Managing the HIV/AIDS Pandemic: 2006-2055

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Abstract

The HIV/AIDS pandemic is undoubtedly one of the greatest challenges facing the modern world. Not only is it a fatal virus, it is a master of elusion. After twenty-five years, no human effort has come near stopping the destruction caused by HIV/AIDS. Further, the problem is so large that determining how to attack it may be one of the more insurmountable difficulties faced thus far.

We outline a plan of attack for understanding and controlling the HIV/AIDS crisis. It begins with a thorough consideration of determining what nations are facing the most critical situations with respect to HIV/AIDS. We accomplish this by modeling an adjusted life expectancy, using a short-term logistic differential equation model, and mathematically defining criticality.

We more deeply analyze the future situations of the most critical nations with a powerful computer simulation model. The model is very versatile and can provide a great deal of information about populations, and has the further advantage of dealing directly with people rather than homogenous populations, as a differential equations model would.

Treatment analysis includes a brief estimation on the amount of foreign aid available through 2055, and then predicts the effects of Antiretroviral Therapy and the possibilities of a preventative HIV/AIDS vaccine. We then consider the ramifications of drug resistant strains and how they may arise.

We conclude with a series of recommendations to the United Nations, for how best to allocate resources to the HIV/AIDS Pandemic.

By continent, we conclude the most critical nations are: Botswana, Thailand, Tonga, Ukraine, Bahamas, and Guyana. We recommend intensive spending on research and development for and HIV/AIDS vaccine in the short term, followed by a global coverage of ARV treatment with heavy emphasis on maintaining adherence.

Introduction

Since first being identified in 1981, the HIV virus has spread rampantly throughout many parts of the world. HIV is a sexually transmitted retrovirus that weakens the immune system, almost inevitably leading to death. It is estimated that approximately 25 million people have already died from complications related to the HIV virus and AIDS. Despite a wide variety of global efforts to control this pandemic, the number of infections and deaths from HIV/AIDS continues to rise. One of the main complications when dealing with a virus such as HIV is that it affects its host at a rate much slower than the disease is spread. This allows HIV positive individuals to spread the disease for some time before they are even aware that they are infected.

HIV and AIDS has become a particularly challenging problem to deal with in the developing world. In countries where poverty and famine are widespread, methods of prevention such as condoms and HIV/AIDS education aren't available. Furthermore, these countries often lack the necessary funding to test citizens for HIV and to treat current patients with antiretroviral drugs (ARV treatment). International funding has become an integral part of managing the HIV/AIDS pandemic in the world today. Funding from private sectors, non-profit organizations, as well as individual governments, provides the majority of the resources with which nations are able to

Restatement of the Problem

While almost everyone will agree that the rapid spread of the HIV virus is an enormous crisis throughout many parts of the world, a highly disputed topic is how funding should be distributed to deal with the current situation. While some will argue that treatment of patients is of utmost importance, many feel that research into preventative measures such as development of a vaccination would provide the most benefit in the long run.

Our goal throughout this model is to access the trade-offs between each of the above approaches, specifically determining the most beneficial way to distribute funding over the next fifty years. We will pay specific attention to factors such as the possible development of a vaccine, changes in ARV treatment, and the possible mutation of the virus into multiple strains.

1.1 Defining Criticality

1.2 Approach

We were charged with the task of determining a country from each continent "most critical in terms of HIV/AIDS." But what exactly makes a country "critical"? The obvious answer is to choose countries with the greatest number of HIV/AIDS cases, or

the greatest proportion of cases, but this is not a complete analysis. A critical situation implies that progress can be made towards a solution. At this point in time, nothing beyond antiretroviral therapy can be done for an HIV/AIDS patient. Therefore, countries with high rates of treatment can do little more for their infected population (although it is important to keep in mind that prevention and education measures are still very applicable). Thus, such countries should not be deemed most critical. The term critical also implies that action is urgent, that HIV/AIDS will be very detrimental in the short term. We believe that the best way to measure the effect of HIV/AIDS on a population is to determine the cumulative number of years of life lost due to infection.

1.3 Assumptions & Terms

- We are not considering people currently receiving treatment, as it is assumed that there is nothing more that can be done with them. Criticality is relevant to determining how urgent it is to act on a situation, so there is no reason to consider those for whom nothing more can be done.
- ARV patients have 100% adherence. That is, a patient either has ARV treatment or does not, there is no middle ground.
- No further intervention occurs within the next five years.
- ARV treatment percentages remain constant.
- No other major causes of death affect the population. Since we are predicting over a relatively short interval of time, it is unlikely that major events such as natural disaster, wars, or other pandemics will significantly affect the population.
- People-year: A unit equivalent to one person times one year. The number of people-years of a population is equal to the sum of all the lifetimes of people in the population.
- To measure the immediate effects of HIV/AIDS on a population receiving no further intervention, we define criticality over the next five years (2006-2010):
    - Absolute Criticality: The total number of people-years lost by a population over the next five years due to HIV/AIDS.
    - Relative Criticality: The average number of people-years lost by a person over the next five years, in other words, the change in life expectancy over the next five years.

1.4 Development

Based on our assumptions and definition of criticality, we then derived a mathematical expression for criticality in terms of various parameters. Mathematically, relative criticality, ζ, is given by:

$$\zeta(\alpha,\beta,\gamma,\delta,\varepsilon) = \alpha(\gamma+\delta)+\beta(\varepsilon)$$

Where:

- α – The average loss of life expectancy due to contracting HIV and without receiving ARV treatment.
- β – The average loss of life expectancy due to contracting HIV and receiving ARV treatment.
- γ - Number of current untreated cases divided by population.
- δ - Number of untreated cases contracted over the next five years divided by population.
- ε - Number of treated cases contracted over the next five years divided by population.

Absolute criticality is then given by:

$$\zeta_{Abs.} = \zeta(\alpha, \beta, \gamma, \delta, \varepsilon)P$$

Where P is the total population of a given country.

It seems counterintuitive that a country should be considered "less critical" if its life expectancy is innately lower, as our model would conclude. What this really means is that for the given country, spending money on HIV/AIDS may be less relevant than spending money on other causes of death. If for instance, most people in a country die at 30 of tuberculosis (without AIDS) then tuberculosis is likely to be a bigger concern for that country even than a raging HIV epidemic. Further, we did not include a parameter for current HIV cases undergoing treatment, because, as we stated above, nothing more can be done for these people, so they should have no impact on the criticality.

1.5 Model A: Adjusting the Life Expectancy

1.6 Approach

In order to determine the effects of HIV/AIDS on a population, we initially determined the life expectancy of a population as if HIV/AIDS did not exist. Furthermore, we then adjusted for the fact that life expectancy is a function of year of birth.

1.7 Assumptions

- The life expectancy does not significantly change within a period of five years, as we assume people of each age group are the same age.
- Life expectancy data does not exist for birth years before 1950, so we assume any person born before 1950 has the life expectancy of someone born in 1950.
- No immigration or emigration occurs.

1.8 Method

Again, we employed the idea of a person-year as the unit for population life expectancy, which is simply a person times one year. Using 2005 population data, we multiply the population for each age group by the life expectancy of the corresponding birth years. This yields the total number of person-years for a given population. Dividing this by the population will then give the age-adjusted life expectancy, denoted Γ_0.

We then determined a life expectancy value for people infected with HIV/AIDS. Research showed that worldwide, the average age for contracting HIV is 23 years old. We then had to distinguish between life expectancy with and without ARV treatment. We assumed here that a person on ARV treatment has 100% adherence and never stops treatment. In developed nations, a person contracting HIV typically lives twelve years, untreated. Few people treated with ARV have died; however, the program began only ten years ago. Current projections claim ARV treated patients will live twenty years after contraction in developed nations. To determine the average life expectancy for a person contracting HIV/AIDS, we used the following formula, where T is the percentage of people currently receiving ARV treatment;

$$\Gamma_{HIV} = \frac{\Gamma_0(35(1-\mathrm{T}) + 43(\mathrm{T}))}{70}$$

We take a weighted average of the life expectancies for untreated and treated patients, and then we account for the difference in life expectancy due to causes other than HIV by multiplying by the unadjusted life expectancy and dividing by 70, an assumed average for the life expectancy of a developed nation.

Now we can derive an expression for the HIV-adjusted life expectancy. Rather than using an algebraic definition, we take a more intuitive approach using set theory.

We have data for the total number of people-years of a population, and given the number of HIV cases, P_{HIV}, and the average life expectancy for HIV patients, we know the total number of HIV people-years. If these people did not have HIV, the number of people-years they contribute to the population would increase. Therefore, adding the number of people-years the HIV infected population loses due to premature death to the unadjusted number of people-years for a population will yield the adjusted people-years, and consequently an HIV-adjusted life expectancy for that population.

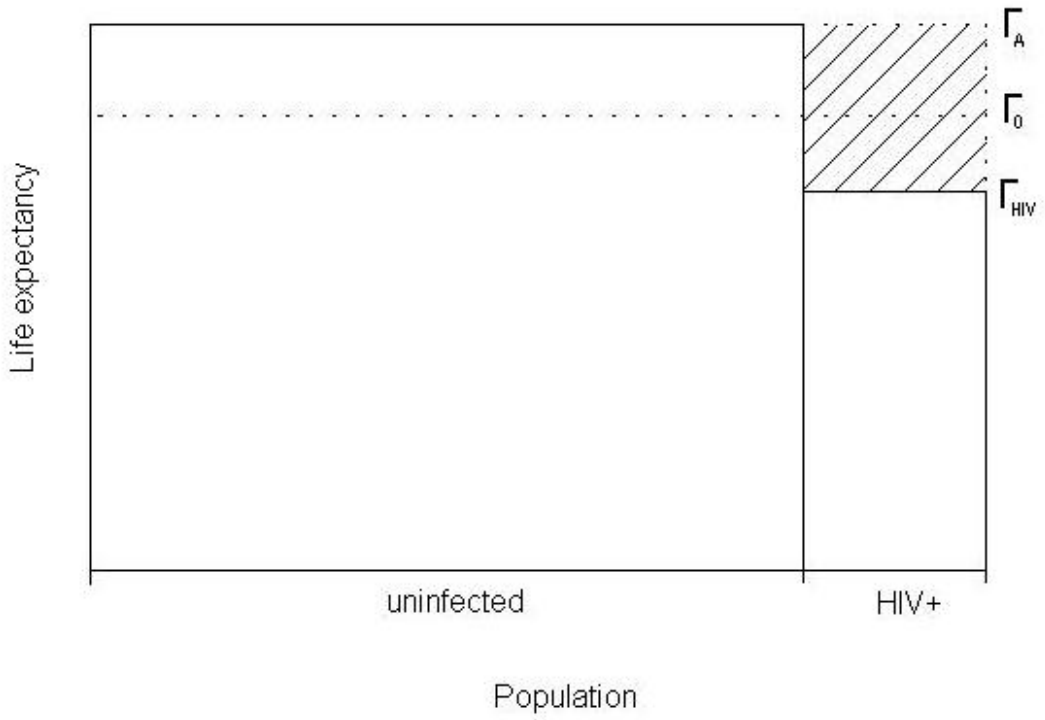

Figure 1: Schematic for HIV/AIDS Adjusted Life Expectancy

The formula for HIV-adjusted life expectancy, Γ_A, is then:

$$\Gamma_A = \frac{P\Gamma_0 + P_{HIV}(\Gamma_0 - \Gamma_{HIV})}{P}.$$

1.9 Expectations & Results

If our model is appropriate, a few things should certainly occur.

- The HIV-adjusted life expectancy should always be greater than the unadjusted life expectancy.
- The difference between the HIV-adjusted life expectancy and the unadjusted life expectancy should be proportional to the percentage of the population infected with HIV.

We found that no country showed a decrease in life-expectancy, and by taking the difference between the HIV-adjusted life expectancy and the unadjusted life expectancy and dividing by the percentage of the population infected with HIV found that there is strong evidence for proportionality.

Table 1: Sampling of Data for Adjusted Life Expectancy

Country	$\%P_{HIV}$	Γ_A	Γ_0	$\Gamma_A - \Gamma_0$	$\frac{\Gamma_A - \Gamma_0}{\%P_{HIV}}$
South Africa	9.208447	54.43419765	47.8859661	6.548231545	0.71111141
Swaziland	12.70692	59.90673829	49.96840014	9.938338147	0.782120455
Benin	0.972634	45.78348032	45.19888046	0.584599864	0.601048416
Burkina Faso	3.099645	50.7415497	48.63499062	2.106559077	0.679612974
Côte d'Ivoire	4.541394	48.28076085	45.42957291	2.85118794	0.627822243
Gambia	0.987929	53.35998887	52.63296005	0.727028811	0.735911985
Ghana	1.711382	43.27133889	42.32572913	0.945609759	0.552541587
Mali	0.858596	44.17979029	43.68821152	0.491578764	0.572537707
Nigeria	2.295766	49.68537808	48.15856453	1.526813551	0.665056312

1.10 Model B: Logistic Growth

1.11 Approach

In order to use our definition of criticality, it was necessary to be able to predict the number of HIV/AIDS cases (both treated and untreated) over the next five years. We decided to employ a logistic growth model since it would be reasonably easy to work with, while providing estimates that are necessary to determine which countries are most critically in need of aid. Furthermore, the logistic model incorporates a maximum sustainable population, something that is clearly applicable in situations such as fatal epidemics, at least in the short term. We will later develop a more detailed computer simulation that will hopefully provide more accurate results for the selected countries.

1.12 Assumptions

- Birth and death trends remain similar over the next five years. Since the data collected is dependent upon these trends, it is assumed that there will be no significant variation of these trends over the next five years.
- The incidence of HIV/AIDS is constant within each of the 12 selected regions. We chose 12 representative regions (including some individual countries and continents) which we feel have minimal variation in HIV/AIDS growth rates: Africa, South East/Central Asia, North/East Asia, Oceania, Brazil, South America excluding Brazil, Canada, the United States, Mexico, Latin/Central America, the Caribbean, and Europe.

1.13 Development

The logistic growth model describes a population that grows proportionally to the current size of the population, in addition to factoring in a carrying capacity, or in this case, a maximum sustainable AIDS population. The general form of the differential equation is:

$$\frac{dP}{dt} = \frac{rP(K-P)}{K} = rP(1-\frac{P}{K})$$

Where P is the total HIV/AIDS population size, r is the maximum population growth rate, and K is the maximum sustainable population. The above equation indicates that as the population gets closer and closer to the maximum sustainable population, its growth rate becomes a smaller proportion of the maximum growth rate, r. The general solution to the differential equation is:

$$P(t) = \frac{r}{ce^{-rt} + r/k}.$$

Where c is a constant determined by an initial condition. However, since we do not know the value of k or r, we devised a method for determining these values. We began by collecting data for the number of HIV/AIDS case over the past 5-20 years. We then multiplied out the differential equation:

$$\frac{dP}{dt} = rP - \frac{r}{K}P^2.$$

We then defined $a = r$ and $b = -r/k$, to arrive at the equation:

$$\frac{dP}{dt} = aP + bP^2.$$

Next, we divided both sides of the equation by P to obtain:

$$\frac{1}{P}\frac{dP}{dt} = a + bP.$$

Since the right hand side of the above equation is now linear, we plotted successive values of

$$(P(t_i), \frac{P'(t_i)}{P(t_i)})$$

and then fit a linear regression to the data, which will have a slope of *b* and a y-intercept of *a*. To obtain values for $P'(t_i)$, we decided to plot population versus time data using computer software, and then estimate the derivative at a point by the slope of the secant line connecting the point before and the point after the chosen point. A visualization of this is provided in the figure below.

