</tbody>
</table>

Table 7.7 Scenario 4 Idea Spread Results

<table>
<thead>
<tr>
<th>#</th>
<th>Weak Tie Probability</th>
<th>Fraction of out of Province Friendships</th>
</tr>
</thead>
<tbody>
<tr>
<td>5</td>
<td>0.1</td>
<td>0.19</td>
</tr>
<tr>
<td>6</td>
<td>0.3</td>
<td>0.47</td>
</tr>
<tr>
<td>7</td>
<td>0.5</td>
<td>0.64</td>
</tr>
</tbody>
</table>

Table 7.8 Scenarios 5-7 Parameters

<table>
<thead>
<tr>
<th>#</th>
<th>Max Agents reached</th>
<th>Advocate to Peer Spread</th>
<th>Peer to Peer Spread</th>
<th>Relapsed</th>
<th>Vulnerable</th>
<th>Non-Transmitter</th>
<th>HIV Prevalence</th>
<th>Fraction of Provinces not Reached</th>
</tr>
</thead>
<tbody>
<tr>
<td>5</td>
<td>402</td>
<td>346</td>
<td>51</td>
<td>5</td>
<td>1598</td>
<td>398</td>
<td>31</td>
<td>0.36</td>
</tr>
<tr>
<td>6</td>
<td>425</td>
<td>342</td>
<td>75</td>
<td>8</td>
<td>1574</td>
<td>417</td>
<td>30</td>
<td>0.12</td>
</tr>
<tr>
<td>7</td>
<td>429</td>
<td>339</td>
<td>81</td>
<td>9</td>
<td>1571</td>
<td>420</td>
<td>20</td>
<td>0.06</td>
</tr>
</tbody>
</table>

Table 7.9 Scenarios 5-7 Results
In Scenario 5, approximately 19% of friendships are between agents of two different provinces. In Scenario 7, more than half of the friendships are between agents of different provinces. The maximum number of agents reached by intervention and the number of agents that retain the good idea at the end of the simulation increases with the increase in Fraction of out of Province Friendships. Therefore, the number of agents that are never reached also decreases. However, the number of agents that revert from non-transmitter to vulnerable increases with greater out of province friendships or more diverse social networks. The number of agents reached by advocates decreases with social diversity, while the number of agents that were influenced by their neighbors increases.

HIV prevalence in Scenarios 4-6 is roughly the same level. In these circumstances, an intervention of twenty advocates promoting HIV awareness in a population of 2000 does not avert a significant number of HIV infections. By increasing the number of advocates in the social network, idea spread will be more extensive and more cases of HIV will be averted. Scenarios 8-11 use a weak tie probability of 0.1 such that on average 20% of friendships are between agents from different provinces, representing the isolation that may be typical of Papua New Guinean villages. The number of advocates is increased for the following scenarios:

<table>
<thead>
<tr>
<th>#</th>
<th>Number of Advocates</th>
<th>Fraction of out of Province Friendships</th>
</tr>
</thead>
<tbody>
<tr>
<td>8</td>
<td>40</td>
<td>0.19</td>
</tr>
<tr>
<td>9</td>
<td>80</td>
<td>0.19</td>
</tr>
<tr>
<td>10</td>
<td>160</td>
<td>0.19</td>
</tr>
<tr>
<td>11</td>
<td>320</td>
<td>0.19</td>
</tr>
</tbody>
</table>

*Table 7.10 Scenarios 8-11 Parameters*

One hundred iterations were executed for each scenario. The number of advocates is doubled in successive scenarios.
In Scenarios 5-7, HIV prevalence is approximately 30 agents when 20 advocates are spreading ideas through their social networks, while in Scenario 11, prevalence is 18 agents. The impact of the advocates seems minor, as only 12 cases are averted when the number of agents is increased by 16, from 20 to 320. However, the first three years of the epidemic is a period when the virus is moving relatively slowly. Once highly connected individuals in a scale-free sexual network have been infected, HIV will spread more rapidly.

Ultimately, the number of agents that are non-transmitters is a better indicator of the trajectory of the epidemic. In Scenario 8, on average, each advocate directly or indirectly influences 17 agents. In Scenario 11, each advocate influences about 10 agents. Although only 331 agents in the population are vulnerable at the end of the simulation in Scenario 11, the effectiveness of each of the 320 agents is much less than each of the 20 advocates in Scenario 5. Because advocates already have some similarity with those agents in their social networks (because idea
spread probability is based on percentage of shared attributes and 0.1 weak tie probability guarantees that advocates are from the same province as most of their peers), each advocate reaches approximately the same number of agents in their social networks—17 agents—in Scenarios 5 and 8. In Scenario 10, 160 agents are randomly dispersed in 100 provinces, thus efficiency decreases because more than one advocate is working among the same social network. Advocate efficiency dramatically decreases in Scenario 11 for the same reason.

Discussion

Impact of Network Topology

Sexual and social network topology may affect the rate at which HIV is spread within a population and the efficiency of HIV/AIDS education campaigns. In sexual networks, increasing randomness will increase the spread of the epidemic. On the other hand, random social networks (far links, as opposed to highly clustered, sparsely interlinked with each other) is more desirable when spreading ideas of behavioral risk reduction and acceptance of PLWHAs. Groups that are isolated from mainstream education or media campaigns will be at more risk than those that interact with the society at large. Sexual networks with more concurrent partnerships may have higher prevalence of STIs. Depending on the distribution of disease burden among isolated communities, HIV incidence rates seen in the initial years of the epidemic are not indicative of stabilizing levels of HIV.

The less isolated are social groups, the better access individuals in these groups have to different sources of information. However, social groups that are more diverse also tend to be influenced by a greater number of ideas and learning may be transient. Thus HIV awareness programs and safe sex practices may be a short term trend if overwhelmed by alternative beliefs and practices which are also proliferating within a social group.
Advocates have greater influence in more socially isolated groups, as few alternate ideas enter the homogenous sub-network. Agents are less likely to revert back to unsafe practices as the growing proportion of their social group have been positively impacted by the intervention and become non-transmitters. Once an advocate convinces a proportion of the group to use safe sex practices, this idea will be maintain in isolated groups as shared norms in social networks reinforce this intervention. Advocates are most effective when distributed among all isolated groups, such that most social networks had at least one advocate. Idea spread through the peer network (agent to agent), is more efficient in diverse social networks than in isolated sub-networks as the diversity of social ties allowed for faster access to ideas in the social network. On the other hand, greater diversity of social ties also makes it difficult to maintain one idea, such that the number of agents that converted back to the negative idea is highest in the most diverse social network.

Limitations and Extensions of the Model

This model may be extended to represent the population distribution and social mobility of Papua New Guinea. It is possible to represent urban cities by creating a few large clusters with many connections throughout the network and many clusters with few distant connections. The placement of advocates in urban areas and isolated provinces may be analyzed to determine the most efficient allocation of resources.

In this model, vulnerability to HIV infection is determined by a Boolean value which symbolizes the agent’s behavioral practices to prevent HIV. However, positive and negative ideas may not have equal efficiency in diffusion. In societies like Papua New Guinea, where there are severe social repercussions to disclosing infection status, such as social exile (as cited in Chapter Three), negative idea spread may have a greater influence than the acceptance of safe
sex practices and status disclosure to partners. The power of positive and negative ideas may be represented by changing the probability of idea acceptance (i.e. an agent is twice as more likely to pass on a negative idea than the positive idea).

Vertical transmission of HIV is also an important source of infection in developing countries, especially in the early phases of the epidemic when ARTs are not available to decrease the probability of mother-to-child transmission. Furthermore, such relationships may be important to capture, as HIV knowledge and attitudes may be passed on to the child, as the mother or family have had personal experience with the devastating affects of AIDS opportunistic infections.

