

MODELLING AN HIV/AIDS EPIDEMIC WITH DISTRIBUTED SYSTEM PROGRAMMING

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Abstract- This paper presents the application of distributed systems high performance cluster in modelling the spread of HIV in a given population. A population of a complex ecosystem such as a community of sexually related individuals has been modelled around distributed objects. An object modelled one individual and its communication with other objects represents social interaction between individuals. This research focuses on the heterosexual transmission of HIV and uses the probability of infection as determined by medical research work. The probability of infection is dependent on a number of factors; one) viral load of the infected person as well as two) the CD4+ +CCR5 receptor cell count of the person at risk and three) use of ARVs on mortality and transmission rate is also considered. The experiment was run on a cluster of 70 connected computers each capable of running hundreds of objects (individuals). These objects are implemented in Java in a distributed programming environment called CORBA that enables object across a network to communicate. The results obtained show patterns consistent with the epidemiological nature of the HIV as well as impact of the behavioural properties of the people. The results have clearly demonstrated the ability for the high performance computer cluster to play out different scenarios and provide predictions and answers to “what if?” questions especially those of intervention programmes.

Keywords- Epidemiology, HIV/AIDS, Computer Modelling, Distributed Systems Programming,

I. INTRODUCTION

This research models the spread of HIV in a population by use of distributed objects, spread across a number of nodes on a High Performance Cluster. Some of the ideas used in this model are drawn from agent based models that have been developed in the study of the spread of epidemics [1].

The model takes as parameters the initial population described as number of males and females in the population as well as length of time the experiment is to be run. Each individual is created with a set of attributes which includes name, gender, HIV status, CD4 count, viral load, patterns of condom

use, number of partners and length of relationships. A ‘maximum number of partners’ value is also set as a characteristic of the population. Each male will then pick a random number between 0 and that maximum number, as their own individual choice of number of partners. [2,3,4,5]

Relationships are formed between males and females and are initiated by males in the population. Depending on the number of partners a male may have, each male chooses females at random to form relationships with. The length of a relationship is a random number also picked by the male. This accommodates both long and short term relationships [7,9]. A male will then at random pick any one of the females he is in relationships with to interact with and may have only one interaction per day. Once the length of the relationships expires males are free to choose new partner(s)[10,11,12,13].

During an interaction between a male and a female, the probability of transmission is calculated if one of the individuals is HIV infected. This probability is then used to determine if transmission is successful. Once transmission takes place the infected individual experiences progression of the infection. Anti Retroviral Therapy (ARV) is also introduced in the model and its effect on the viral load and CD4+T cell was monitored. The model has a monitor that records the vital HIV statistics about the population. These are saved to a file for future reference and comparison of different experiments with different scenarios [14,15,16,17,19].

II. THE OBJECT ORIENTED APPROACH

An object oriented approach was used because of its natural provision of describing the internal structures and behaviours of entities in an environment, as well as interactions and changes in their states over time, and as a result of these interactions. The humans in the ecosystem population are modelled as person objects as described in Figure 1.