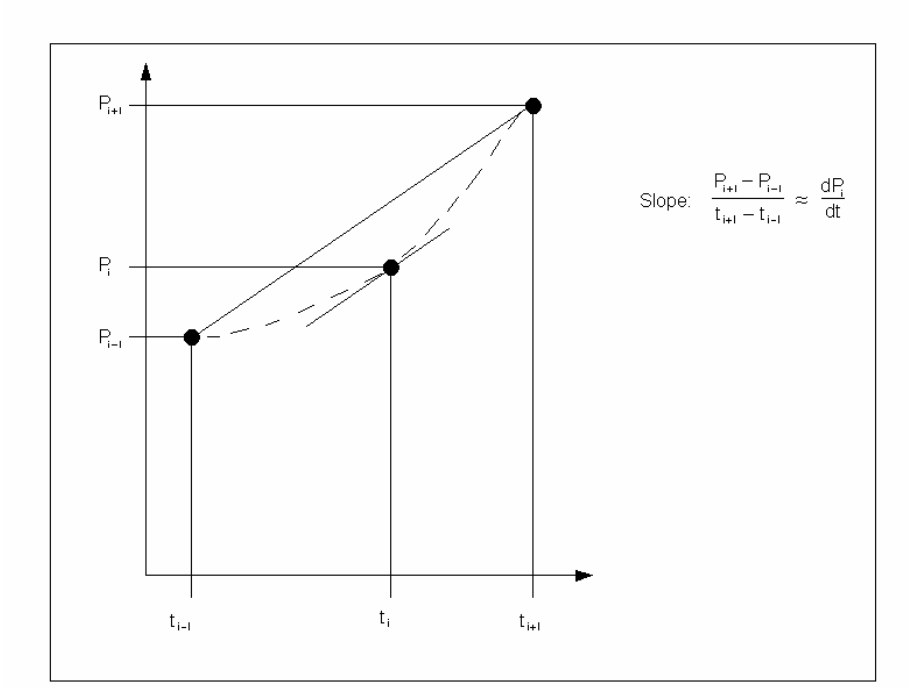

Figure 2: Estimating P'(t) Using the Slope of Secant Line Connecting Adjacent Points

1.14 Results

Initially we used the above procedure to determine a function for the size of the HIV/AIDS population at a given time, *P(t)*. It was then necessary to predict the number of new cases that will occur over the next five years, an important parameter in our criticality function. To do this we evaluated the function at 2010, and then subtracted from this the value of the function evaluated at 2005. Below is an example of the data collected for Africa, with the logistic fit superimposed on the graph. Appendix 1 provides graphs illustrating the logistic curve model for all of the 12 selected regions.

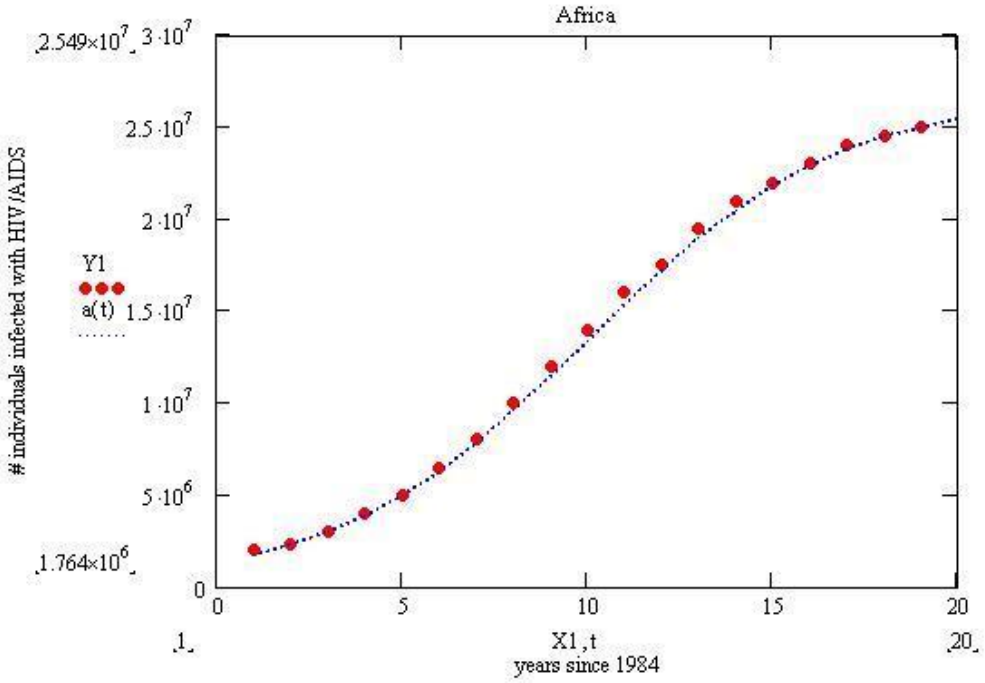

Figure 3: Logistic Growth Model for African Region

1.15 Putting it all together

Given the HIV-adjusted life expectancy, we can determine the values for α and β for each country;

$$\alpha = \Gamma_A - 35(\frac{\Gamma_0}{70})$$

$$\beta = \Gamma_A - 43(\frac{\Gamma_0}{70})$$

Armed with a logistic model for the HIV/AIDS infected population of each region, we can extrapolate to determine the number of cases that will arise over the next five years, by region. This simply involves determining the total number of cases predicted in 2010 and subtracting the number of cases in 2005. We then make two assumptions for determine the values of γ and ε for each country:

1.16 Additional Assumptions

- The proportion of HIV/AIDS cases which are treated by ARV will remain unchanged over the next five years, as no new interventions will occur.
- The proportion of HIV/AIDS cases of each country within its respective region will remain unchanged, we call this proportion $\mathrm{H}_{relative}$.

$$\gamma = \frac{(1-\mathrm{T})(P(26)-P(21))\mathrm{H}_{relative}}{P}$$
$$\varepsilon = \frac{\mathrm{T}(P(26)-P(21))\mathrm{H}_{relative}}{P}$$

Finally, the number of current HIV/AIDS cases is given by our data, so

$$\delta = \frac{(1-\mathrm{T})\mathrm{H}}{P}$$

1.17 Results

We determined absolute and relative criticality values for each country for which all the data used in computing parameters was available (108 countries). We then used relative criticality in selecting our most critical countries, by continent. Had we used absolute criticality it would have given precedence to large nations, despite relatively mild HIV/AIDS situations.

Table 2: Most Critical Countries by Continent

Country	Continent	Criticality (Relative)
Botswana	Africa	4.097469
Thailand	Asia	0.283505
Tonga	Australia	0.06667
Ukraine	Europe	0.135426
Bahamas	North America	0.614664
Guyana	South America	0.4312

Table 3: 15 Most Critical Counties Worldwide

Country	Continent	Criticality (Relative)
Botswana	Africa	4.097469
Lesotho	Africa	3.917542
Zimbabwe	Africa	2.948378
Swaziland	Africa	2.936501
Namibia	Africa	2.061595
South Africa	Africa	1.696884
Zambia	Africa	1.134822
Malawi	Africa	0.778267
Central African Republic	Africa	0.770965
Djibouti	Africa	0.765548
Mozambique	Africa	0.700727
Burundi	Africa	0.652575
Bahamas	North America	0.614664
Tanzania	Africa	0.571731
Côte d'Ivoire	Africa	0.565031

1.18 Discussion

Analysis of the criticality equation allowed us to select the most critical nations by continent; Botswana, Thailand, Tonga, Ukraine, Bahamas, and Guyana. We also observed that fourteen of the fifteen most critical nations, worldwide, are located in Africa. This will be important in formulating recommendations for foreign spending in fighting the AIDS pandemic.

2.1 Determining Growth Rates Among HIV/AIDS Populations

2.2 Model C: Simulation of a Country with HIV/AIDS

2.3 Approach

While a logistic model proved a remarkably good fit for the data we had, we wanted a more detailed and elaborate model to use for forecasting the long-term behavior of HIV/AIDS in the populations of the particular countries selected as the most critical. This was partly to address the role of births and deaths in the behavior of the virus; while it is plausible to assume, as the logistic model requires, that the role of these may be relatively small over a five-year period, a fifty-year period presents another question entirely. Another reason to have this would be to get a deeper understanding of the

mechanisms behind the disease. With the logistic model we used, the carrying capacity was derived simply as a consequence of the curve fitting; it is preferable that the carrying capacity ought to arise naturally as a consequence of other parameters in the model, both from an aesthetic standpoint and from a desire to know how to go about altering the course of the disease.

We considered attempting to use another, more sophisticated differential-equation based model to improve our understanding of the disease and our ability to predict it over time. For instance, we could have modeled separate populations of infected and uninfected persons, and the effects of these populations on each other. While the logistic model is technically a very simple model of this sort, a more complicated model might be able to predict the ultimate behavior of the disease based on assumptions about rates of birth, death, and infection, rather than simply assuming the existence of a carrying capacity. However, we felt that this approach would still exclude certain key features of the spread of the disease, most notably the extensive demographic variation in its rate of spreading. HIV/AIDS has a history of exploding in one demographic group, for instance intra-venous drug users and homosexually active males, and then being transferred to another, for instance heterosexuals of both genders. A relatively simple differential-equation model based on separate populations of infected and uninfected persons would not easily be able to accommodate this sort of occurrence, as differential equation models are classically derived based on assumptions of homogeneity. A more complicated differential equation system that treats demographic groups differently would likely be unwieldy, particularly since demographic groups often overlap. Thus, we opted for a different sort of model altogether: a discrete computer simulation of the interactions of individuals. An advantage of such a model is that it is much better able to cope with complicated demographic combinations, as the objects of the model are persons rather than homogeneous populations. A disadvantage is that directly simulating an entire country's population in this way is not feasible.

2.4 Assumptions

- Key Assumption- An entire country may be modeled by modeling the course of the disease over a small, representative community (population on the order of one thousand).
- By allowing the simulation to run for ten years before introducing HIV, this will allow for a base of existing relationships to form.
- With the exception of contraction before or during birth, all transfers of HIV occur as a result of a consensual event (drug or sex-related) between two people in a consensual relationship between those two people.
- A person's probability of dying of natural causes is directly proportional to their age.
- The effect of HIV is to multiply by some factor what would otherwise be a person's probability of dying of all other causes. This effect depends solely on

whether or not a person has the virus; other factors, such as amount of time since the virus was contracted, need not be considered.

- The sexual behavior of persons regarding number of partners, frequency of sex, etc. is essentially the same, regardless of their gender and sexual orientation. The only exception is that only females can be sex workers and only males can be clients of sex workers.
- The population of female homosexuals and bisexuals can be neglected.
- People's characteristics do not change as they grow older, except for changing stages from infant to child at age 2 and from child to adult at age 16.
- Only adults will have sexual relationships or share intravenous drugs.
- A needle-sharing or sexual encounter with an infected person will automatically result in the transfer of the virus.

2.5 Development

Relationships

The basic tools that we used to model the spread of the disease were relationships and events. A relationship occurs between two people. It can be initiated by either and must be accepted by the other. An event occurs within a relationship and may result in the transfer of a virus, or multiple strains of a virus, between persons. Like a relationship, an event can be initiated by either person but must be accepted by the other. Different people have tendencies to engage in different sorts of relationships and events, and may thereby be classified into relevant demographic groups. The relationships types we used included sexual relationships, mother-child relationships, and relationships for the social use of intravenous drugs.

Availability pools

The mechanism for the formation of relationships was based on availability pools. Depending on their characteristics and on existing relationships, persons are placed into availability pools for particular sorts of relationships. A person seeking a relationship will choose the appropriate availability pool, which they may or may not belong to themselves, and query it for a possible match. The availability pool will choose a potential match using an algorithm that attempts to preserve efficiency of data structures while providing some measure of randomness, and the chosen person is given the option of accepting or refusing the offered relationship. Either person may choose to end a relationship.

Events

In general, each person who engages in relationships of a given category has a desired rate of events of that category. The chance of accepting an event or of requesting an

event in a given cycle is based on whether or not the person has reached their satiation point for the given event.

Drug use relationships

Every intravenous drug user belongs to the drug use availability pool. Each drug user has a preferred number of "drug buddies"; the rate of requesting a new buddy relationship and the probability of accepting a request are both proportional to the difference between the current number of relationships and the preferred number, with different constants of proportionality that are also different for different drug users. Events represent sharing needles.

Mother-child relationships

It is assumed that every infant and every child wants to have a mother. When a woman gives birth, a mother-child relationship is automatically formed. An infant or child whose mother has died will request a new relationship with a surrogate mother at every opportunity. The availability pool for such requests consists of all adult women. Each woman has a probability per year of accepting such a request, corresponding to the adoption rate of orphans. An event in this relationship consists of a breast-feeding event that will, if appropriate, transfer the HIV virus. Only infants will request this event; they will do so with an approximate probability of .05 per year, based on the probability of an infant whose mother has HIV contracting HIV from breastfeeding in the first two years of life. Every request for such an event will be honored by the mother, assuming the child has a mother. The presence or absence of a mother-child relationship has an effect on the death rate of the infant or child (to be addressed later). The model does not consider the impact of father-child relationships.

Sexual relationships

Sexual relationships are classified into heterosexual and male homosexual relationships, and also into monogamous relationships, casual relationships, and prostitutional relationships; thus, there are a total of six availability pools. Additionally, the three heterosexual availability pools are subdivided into males and females. When seeking a relationship of a particular level of commitment, bisexuals will choose randomly whether to request from the heterosexual or the homosexual pool. Forming a monogamous relationship automatically excludes a person from all sexual availability pools for as long as the relationship lasts, although "monogamous" partners may still maintain and request casual and prostitutional relationships. An event for such a relationship consists of a sexual encounter, which can result in the transfer of a virus and/or in the pregnancy of a woman. Prostitutional relationships only last for the duration of a single event. Behavior with respect to sexual relationships is rather complex. There are four basic patterns of

sexual behavior to which a person may belong: these may be called abstinence, monogamy, casuality, and prostitution.

Abstinence

Persons who practice this form of behavior are not in any sexual availability pools and do not request any sexual relationships.

Monogamy

Persons who practice this form of behavior will only be in the monogamous availability pool(s), will only request monogamous relationships, and will never have on-the-side sexual relationships. Also, they will never instigate the end of a relationship.

Casuality

This form of behavior is by far the most complex; it is also the form practiced by the majority of adults, partially because it encompasses a wide range of behaviors. Persons who practice casuality may seek relationships of all three commitment levels, and when not in monogamous relationships are in the availability pools for monogamous and casual relationships. Such a person has a probability of accepting a monogamous proposal and a probability per year of requesting a monogamous proposal, as well as a probability per year of ending a monogamous relationship. When not in a monogamous relationship, a person's treatment of casual relationships is the same system used for drug use relationships; the preferred number of simultaneous relationships may be one or greater, and the likelihood of initiating or accepting a relationship is proportional to the difference between the preferred number of relationships and the actual number of relationships. When such a person is in a monogamous relationship, the monogamous partner counts for two casual partners, so that if the preferred number of partners is less than or equal to two, no new casual relationships will be formed. Additionally, the probability of forming a relationship or requesting a sexual event outside the relationship is reduced by a faithfulness factor that may vary from person to person. Prostitutional relationships, which last only for the duration of a single sexual encounter, are formed when the person's sex event count is below the desired level. However, there is also an inhibition factor that reduces the likelihood of forming a prostitutional relationship. (For women, the inhibition factor removes the possibility of forming a prostitutional relationship.) If the person is in a monogamous relationship, the likelihood of forming a prostitutional relationship when lacking in sex events is further reduced by the faithfulness factor.

Prostitution

The persons, all women, who practice this sort of sexual behavior are always and only in the prostitutional availability pool. They never request relationships, and will accept all relationships up to a maximum rate that varies somewhat among prostitutes.

Birth and Death Rates

For every adult woman who is not already pregnant, a sexual encounter with a man has a fixed probability of resulting in pregnancy. (Menopause is not taken into consideration.) Every pregnancy results in the live birth of a baby nine months after conception, unless the mother dies before that.

The probability of death by natural causes is assumed to be directly proportional to age. Additionally, children and especially infants without mothers have a constant term added to their probability of dying. When HIV is present, the death rate is calculated as if it were not, and is then multiplied by some fixed constant; in a sense, the virus reduces a person's "death resistance."

2.6 Justification of Parameters Used in Simulation

Mother to Child Transfer

Research revealed that the risk of a child contracting HIV during pregnancy and birth ranged from 15 to 30%, and we took this range directly into the program. The research went further, stating that risk increased another 10 to 15% due to breastfeeding over the first two years of life. We simply divided this range in half to determine the rate per year of breastfeeding contraction. (Orendi)

Demographic Data

The demographic data used in the program came largely from the CIA world fact book, including gender values, infant mortality rates, and fertility rates. These data often had to be scaled to run correctly with in the program. For example, the fertility rate was given in births per woman per lifetime. To determine the likelihood of a particular sexual encounter producing a pregnancy, we found the number of births per woman per year that should occur by dividing the fertility rate by the length of time a woman is fertile. Next, we took the number of sexual events per year by the number of women involved in them. Finally we took the number of births per woman and divided by the number of sexual events per woman to determine the number of births per sexual event, a value on the order of thousandths.