One positive aspect of ABMs are the ability to model behavior and decision making at the individual level so that intervention efficiency can be estimated or compared for various scenarios. Simulating partner choice and idea exchange along networks also allows the modeler to think about interventions that are based on relationships and peer structure. It is possible to simulate policies that focus on network structures and persistent interactions. For example, the allocation of resources and placement of intervention programs may depend on the topology of the sexual network, specifically meeting places for commercial sex workers and their clients and places were risky behavior may occur, such as hotels and clubs. However, like all simulations of reality, results are sensitive to the assumptions and framework of the underlying model. Therefore, the model presented in this thesis aims to minimize complexity and present the most important factors in an epidemic in a country like Papua New Guinea, where social isolation and cultural belief systems may be major factors for HIV persistence in the country.
8 Policy Implications

Brazil: Successful HIV Reduction

The HIV epidemic in Brazil epidemic peaked in the mid-90s with 24,000 new cases in 1998 alone. By 2000, incidence was reduced to 15,000. This success was attributed to the following: early government intervention; strong civil society participation at all decision levels; multi-sectoral mobilization; a balanced prevention and treatment approach; and a human rights perspective in all strategies and actions. Preventive measures centered around HIV screening, promotion of condom use, provision of disposable syringes, and promotion of pre-natal testing to avoid mother to child transmission. One important factor in the success was the mobilization of different groups to fight discrimination. The first goal of these groups was to fight stigma and promote open discussion of HIV status so that the epidemic would not be exacerbated by dread of realizing one’s HIV status and by HIV spread through non-disclosure in sero-discordant partnerships. Homosexual individuals were first to create non-government organizations (NGO) focused on the rights of PLWHA in the work place and medical centers. HIV positive individuals went public with their status and fought against discrimination and for civil rights. Other community and religious groups also worked with these NGO’s to support their efforts. The government also promoted equal treatment of PLWHAs and in 1996, passed a federal law mandating the free provision of ARTs (Levi and Vitoria, 2002). It is apparent that the fight against AIDS must be taken by governments around the world, not only to provide treatment for those with HIV/AIDS, but also to support behavior change policies and to fight discrimination and stigma associated with this disease.
Prevention of AIDS in Papua New Guinea

While government support and community-based advocates are important aspects of fighting the spread of HIV within a country, the epidemic in Papua New Guinea may not progress like other regions with high incidence rates. Because high risk behavior is practiced by many individuals (frequent occurrence of rape and cultural practices that may result in HIV transmission), HIV spread may occur among low risk individuals in the population and interventions which have succeeded in other countries may not be applicable or efficient.

One positive aspect of ABMs is the ability to model persistent interactions of individuals and influences of family or peer networks. Thinking about disease along networks allows one to think of policy interventions along the social and risk networks. In sexual networks which exhibit preferential attachment, prevention programs should focus on individuals that contribute most heavily to the epidemic—those with concurrent or multiple partnerships and unsafe sex. However, as seen in virus spread among the internet, in scale-free networks, disease may spread and persist even though the probabilities of transmission are surprisingly small. Some researchers feel that some diseases could never be eliminated through a biomedical intervention aimed at reducing transmission probabilities, reflecting the fact that redundancy of connections in a scale-free network causes error resistance. Therefore, an epidemic could be stopped only by alterations that reduce the network of contacts over which the infections spread (Schneeberger et al, 2001).

Given the propensity for violence and discrimination against PLWHAs, it is difficult for individuals in Papua New Guinea to lead campaigns to fight stigma or to gather together and lobby for better support from the government. One difficulty in small isolated communities is the lack of privacy, which may prevent individuals from seeking treatment or limits how one can
access resources like condoms and HIV tests. For example, visiting VCTs may be highly conspicuous in small rural villages and individuals may not use these services for fear of being marked as a HIV positive or adulterous individual.

In countries where HIV has been extensively spread throughout the country, there are many non-government programs which provide home-base care for PLWHAs. These programs were developed out of the necessity to treat those with AIDS and are not mobile enough to reach treatment centers. Home-based care programs usually recruit volunteers to be health care workers in a community. These volunteers attend weekly seminars on how to treat common infectious diseases and IDS related opportunistic infections. Volunteers then visit households that chose to participate in the program. In Lusaka, Zambia, many women volunteer their services to these programs because they desire to know how to care for their own family in case of illness, and have no access to such education programs otherwise. These women are exposed to AIDS victims on a daily basis, but also receive training and education on HIV etiology and prevention. Such knowledge is valuable to pass onto the family, especially as the next generation reaches sexual maturity.

Home-based care programs are a response to the heavy burden of HIV in the country and lack of public health services to care for PLWHAs. Volunteers are given basic supplies to care for illnesses due to dehydration, malaria, tuberculosis, etc., depending on the country. Essentially, HIV awareness is spread through community volunteers that have incentive to have better access to health education and treatment for their own families.

Instead of being a response to heavy HIV burden, such health programs may be used as a preventative intervention to spread health awareness through peer and family networks. Such

---

20 I interviewed several women from the Catholic Archdiocese of Lusaka in Zambia, one of the largest home-based care programs in the city. They expressed the desire to know how to take care of sickness in their family, thus felt that volunteering their time in these programs were beneficial.
programs may be highly relevant for Papua New Guinea. It is empowering for women to have the knowledge and resources to care for their families and community members. By learning more about health risks for the community, they can also spread AIDS awareness within the family.

Ultimately, the purpose of HIV transmission models is to hypothesize about drivers of the epidemic which will then shed light on appropriate interventions and prevention measures. While DE and ABMs may have similar results in epidemic curves (Rahmandad and Sterman), the framework and foundations of the model open policy makers to different interventions and policy decisions. The results of the mixing models presented in Chapter Four were interventions targeting HIV spread from core group transmitters to the general population. On the other hand, network-based interventions are important in Papua New Guinea because of the geographic isolation of many communities throughout the country and great diversity between groups of people. The close social connections within the wantok is an important source to leverage in terms of community or network-based health policy. Already, values and resources are shared in the community through the wantok. Other community based interventions, such as home-base care programs, will have great promise in Papua New Guinea and agent-based models may assist in the planning and development of health policy in this country.
References


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UNAIDS, (1999), *Sexual Behavioural Change for HIV: Where have Theories taken us?*, Geneva, UNAIDS.

UNAIDS, (1999), *Trends in HIV incidence and prevalence: natural course of the epidemic or results of behavioral change?* UNAIDS in collaboration with Wellcome Trust Centre for the Epidemiology of Infectious Disease, Switzerland.


Appendix

Project: HIV

<table>
<thead>
<tr>
<th>Global</th>
<th>Event scheduling algorithm</th>
<th>Deterministically</th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td>Import</td>
<td>import java.util.*</td>
</tr>
</tbody>
</table>

Package: hiv

Stochastic SI model defined by: Kretzschmar & Morris in “Measures of Concurrency in Networks and the Spread of Infectious Disease” and Robert Axelrod, “The Complexity of Cooperation”

- Assumes infectious disease is chronic, no recovery, in AIDS phase, agents not infectious
- Heterogeneous partnerships only, equal distribution of females/males
- Constant # of partnerships, varying distribution of partnerships over population

Three parameters must be defined before model is executed:

a. mixingType (sexual network)
b. networkType (social network)
c. SimulationTimeEnd (model execution end)

- Other variables that may be changed for iterations of model are listed under Main - Parameters
- Other important parameters that may be changed are:
  a. weakTieProb (for caveman social network, the probability that an agent has a friendship with another agent from a different province)
  b. numIdeaBearers (number of advocates at model start)
  c. numHIV (number of agents with HIV at model start)

New to Versions 1.1

- methods to calculate K
- methods to connect to MS access db
- new states (primaryinfection, acuteHIV, latentHIV)
- Custom assimilation method

New to Version 2.1

- Axelrod model of diffusion of ideas
- Agent characteristics: sex, province, education level completed, age, idea (good/bad)
- Social network: connected caveman
New to Version 2.2
- number of friends & population must be divisible
- randomly connect cavemen via weakTieProb
- created Partnership object to add to Vector allPartnerships
- this is to prevent too many partnerships in scale free network by giving those with more partnerships more probability that these break up

New to Version 2.3
- Assortive Sexual Network, takes into account village location and partnership degree