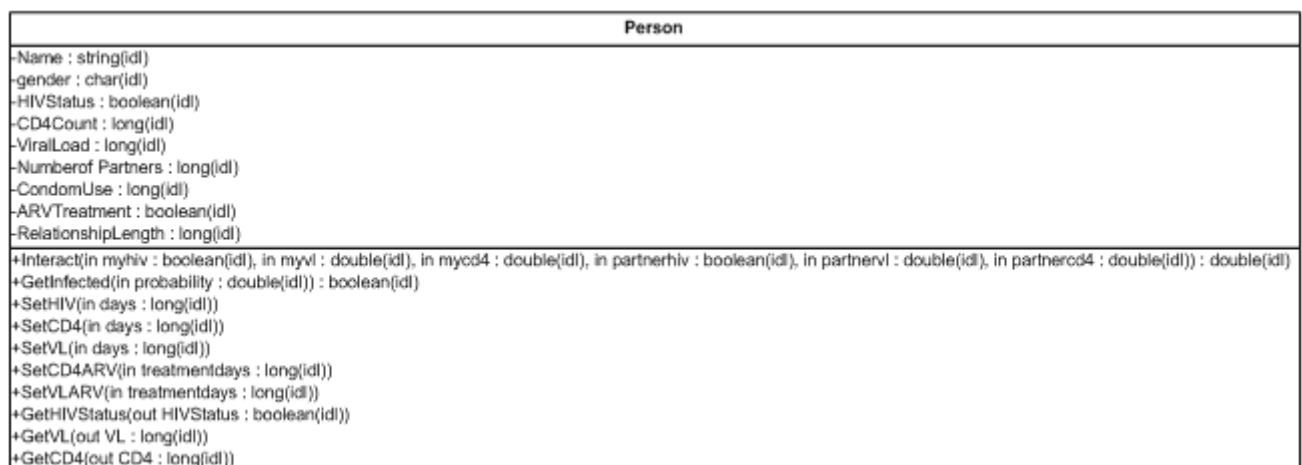


Figure. 1: Class Diagram of thePerson

III. THE DISTRIBUTED SYSTEMS APPLICATION

The model was developed as a distributed system and the Common Object Request Broker architecture (CORBA) was used to facilitate the communication between the distributed objects. CORBA is a distributed object management technology specification that provides a high level object oriented interface between objects on an open distributed computing environment. It is based on a client-server technology, where the client requests for services from the server. In order to facilitate the routing of these requests, a standard interface is specified using an interface definition language (IDL). Once this is specified and compiled, communication is independent of the physical location, operating system platform, programming language, or networking protocol.

IV. DEVELOPMENT PROCESS

First an IDL interface specification was written to describe the interfaces to the objects. IDL supports the communication between the person objects that are distributed over the numerous nodes of the cluster. The communication represents their interactions in the model (Code 1).

```
module PersonApp
{ interface Person
{
double Interact(in boolean myHIV, in double myVL, in
double myCD4+ , in boolean pHIV, in double pVL, in
double CD4+ );
boolean getInfected(in double probability);
oneway void setVL(in long days);
oneway void setVLARV(in long treatdays);
oneway void setCD4+ (in long days);
oneway void setCD4+ ARV(in long treatdays);
oneway void setHIV(in boolean hiv);
boolean getHIVstatus();
double getVL();
double getCD4+ ();
oneway void shutdown();
};
};
```

Code 1: IDL Interface Specification For The Person Object

The following is an IDL interface specification that supports the communication between the person objects and the monitor object.

```
module MonitorApp
{ interface Monitor
{ oneway void countPop();
oneway void countHIV();
oneway void countMHIV();
oneway void countFHIV();
oneway void countDead();
oneway void countFDead();
oneway void countMDead();
oneway void countARV();
oneway void countFARV();
oneway void countMARV();
oneway void createResultsFile(in string file);
oneway void showStats(in long i);
oneway void closeResultsFile();
oneway void shutdown();
};
};
```

Code 2: IDL Interface Specification For The Monitor Object.

The communication is required for the person objects to register themselves with the monitor for it to keep track of the population. Person objects also report their status to the monitor object which in turns maintains a count of both male and female in the population as well as the infected population. The monitor also writes the results to a file.

V. PERSON IMPLEMENTATION

The Person implementation class, "PersonImpl" [Code 3], is then defined and it extends the PersonPOA generated above. In this class all the operations that are defined in the Person.idl interface specification are coded.

```
//PersonImpl.java
class PersonImpl extends PersonPOA
{
private ORB orb;
private boolean HIVStat;
private double VL;
private double CD4;
private int noofpartners;
private int ARVdays = 0;
// implements Interact() method and returns a probability
of HIV transmission.
public double Interact(boolean myhiv, double myvl,
double mycd4, boolean phiv, double pvl, double pcd4)
{
}
// implements getInfected() method returns HIVstatus
public boolean getInfected(double probability)
{
}
// implements setVL() method
public void setVL(int days)
{
}
public void setVLARV(int treatdays)
{
}
public void setCD4(int days) // days after infection
{
}
//implements setCD4ARV() method
public void setCD4ARV(int treatdays)
{
}
//implements getCD4() method and returns the CD4
count
public double getCD4()
{
}
//implements getVL() method and returns the viral load
public double getVL()
{
}
//implements setHIV() method. Sets the HIV status if a
person gets infected
public void setHIV(boolean hiv)
{
}
//implements getHIVstatus() method and returns the HIV
status as Boolean.
```

```
public boolean getHIVstatus()
{
}
}
```

Code 3: Outline Of The Person Implementation Class

The method Interact() uses the HIV status and CD4 T-cell count of both the female and male involved in the interaction. If one of the individuals is infected with HIV, their viral load is used to calculate the probability of transmission during that interaction. i.e. It takes as input, myCD4, myVL, myHIV status as well as my partner's phiv, pvl and pcd4.