Intravenous Drug Use

We determined the percentage of the population using IV drugs by assuming that this value was equal to that of the surrounding region, which we looked up from the United Nations Office of Drug Control. For example, Botswana was considered to have an IV drug population comparable to that of southern Africa. To determine the acceptance, seeking, and breaking rates for drug relationships, we made reasonable assumptions based on reading about the typical social behavior of IV drug abusers. Such an approach was also used in determining the maximum number of drug relationships and the rate of drug relationships per year. (UNODC)

HIV Vulnerability

This parameter comes directly from the HIV-adjusted life expectancy model, and is simply an adjusted ratio of the HIV life expectancy and the unadjusted life expectancy. It is meant to discern between how threatening HIV is in each of the selected nations.

Sex

We discern nearly all of the parameters for the sexual relationships from two sources; the International Encyclopedia of Sexuality and the Penguin Atlas of Human Sexual Behavior. Most of the figures given in these texts are either average values or ranges, and consequently we were forced to make a number of assumptions when applying them to our model. Fortunately, as more concrete data becomes available, this only ensures further accuracy of the model. Again, most of the mathematics involved in converting the data to our program is simple scaling and unit conversion, and we omit the majority of it here.

The yearly number of sexual relationships was expanded to ranges from average values for respective countries, while the various ratios for acceptance, proposal and breaking of a relationship were discerned from worldwide averages for number of relationships per year. A similar method was used to describe the distribution for number of partners per year. Prostitution data was assumed to be constant worldwide, and based on available country-specific data, this seemed a reasonable conjecture. The maximum customers parameter essentially assumed a typical prostitute as having between five and seven maximum clients per week. Finally, the adoption rates were taken from average numbers of adoptions in countries and comparing them to the available "mother pool," that is all potential females who could support a child.

Aging Constant

In our assumption that a person's probability of dying is directly proportional to the person's age, we wanted to be able to calculate the constant of proportionality k based on the life expectancy. The statement about the death rate might be expressed

$$-\frac{dP/dt}{P} = kt\,,$$

where t represents time and P represents the probability of a person being alive. (On another scale, P represents the number of people born in, say, the same year who remain alive after time t.) Applying separation of variables, we get that

$$\frac{dP}{P} = -kt\ dt$$

$$\ln(P) = -\frac{1}{2}kt^2 + C$$

$$P = P_0 e^{-\frac{1}{2}kt^2}$$

Surprisingly (or not, if you are already familiar with this model for human aging, which we weren't), the solution to this differential equation turns out to be the right half of the Gaussian distribution. The following is a graph of (P/P_0) vs. time for k=.001:

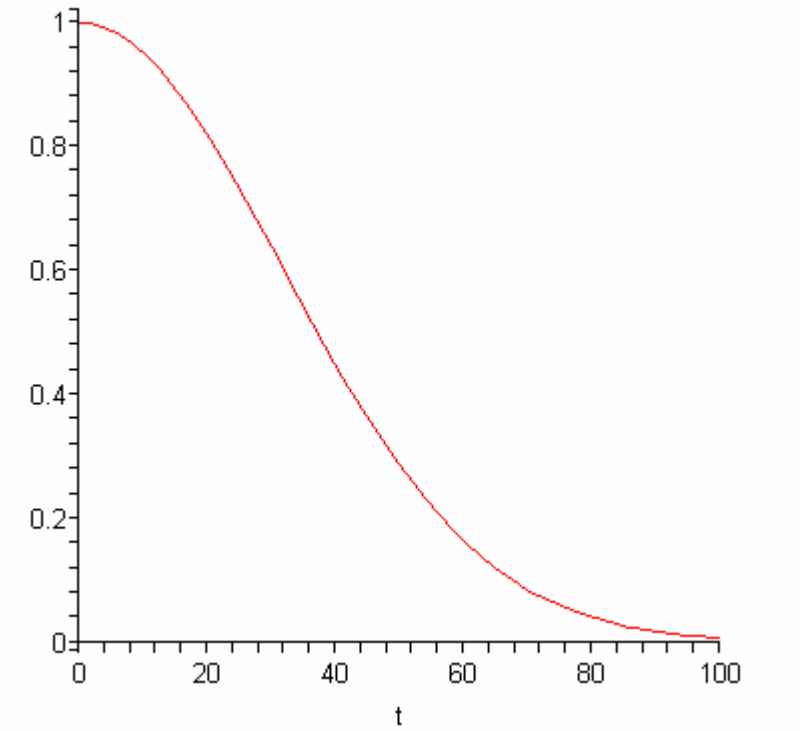

Figure 4: Aging Function

To combine this equation with life expectancy, let *r* represent the death rate and consider that for a differential time quanitity, *-r dt* represents a differential quantity of the number of people who die at a given age *t*. Hence, the average age of death, or life expectancy, would be

$$\frac{1}{P_0}\int_0^\infty rt\ dt = \int kt^2 e^{-\frac{1}{2}kt^2}$$

Although performing this integral is either nontrivial or impossible, it is possible to calculate it numerically as a function of k. We used Maple to solve numerically for setting this expression equal to the life expectancies that we had calculated from other data for the countries of interest, thereby obtaining the appropriate values of k.

2.7 Results & Discussion

After running the fifty year simulation a number of times, we noticed a few things concerning the HIV/AIDS population in each of the critical countries. We first noticed that there was almost always an initially explosion of HIV cases in the first few years, followed by a much slower growth of the HIV/AIDS population. This is likely the result of our assumption that every encounter results in the transmission of HIV. Because of this, HIV spread very quickly throughout relationships that were already in place at the beginning of the fifty year period. Additionally, we noticed that as time progressed, the HIV/AIDS population appeared to somewhat approach a steady-state population, or infected carrying capacity. Below is the graph for Ukraine's HIV/AIDS population and total population over the next fifty years. Data for all of the critical countries can be found in appendix 2.

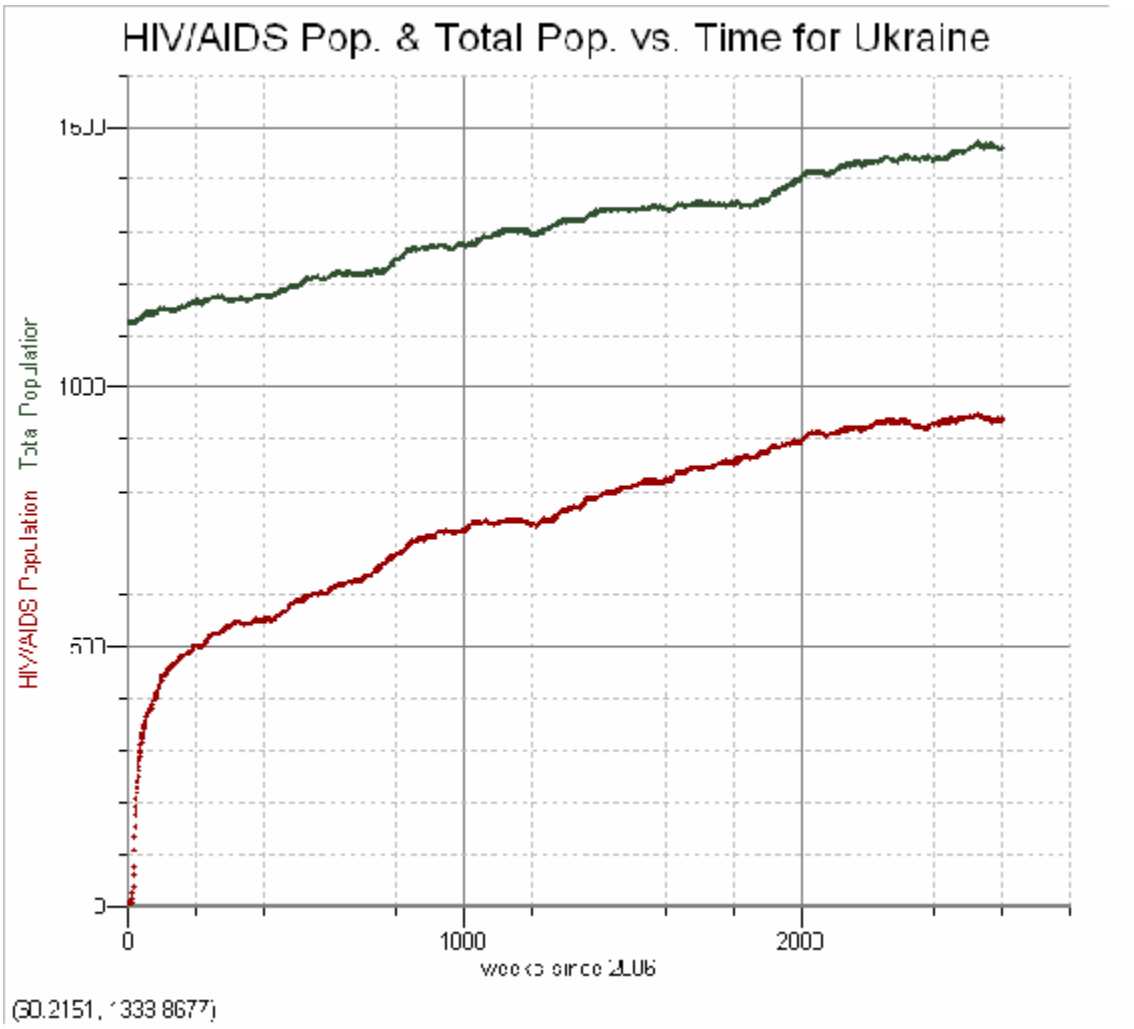

Figure 4: HIV/AIDS Pop. & Total Pop. Vs. Time for Ukraine

We then decided to investigate why the HIV/AIDS population seemed to stabilize at some steady-state value. We realized that based on the structure of our model, it is likely that the majority of the adult population ends up being infected with HIV, while only a small portion of the children contract the virus. Thus, it is possible that this steady state value of HIV/AIDS population could merely be a high percentage of the steady-state value for the adult population. To test this idea, we had the simulation give us data for the number of HIV positive and negative people left at the end of the simulation as a function of age. From the figure below, it is clear that nearly all of the young population left at the end of the simulation is HIV negative, while most of the older population is HIV positive. Thus, our speculations were confirmed.

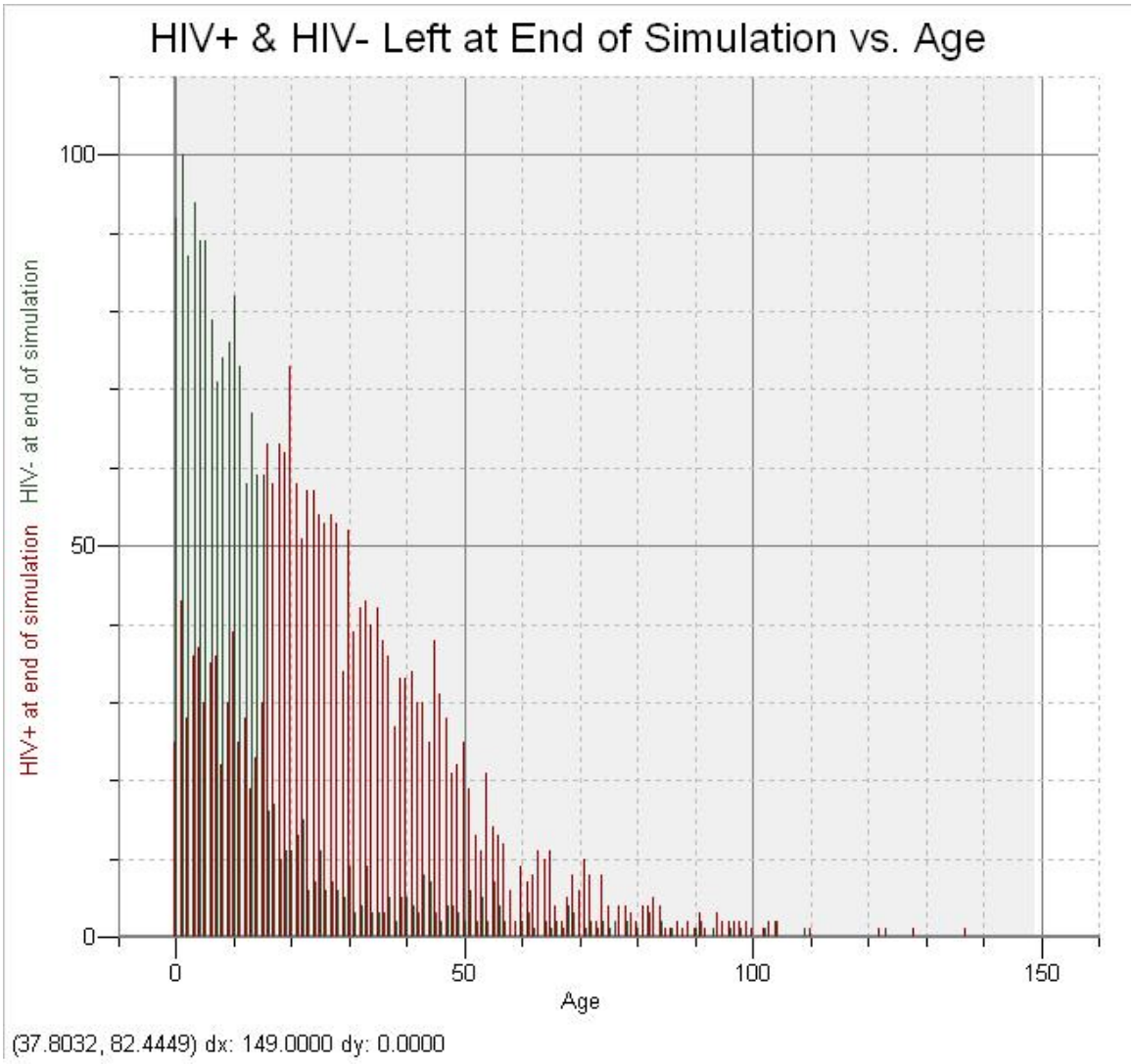

Figure 5: HIV+ and HIV- Left at End of Simulation vs. Age

3.1 Model D: Treating the Pandemic

3.2 Approach

There is a definite political and social impetus for increasing worldwide funding for dealing with the HIV/AIDS pandemic. What is unknown is how best to spend the available money. We answer this question in stages. First, we determine the amount of available funding to each of the critical countries and to the world as a whole, for the years 2005-2050. Then, we add additional parameters to the computer simulation model to determine the effects of increased antiretroviral therapy and preventative vaccination. Further simulation of the model, devoting different proportions of the available funding

to ARV and vaccinations allows us to determine the best way to spend both national and worldwide HIV/AIDS funding.

3.3 Assumptions

- Economic trends remain relatively stable over time.
- The inflation of the cost of HIV treatment is comparable to that of the rest of the world economy.
- Antiretroviral patients have 100% adherence.
- Vaccination, when developed, is 100% effective in preventing contraction of HIV.

3.4 Development

Finding Aid

To determine worldwide aid figures, we began by examine current available funding. In 2004, \$6.1 billion was provided in foreign aid, worldwide. (Global Fund) To account for the growth of the world economy and the increasing awareness with respect to HIV funding, we model the available funding A exponentially, choosing the growth rate of the function as an assumption based on an interpretation of the recent progress in funding HIV/AIDS.

$$A_{world}(t) = \$6{,}100{,}000{,}000(1.05)^t$$

We then analyze the funding available to each of the six critical countries. Research revealed an interesting trend among countries fighting HIV/AIDS, excluding the major developed countries. We found in that 85% of funding for HIV/AIDS in these developing/semideveloped nations came from foreign aid, and the remaining 15% from domestic spending. We make the assumption that each government spends one twentieth of one-percent of its GDP on HIV/AIDS each year. Botswana, Tonga, Bahamas, and Guyana reasonably fit this 85/15 rule; however we felt that Thailand and Ukraine were too developed for this assumption to apply, and imposed a 25/75 analog. From this the equations for funding are as follows, where ρ is the growth rate of the GDP for each nation.

$$A_{developing}(t) = (.0005)(GDP)(\rho)^t + (.0005)(GDP)(1.05)^t(\frac{17}{3})$$

$$A_{developed}(t) = (.0005)(GDP)(\rho)^t + (.0005)(GDP)(1.05)^t(\frac{1}{3})$$

We know the predicted cost of supplying ARV treatment to be \$1100 per person per year of treatment, and we assume that a person will continue receiving ARV treatment until

death. We account for the potential inflation of the said costs, again using an exponential function, with growth rate equal to 1.02. It then follows that the maximum number of ARV patients a nation can treat is equal to the total funding divided by the current cost per person per year.