New to Version 3.1
- Changed M/F object to just People with sex assigned

New to Version 3.2
- Diffusion of idea data

New to Version 3.3
- Description of major variables, parameters, methods

**Active Object: Main**

<table>
<thead>
<tr>
<th>General</th>
</tr>
</thead>
</table>
| **Import** | import java.net.URL;  
import java.sql.*;  
import java.lang.*;  
import java.util.Date;  
import java.util.logging.*; |
| **Startup code** | initCounters();  
createSexualNetwork(); //create network until equilibrium conditions reached  
createSocialNetwork(); |
| **Additional class code** | final static int RANDOM = 1;  
final static int SCALE_FREE = 2;  
final static int RANDOMNETWORK = 3;  
final static int CONNECTCAVEMAN = 4;  
final static int GOOD_IDEA = 5;  
final static int BAD_IDEA = 6;  
static int SimulationTimeEnd;  
static int[][] prevalence = new int[SimulationTimeEnd][];  
static int RunID; |
static Vector allPartnerships = new Vector();
double totalAverPartners;
static DataSet durationData = new DataSet();
double averDuration;
static Vector ideaBearers = new Vector();
static DataSet totPartners = new DataSet();
static DataSet friendShips = new DataSet();
static DataSet concurrency = new DataSet();
double kThree;

// used to check distribution of concurrency
double partnerzero=0;
double partnerone=0;
double partnertwo=0;
double partnerthree=0;
double partnerfour=0;
double partnerfive=0;
int averPartners;
int nSingles = population;
double countOutOfProvincePartnership;
double countOutOfProvinceFriendship;

public void initCounters(){
// used to reset all counters between iterations of model run
intervalCounter=0;
nSingles = population;
maxPartnrsobserved=3;
averPartners=0;
totalAverPartners=0;
averDuration=0;
countOutOfProvincePartnership=0;
countOutOfProvinceFriendship=0;

allPartnerships.clear();
durationData.reset();
ideaBearers.clear();
totPartners.reset();
friendShips.reset();
concurrency.reset();
kThree=0;
partnerzero=0;
partnerone=0;
partnertwo=0;
partnerthree=0;
partnerfour=0;
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<th>Default Value</th>
<th>Description</th>
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<td></td>
</tr>
<tr>
<td>pairsep_prob</td>
<td>double</td>
<td>.005</td>
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</tr>
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<td>availPartnerships</td>
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<td></td>
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<td>--------------------</td>
<td>-------------------</td>
<td></td>
<td></td>
</tr>
<tr>
<td>Type</td>
<td>integer</td>
<td></td>
<td></td>
</tr>
<tr>
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<td>population/2</td>
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</thead>
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<tr>
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</table>

<table>
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<tr>
<th>Name</th>
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</tr>
<tr>
<td>Modifier</td>
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<table>
<thead>
<tr>
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</tr>
</thead>
<tbody>
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</tr>
<tr>
<td>Modifier</td>
<td>Global</td>
</tr>
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</table>

<table>
<thead>
<tr>
<th>Name</th>
<th>numFriends</th>
</tr>
</thead>
<tbody>
<tr>
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<tr>
<td>Default value</td>
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</tr>
<tr>
<td>Modifier</td>
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</table>

<table>
<thead>
<tr>
<th>Name</th>
<th>maxPartnrsobserved</th>
</tr>
</thead>
<tbody>
<tr>
<td>Type</td>
<td>integer</td>
</tr>
<tr>
<td>Default value</td>
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</tr>
<tr>
<td>Modifier</td>
<td>Global</td>
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<table>
<thead>
<tr>
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</tr>
<tr>
<td>Name</td>
<td>Type</td>
</tr>
<tr>
<td>-----------------</td>
<td>------------</td>
</tr>
<tr>
<td>numIdeaBearers</td>
<td>integer</td>
</tr>
<tr>
<td>numHIV</td>
<td>integer</td>
</tr>
<tr>
<td>dataTimeInterval</td>
<td>integer</td>
</tr>
<tr>
<td>intervalCounter</td>
<td>integer</td>
</tr>
<tr>
<td>xi</td>
<td>double</td>
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</table>
### Structure

<table>
<thead>
<tr>
<th>Timers</th>
<th>Variables related to Idea Spread</th>
</tr>
</thead>
<tbody>
<tr>
<td>startEpidemic</td>
<td>advocateEffectiveness</td>
</tr>
<tr>
<td>pairFormation</td>
<td>goodIdeaSpread</td>
</tr>
<tr>
<td>pairSeparation</td>
<td>maxAgentsReached</td>
</tr>
<tr>
<td>IdeaSpread</td>
<td>countGoodtoBad</td>
</tr>
<tr>
<td>copyIdeaCarrier</td>
<td>countBadIdea</td>
</tr>
<tr>
<td>gatherStats</td>
<td>countBadtoGood</td>
</tr>
<tr>
<td>enterDB</td>
<td>countProvinceNoGoodIdeaBearers</td>
</tr>
</tbody>
</table>

#### Variables related to HIV/AIDS prevalence

- nSusceptible
- nPrimaryInfected
- nAcuteHIV
- nLatentHIV
- nAIDS
- totalPrevalence

**ChartTimer**: startEpidemic

**Description**: Chooses advocate and diseased individuals after social and sexual networks are created.

**Timeout**: 1

**Expiry Action**: 
- Engine.log.println("Starting epidemic and idea spread....");
- chooseDisease();
- chooseAdvocates();

**ChartTimer**: copyIdeaCarrier

**Description**: Algorithm for idea spread from an advocate of HIV awareness, adapted from Haggith et al, Infectious Ideas: Modeling the Diffusion of Ideas across Social Networks.

**Timeout**: 1.0

**Expire At Startup**: No

**Expiry Action**: 
//at each time step, each advocate acts like a proseltizer, and one person from //their social network may copy his/her idea

```
Iterator i = ideaBearers.iterator();
```
while (i.hasNext()) {
    Person pi = (Person)i.next();

    if (pi.getNumFriends() != 0) {
        Person pj = pi.getFriend(uniform_discr(pi.getNumFriends() - 1));

        if (randomTrue(calcIdeaPropProb(pi, pj))) {
            pj.copyIdeaFrom(pi);
            pj.isIdeaFromAdvocate = true;
        }
    }
}

### ChartTimer

<table>
<thead>
<tr>
<th>Description</th>
<th>ideaSpread</th>
</tr>
</thead>
<tbody>
<tr>
<td>Algorithm for idea spread as defined by Axelrod's model for cultural diffusion. Probability for idea spread between two agents dependant on the number of characteristics held in common.</td>
<td></td>
</tr>
</tbody>
</table>

| Timeout | 1.0 |
| Expire At Startup | No |

**Expiry Action**

```java
int i = uniform_discr(population - 1);

Person a = getPerson(i);
int friendIndex = a.getNumFriends();

if (friendIndex > 0) {
    Person b = (Person)a.getFriend(uniform_discr(a.getNumFriends() - 1));

    if (randomTrue(calcIdeaPropProb(a, b))) {
        a.copyIdeaFrom(b);
    }
}
```

### ChartTimer

<table>
<thead>
<tr>
<th>Description</th>
<th>enterDB</th>
</tr>
</thead>
<tbody>
<tr>
<td>Enters all parameters used and data collected for model run. Iterations for same parameters are defined by same RunID. Queries to average multiple runs are defined in MS Access HIV.mdb</td>
<td></td>
</tr>
</tbody>
</table>

| Timeout | SimulationTimeEnd-1 |
| Expire Action | boolean dataEntered = false; Connection connect = null; |
Driver driver = null;
String modelVersion = "3.3";
String comments = "test";

boolean insertOK = false;

checkPartnerDistribution();
countIdeaSpread();
checkSocialNetworkCohesion();
countProvinceData();

Engine.log.println("Total HIV and AIDS prevalence at model end: "+totalPrevalence);
Engine.log.println("\n");
Engine.log.println("\n");
Engine.log.println("\n");