The probability of successful transmission from male to female has been given as $P = X_1^{0.778} X_2^{0.604}$ where X_1 is the viral load, or the concentration of the virus in the sexual secretions, and X_2 is the number of receptor cells in the mucosal layer of the reception area (ref). The method returns the probability of infection. The probability of infection returned from the above method is then used to determine if the susceptible person in the interaction gets infected or not.

VI. PROGRESSION OF HIV INFECTION

Once a person object is infected, its viral load starts to grow while the CD4-T-cell count starts to decline as shown by the following graph and described in previous sections.

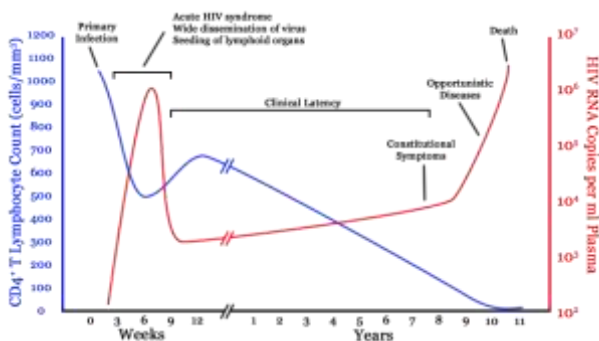


Figure 2: Changes In HIV Viral Load And CD4 T Cell Count In An Infected Person Without ARV Therapy [22]

The method setVL() below, uses the number of days after initial infection to calculate the viral load of the infected individual. It takes into consideration all the phases an individual patient goes through without the benefit of anti-retroviral (ARV) therapy.

```
public void setVL(int days)
{
    if (days < 43)//primary infection{
        VL = 2*(Math.pow(10,6))*days/42;
    }
    if (days > 42)&& (days < 64)//acute phase{
        VL = 5995000 - ((1997500*days)/21);
    }
    if (days > 63)&& (days < 3277)//chronic phase or clinical latency
    {VL = (108.93246187363834*(days/7)) + 1519.6078431372548;
    }
    if (days > 3276)//AIDS Phase
    {VL = (31714.74358974359*(days/7))-14790000;
    }
}
```

Code 4: setVL() Method

The setCD4() method [Code 6], uses the number of days after initial infection to calculate the viral load of the infected person. It also takes into consideration all the phases an individual patient goes through without the benefit of anti-retroviral (ARV) therapy.

```
public void setCD4(int days) // days after infection
{
    //primary infection
    if (days < 43)
    {CD4 = 1100 - ((640/6)*days/7);
    }
    // acute phase
    if (days > 42)&& (days < 85)
    {CD4 = ( 30*(days/7)) + 280;
    }
    // chronic phase or clinical latency period
    if (days > 84)&& (days < 1821)
    {CD4 = 648.7096774193549 - (0.7258064516129032*(days/7));
    }
    if (days > 1820)&& (days < 3277)
    {CD4 = 785 -(1.25*(days/7));
    }
    if (days > 3276)&& (days < 3641)
    {CD4 = 1100 -(1.9230769230769231*(days/7));
    }
    //AIDS
    if (days > 3640)
    {CD4 = 600 - (0.9615384615384616*(days/7));
    }
}
```

Code 5: setCD4() method

VII. PROGRESSION OF HIV INFECTION WITH ANTI-RETROVIRAL (ARV) THERAPY

The method setVLARV() uses the number of days a person has been on treatment to calculate the viral load of the infected individual. The Viral load is calculated as $20 + (((10^{8.5}) / (10w)^2) / (2w))$ where w is the number of weeks the individual has been on treatment (Figure 3). It takes into consideration the trend shown by the graph below to estimate the viral load in positive response to ARV therapy.

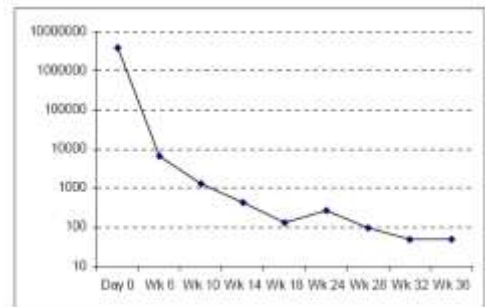


Figure 3: Decline in HIV Viral Load as a Result of ARV Therapy

The method setCD4ARV() uses the number of days a person has been on treatment to calculate the CD4-T-cell count of the infected individual. It takes into consideration the trend shown by the graph below to estimate the CD4-T-cell count in positive response to ARV therapy.