But what are the effects on the population given an increased number of patients treated with ARV? Dr. Kholoud Porter reveals the most important factor in the Lancet Medical Journal. People strictly adhering to ARV treatment have extremely suppressed HIV virus figures. This means that is nearly impossible for a correctly treated ARV patient to transfer the virus to an uninfected person. Therefore, in our modification of the computer simulation, we prevent any person treated with ARV from transferring HIV to other people. This should lead to a significant decrease in the number of new HIV cases per year in comparison to the original model. In theory, if all HIV cases are treated with ARV, over time the virus should be removed from the population.

We assume in determining when a preventative vaccination for the HIV/AIDS virus that funding for such research is generated from the worldwide aid pool and that changes in the amount of funding do not have a significant effect on when a vaccine will be found. Thus the probability of finding a preventative vaccine in a given year should be a function of time. Multiple sources state that a vaccine will not be found within the next ten years, so we define the probability of a vaccine being discovered in a given year as:

$$S(t) = .03(t - 10) \quad \forall \quad 10 < t < 43.33$$

where time is measured in years after 2005. This probability function assumes that in 26.67 years, there will be a 50% chance of a vaccine being discovered.

3.5 Modeling E: Preventative Vaccination Distribution

3.6 Approach

In order to model the rate at which the vaccine is introduced into the population, we decided to use a logistic growth model. This makes sense in the context of this particular situation, since when the vaccine is first introduced, it will likely take some time for it to be frequently administered. Additionally, as time passes, the vaccine rates will approach a maximum percent vaccinated.

3.7 Assumptions & Terms

- The steady-state percentage of the population vaccinated will be equal to that of DTP_3 and Tetanus for infants and adults respectively, as reported by the WHO in 2002.

- The steady-state percentage value will remain constant over the next fifty years.
- Assume that the growth rate is consistent among the six critical nations.

3.8 Development

We began by using the standard logistic growth model:

$$\frac{dV}{dt} = \lambda V(1 - \frac{V}{D})$$

Where λ is the percent vaccinated growth rate, V is the percent vaccinated as a function of time, and D is the maximum percent vaccinated. This differential equation has an associated solution:

$$V(t) = \frac{D}{Ce^{-\lambda t} + 1}$$

However, since both λ and C are unknown, we decided to define initial conditions that would allow us to determine these values. We began by assuming that in 10 years, the vaccination rate would reach 95% of its maximum value. Furthermore, after one year, it would reach approximately 10% of its maximum value. From this we can derive the following equations, and subsequently solve for C and λ.

$$V(1) = \frac{D}{10} = \frac{D}{Ce^{-\lambda} + 1} \qquad V(10) = \frac{19}{20}D = \frac{D}{Ce^{-10\lambda} + 1}$$

Solving these for C we obtain:

$$C = 9e^{\lambda} \qquad C = \frac{1}{19}e^{10\lambda}$$

Setting these two equal, we then solve for λ.

$$\lambda = \frac{\ln(171)}{9} \approx 0.57129595$$

We can then plug this value into one of the equations for C to obtain:

$$C = 9(19)^{1/9}(3)^{2/9} \approx 15.935$$

Thus, the equation for the percent vaccinated in terms of the maximum percent vaccinate, D, becomes:

$$V(t) = \frac{D}{15.935e^{-0.57129595t} + 1}$$

Table 4: D-Values for Critical Countries

Country	Max. Percent Vaccinated Child	Max. Percent Vaccinated Adult
Botswana	87	49
Thailand	96.5	89.6
Tonga	90.1	93.4
Ukraine	99	37
Bahamas	86	1.4
Guyana	91	1.4

4.1 Model F: Resistant Strains and Mutations

4.2 Approach

One of the most dangerous aspects of the HIV virus is its ability to mutate quickly. Constant vigilance must be maintained to ensure that new strains of virus do not manifest themselves, making the current treatment plans largely ineffectual. Chemical or biological treatment of any bacteria or virus carries with it the risk of producing resistant strains. Global concerns of "supergerms" have begun to be realized over the last decade. The principle is simple, if a regimen of treatment does not destroy or incapacitate all of the viruses in a system, only the strong ones will remain to repopulate, over time forming a dangerous resistance which renders the drug useless.

The antiretroviral therapy associated with the HIV virus is difficult. Patients must take scores of pills, multiple times per day, essentially for the rest of their lives. With such a difficult lifestyle, it can not be expected that people complete their regimen 100% of the time. We define this ratio of completeness as adherence, and quantify its effects on a population facing HIV/AIDS.

4.3 Assumptions

- All people receiving ARV treatment intend to maintain 100% adherence. No patients are opposed to being treated for psychological, ethical or spiritual reasons.
- No patient is guaranteed to succeed in maintaining 100% adherence. We assume that "life intervenes" in some cases.

- A person with cumulative adherence below 90% has a 5% chance of developing a resistant strain.
- The opportunity for a resistant strain to develop occurs every time a treatment occurs in which cumulative adherence is below 90%.
- ARV treatment for a resistant strain will not be available before the year 2050. This allows us to make the simplification that only one resistant strain will exist.
- Resistant strains can be vaccinated, but a new vaccine will have to be developed.
- The only property of a resistant strain that distinguishes it from the original HIV is the resistance to ARV treatment. The effects on the human body and life expectancy remain constant.
- The resistant strain, if it exists, takes precedence over the original strain, that is, a person will not carry both strains.

4.4 Development

We begin with one major assumption, for which no data exists at the present time. We assume that a person will adhere completely to a year of treatment 99% of the time. From this basis, we can extrapolate the effects of adherence to the population. The model is very flexible, so if data is taken to determine the level of adherence in a particular nation, new results can quickly be generated to give a more accurate idea of what occurs.

By creating a new parameter within the main simulation, we can simulate the adherence behavior of every ARV patient within the model. A second parameter will randomly decide whether a person with sufficiently low adherence (less than 90%) will cause the production of a resistant strain. We introduce a constraint on this behavior, however, not allowing any resistant strains to occur within a person until three years of treatment have occurred. This minimizes the skewing effects that could occur if a person developed a resistant strain after missing the first treatment, which is biologically nonsensical, as the virus would have nothing to resist. The computer simulation would then run as normal, allowing for a resistant strain to occur. This strain would not be affected by ARV treatment or vaccination, and thus resistant strain infected people would behave just as HIV infected people who remain untreated.

Given that second and third-line ARV treatment drugs are so expensive, we assume none of the nations we consider will have access to them. We do, however, believe that a vaccination could be formed for the resistant strain, and define a function for that probability.

$$S_{resistant}(t) = .03t \quad t \in (0, \frac{100}{3})$$

where t is the number of years since finding the original vaccine.

We assume that the costs associated with this vaccine are identical to those of the original vaccine, and simply add the new vaccine as another parameter in the population simulation.

4.5 Discussion of Models D-F

Due to time constraints, we were unable to collect a significant amount of data from the respective modifications to the main computer simulation. However, we can analyze some basic trends apparent in our models which are important in formulating recommendations.

Assuming no significant economic disasters over the next fifty years, the world economy is will prepared to handle the HIV/AIDS situation and should be able to provide billions of dollars to the cause consistently over this time period. The question is not about availability of money, but where to spend it.

Antiretroviral therapy is a powerful weapon against the HIV/AIDS pandemic, for the obvious reason that it almost certainly prevents transfer to uninfected people. Intuitively, running the computer simulation will show that one a majority of infected people are treated with ARV therapy, the number of new cases rapidly decreases to a new steady state much closer to zero.

There is, however, a danger with the antiretroviral therapy, that of the production of resistant strains of HIV. These strains would be extremely dangerous if they became widespread, as the current set of treatments may be largely ineffective. It is vital that the implementation of ARV programs be done cautiously and with a great emphasis on maintaining adherence to the program. If used correctly, ARV drugs can be a great asset in the fight against HIV/AIDS, but mishandled they could make the situation even worse that it already is.

Finally, we consider the possibility of producing a preventative vaccine for the HIV/AIDS virus. This would provide another way to quickly stall the number of new cases and bring the disease down to a manageable level. Although it is very unlikely that a vaccine will be developed in the near future, we believe it to be probable that one will be discovered within the next twenty-five to forty years. It is then, important to devote resources to the research and development associated with a preventative vaccine.

We suggest that funds be allocated largely to ARV treatment in the next few years to bring raging epidemics in the critical nations under control, followed by a phasing in of an intense vaccine development program beginning in approximately ten years.

Conclusion

Our analysis has yielded a powerful tool in studying the HIV/AIDS pandemic. The computer simulation model we developed has the potential to reveal the inner mechanisms underlying the spread and vitality of the HIV virus, and therefore the keys to its demise. With intensive data collection and a significant amount of time and effort, many answers to the HIV/AIDS crisis may be discerned out of this model.

Our recommendations are based upon an objective analysis, letting the data speak for itself, but not without a touch of detective work in sifting through it all. The critical nations of Botswana, Thailand, Tonga, Ukraine, Bahamas, and Guyana are a springboard for a global control effort of the HIV/AIDS pandemic.

Foreign aid should be focused on the most critical nations, not necessarily by continent, but worldwide. Treatment should begin with sweeping programs of antiretroviral therapy focused on maintaining 100% adherence. Simultaneously, research should begin on developing a preventative vaccination, which could begin distribution immediately and reach stable levels within ten years.

This combination of treatments best manages the wide range of tools and capital we have available to us in controlling and defeating the HIV/AIDS epidemic.

Strengths, Weaknesses, & Further Recommendations

It is a peculiar paradox that the great complexity of the computer simulation is at once its greatest strength and its greatest weakness. This is a great strength inasmuch as the model has a great deal of power to study the particular characteristics of the spread of the disease. For instance, unlike a simplistic differential equation model, this simulation contains full data on the webs of relationships whereby the disease is spread; this allows analysis of whether certain demographic groups might be most at risk for spreading the disease to others, so that given limited funding it might be advantageous to concentrating or treating these in order to slow the spread of the disease throughout the population. Similarly, the model could be used to study what sorts of behavior put the individuals who practice them at the greatest risk, and so assist in education-based prevention. Typically, a differential equation model reflects trends that the modeler envisioned, where the primary goal is to quantify what is going on; in a computer simulation like ours, it is quite possible to get results that are qualitatively surprising. This parallels the situation in the real world, but can also be an enormously useful tool because, unlike the situation in the real world, the resourceful model programmer has complete access to all the data and can thereby track down with great precision the cause of unexpected events.

At the same time, however, performing such detective work on a model of this complexity is still no mean feat. If a simple model proves a good match for the real data, the modeler can be reasonably confident that he has some idea of the mechanism behind why it does so. If a complex model fits the data, it may still require a great deal of intensive analysis to determine the mechanisms at play within the simulation. Likewise, if a simple model is failing, it can be relatively obvious to test different changes of parameters to see if it can easily be repaired. A complex simulation has so many parameters that setting them so as to make the model match up against past data, for instance, is not really feasible. Intensive analysis may stand a chance of understanding why the model is behaving as it does, and thereby testing current data and conjectured data—this is one of the strengths of the complex model—but the corresponding weakness is that it takes much longer to analyze when simple results are all that is required. In our case, one peculiarity that we noticed was that for some runs of the Tonga simulation, the HIV population, which started very small, would remain so for a time and then suddenly explode much more sharply than, say, a logistic model might predict. If our model is correct, it is strong evidence that a smooth, differential equation model is probably not correct. On the other hand, this could be a result of a very subtle error in setting up the preconditions for our model to be a situation unlikely to occur in real life, for instance, causing the initially infected population to be a population that would normally be at low risk of either transmitting the disease or contracting it in the first place. Because of the complexity of the model, we did not have enough time to extract the data from it that it is capable of providing.

Other weaknesses of the model included assumptions made for simplicity that likely do not hold. For instance, the rapid explosion of HIV cases to include most of the adult population that occurred within about three years in most runs of our model on any country do not seem to correspond to data about the past behavior of HIV in the real world. It seems likely that this is a result of our assumption that every single sexual encounter or sharing of a dirty needle with an HIV-infected person will result in the disease's transmission. However, a corresponding strength of our model is that it would relatively easy to go back and make additions, including a probability of transmission below 1.0 and considerations such as the availability of condoms. Our model would be particularly appropriate for including the simulation of evolving strains of resistant viruses, a problem that naturally lends itself to discrete modeling.

We had several ideas for further developments, beyond simply making use of the capacity that our model already has. For instance, incorporating new demographic concerns such as wealth might yield interesting results, particularly when correlated with such concerns as education and availability of condoms and treatment, which we did not have time to implement. Similarly, if we could receive demographic data about the distribution of the virus in the modeled countries, rather than merely the percentage that have the virus, we might be able to provide a more accurate simulation than we have been doing simply by picking people at random to infect. In a related concern, it might

be possible to treat the model as, in fact, a model of a village rather than generalizing it to an entire country. Using this approach, the most plausible way for the disease to begin, once the village had been established with its standard relationships, would be through the immigration of infected people without existing ties rather than the spontaneous infection of already-entrenched villagers. What might be especially interesting would be to learn the general pattern of the disease's progress in a village and then, armed with that information, to treat the country as a collection of comparatively small communities in a particular geographic distribution. It would then be possible to predict the progress of the virus across the geographic landscape as it moves from village to village.

White Paper to the United Nations:

Prescription for the Management and Funding of the HIV/AIDS Pandemic

Introduction

The HIV/AIDS pandemic has ravaged our world for the past twenty-five years growing more fearsome with every new case. The care, the compassion, the will; these are not what is lacking from the fight against HIV/AIDS. What is needed is a coherent and viable strategy, a prescription for controlling and eventually defeating the HIV/AIDS pandemic. We can succeed in this task, HIV/AIDS is controllable, and with the support of the world and the plan we outline here, we will defeat it.

Recommendations for Resource Allocation

Allocation of resources must occur both across treatment methods and across geography. Our analysis of the current situation and predictions for the future yielded the following recommendations:

A preventative vaccine for HIV/AIDS can be found. If we dedicate a large portion of our funds to the research and development of a vaccine, our analysis predicts the emergence of a vaccine in approximately twenty five years, but potentially within ten years. The vaccines will have a relatively low cost per capita, making funding for them quite feasible. Full distribution of the vaccines is expected to occur over ten years, so within forty years, the majority of the world could be vaccinated against HIV/AIDS. We recommend intensive funding during the next five years to jumpstart research programs and hopefully discover a vaccine earlier than expected.

Antiretroviral Treatment has shown to be very effective in treating patients already infected with the HIV virus. It has the benefits of significantly increasing the life expectancy of an infected person, and even more importantly, vastly reducing the ability

of the virus to spread from person to person. We recommend an extensive program in ARV distribution, as we found when a majority of infected people are treated with ARV; the number of new cases of HIV/AIDS will rapidly decrease.

Thus, we recommend a two-pronged attack on the HIV/AIDS virus, both methods of preventing new cases; one targeting uninfected people and one targeting infected people.

Our geographical analysis involved an extensive model to determine which nations are most critical with respect to the HIV/AIDS pandemic. We determined the following as the most critical nations on each continent: Botswana (Africa), Thailand (Asia), Tonga (Australia/Oceania), Ukraine (Europe), Bahamas (North America), and Guyana (South America). Clearly, significant amounts of funding should go to these nations. If we consider the entire world, however, we find that fourteen of the fifteen most critical countries are in Africa. Therefore, Africa should be the major focus of immediate HIV/AIDS funding. Over time, the funding should move towards a relatively equal distribution over all countries significantly impacted by HIV/AIDS

HIV/AIDS and Its Role in Global Foreign Policy

HIV/AIDS is certainly one of the most pressing issues facing the world today, but how does it compare to other matters of global foreign policy, such as wars, natural disasters and other major epidemics. As guidance for determining the relative importance of these various entities, we turn to our model of HIV-adjusted life expectancy, where we perform an analysis of the loss of life expectancy associated with the HIV/AIDS pandemic. Similarly analyses can be constructed for nearly any other potential situation we could consider, and comparison among these should reveal the relative importance. We ask you to consider one other thing; we have a solid plan for the management of the HIV/AIDS pandemic, something that is difficult to form for wars or natural disasters. In short, HIV/AIDS is something we can control, and this should give it priority as something the world can be proactive about, rather than reactive.