String sql;
try {
    // connection to an ACCESS MDB
    driver = (Driver)Class.forName("sun.jdbc.odbc.JdbcOdbcDriver").newInstance();
    connect = DriverManager.getConnection("jdbc:odbc:Driver= {Microsoft Access Driver (*.mdb)} ;DBQ=HIV.mdb");
    Statement stmt = connect.createStatement();;

    sql = "INSERT INTO SimulationParameters (RunID, kThree, population, partnerships, pairform_prob, pairsep_prob, maxPartnrs, numFemales, numMales, mixingType, averPartners, modelVersion) VALUES (" + RunID + "," + kThree + "," + population + "," + allPartnerships.size() + "," + pairform_prob + "," + pairsep_prob + "," + maxPartnrsobserved + "," + numFemales + "," + numMales + "," + mixingType + "," + averPartners + "," + modelVersion + ")";
    insertOK = stmt.execute(sql);
    sql = null;

    sql = "INSERT INTO Concurrency (RunID, averDuration, mixingType, kThree, nSingles, totalAverPartners, partnerzero, partnerone, partnertwo, partnerthree, partnerfour, partnerfive, countOfProvincePartnership) VALUES(" + RunID + "," + averDuration + "," + mixingType + "," + kThree + "," + nSingles + "," + totalAverPartners + "," + partnerzero + "," + partnerone + "," + partnertwo + "," + partnerthree + "," + partnerfour + "," + partnerfive + "," + countOfProvincePartnership + ")";
    insertOK = stmt.execute(sql);
}
sql = null;

Engine.log.println("Percentage of Provinces with No Good Ideas Bearers "+countProvinceNoGoodIdeaBearers);

sql = "INSERT INTO IdeaSpread (RunID,countProvinceNoGoodIdeaBearers, goodIdeaSpread, advocateEffectiveness, countOutOfProvinceFriendship,numFriends, totalPrevalence , weakTieProb, networkType, mixingType, numIdeaBearers, maxAgentsReached, countGoodtoBad, countBadIdea, countBadtoGood) VALUES(" + RunID+ "," + countProvinceNoGoodIdeaBearers + "," + goodIdeaSpread+ "," + advocateEffectiveness + "," +countOutOfProvinceFriendship + "," +numFriends+ "," +totalPrevalence + "," + weakTieProb+ "," + networkType+ "," + mixingType+ "," + numIdeaBearers+ "," + maxAgentsReached + "," + countGoodtoBad + "," + countBadIdea + "," + countBadtoGood + ");";
insertOK = stmt.execute(sql);
sql = null;

for(int i = 0; i<prevalence.length;i++){
    String dataString ="";
    for (int j = 0; j<prevalence[i].length;j++){
        dataString=dataString+ prevalence[i][j] +",";
    }
    int lastComa = dataString.lastIndexOf(","); //take off last coma
    dataString = dataString.substring(0,lastComa);

    sql = "INSERT INTO Prevalence (RunID, nSusceptible, nPrimaryInfected, nAcuteHIV, nLatentHIV,nAIDS, getTime) VALUES (" + dataString + ");"
    insertOK = stmt.execute(sql);
}
stmt.close();

catch (Exception e) {
e.printStackTrace();
}
finally {
    try {
        if (connect != null) connect.close();
    }
    catch (Exception e) {
        e.printStackTrace();
    }
}

gatherStats

<table>
<thead>
<tr>
<th>ChartTimer</th>
<th>Description</th>
<th>Timeout</th>
<th>Expire At Startup</th>
<th>Expiry Action</th>
</tr>
</thead>
</table>
| gatherStats | Collects prevalence data at each dataTimeInterval | dataTimeInterval | No | int time = (int) Engine.getTime();
int[] a = {RunID,nSusceptible,
nPrimaryInfected,nAcuteHIV,nLatentHIV,nAIDS,time};
prevalence[intervalCounter] = a;
intervalCounter++;

<table>
<thead>
<tr>
<th>ChartTimer</th>
<th>Description</th>
<th>Timeout</th>
<th>Expire At Startup</th>
<th>Expiry Action</th>
</tr>
</thead>
</table>
| pairSeperation | For each partnership that exists at the beginning of time t, with probability "pairsep_prob" choose a couple to split up. | 1.0 | No | double j;
int pickPartner;
Person p = null;
boolean noPrtnerFound;

for(int i = 0; i < allPartnerships.size();i++) {
    j = uniform(1);
    if (j < pairsep_prob) //seperate a partnership
        int randomCoupleIndex = uniform_discr(allPartnerships.size()-1);
Partners randomCouple = (Partners)allPartnerships.get(randomCoupleIndex);
allPartnerships.remove(randomCoupleIndex);

Person male = randomCouple.male;
Person female = randomCouple.female;

int hisPartnerIndex = male.partners.indexOf(female);
int herPartnerIndex = female.partners.indexOf(male);

male.removePartner(female); //randomly choose person o from p's list of partners
female.removePartner(male);

Double time = (Double) male.removePartnerDuration(hisPartnerIndex);
if (time.intValue() != 0) durationData.add(Engine.getTime()-
time.doubleValue());
//those partnerships created at time 0 are not counted
female.removePartnerDuration(herPartnerIndex);

availPartnerships++;
nSingles = nSingles + 2;
}
}

<table>
<thead>
<tr>
<th>ChartTimer</th>
<th>pairFormation</th>
</tr>
</thead>
<tbody>
<tr>
<td>Description</td>
<td>Iterative loop: For each available partnership at the beginning of time t, form a partnership with probabliy &quot;pairform_prob&quot;</td>
</tr>
<tr>
<td>Timeout</td>
<td>1</td>
</tr>
<tr>
<td>Expire At Startup</td>
<td>No</td>
</tr>
</tbody>
</table>