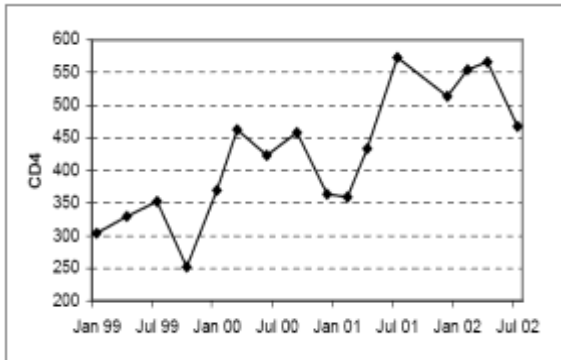


Figure 4: Increase in CD4 T Cell Count as a Result of ARV Therapy

```
public void setCD4ARV(int treatdays)
{ int months = treatdays / 30;
  if (months <= 30)
  { VL = ((25*months)/3) +200;}
  if (months > 30)
  { VL = ((25*months)/6) +325;}
}
```

Code 6: Java Coding of setCD4ARV() method.

A. Running the Model

The Monitor is run as a separate process and the following command starts the monitor.

```
start java HIVMonitor %runperiod% %filename%
```

where

- %runperiod% is the number of days the monitor must run.
- %filename% is the name of the file you would like the monitor to create and write results to.

The results file will be created in the same host that the monitor is running in.

Each individual person is created and run as a separate process. The following is the format of the command that creates a person process, assigning it its unique identity and characteristics.

```
start java PersonSvr
%ID% %gender% %HIVStatus% %partners% %popul% %condom
use% %ARV% %runperiod% %hostformonitor% %hostforpartners%
where
```

- %ID% is a serial number identifying the person
- %gender% is the gender of person, either 'male' or 'female'
- %HIVStatus% is the HIV status of the person, either 'negative' or 'positive'
- %partners% is the maximum number of partners the individual may have
- %popul% population of each gender in the population
- %condomuse% is a percentage representing pattern of condom use
- %ARV% is the availability of ARV therapy and is TRUE if available and FALSE otherwise
- %runperiod% is the number of days you would like the experiment to run
- %hostformonitor% is the network name of the host node where the monitor is running
- %hostforpartners% is the network name of the host node where this person may find partners

In order to generate a large population, a batch program was created. The following example is a batch program that generated 40 males and 40 females, where the monitor was hosted on one host and both the male and female groups were created on the same host.

```
SETLOCAL
```

```
SET Partners=3
```

```
SET popul=100
SET ID=0
set Monitorhost=cslab117-002
set partnerhost=localhost
```

```
:BEGIN
```

```
SET /ID ID=%ID%+1
```

```
start java PersonSvr %ID% %gender% %HIVStatus%
%partners% % popul% %condomuse% %ARV%
%runperiod% %hostformonitor% %hostforpartners%
start java PersonSvr %ID% %gender% %HIVStatus%
%partners% % popul% %condomuse% %ARV%
%runperiod% %hostformonitor% %hostforpartners%
```

```
IF %ID% LSS %popul% GOTO BEGIN
```

Code 7: Sample Batch Program That Generates The Population

B. The Relationships

There are different types of sexual relationships that exist in real life, but this research only considers heterosexual relationships as they are the main route through which HIV is spread. Human beings are also very complex organisms, each with unique characteristics and interests. Modelling all these combinations of characters is complex due to the complex nature of the human race, but an attempt has been made to model this as much as possible by means of randomizing their behaviours.

The way relationships are formed is not predictable, nor can it be described in a formal and logical systematic manner so as to enable programming. In other words, it is impossible to deduce the behaviour of a complex set of interacting individuals on purely logical grounds. Their personalities and choices are as unique as they each are. Behaviour has therefore been randomised within the confines of the parameters set.

- i. Partners are randomly selected by each individual within the given population.
- ii. The number of partners an individual has is chosen at random within a given maximum.
- iii. The number of times an individual interacts with any single one of his or her partners is selected randomly.
- iv. The frequency of change of partners is randomly picked by each individual person object.
- v. Those who are initialized with HIV infection are randomly assigned a CD4 count and a viral load that corresponds with the number of days,

- months or years they have lived with the infection.
- vi. Those who are initialized without the HIV infection are randomly assigned a CD4 count ranging between 152 and 1282. This is the range identified by NACA in 2003 [11] among healthy HIV negative Batswana.

These random characteristics enable adequate description of each individual as unique as any individual in a real population, such that results of their interactions cannot be predictable.

C. The Interactions

The system simulates sexual relationships between male and female individuals.