Recommendation for Donor Coordination

Donors are an integral part of funding the management and control of the HIV/AIDS epidemic, their funds are a large portion of worldwide available aid, and it is important that we have a system catering to ease of donation and satisfaction of the donor. To this end, a donation system should allow the donors as much freedom as possible, with respect to how much to donate, what programs/countries to donate to, and what specific treatments the donation be spent on. We should openly praise donors, providing significant recognition of their gifts to humanity, this will encourage potential donors to "make the leap" and join our cause. Finally, the system of donation should be streamlined, a centralized donation organization which doles out funds as needed by the

various treatment groups and nations. This will provide donors with the easiest methods for donation, while ensuring that the money always reaches where it is needed.

Conclusions

The HIV/AIDS pandemic is something we can overcome. We have the tools, the funds, and the knowledge to defeat this disease which has been so painful in the past twenty-five years. The plan we lay forth is the most effective use of the global funding we have available. Effective management of the incredible resources we posses will surely allow us all to see the end of HIV/AIDS in this world.

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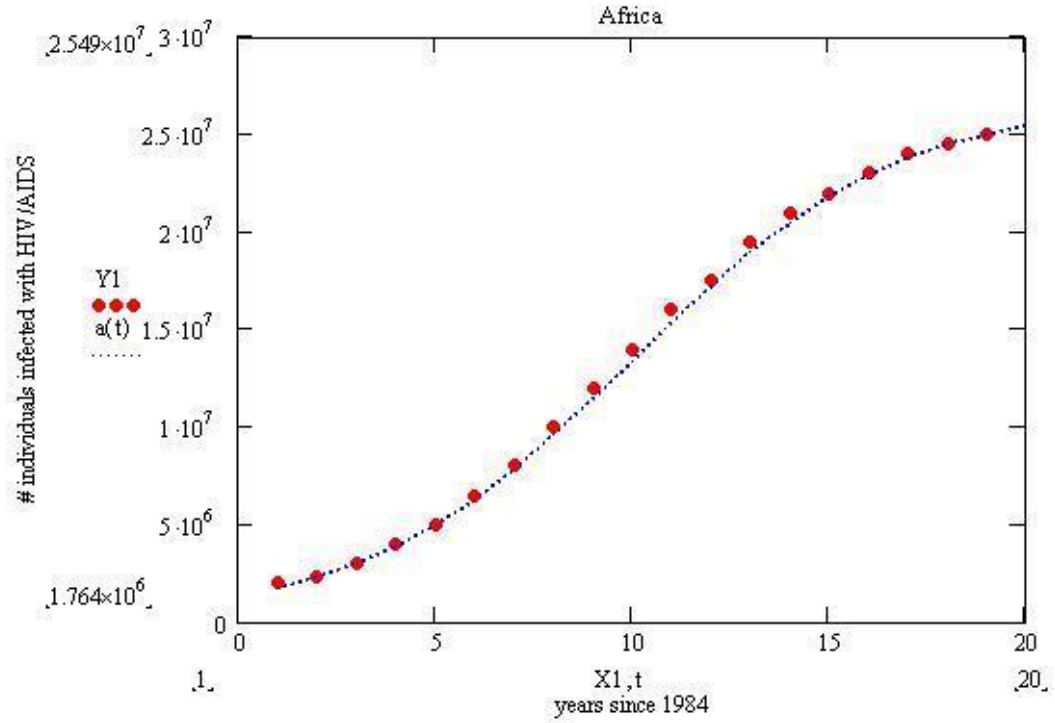
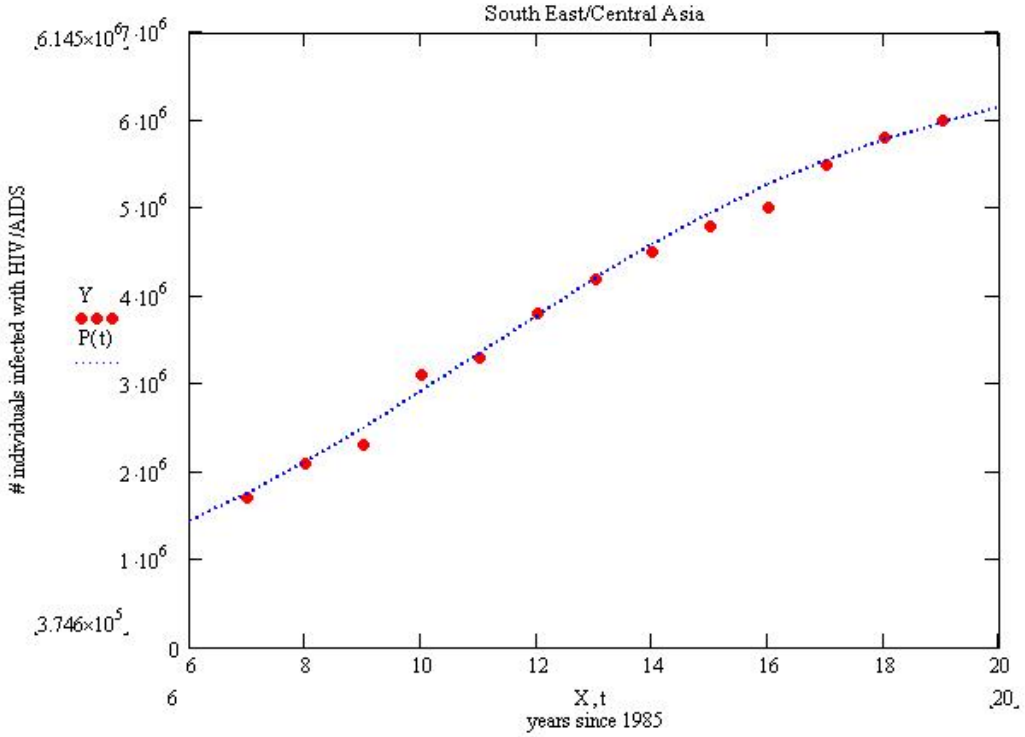
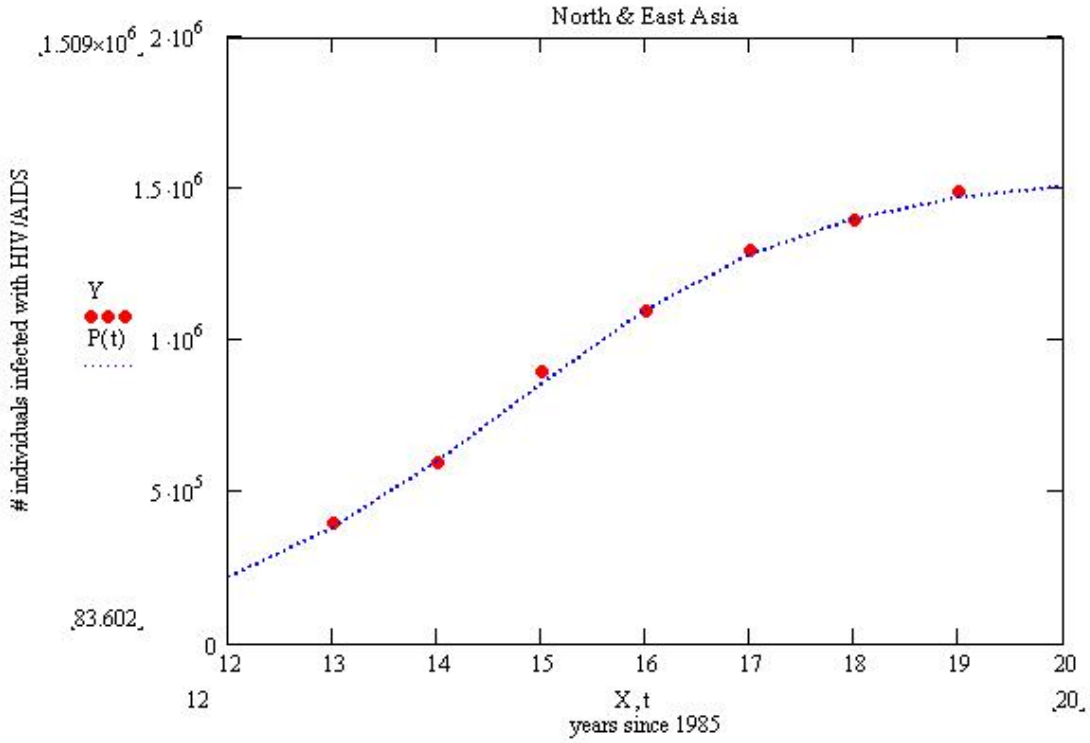
Appendix 1: Logistic Growth Curves for HIV/AIDS Infections






North & East Asia
individuals infected with HIV/AIDS
1.509×10^6
2·10^6
1.5·10^6
1·10^6
5·10^5
83.602
0
Y
P(t)
12
13
14
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16
17
18
19
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12
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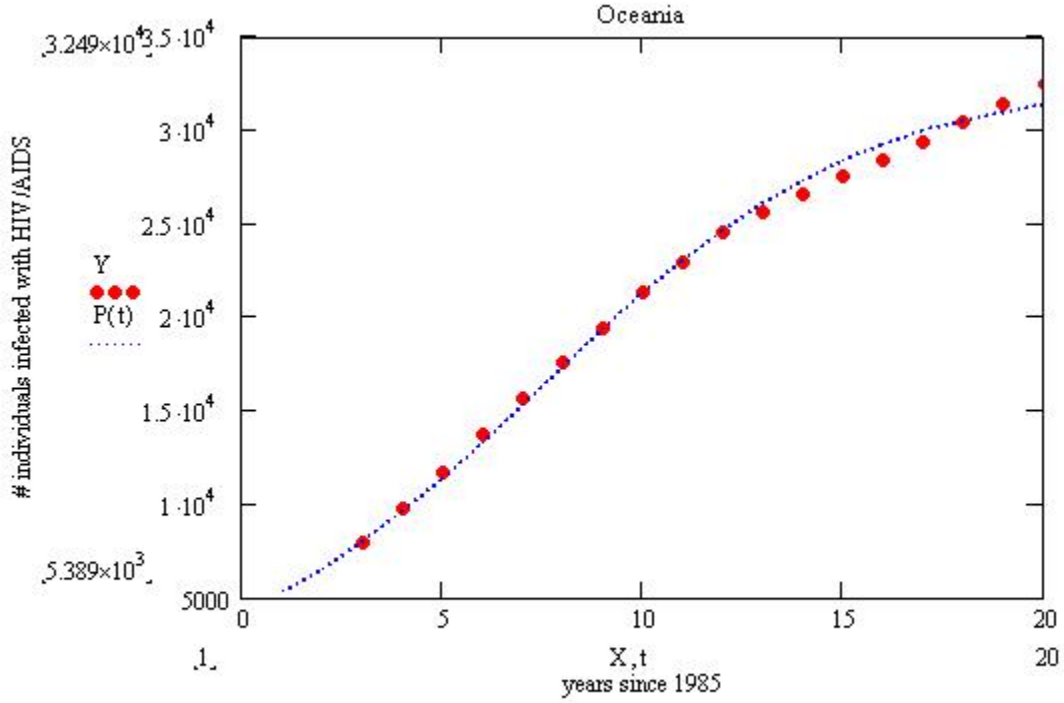
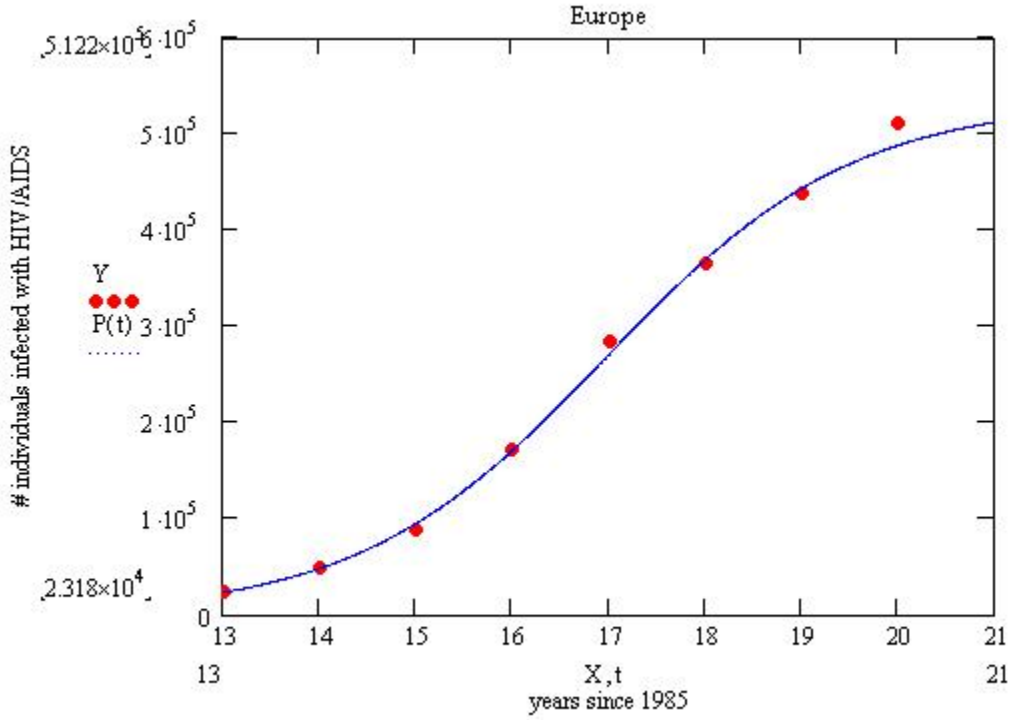
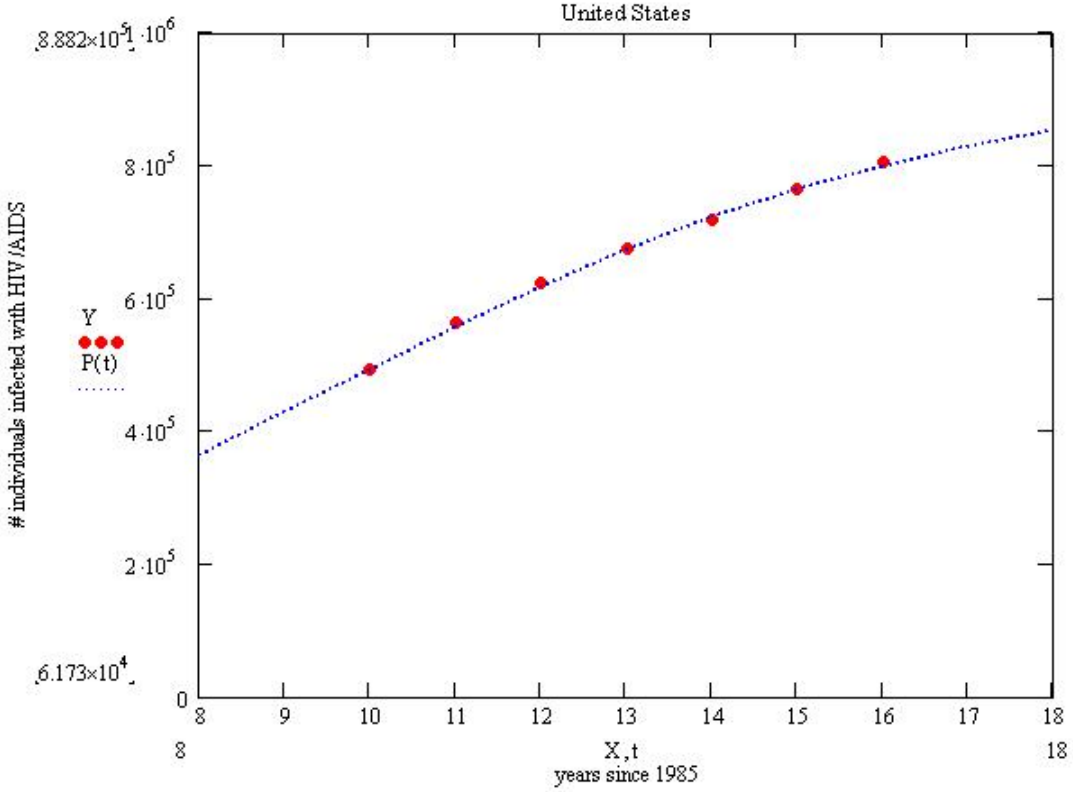
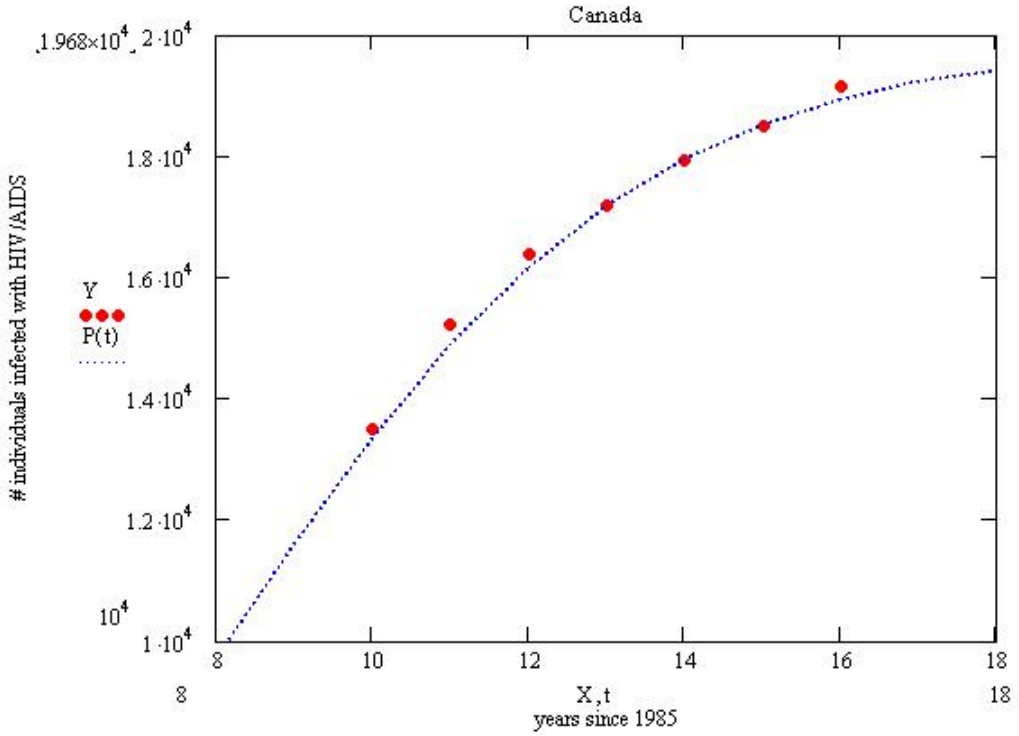
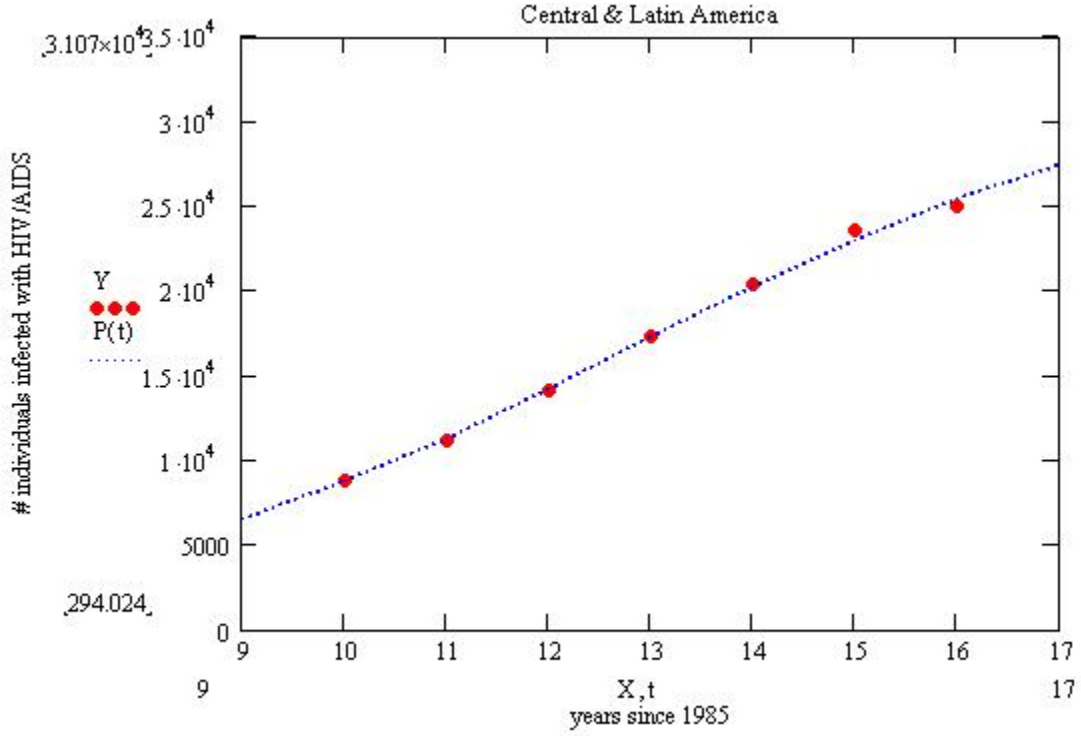
20
years since 1985