<table>
<thead>
<tr>
<th>Expiry Action</th>
</tr>
</thead>
</table>
| int i=0;
| boolean pairFormed = false;
| boolean has;
| double j;
| double k;
| Person m;
| Person f;
| int a = availPartnerships;
| while(i < a) {
| i++;
| } |
```java
j = uniform(1);
if (j < pairform_prob) {
pairFormed = false;

while (pairFormed == false) {

do {
    m = getRandomMale();
    f = getRandomFemale();
    has = m.partners.contains(f);
}
while (has);

Partners partnership = new Partners();
partnership.male = m;
partnership.female = f;

k = uniform(1);
if (k < phi(m, f)) { // test mixing function
    f.addPartner(m);
    m.addPartner(f);
    f.partnersDuration.add(new Double(Engine.getTime()));
    m.partnersDuration.add(new Double(Engine.getTime()));
    allPartnerships.add(partnership);
    availPartnerships--;
    f.totalPartners++;
    m.totalPartners++;
    pairFormed = true;
    nSingles = nSingles - 2;
    // get number of max partners observed here and update it if its increased
}
}
}

<table>
<thead>
<tr>
<th>Variable</th>
<th>countProvinceNoGoodIdeaBearers</th>
</tr>
</thead>
<tbody>
<tr>
<td>Description</td>
<td>Percentage of provinces that have no agents with good idea, but may at one point have had, but lost</td>
</tr>
<tr>
<td>Variable type</td>
<td>double</td>
</tr>
<tr>
<td>Initial value</td>
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</tr>
<tr>
<td>Variable</td>
<td>goodIdeaSpread</td>
</tr>
<tr>
<td>-----------------------</td>
<td>--------------------------------------------------------------------------------</td>
</tr>
<tr>
<td>Description</td>
<td>Number of agents that currently have good idea, having received idea from social network</td>
</tr>
<tr>
<td>Variable type</td>
<td>integer</td>
</tr>
<tr>
<td>Variable</td>
<td>advocateEffectiveness</td>
</tr>
<tr>
<td>Description</td>
<td>Number of agents that currently have good idea, having received idea from advocate</td>
</tr>
<tr>
<td>Variable type</td>
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</tr>
<tr>
<td>Initial value</td>
<td>0</td>
</tr>
<tr>
<td>Variable</td>
<td>totalPrevalence</td>
</tr>
<tr>
<td>Description</td>
<td>Total prevalence of HIV and AIDS together</td>
</tr>
<tr>
<td>Variable type</td>
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</tr>
<tr>
<td>Initial value</td>
<td>0</td>
</tr>
<tr>
<td>Variable</td>
<td>maxAgentsReached</td>
</tr>
<tr>
<td>Description</td>
<td>Maximum number of agents that have received good idea at some point during model execution</td>
</tr>
<tr>
<td>Variable type</td>
<td>integer</td>
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<tr>
<td>Initial value</td>
<td>0</td>
</tr>
<tr>
<td>Variable</td>
<td>countGoodtoBad</td>
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<td>Description</td>
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<td>Variable</td>
<td>countBadIdea</td>
</tr>
<tr>
<td>Description</td>
<td>Number of agents that never received good idea</td>
</tr>
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<td>Variable type</td>
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<td>---------------</td>
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<td>------------</td>
<td>--------------</td>
</tr>
<tr>
<td>Description</td>
<td>Number of agents that do not have HIV or AIDS</td>
</tr>
<tr>
<td>Variable type</td>
<td>integer</td>
</tr>
<tr>
<td>Initial value</td>
<td>population</td>
</tr>
<tr>
<td>Auto collect dataset</td>
<td>Yes</td>
</tr>
<tr>
<td>Object</td>
<td>people</td>
</tr>
<tr>
<td>Type</td>
<td>hiv.Person</td>
</tr>
<tr>
<td>Number of objects</td>
<td>population</td>
</tr>
<tr>
<td>Comment</td>
<td>textBox2</td>
</tr>
<tr>
<td>Text</td>
<td>Variables related to HIV/AIDS prevalence</td>
</tr>
<tr>
<td>Comment</td>
<td>textBox1</td>
</tr>
<tr>
<td>Text</td>
<td>Timers</td>
</tr>
<tr>
<td>Comment</td>
<td>textBox</td>
</tr>
<tr>
<td>Text</td>
<td>Variables related to Idea Spread</td>
</tr>
</tbody>
</table>

### Algorithmic Functions

<table>
<thead>
<tr>
<th>Name</th>
<th>calcIdeaPropProb</th>
</tr>
</thead>
<tbody>
<tr>
<td>Description</td>
<td>Calculates the probability of idea propagation based on 4 characteristics of the two agents selected</td>
</tr>
<tr>
<td>Body</td>
<td>double probability = 0; if(a.getDwelling()==b.getDwelling()) probability=probability + .167; if(a.getEducLevel()==b.getEducLevel()) probability = probability + .167; if(a.getBeliefGroup()==b.getBeliefGroup())probability = probability + .167; if(a.getSex()==b.getSex()) probability = probability + .167; if(a.getAge()==b.getAge()) probability = probability + .167;</td>
</tr>
</tbody>
</table>
if(a.getProvince()==b.getProvince()) probability = probability +.167;
return probability;

<table>
<thead>
<tr>
<th>Name</th>
<th>checkPartnerDistribution</th>
</tr>
</thead>
<tbody>
<tr>
<td>Type</td>
<td>void</td>
</tr>
<tr>
<td>Description</td>
<td>This method is executed at the end of the simulation. Data statistics are collected on the distribution of partnerships, number of lifetime partnerships, and average number of friendships. This method prints out distribution data.</td>
</tr>
</tbody>
</table>
| Body         | double temp=0;
for(int i = 0; i<population; i++){
    Person p = getPerson(i);
    Iterator it = p.getPartnersIterator();
    while (it.hasNext () {
        Person pi = (Person)it.next();
        if(p.getProvince()! =pi.getProvince()){
            countOutOfProvincePartnership++;
        }
    }
    totPartners.add(p.totalPartners);
    friendships.add(p.getNumFriends());
    if (p.getDegree()==0) {
        partnerzero++;
    }
    if (p.getDegree()==1) {
        partnerone++;
    }
    if (p.getDegree()==2){
        partnertwo++;
    }
    if (p.getDegree()==3) {
        partnerthree++;
    }
    if (p.getDegree()==4) {
        partnerfour++;
    }
    if (p.getDegree()>5) {
        partnerfive++;
    } |
temp=temp+p.getDegree();
    concurrency.add(p.getDegree());
}

double allDegrees = partnerzero +
    partnerone + partnertwo + partnerthree + partnerfour + partnerfive;

double total = allPartnerships.size();
    partnerzero = partnerzero / allDegrees;
    partnerone = partnerone / allDegrees;
    partnertwo = partnertwo / allDegrees;
    partnerthree = partnerthree / allDegrees;
    partnerfour = partnerfour / allDegrees;
    partnerfive = partnerfive / allDegrees;

countOutOfProvincePartnership = ((countOutOfProvincePartnership / 2) / total);
    totalAverPartners = totPartners.mean();
    averDuration = durationData.mean();

    kThree = (concurrency.variance() / concurrency.mean()) + concurrency.mean() - 1;
    Engine.log.println("CONCURRENCY DATA");
    Engine.log.println("Average number of partners per person:" +
        totalAverPartners);
    Engine.log.println("kthree (concurrency metric): " + kThree);
    Engine.log.println("Percentage of singles: " + partnerzero);
    Engine.log.println("Percentage of monogamous couples: " + partnerone);
    Engine.log.println("Percentage of agents with 2 partners: " + partnertwo);
    Engine.log.println("Percentage of agents with 3 partners: " + partnerthree);
    Engine.log.println("Percentage of agents with 4 partners: " + partnerfour);
    Engine.log.println("Percentage of agents with 5 partners: " + partnerfive);
    Engine.log.println("Percentage out Of Province Partnerships: " +
        countOutOfProvincePartnership);
    Engine.log.println("Average duration of partnerships: " + averDuration);
    Engine.log.println(" ");

<table>
<thead>
<tr>
<th>Name</th>
<th>checkSocialNetworkCohesion</th>
</tr>
</thead>
<tbody>
<tr>
<td>Type</td>
<td>void</td>
</tr>
</tbody>
</table>