- Each individual may form relationships with other individuals based on the number of sexual partners they typically keep.
- The system effects infection from one person to another as sexual interactions occur based on the probability of infection calculated using viral load and CD4 count if one of the partners is infected.
- Individuals may change partners after a random period of time which they pick themselves. This accommodates both short and long term relationships including casual encounters.

Data

- The experiment was run with a population of 1000 individuals between the ages of 15 and 45 with a 1:1 ratio of males to females.
- In a survey that was conducted by Selohilwe et al.[[13]] that involved 1327 students of the University of Botswana, whose ages range between 18 and 45, only 803 of them answered the question on condom use relating to their last sexual act. The assumption here is that the rest were not sexually involved. It is therefore assumed that 60% (803/1327) of the population is sexually active.
- The population was initialised with a 6% HIV prevalence, balanced between both male and female members of the population.
- Patterns of condom use were set at 0% where there was no condom use, 50% where condoms were used sometimes, and 90% where condoms were used most of the time.
- The experiment used a maximum of 3 partners where multi-partner relationships are modelled.

VIII. RESULTS

The experiment focused on answering a number of questions relating to the effect of intervention programs on the infection rate, mortality and need for ARV treatment. It was configured to run with different scenarios in order to answer different “What if ...?” questions. What would happen if no intervention programs are implemented?

- What if all people stick to only one sexual partner at a time?
- What if all people who are sexually active use condoms consistently?
- What if all persons infected with HIV receive ARV?

- What if all the above are combined as an HIV control strategy?
- How many people would die if no ARV therapy is available?
- What difference would it make if only part of the population used condoms consistently?
- What difference would it make if condoms are used only sometimes as compared to all the time, or never?

A. Results

Experiment 1 : Single Partner Relationships With No Condom Use And No ARV

In the first experiment, individuals had only one partner at a time. No condoms were used at all during the interactions. By the end of the second year, HIV prevalence had increased from an initial 6% to 18%. By the fifth year HIV had spread to 36% of the population, reaching 52% by the end of seventh year and finally 60% by the tenth year. At the end of this ten year run, the entire sexually active population had been infected. 7% had died due to AIDS (Figure 5).

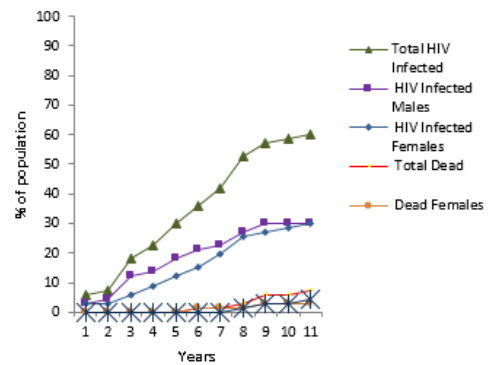


Figure 5: Results Of The Experiment with Single Partner Relationships, No Condom Use And No ARV

Experiment 2: Single Partner Relationships And 50% Condom and No ARV

The second experiment was where the individuals had only one partner at a time. Condoms were used only 50% of the times during interactions. The results show that by the second year, the HIV prevalence had increased from an initial 6% to 18%. By the fifth year it had reached 30%, and 50% by the seventh year. It finally reached 60% by the end of the tenth year. This means that by the end of the ten year run, the entire sexually active population had been infected. There was also evidence of AIDS mortality at 12% by the end of the run period (Figure 6).

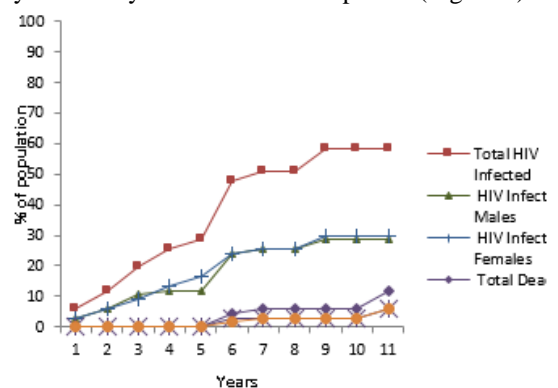


Figure 6: Results Of The Experiment With Single Partner Relationships, 50% Condom Use And No ARV

Experiment 3 : Single Partner Relationships, 90% Condom Use And No ARV

In the third experiment, individuals had only one sexual partner at a time, and condoms were used 90% of the time during interactions. In the first two years, results show a small increase in HIV prevalence from 6% to 7%. By the end of the fifth year, HIV prevalence had reached 18%, continuing to increase to 34% by the end of the tenth year. There was a 6% AIDS related mortality by the end of the 10 year run (Figure 7)