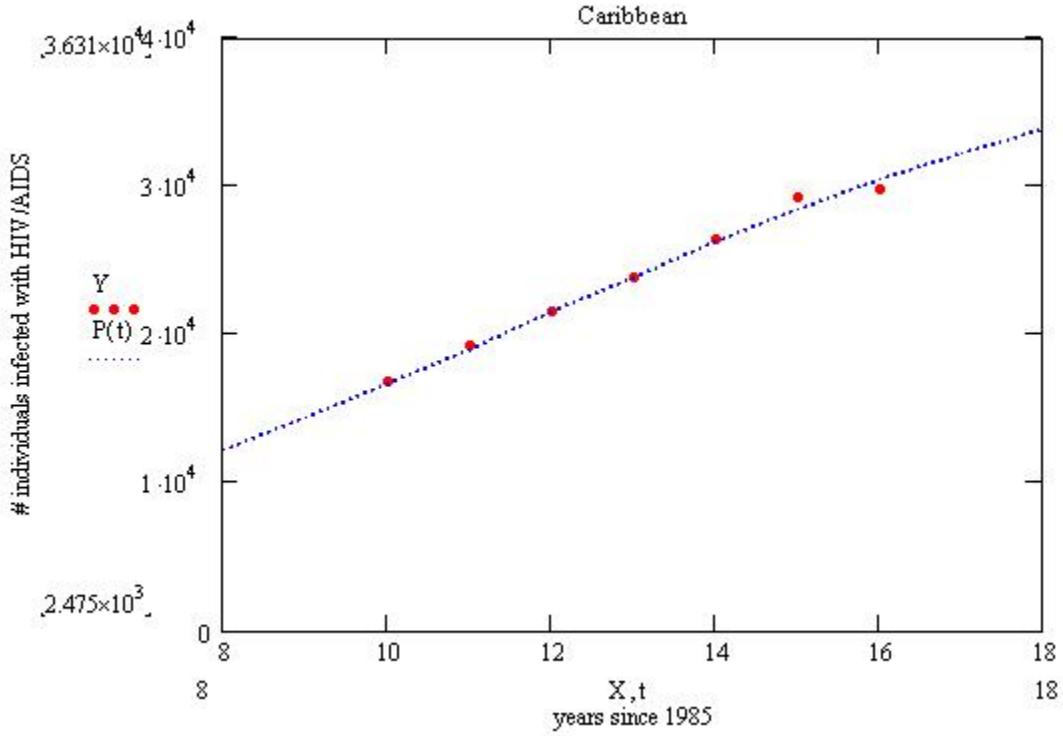

Oceania
individuals infected with HIV/AIDS
3.249×10^4
3.5·10^4
3·10^4
2.5·10^4
2·10^4
1.5·10^4
1·10^4
5.389×10^3
5000
Y
P(t)
0
5
10
15
20
1
X, t
20
years since 1985

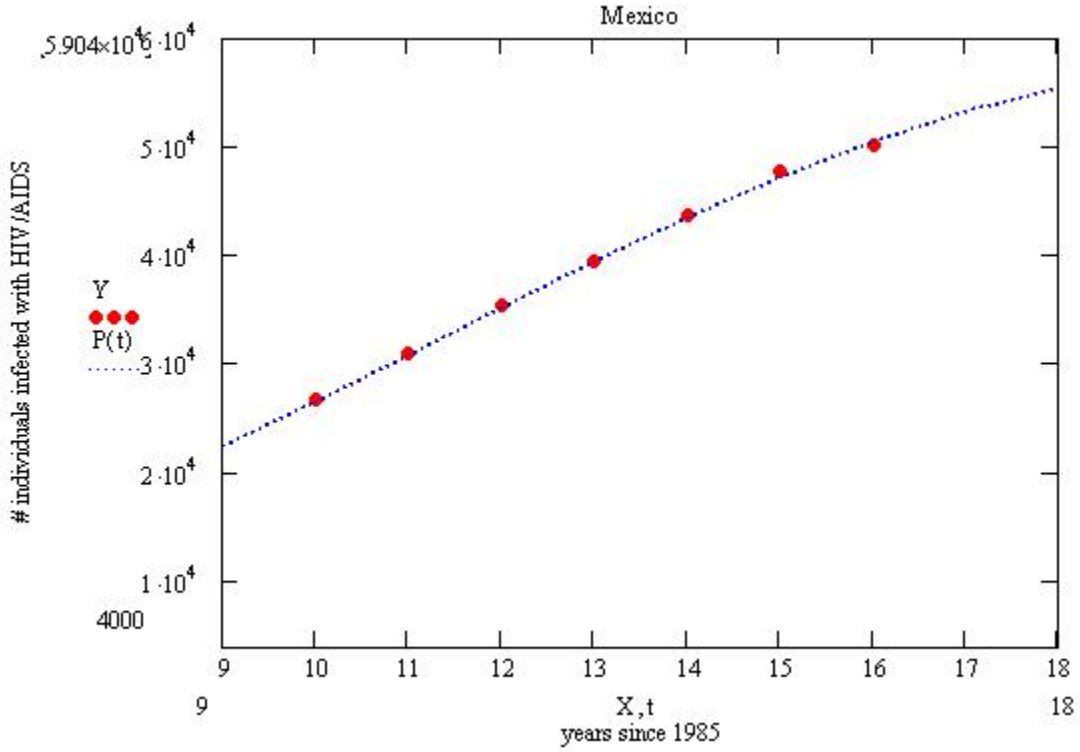

Europe
individuals infected with HIV/AIDS
Y
P(t)
5.122×10^5
6·10^5
5·10^5
4·10^5
3·10^5
2·10^5
1·10^5
2.318×10^4
0
13
14
15
16
17
18
19
20
21
X, t
years since 1985

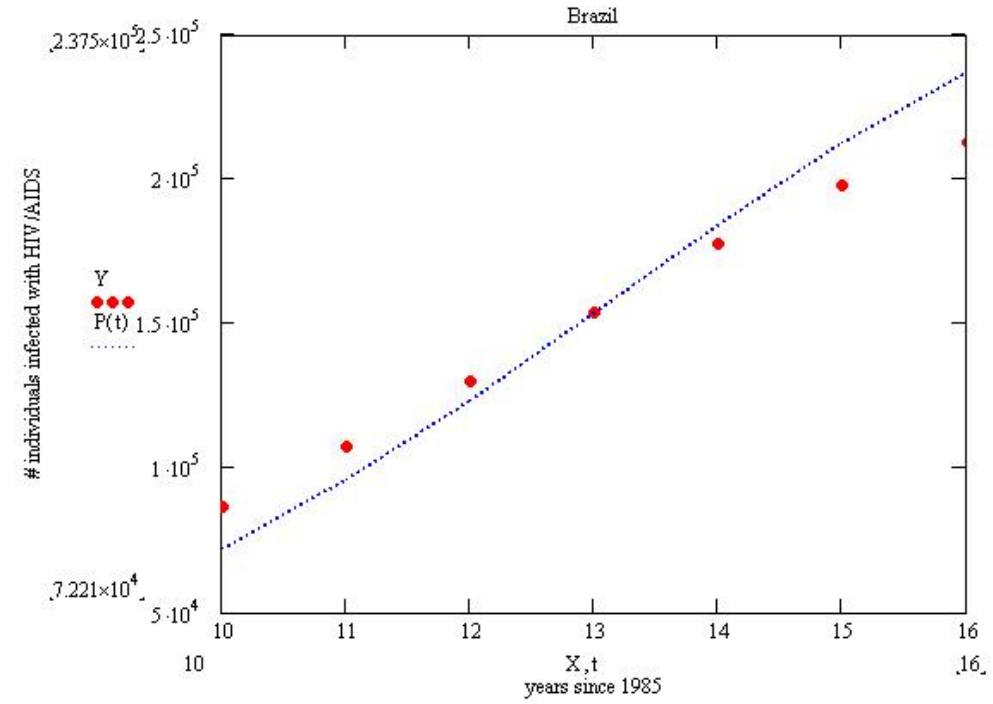

United States
individuals infected with HIV/AIDS
Y
P(t)
8.882×10^5
1·10^6
8·10^5
6·10^5
4·10^5
2·10^5
6.173×10^4
0
8
9
10
11
12
13
14
15
16
17
18
X, t
years since 1985

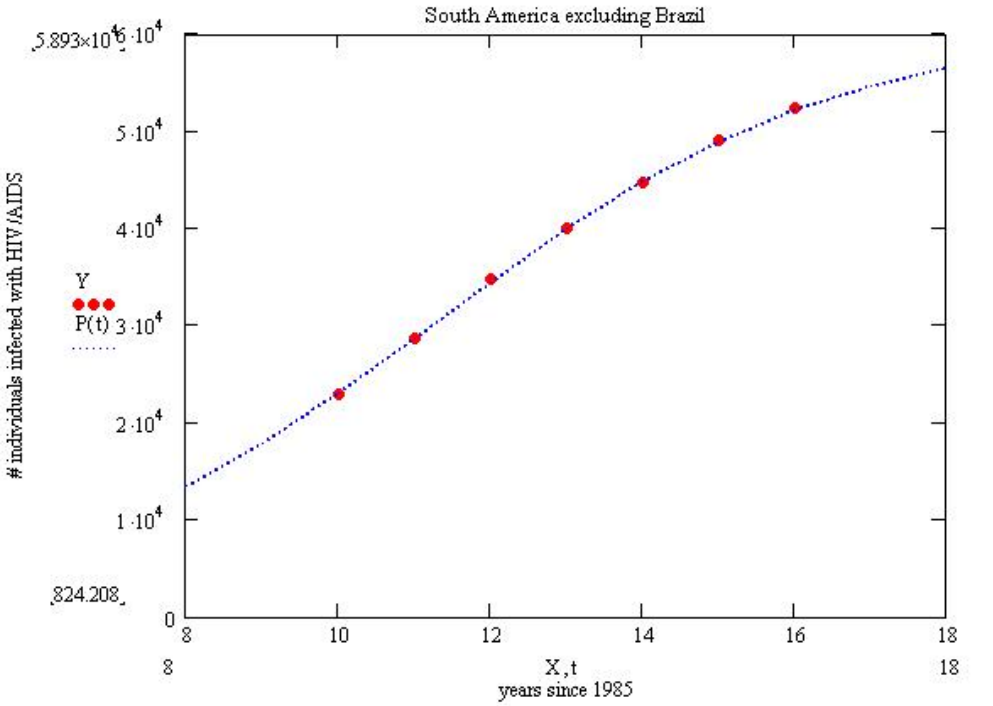

Canada
individuals infected with HIV/AIDS
Y
P(t)
X, t
years since 1985


Central & Latin America
individuals infected with HIV/AIDS
Y
P(t)
X, t
years since 1985


Caribbean
3.631×10^4
4·10^4
3·10^4
2·10^4
1·10^4
2.475×10^3
0
Y
P(t)
# individuals infected with HIV/AIDS
8
10
12
14
16
18
8
X, t
18
years since 1985