| Description           | Calculates the percentage of out of province friendships in social network. This
                        is directly correlated with weakTieProb. Higher weakTieProb, higher proportion
                        of out of province friendships, more idea spread, more transience of good idea
                        retention.                        |
| Body                  | double total = 0;
                        for(int i = 0; i<population; i++){
                            Person p = getPerson(i);
                            total = total + p.getNumFriends(); |
Iterator it = p.getFriendsIterator();
while (it.hasNext () ) {
    Person pi = (Person)it.next ();
    if(p.getProvince() != pi.getProvince()){
        countOutOfProvinceFriendship++;
    }
}

countOutOfProvinceFriendship=countOutOfProvinceFriendship/total;

Engine.log.println("Percent out of province friendships " +
countOutOfProvinceFriendship);

<table>
<thead>
<tr>
<th>Name</th>
<th>chooseAdvocates</th>
</tr>
</thead>
<tbody>
<tr>
<td>Type</td>
<td>void</td>
</tr>
<tr>
<td>Description</td>
<td>Randomly chooses agents to be advocates of HIV education. Number of advocates is determined by numIdeaBearers parameter.</td>
</tr>
</tbody>
</table>
| Body       | int temp = numIdeaBearers;
    while(numIdeaBearers!=0){
        Person p = getPerson(uniform_discr(population-1));
        if(!ideaBearers.contains(p)){
            ideaBearers.add(p);
            p.makeAdvocate();
            numIdeaBearers--;
        } 
    }
    numIdeaBearers=temp;
    Iterator i = ideaBearers.iterator();
    while (i.hasNext () ) {
        Person pi = (Person)i.next();
    }
    Engine.log.println(" "); |

<table>
<thead>
<tr>
<th>Name</th>
<th>chooseDisease</th>
</tr>
</thead>
<tbody>
<tr>
<td>Type</td>
<td>void</td>
</tr>
<tr>
<td>Description</td>
<td>Random selection of agents to have HIV at model start. Number of individuals infected with HIV is defined by numHIV</td>
</tr>
</tbody>
</table>
| **Body** | for(int i = 0; i < numHIV; i++){  
|   |     Person p = people.item(uniform_discr(population-1));  
|   |     p.statechart.fireEvent("Infected");  
| **Name** | countIdeaSpread  
| **Type** | void  
| **Description** | Calculates distribution of idea spread. maxAgents Reached: maximum number of agents reached that have ever had a good idea countBadtoGood: number of agents that currently have good idea countGoodtoBad: number of agents that reverted from having good to bad idea countBadIdea: number of agents that were never reached from advocate or through their social network goodIdeaSpread: from social network, as opposed to advocate  
| **Body** | for(int i = 0; i< population; i++){  
|   |     Person p = getPerson(i);  
|   |     if(p.getIdea()==BAD_IDEA){  
|   |         if(p.hasReceivedIdea()==true){  
|   |             countGoodtoBad++;  
|   |             //this agent was convinced from good idea to bad  
|   |         }else{  
|   |             countBadIdea++;  
|   |             //no one has reached this agent for him to receive good idea  
|   |         }  
|   |     }else if(p.getIdea()==GOOD_IDEA){  
|   |         if(p.isIdeaFromAdvocate){  
|   |             advocateEffectiveness++;  
|   |         }else{  
|   |             goodIdeaSpread++; //from social network, as opposed to advocate  
|   |         }  
|   |         countBadtoGood++;  
|   |         //count people with good idea  
|   |     }  
|   |     maxAgentsReached = countBadtoGood + countGoodtoBad;  
|   |     Engine.log.println("IDEA SPREAD DATA ");  
|   |     Engine.log.println("Maximum number of agents reached with good idea: " + 
|   |         maxAgentsReached);  
|   |     Engine.log.println("Number of agents that currently have good: " + 
|   |         countBadtoGood);  
|   |     Engine.log.println("Number of agents that reverted from having good to bad: " + 
|   |         countGoodtoBad);  
|   |     Engine.log.println("Number of agents that were never reached: " + 
|   |         countBadIdea);  
| } }
countBadIdea);

<table>
<thead>
<tr>
<th>Name</th>
<th>countProvinceData</th>
</tr>
</thead>
<tbody>
<tr>
<td>Type</td>
<td>void</td>
</tr>
<tr>
<td>Description</td>
<td>Calculates idea spread data based on province</td>
</tr>
</tbody>
</table>
| Body       | int provinceCountGoodtoBad=0;  
             int provinceCountBadIdea=0;  
             int provinceAdvocateEffectiveness=0;  
             int provinceGoodIdeaSpread=0;  
             int provinceCountBadtoGood=0;  
             
             Engine.log.println("PROVINCE DATA");  
             for(int province = 1; province<(population/numFriends)+1;  
                 province++) { //hardcoded for each of the provinces  
                 for(int i = 0; i<population;i++){
                     Person p = getPerson(i);  
                     if(p.getProvince()==province){  
                         if(p.getIdea()==BAD_IDEA){  
                             if(p.hasReceivedIdea()==true){  
                                 provinceCountGoodtoBad++;  
                                 //this agent was convinced from good idea to bad  
                             }else{  
                                 provinceCountBadIdea++;  
                                 //no one has reached this agent for him to receive good idea  
                             }
                         }else if(p.getIdea()==GOOD_IDEA){  
                             if(p.isIdeaFromAdvocate) {  
                                 provinceAdvocateEffectiveness++;  
                             }else{  
                                 provinceGoodIdeaSpread++; //from social network, as opposed to advocate  
                             }  
                         }  
                         provinceCountBadtoGood++;  
                         //count people with good idea  
                     }
                 }
             }  
             if(provinceCountBadtoGood==0){
<table>
<thead>
<tr>
<th>Name</th>
<th>createSexualNetwork</th>
</tr>
</thead>
<tbody>
<tr>
<td><strong>Type</strong></td>
<td>void</td>
</tr>
<tr>
<td><strong>Description</strong></td>
<td>Creates sexual network, type defined by mixingType as defined in Experiments - Custom</td>
</tr>
<tr>
<td><strong>Body</strong></td>
<td>int i=0;</td>
</tr>
<tr>
<td></td>
<td>boolean pairFormed;</td>
</tr>
<tr>
<td></td>
<td>boolean has=false;</td>
</tr>
<tr>
<td></td>
<td>double k;</td>
</tr>
<tr>
<td></td>
<td>Person m;</td>
</tr>
<tr>
<td></td>
<td>Person f;</td>
</tr>
<tr>
<td></td>
<td>double d = (pairform_prob<em>population)/(2</em>(pairform_prob+pairsep_prob));</td>
</tr>
<tr>
<td></td>
<td>int steadyStatePrtnrshps = (int)d;</td>
</tr>
<tr>
<td></td>
<td>while(i &lt; steadyStatePrtnrshps</td>
</tr>
<tr>
<td></td>
<td>i++;</td>
</tr>
<tr>
<td></td>
<td>pairFormed=false;</td>
</tr>
<tr>
<td></td>
<td>while(pairFormed==false){</td>
</tr>
<tr>
<td></td>
<td>do{</td>
</tr>
<tr>
<td></td>
<td>m =getRandomMale();</td>
</tr>
<tr>
<td></td>
<td>f = getRandomFemale();</td>
</tr>
<tr>
<td></td>
<td>has=m.checkPartners(f); //check that they arent already partners</td>
</tr>
<tr>
<td></td>
<td>}while (has);</td>
</tr>
<tr>
<td></td>
<td>Partners partnership = new Partners();</td>
</tr>
</tbody>
</table>
partnership.male = m;
partnership.female=f;

k = uniform(1);

if (k< phi(m,f)) { //test mixing function
    f.addPartner(m);
    m.addPartner(f);
    f.addPartnerDuration(new Double(Engine.getTime()));
    m.addPartnerDuration(new Double(Engine.getTime()));
    allPartnerships.add(partnership);
    availPartnerships--;
    f.incrementTotalPartnerships();
    m.incrementTotalPartnerships();
    pairFormed=true;
    nSingles= nSingles-2;
}
}

Engine.log.println("Sexual network created...");

<table>
<thead>
<tr>
<th>Name</th>
<th>createSocialNetwork</th>
</tr>
</thead>
<tbody>
<tr>
<td>Type</td>
<td>void</td>
</tr>
<tr>
<td>Description</td>
<td>Creates sexual network, type defined by networkType as defined in Experiments - Custom</td>
</tr>
<tr>
<td>Body</td>
<td>switch( networkType ) {</td>
</tr>
<tr>
<td></td>
<td>case RANDOMNETWORK:</td>
</tr>
<tr>
<td></td>
<td>boolean has;</td>
</tr>
<tr>
<td></td>
<td>// Person pj;</td>
</tr>
<tr>
<td></td>
<td>int chooseRandomFriend;</td>
</tr>
<tr>
<td></td>
<td>double plink = (double)numFriends / ( population - 1 );</td>
</tr>
<tr>
<td></td>
<td>// everybody knows numFriends other people</td>
</tr>
<tr>
<td></td>
<td>for( int i=0; i &lt; population-1; i++ ) {</td>
</tr>
<tr>
<td></td>
<td>Person pi = getPerson(i);</td>
</tr>
<tr>
<td></td>
<td>for( int j=i+1; j&lt;population-1; j++ ) {</td>
</tr>
<tr>
<td></td>
<td>if( uniform() &lt; plink ) {</td>
</tr>
</tbody>
</table>
Person pj = getPerson(j);

has=pi.contains(pj); //check that they arent already partners
if(!has){
    pi.addFriend( pj);
    pj.addFriend( pi);
}
}
}
} break;

case CONNECTCAVEMAN: //taken from UNIFORM
//everybody knows everybody else

int nextFriend = population/numFriends; //increment to jump through population

for(int i = 0; i<nextFriend; i++){
    linkCaveman(numFriends, i, nextFriend, i);
}

double createLongLink = (weakTieProb*numFriends)/(population-
numFriends-1);

for( int i=0; i<population-1; i++ ) {
    Person pi = getPerson(i);

    for( int j=0; j<population-1; j++ ) {
        Person pj = getPerson(j);
        if( i!=j & & !pi.contains( pj ) & & randomTrue(createLongLink) ) {
            //randomly choose a friend to disconnect

            if(pi.getNumFriends()!=0){
                Person removedFromPi =
                (Person)pi.removeFriend(uniform_discr( pi.getNumFriends()-1));
                removedFromPi.removeFriend(pi);
            }

            pi.addFriend(pj);
            pj.addFriend(pi);
        }
    }
}
Engine.log.println("Social network created... ");

<table>
<thead>
<tr>
<th>Name</th>
<th>getRandomFemale</th>
</tr>
</thead>
<tbody>
<tr>
<td>Type</td>
<td>Person</td>
</tr>
<tr>
<td>Description</td>
<td>Retrieves random female from population</td>
</tr>
<tr>
<td>Body</td>
<td>boolean notFound = true; Person f= null; while(notFound){ f = getPerson(uniform_discr(0,population-1)); if (f.getSex()==1) { notFound=false; } } return f;</td>
</tr>
</tbody>
</table>

<table>
<thead>
<tr>
<th>Name</th>
<th>getRandomMale</th>
</tr>
</thead>
<tbody>
<tr>
<td>Type</td>
<td>Person</td>
</tr>
<tr>
<td>Description</td>
<td>Retrieves random male from population</td>
</tr>
<tr>
<td>Body</td>
<td>boolean notFound = true; Person m=null; while(notFound){ m = getPerson(uniform_discr(0,population-1)); if (m.getSex()==0) { notFound=false; } } return m;</td>
</tr>
</tbody>
</table>

<table>
<thead>
<tr>
<th>Name</th>
<th>linkCaveman</th>
</tr>
</thead>
<tbody>
<tr>
<td>Type</td>
<td>void</td>
</tr>
<tr>
<td>Arguments</td>
<td>Type  Name</td>
</tr>
<tr>
<td></td>
<td>int    myFriends</td>
</tr>
<tr>
<td></td>
<td>int    index</td>
</tr>
<tr>
<td></td>
<td>int    step</td>
</tr>
<tr>
<td></td>
<td>int    province</td>
</tr>
</tbody>
</table>

121
<table>
<thead>
<tr>
<th>Description</th>
<th>Body</th>
</tr>
</thead>
<tbody>
<tr>
<td>Used to create a group of numFriends to each other</td>
<td>if (myFriends!=0){</td>
</tr>
<tr>
<td></td>
<td>Person p = getPerson(index);</td>
</tr>
<tr>
<td></td>
<td>p.setProvince(province);</td>
</tr>
<tr>
<td></td>
<td>for(int i = index + step; i&lt;population; i=i+step){</td>
</tr>
<tr>
<td></td>
<td>linkFriends(index, i);</td>
</tr>
<tr>
<td></td>
<td>}</td>
</tr>
<tr>
<td></td>
<td>linkCaveman(myFriends-1, index+step, step, province);</td>
</tr>
<tr>
<td></td>
<td>}</td>
</tr>
</tbody>
</table>

<table>
<thead>
<tr>
<th>Name</th>
<th>linkFriends</th>
</tr>
</thead>
<tbody>
<tr>
<td>Type</td>
<td>void</td>
</tr>
<tr>
<td>Arguments</td>
<td>Type  Name</td>
</tr>
<tr>
<td></td>
<td>int   a</td>
</tr>
<tr>
<td></td>
<td>int   b</td>
</tr>
</tbody>
</table>

<table>
<thead>
<tr>
<th>Description</th>
<th>Used to link to agents to each other</th>
</tr>
</thead>
<tbody>
<tr>
<td>Body</td>
<td>Person first = getPerson(a);</td>
</tr>
<tr>
<td></td>
<td>Person second = getPerson(b);</td>
</tr>
<tr>
<td></td>
<td>first.addFriend(second);</td>
</tr>
<tr>
<td></td>
<td>second.addFriend(first);</td>
</tr>
</tbody>
</table>

<table>
<thead>
<tr>
<th>Name</th>
<th>phi</th>
</tr>
</thead>
<tbody>
<tr>
<td>Type</td>
<td>double</td>
</tr>
<tr>
<td>Arguments</td>
<td>Type  Name</td>
</tr>
<tr>
<td></td>
<td>Person   perA</td>
</tr>
<tr>
<td></td>
<td>Person   perB</td>
</tr>
</tbody>
</table>

<table>
<thead>
<tr>
<th>Description</th>
<th>Mixing function as defined by Kretzschmar &amp; Morris.</th>
</tr>
</thead>
<tbody>
<tr>
<td>Body</td>
<td>switch( mixingType ) {</td>
</tr>
<tr>
<td></td>
<td>case RANDOM:</td>
</tr>
<tr>
<td></td>
<td>if(perA.getDegree() == 0 &amp;&amp; perB.getDegree() == 0 ) {</td>
</tr>
<tr>
<td></td>
<td>return 1;</td>
</tr>
<tr>
<td></td>
<td>} else {</td>
</tr>
<tr>
<td></td>
<td>return xi;</td>
</tr>
<tr>
<td></td>
<td>}</td>
</tr>
<tr>
<td></td>
<td>case SCALE_FREE:</td>
</tr>
<tr>
<td></td>
<td>double d = .1 + (.9 *</td>
</tr>
<tr>
<td></td>
<td>((perA.getDegree()<em>perB.getDegree())/(maxPartnrsoberved</em>maxPartnrsoberved))</td>
</tr>
</tbody>
</table>
if (perA.getProvince() == perB.getProvince()) {
    return d;
} else {
    return d * .01; // 100 provinces, probability that provinces are equal is 1%
}
return 0;

Active Object: Person

<table>
<thead>
<tr>
<th>Additional class code</th>
<th></th>
</tr>
</thead>
</table>
| public void addFriend(Person p) {
  this.friends.add(p);
} |
| public void addPartner(Person p) {
  this.partners.add(p);
  if (this.partners.size() > model.maxPartnrsobserved) {
    model.maxPartnrsobserved = this.partners.size();
  }
} |
| public void addPartnerDuration(Double d) {
  this.partnersDuration.add(d);
} |
| public double calcTransProb(Person p) {
  double gamma = .001;
  return gamma;
} |
| public boolean checkPartners(Person p) {
  return this.partners.contains(p);
} |
| public boolean contains(Person p) {
  return this.friends.contains(p);
} |
| public void copyIdeaFrom(Person p) {
  this.setIdea(p.getIdea());
} |
public int findIndex(Object o) {
    return this.partners.indexOf(o);
}

public int getAge() {
    return this.age;
}

public int getBeliefGroup() {
    return this.beliefGroup;
}

public int getDegree() {
    return this.partners.size();
}

public int getDwelling() {
    return this.dwelling;
}

public int getEducLevel() {
    return this.educLevel;
}

public Person getFriend(int index) {
    return (Person) this.friends.elementAt(index);
}

public Iterator getFriendsIterator() {
    return this.friends.iterator();
}

public int getIdea() {
    return this.idea;
}

public int getNumFriends() {
    return this.friends.size();
}

public Iterator getPartnersIterator() {
    return this.partners.iterator();
}

public int getProvince() {
    return this.province;
public int getSex() {
    return this.sex;
}

public boolean hasPartners() {
    return !this.partners.isEmpty;
}

public boolean hasReceivedIdea() {
    return this.goodIdeaReceived;
}

public void incrementTotalPartners() {
    this.totalPartners++;
}

public void makeAdvocate() {
    this.idea = model.GOOD IDEA;
    this.goodIdeaReceived = true;
    this.isAdvocate = true;
}

public Person removeFriend(int index) {
    Object p = this.friends.remove(index);
    return (Person)p;
}

public void removeFriend(Object o) {