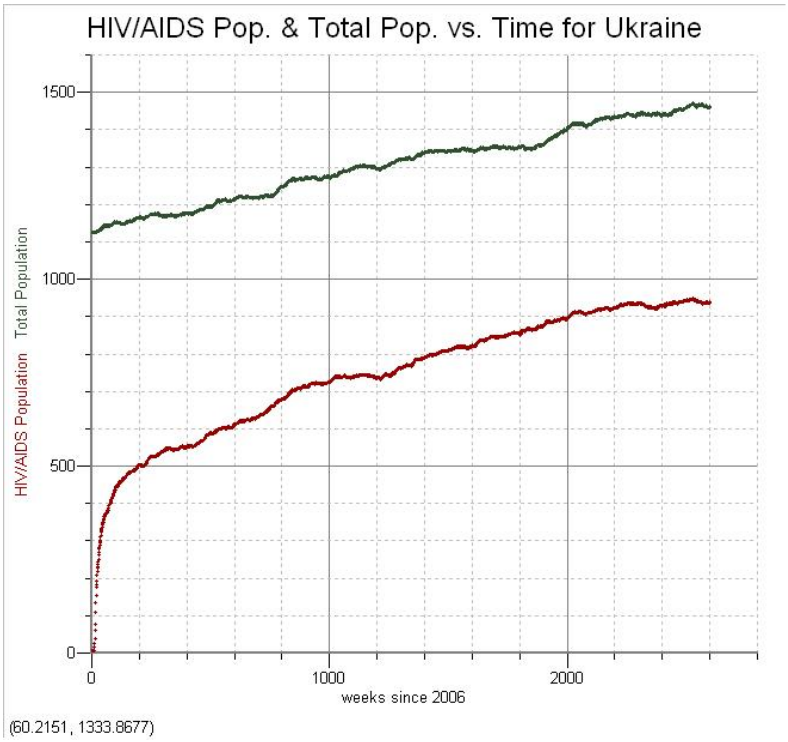

Mexico
5.904×10^4
6·10^4
5·10^4
4·10^4
3·10^4
2·10^4
1·10^4
4000
Y
P(t)
# individuals infected with HIV/AIDS
9
10
11
12
13
14
15
16
17
18
9
X, t
18
years since 1985

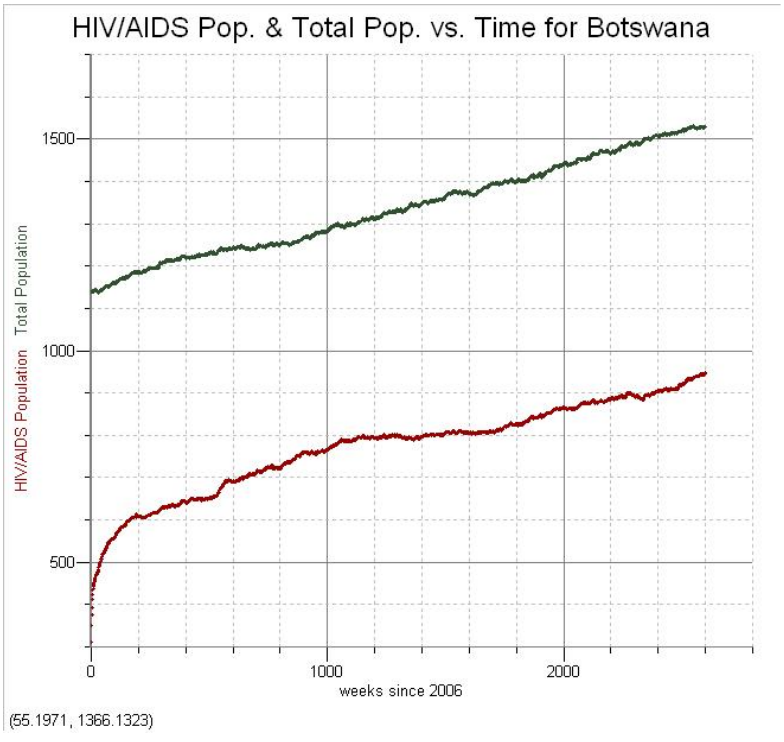


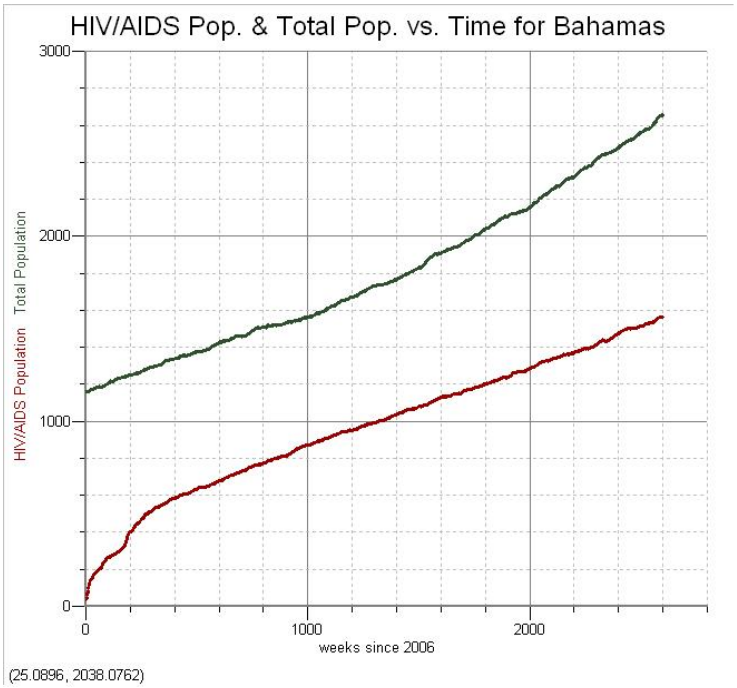


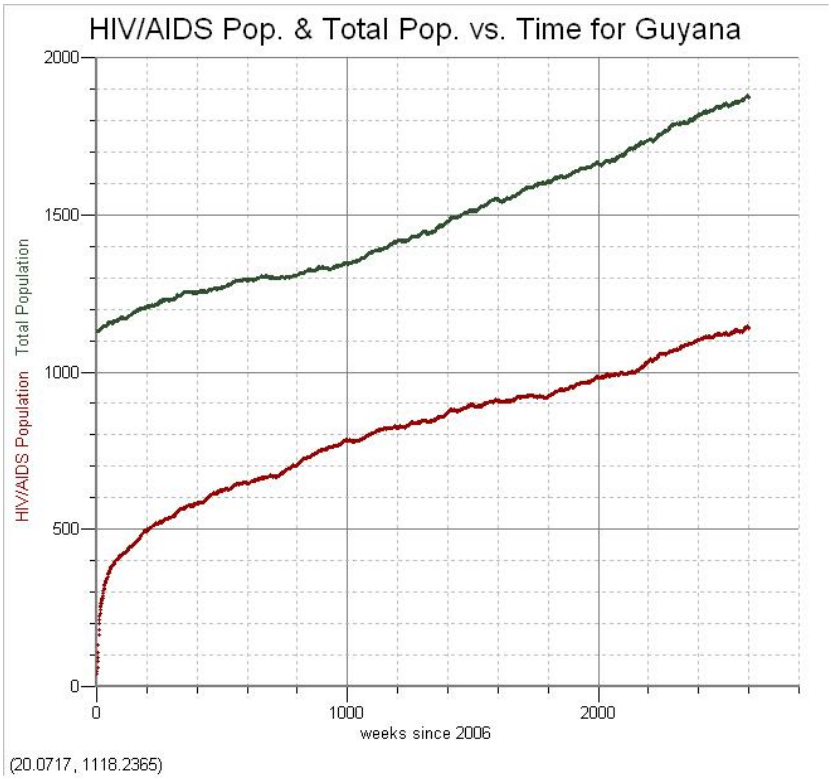
Source of Above Data: Hepatitis and AIDS Research Trust-S. America, Latin & Central America, Brazil, Mexico, Caribbean, US, Canada; Avert-Australia; EuroHIV-Europe; UNAIDS-Africa; All of Asia- UN development programme.

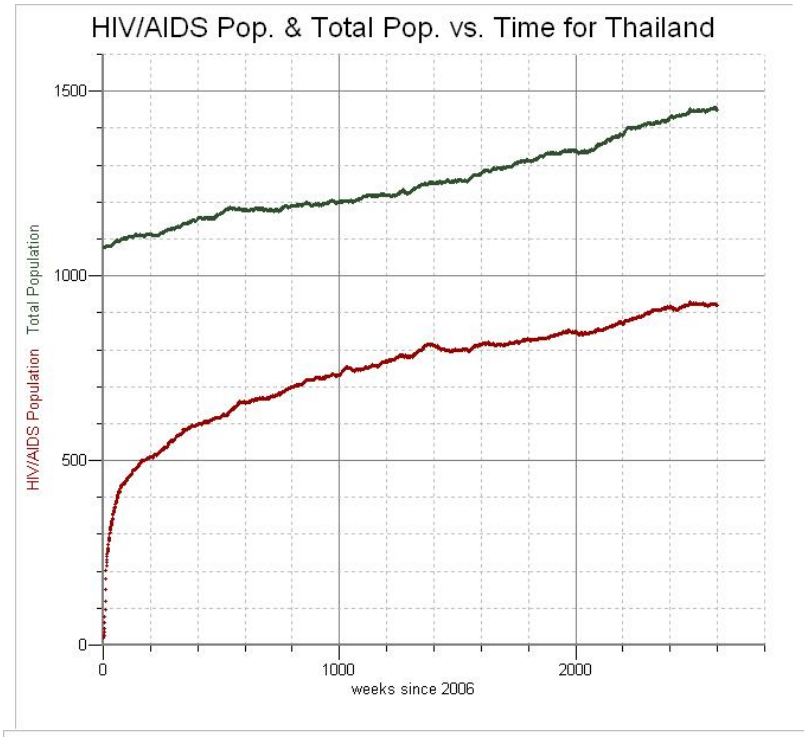
Appendix 2: Simulation Results for Each Critical Country

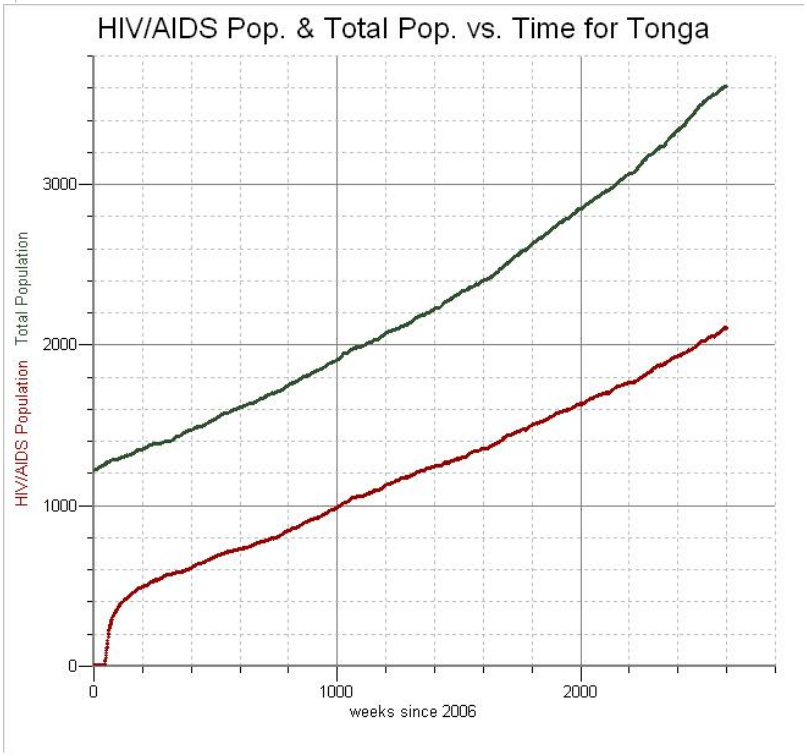





HIV/AIDS Pop. & Total Pop. vs. Time for Bahamas
3000
2000
1000
0
HIV/AIDS Population Total Population
0
1000
2000
weeks since 2006
(25.0896, 2038.0762)


HIV/AIDS Pop. & Total Pop. vs. Time for Guyana
2000
1500
1000
500
0
HIV/AIDS Population Total Population
0
1000
2000
weeks since 2006
(20.0717, 1118.2365)


HIV/AIDS Pop. & Total Pop. vs. Time for Thailand
1500
1000
500
0
HIV/AIDS Population Total Population
0
1000
2000
weeks since 2006


HIV/AIDS Pop. & Total Pop. vs. Time for Tonga
3000
2000
1000
0
HIV/AIDS Population Total Population
0
1000
2000
weeks since 2006

Appendix 3: Representative Portions of Simulation Code

Cycler

```
package task1.general;

import java.util.*;

public class Cycler {

	private double fractionToInfect = .0025;



	//starting population
	private final int startingPop = 1000;
	public static final int CYCLES_PER_YEAR = 52;

	private int maxCycles = CYCLES_PER_YEAR*50;
	private int preCycles = CYCLES_PER_YEAR*10;
	private Set<Person> persons= new HashSet<Person>();
	private Set<AvailabilityPool> pools = new HashSet<AvailabilityPool>();
	private Set<Person> toAdd = new HashSet<Person>();
	private Set<Person> toRemove = new HashSet<Person>();

	//Choose PersonFactory based on demographics of scenario to be simulated
	private PersonFactory myFactory = new DefaultPersonFactory();

	private int numInfected = 0;
	private int[] infectionData = new int[maxCycles];
	private int[] populationData = new int[maxCycles];
	private int[] prePopulationData = new int[preCycles];
	private int numBirths = 0;
	private int numNewInfections = 0;

	private static int numSexEvents =0;

	private static int currentSexRelationships = 0;
	private static int maxSimultaneousRelationships = 0;
	private static int relationshipsBroken = 0;
//	private static boolean allowBreaking = false;

	public PersonFactory getFactory() {
```

```
            return myFactory;
        }

        public Cycler() {
            List<Integer> newCases = new ArrayList<Integer>();

            System.out.println("Starting");
            pools.add(new AvailabilityPool(RelTypes.DRUG_USE));
            pools.add(new AvailabilityPool(RelTypes.GAY_CASUAL));
            pools.add(new AvailabilityPool(RelTypes.GAY_MONO));
            pools.add(new AvailabilityPool(RelTypes.GAY_POLY));
            pools.add(new AvailabilityPool(RelTypes.MOTHER_CHILD));
            pools.add(new SplitAvailabilityPool(RelTypes.STRAIGHT_CASUAL));
            pools.add(new SplitAvailabilityPool(RelTypes.STRAIGHT_MONO));
            pools.add(new SplitAvailabilityPool(RelTypes.STRAIGHT_POLY));

            Virus hiv = new Virus(){ };

            for (int i = 0; i < startingPop; i++) {
                Person person;
                persons.add(person = myFactory.makePerson(this));
//              if (i < 10) person.receiveVirus(hiv);
            }

            for (int t = 0; t < preCycles; t++) {
//              System.out.println("AZZ "  + t);
                for (Person current : persons) {
//                  System.out.println("BZZ");
                    current.doCycle();
                }
//              System.out.println("GGG");
                for (Person adding : toAdd) {
                    persons.add(adding);
                }
//              System.out.println("LLL");
                toAdd.clear();
                for (Person removing : toRemove) {
                    persons.remove(removing);
                }
//              System.out.println("PPP");
                toRemove.clear();

//              infectionData[t] = numInfected;
```

```
                prePopulationData[t] = persons.size();
            }

            System.out.println("\n" + numBirths + "\n" + numSexEvents + "\n" +
Cycler.maxSimultaneousRelationships);
            System.out.println(Cycler.relationshipsBroken);
            System.out.println();

            for (int p : prePopulationData) {
                System.out.println(p);
            }

            int numStartInfected = 0;
            int num = persons.size();
            for (Person toInfect : persons) {
                if (Math.random() < fractionToInfect) {
                    toInfect.receiveVirus(hiv);
                    numStartInfected++;
                }
            }
            System.out.println((1.0*numStartInfected)/num + " " + fractionToInfect);

            for (int t = 0; t < maxCycles; t++) {
//                  System.out.println("AZZ "  + t);
                    for (Person current : persons) {
//                      System.out.println("BZZ");
                        current.doCycle();
                    }
//                  System.out.println("GGG");
                    for (Person adding : toAdd) {
                        persons.add(adding);
                    }
//                  System.out.println("LLL");
                    toAdd.clear();
                    for (Person removing : toRemove) {
                        persons.remove(removing);
                    }
//                  System.out.println("PPP");
                    toRemove.clear();

                    infectionData[t] = numInfected;
                    populationData[t] = persons.size();
                    if ((t+1) % Cycler.CYCLES_PER_YEAR == 0) {
```

```
                        newCases.add(numNewInfections);
                        numNewInfections = 0;
                }

        }

        System.out.println("\n" + numBirths + "\n" + numSexEvents + "\n" +
Cycler.maxSimultaneousRelationships);
        System.out.println(Cycler.relationshipsBroken);
        System.out.println();

        for (int t = 0; t < infectionData.length; t++) {
                System.out.println(infectionData[t] + " " + populationData[t]);
        }


        System.out.println("\nNumber of New Infections in each year:");
        for (Integer inf : newCases) {
                System.out.println(inf);
        }
        List<int[]> ages = new ArrayList<int[]>(150);
        for (int i = 0; i < 150; i++) {
                int[] toPut = {0, 0};
                ages.add(toPut);
        }
        for (Person pers : persons) {
                int[] using = ages.get(pers.getAge() / CYCLES_PER_YEAR);
                if (pers.hasVirus()) using[0]++;
                else using[1]++;
        }
        int someIntName = 0;
        for (int[] using : ages) {
                System.out.println(someIntName + " " + using[0] + " " + using[1]);
                someIntName++;
        }

}

/**
 * @param args
 */
public static void main(String[] args) {
        long time = System.currentTimeMillis();
```

```
                new Cycler();
                time = System.currentTimeMillis() - time;
//              System.out.println(time/1000.0);
        }

        /**
         * This should only be called from a person's "die" method; it removes that person
from
         * the list and records the statistics based on information-getting methods from the
         * person.
         * @param p
         */
        public void kill(Person p) {
                doStatistics(p, false);
                toRemove.add(p);
        }

        public Iterable<AvailabilityPool> getPools() {
                return pools;
        }

        /**
         * This method should ONLY be called from the constructor of a Person.
         * @param p
         */
        public void add(Person p) {
//              doStatistics(p, true);
                toAdd.add(p);
        }

        /**
         *
         * @param p
         * @param b
         */
        private void doStatistics(Person p, boolean birth) {
                if (p.hasVirus() && !birth) numInfected--;
        }

        public void recordInfection() {
                numInfected++;
                numNewInfections++;
        }
```

```
	public void recordBirth() {
		numBirths++;
	}

	public static void reportSexEvent() {
		numSexEvents++;
	}

	public static void relationshipFormed() {
		Cycler.currentSexRelationships++;
		if (currentSexRelationships > maxSimultaneousRelationships)
Cycler.maxSimultaneousRelationships = Cycler.currentSexRelationships;
	}

	public static void relationshipEnded() {
		Cycler.currentSexRelationships--;
		Cycler.relationshipsBroken++;
	}

/*	public static boolean breakingAllowed() {
		return allowBreaking ;
	}
	*/
}
```