    this.friends.remove(o);
}

public Object removePartner(int index) {
    Object p = this.partners.remove(index);
    return p;
}

public void removePartner(Object o) {
    this.partners.remove(o);
}

public void removePartnerDuration(Object o) {
    this.partnersDuration.remove(o);
}
public Object removePartnerDuration(int index) {
    Object p = this.partnersDuration.remove(index);
    return p;
}

public void setIdea(int idea) {
    if (!this.isAdvocate) {
        if ((idea == model.GOOD_IDEA) && (!this.goodIdeaReceived)) {
            this.goodIdeaReceived = true;
        }
        this.idea = idea;
    }
}

public void setProvince(int p) {
    this.province = p;
}

Icon

<table>
<thead>
<tr>
<th>Picture</th>
</tr>
</thead>
<tbody>
<tr>
<td><img src="image" alt="Icon" /></td>
</tr>
</tbody>
</table>

Structure

<table>
<thead>
<tr>
<th>Picture</th>
</tr>
</thead>
<tbody>
<tr>
<td><img src="image" alt="Structure" /></td>
</tr>
</tbody>
</table>

Variable

<p>| isIdeaFromAdvocate |</p>
<table>
<thead>
<tr>
<th>Description</th>
<th>Boolean set to true if agent received good idea directly from advocate (as opposed to idea spread within a social group)</th>
</tr>
</thead>
<tbody>
<tr>
<td>Variable type</td>
<td>boolean</td>
</tr>
<tr>
<td>Initial value</td>
<td>false</td>
</tr>
<tr>
<td>Variable</td>
<td>beliefGroup</td>
</tr>
<tr>
<td>Description</td>
<td>Uniform distribution of belief groups. Could represent groups such as Catholics, Protest, animists.</td>
</tr>
<tr>
<td>Variable type</td>
<td>integer</td>
</tr>
<tr>
<td>Initial value</td>
<td>uniform_discr(1, 2)</td>
</tr>
<tr>
<td>Variable</td>
<td>isAdvocate</td>
</tr>
<tr>
<td>Description</td>
<td>Boolean set to true if agent is chosen to be advocate</td>
</tr>
<tr>
<td>Variable type</td>
<td>boolean</td>
</tr>
<tr>
<td>Initial value</td>
<td>false</td>
</tr>
<tr>
<td>Variable</td>
<td>totalPartners</td>
</tr>
<tr>
<td>Description</td>
<td>Number of lifetime partners</td>
</tr>
<tr>
<td>Variable type</td>
<td>integer</td>
</tr>
<tr>
<td>Initial value</td>
<td>0</td>
</tr>
<tr>
<td>Variable</td>
<td>goodIdeaReceived</td>
</tr>
<tr>
<td>Description</td>
<td>Boolean which tracks if a good idea was ever received. Used to track if an agent has received a good idea but reverted to bad idea.</td>
</tr>
<tr>
<td>Variable type</td>
<td>boolean</td>
</tr>
<tr>
<td>Initial value</td>
<td>false</td>
</tr>
<tr>
<td>Variable</td>
<td>age</td>
</tr>
<tr>
<td>Description</td>
<td>Distribution of age groups</td>
</tr>
</tbody>
</table>

127
<table>
<thead>
<tr>
<th>Variable Type</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>integer</td>
<td>Distribution of sex 0 is male 1 is female</td>
</tr>
<tr>
<td>integer</td>
<td>Distribution of education attainment</td>
</tr>
<tr>
<td>integer</td>
<td>Binary value which represents if agent is transmitter of HIV or not. If agent has 'bad idea,' he/she may get infected with HIV and pass on virus. Otherwise, he/she will not become infected or transmit as long as the good idea is retained.</td>
</tr>
<tr>
<td>integer</td>
<td>Uniform distribution between urban and rural dwelling types</td>
</tr>
<tr>
<td>integer</td>
<td>Uniform distribution of provinces</td>
</tr>
</tbody>
</table>

<table>
<thead>
<tr>
<th>Initial Value</th>
<th>sex</th>
</tr>
</thead>
<tbody>
<tr>
<td>uniform_discr(0,1);</td>
<td></td>
</tr>
<tr>
<td>uniform_discr(0,1);</td>
<td></td>
</tr>
<tr>
<td>uniform_discr(1, 2)</td>
<td></td>
</tr>
<tr>
<td>model.BAD_IDEA</td>
<td></td>
</tr>
<tr>
<td>dwelling</td>
<td>Uniform distribution between urban and rural dwelling types</td>
</tr>
<tr>
<td>province</td>
<td>Uniform distribution of provinces</td>
</tr>
<tr>
<td>integer</td>
<td></td>
</tr>
<tr>
<td>Variable</td>
<td>Description</td>
</tr>
<tr>
<td>----------------</td>
<td>--------------------------------------------------</td>
</tr>
<tr>
<td>friends</td>
<td>Vector of friends in social network</td>
</tr>
<tr>
<td>partnersDuration</td>
<td>Vector which maintains duration data for each agent's partnerships</td>
</tr>
<tr>
<td>partners</td>
<td>Vector of sexual partners</td>
</tr>
<tr>
<td>model</td>
<td>Used for Person object to refer to parameters defined in Main</td>
</tr>
</tbody>
</table>

**Statechart**

States represent phases of HIV and AIDS. Agent transitions through phases by a number of days given for each phase.
<table>
<thead>
<tr>
<th>Name</th>
<th>statechart</th>
</tr>
</thead>
<tbody>
<tr>
<td>Picture</td>
<td></td>
</tr>
<tr>
<td>Transition</td>
<td>transition4</td>
</tr>
<tr>
<td>Source/target</td>
<td>AIDS=&gt;death</td>
</tr>
<tr>
<td>Fire</td>
<td>Timeout</td>
</tr>
<tr>
<td>Timeout</td>
<td>365</td>
</tr>
<tr>
<td>Transition</td>
<td>infected</td>
</tr>
<tr>
<td>Source/target</td>
<td>susceptible=&gt;primaryInfection</td>
</tr>
<tr>
<td>Fire</td>
<td>Signal event occurs</td>
</tr>
<tr>
<td>Guard</td>
<td>(idea==model.BAD_IDEA)</td>
</tr>
<tr>
<td>Signal event</td>
<td>&quot;Infected&quot;</td>
</tr>
<tr>
<td>Transition</td>
<td>acuteHIVInfecPartner</td>
</tr>
<tr>
<td>Source/target</td>
<td>acuteHIV=&gt;acuteHIV</td>
</tr>
<tr>
<td>Fire</td>
<td>Timeout</td>
</tr>
<tr>
<td>Guard</td>
<td>(idea==model.BAD_IDEA)</td>
</tr>
<tr>
<td>Timeout</td>
<td>1</td>
</tr>
</tbody>
</table>
| Action | double d=0; 
|        | Iterator i = partners.iterator(); 
|        | Person partner; 
|        | while(i.hasNext()) { //iterate through the vector of partners 
|        | d = uniform(1); 
|        | partner = (Person)i.next(); 
|        | if (d < calcTransProb(partner)) { 
|        |     partner.statechart.fireEvent("Infected"); //if partner is already no transition occurs 
|        | } 
|        | } |
| Transition | transition |
| Source/target | acuteHIV=>latentHIV |
| Fire | Timeout |
| Timeout | 14 |
| Transition | latentHIVInfectPartner |
| Source/target | latentHIV=>latentHIV |
| Fire | Timeout |
| Guard | (idea==model.BAD.idea) |
| Timeout | 1 |
| Action | double d; 
|        | Iterator i = partners.iterator(); 
|        | Person partner; 
|        | while(i.hasNext()) { //iterate through the vector of partners 
|        | d = uniform(1); 
|        | partner = (Person)i.next(); 
|        | if (d < calcTransProb(partner)) { 
|        |     partner.statechart.fireEvent("Infected"); //if partner is already no transition occurs 
|        | } 
<p>|        | } |</p>
<table>
<thead>
<tr>
<th>Transition</th>
<th>transitionAIDS</th>
</tr>
</thead>
<tbody>
<tr>
<td>Source/target</td>
<td>latentHIV=&gt;AIDS</td>
</tr>
<tr>
<td>Fire</td>
<td>Timeout</td>
</tr>
<tr>
<td>Timeout</td>
<td>3285</td>
</tr>
<tr>
<td>Action</td>
<td></td>
</tr>
<tr>
<td>Transition</td>
<td>acutePhase</td>
</tr>
<tr>
<td>Source/target</td>
<td>primaryInfection=&gt;acuteHIV</td>
</tr>
<tr>
<td>Fire</td>
<td>Timeout</td>
</tr>
<tr>
<td>Timeout</td>
<td>26</td>
</tr>
<tr>
<td>Action</td>
<td></td>
</tr>
</tbody>
</table>

**State** primaryInfection

**Entry action**
- `model.nPrimaryInfected++;
- `model.totalPrevalence++;
- `model.setModified();

**Exit action**
- `model.nPrimaryInfected--;`  
- `model.setModified();`  

**State** acuteHIV

**Entry action**
- `model.nAcuteHIV++;`
- `model.setModified();`

**Exit action**
- `model.nAcuteHIV--;`
- `model.setModified();`

**State** AIDS

**Entry action**
- `model.nAIDS++;`
- `model.setModified();`

**State** latentHIV

**Entry action**
- `model.nLatentHIV++;`
- `model.setModified();`

**Exit action**
- `model.nLatentHIV--;`
- `model.setModified();`

**State** susceptible
<table>
<thead>
<tr>
<th>Exit action</th>
<th>model.nSusceptible--;</th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td>model.setModified();</td>
</tr>
</tbody>
</table>