Person Factory

```
package task1.general;

public class DefaultPersonFactory implements PersonFactory {

	/*
	 * For Tonga:
	 */
	private double[] adoptionRate = {.05, .1};
	private double[] monogamousEventRate = {60, 90};
	private double[] polyEventRate = {110, 150};
	private double gayPortion = 0;
	private double drugUsers = 0;
	private double[] ageData = {11.96,  12.23,  12.56,  10.62,  10.75,  7.62,  5.59,
	6.38,  4.83,  3.83,  3.8,  3.18,  2.83,  2.03,  1.75,  1.29,  0.6,  0.43,
	0.02,  0.02,  0};
	private double agingConstant = 1.0 / 2877;
	private double infantOrphanDeathRate = 12.62 / 1000;
	private double vulnOfHIV = 1.512;

	private double fertility = .0027;


	/*
	 * For all the countries we are dealing with:
	 */
	private double[] infantEventRate = {.03, .07};
	//monogamous people:
	private double[] monogamousAcceptance = {.12, .20};
	private double[] monogamousSeeking = {.12, .20};
	//prostitutes:
	private double[] prostCustomers = {250, 356};
	//others:
	private double[] monoAcceptance = {.12, .20};
	private double[] monoSeeking = {.12, .20};
	private double[] monoFaithfulness = {8, 12};
	private double[] monoBreakRate = {.015, .035};
	private double[] polyAccept = {.2, .4};
	private double[] polySeek = {.2, .4};
	private double[] polyBreak = {.2*.2, .4*.4};

	private double childOrphanDeathRate = .1 * infantOrphanDeathRate;
```

```
	private double infant2child = 2.0;
	private double child2adult = 16.0;

	public Person makePerson(Cycler cycler) {
		double totalPop = 0;
		double age = 0;
		for (int i = 0; i < ageData.length; i++) {
			totalPop += ageData[i];
		}
		double rand = Math.random();
		double min = 0;
		for (int i = 0; i < ageData.length && min < rand; i++) {
			min += ageData[i] / totalPop;
			if (min > rand) {
				age = randBetween(5*i, 5*(i+1));
			}
		}

//		System.out.println("making person of age " + age + " years");

		return makePerson(cycler, (int)(age*Cycler.CYCLES_PER_YEAR));

	}

	public Person makeNewborn(Cycler cycler) {
//		System.out.println("new baby born");
		cycler.recordBirth();
		Person toReturn = makePerson(cycler, 0);
		cycler.add(toReturn);
		return toReturn;
	}

	public Person makePerson(Cycler cycler, int age) {
		boolean male = (Math.random() < 0.5);
		return new Person(age,
				cycler, male,
				makeNewManager(male), agingConstant,
infantOrphanDeathRate,
				childOrphanDeathRate, infant2child, child2adult,
vulnOfHIV, fertility);
	}

	private RelationshipManager makeNewManager(boolean gender) {
```

```
		return new ConglomerateManager(makeSexManager(gender),
makeDrugsManager(gender),
				makeMotherManager());
	}

	private RelationshipManager makeMotherManager() {
		return new MotherChildManager(randBetween(adoptionRate),
randBetween(infantEventRate));
	}

	private RelationshipManager makeSexManager(boolean isMale) {
		RelationshipManager toReturn = null;

		double rand = Math.random();
		if (rand < .1) {
			//do abstinence
			toReturn = new AbstinentManager();
		} else if (rand < .1+.1) {
			//monogamous
			toReturn = new
MonogamousSexManager(randBetween(monogamousAcceptance),
					randBetween(monogamousSeeking),
randBetween(monogamousEventRate));

		} else if (rand < .1+.1+.005 && !isMale) {
			//prostitute
			toReturn = new
ProstituteManager(randBetween(prostCustomers));
		} else {
			//everyone else
			double maxPartners;
			double rand2 = Math.random();
			if (rand2 < .5) {
				maxPartners = 1;
			} else if (rand2 < .5 + .25) {
				maxPartners = 2;
			} else if (rand2 < .5 + .25 + .2) {
				maxPartners = randBetween(3, 6.5);
			} else {
				maxPartners = randBetween(6.5, 20);
			}
			double casualInhibition;
			if (isMale) casualInhibition = randBetween(.01, .04);
```

```
                else casualInhibition = 0; //assume there are no women who use
prostitutes, particularly since there are assumed no male prostitutes

                toReturn = new OthersSexualManager(
                                randBetween(monoAcceptance),
                                randBetween(monoSeeking),
                                randBetween(monoFaithfulness),
                                randBetween(monoBreakRate),
                                randBetween(polyAccept),
                                randBetween(polySeek),
                                randBetween(polyBreak),
                                maxPartners,
                                casualInhibition,
                                randBetween(polyEventRate));

        }

        if (!isMale) return new StraightFilter(toReturn);

        rand = Math.random();
        double pureStraight = 1.0 - gayPortion;

        //assume 20% of men who engage in homosexual behavior are bisexual
        double pureGay = 0.8 * gayPortion;

        if (rand < pureStraight) return new StraightFilter(toReturn);
        else if (rand < pureStraight + pureGay) return new GayFilter(toReturn);
        else return toReturn;
    }

    private RelationshipManager makeDrugsManager(boolean gender) {
        if (Math.random() > drugUsers) return new AbstinentManager();
        double eventRate;
        double rand = Math.random();
        if (rand < 0.9) eventRate = randBetween(20, 30);
        else if (rand < .9 + .05) eventRate = randBetween(1, 2);
        else eventRate = randBetween(100, 150);

        double maxBuddies;
        if (Math.random() < .5) maxBuddies = 1;
        else maxBuddies = randBetween(2, 10);

        double acceptance = randBetween(.3, .7);
```

```
                double seek = randBetween(.3, .7);
                double breakRate = randBetween(.02, .1);

                return new DrugShipManager(maxBuddies, acceptance, seek, breakRate,
eventRate);

        }

        private static double randBetween(double[] a) {
                return (Math.random()*(a[1] - a[0])) + a[0];
        }

        private static double randBetween(double a, double b) {
                return (Math.random()*(b-a)) + a;
        }

}
```

Sexual Manager

```
package task1.general;

import java.util.*;

/**
 * This is a confusing manager because of the three tiers of relationships to be handled.
 * @author mcm-16
 *
 */
public class OthersSexualManager implements RelationshipManager {
	private Person myPerson;
	private boolean active;
	private Relationship monoShip = null;
	private Pool2<Relationship> polyShips = new Pool2<Relationship>();
	private Relationship casualShip = null;

	private Set<AvailabilityPool> monoPools = new HashSet<AvailabilityPool>(2);
	private Set<AvailabilityPool> polyPools = new HashSet<AvailabilityPool>(2);
	private Set<AvailabilityPool> casualPools = new HashSet<AvailabilityPool>(2);

	private double monoAcceptance;
	private double monoSeeking;
	private double monoFaithfulness;
	private double monoBreakRate;

	private double polyAcceptance;
	private double polySeeking;
	private double polyBreakRate;
	private double maxPartners;

	/*
	 * This should be 0-1 and represents inhibition the person may feel (or perhaps
	 * financial inhibitions also?) about going to prostitutes.
	 */
	private double casualInhibition;

	private double eventRate;
	private int numEvents = 0;

	public OthersSexualManager(double monoAcceptance, double monoSeeking,
double monoFaithfulness,
```

```
                        double monoBreakRate, double polyAcceptance, double
polySeeking,
                        double polyBreakRate, double maxPartners, double
casualInhibition, double eventRate)
        {
                this.monoAcceptance = monoAcceptance;
                this.monoSeeking = monoSeeking;
                this.monoFaithfulness = monoFaithfulness;
                this.monoBreakRate = monoBreakRate;

                this.polyAcceptance = polyAcceptance;
                this.polySeeking = polySeeking;
                this.polyBreakRate = polyBreakRate;
                this.maxPartners = maxPartners;

                this.casualInhibition = casualInhibition;

                this.eventRate = eventRate;
        }

        public void setPerson(Person p) {
                myPerson = p;
        }

        public void setStage(int newStage) {
                active = (newStage == Person.ADULT);
        }

        public void proposePool(AvailabilityPool current) {
                Object type = current.getType();
                if (!(active && RelTypes.isSexType(type))) {
                        current.remove(myPerson);
                } else if (RelTypes.isMono(type)) {
                        monoPools.add(current);
                        if (monoShip == null) current.add(myPerson);
                        else current.remove(myPerson);
                } else if (RelTypes.isPoly(type)) {
                        polyPools.add(current);
                        if (monoShip == null) current.add(myPerson);
                        else current.remove(myPerson);
                } else if (RelTypes.isCasual(type)) {
                        casualPools.add(current);
                        current.remove(myPerson);
```

```
		}
	}

	public void breakOffAll() {
		if (monoShip != null) monoShip.breakOff();
		polyShips.applyToAll(new Applyable<Relationship>() {
			public void applyTo(Relationship object) {
				object.breakOff();
			}
		});
	}

	/**
	 * This method will never be called when in a monogamous relationship.
	 */
	public Relationship requestedRelationship(Person seeker, Object type) {
		if (monoShip != null) return null;
		if (RelTypes.isMono(type)) {
			if (Math.random() < (monoAcceptance))
				return new Relationship(seeker, myPerson, type);
			else return null;
		} else if (RelTypes.isPoly(type)) {
			if (polyShips.contains(new SemiShip(myPerson, seeker, type)))
return null;
			if (Math.random() < (polyAcceptance)*(maxPartners -
polyShips.size()))
				return new Relationship(myPerson, seeker, type);
			else return null;
		} else return null;
	}

	public void doCycle() {
//requesting relationships
		//mono relationships
		if ((!monoPools.isEmpty()) && monoShip == null && Math.random() <
monoSeeking / Cycler.CYCLES_PER_YEAR)
			getMonoPool().seekRelationship(myPerson);
		else {
		//poly relationships
			AvailabilityPool pool = getPolyPool();
			double faithFactor = 1;
			double max = maxPartners;
			if (monoShip != null) {
```

```
                        max -= 2;
                        faithFactor = 1.0/monoFaithfulness;
                    }
                    if (pool != null && Math.random() < faithFactor*(polySeeking /
Cycler.CYCLES_PER_YEAR)*(max - polyShips.size())) {
                        pool.seekRelationship(myPerson);
                    } else {
                //casual relationships
                        pool = getCasualPool();
                        if (pool != null && Math.random() <
casualInhibition*faithFactor*(eventRate / Cycler.CYCLES_PER_YEAR > numEvents ?
1 : 0))
                            pool.seekRelationship(myPerson);
                    }
                }
//requesting events
                //mono first
                if (monoShip != null && (eventRate / Cycler.CYCLES_PER_YEAR >
numEvents)) {
                    monoShip.requestEvent(myPerson);
                }
                //then poly
                double faithFactor = (monoShip == null ? 1.0 : 1.0/monoFaithfulness);
                if (polyShips.size() > 0 && (Math.random() < faithFactor) && (eventRate
/ Cycler.CYCLES_PER_YEAR > numEvents)) {
                    polyShips.getOne().requestEvent(myPerson);
                }
                //then casual
                if (casualShip != null && (eventRate / Cycler.CYCLES_PER_YEAR >
numEvents)) {
                    casualShip.requestEvent(myPerson);
                }

//breaking off relationships
                //mono first
                if (monoShip != null && Math.random() < monoBreakRate /
Cycler.CYCLES_PER_YEAR)
                    monoShip.breakOff();
                //then poly
//                  double max = maxPartners;
//                  if (monoShip != null) max -= 2;
```

```
            if (polyShips.size() > 0 && Math.random() < (polyBreakRate /
Cycler.CYCLES_PER_YEAR)*polyShips.size()) {
                polyShips.getOne().breakOff();
            }

            //then casual
            if (casualShip != null) casualShip.breakOff();

            numEvents = 0;

        }

        private AvailabilityPool getCasualPool() {
            int i = (int) Math.random()*2;
            AvailabilityPool toReturn = null;
            Iterator<AvailabilityPool> iter = casualPools.iterator();
            for (int j = 0; j <= i && iter.hasNext(); j++) {
                toReturn = iter.next();
            }
            return toReturn;        }

        private AvailabilityPool getPolyPool() {
            int i = (int) Math.random()*2;
            AvailabilityPool toReturn = null;
            Iterator<AvailabilityPool> iter = polyPools.iterator();
            for (int j = 0; j <= i && iter.hasNext(); j++) {
                toReturn = iter.next();
            }
            return toReturn;
        }

        private AvailabilityPool getMonoPool() {
            int i = (int) Math.random()*2;
            AvailabilityPool toReturn = null;
            Iterator<AvailabilityPool> iter = monoPools.iterator();
            for (int j = 0; j <= i && iter.hasNext(); j++) {
                toReturn = iter.next();
            }
            return toReturn;
        }

        public boolean hasMother() {
            return false;
```

```
	}

	public boolean acceptEvent(Relationship rel, Person instigator) {
		boolean toReturn = ((eventRate / Cycler.CYCLES_PER_YEAR >
numEvents));
		if (toReturn) numEvents++;
		return toReturn;
	}

	public void addRelationship(Relationship relationship) {
		Object type = relationship.getType();
		if (RelTypes.isMono(type)) {
			for (AvailabilityPool pool : monoPools) {
				pool.remove(myPerson);
			}
			for (AvailabilityPool pool : polyPools) {
				pool.remove(myPerson);
			}
			monoShip = relationship;
		} else if (RelTypes.isPoly(type)) {
			polyShips.add(relationship);
		} else if (RelTypes.isCasual(type)) {
			casualShip = relationship;
		}
	}

	public void breakOff(Relationship relationship) {
		Object type = relationship.getType();
		if (RelTypes.isMono(type)) {
			for (AvailabilityPool pool : monoPools) {
				pool.add(myPerson);
			}
			for (AvailabilityPool pool : polyPools) {
				pool.add(myPerson);
			}
			monoShip = null;
		} else if (RelTypes.isPoly(type)) {
			polyShips.remove(relationship);
		} else if (RelTypes.isCasual(type)) {
			casualShip = null;
		}
	}
}
```