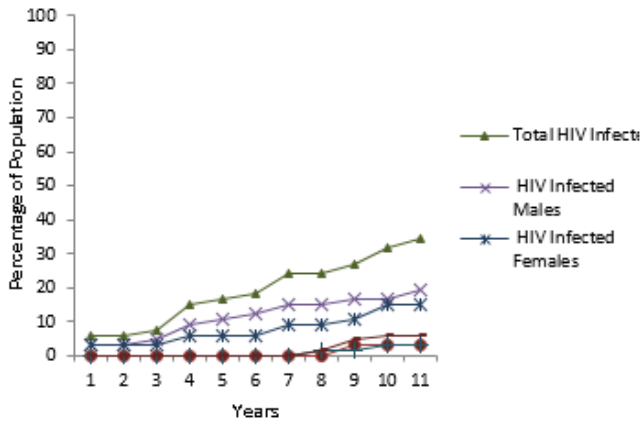


Figure 7: Results Of The Experiment With Single Partner Relationships, 90% Condom Use And No ARV

Experiment 4 : Single Partner Relationships, With ARV And No Condom Use

In the fourth experiment, individuals had only one partner at a time, no condoms were used and anti-retroviral therapy was given to all infected individuals whose CD4-T cell count fell below 200 cells/μl of blood. The results show an increase in HIV prevalence from the initial 6% to 10% in the first two years, reaching 33% by the end of the fifth year and eventually 55% by the end of the tenth year. There were no AIDS related deaths recorded, 9% of the population was on ARV treatment (Figure 8).

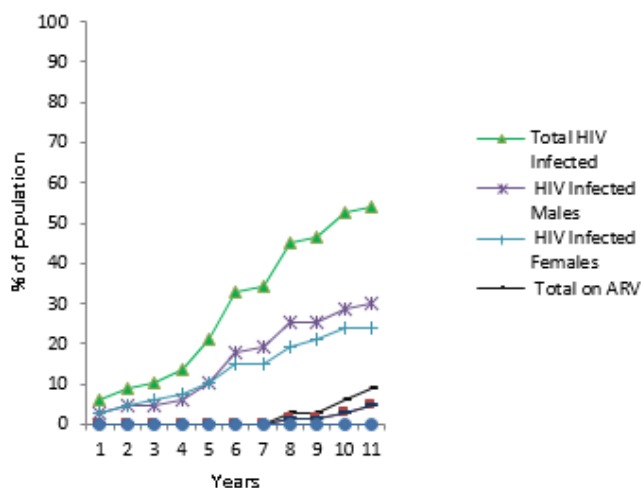


Figure 8: Results Of The Experiment With Single Partner Relationships, With ARV And No Condom Use

Experiment 5 : Single Partner Relationships, with ARV and 50% condom use

In the fifth experiment, individuals had only one partner and used condoms only 50% of the time during sexual interactions. ARV was given to all those infected people whose CD4 T cell count fell below 200 cells/μl of blood. By the end of the second year, results show that HIV prevalence had increased from an

initial 6% to 18%, reaching 28% by the end of the fifth year. Eventually HIV prevalence reached 55% by the end of the tenth year. There were no AIDS related deaths and 7% of the population was on ARV treatment (Figure 9).

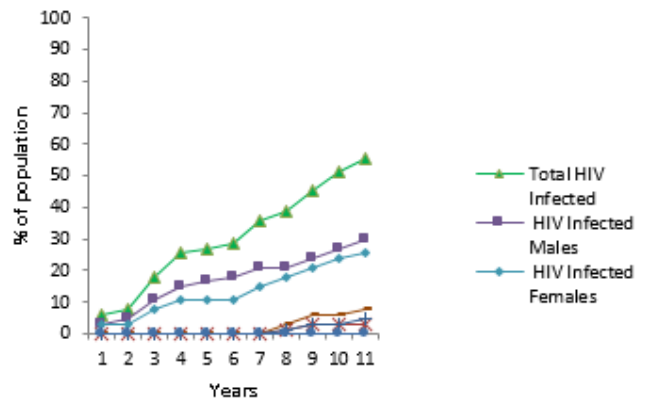


Figure 9: Results Of The Experiment With Single Partner Relationships, With ARV And 50%

Experiment 7 :Multiple Partner Relationships, No Condom Use And No ARV

The seventh experiment was where individuals had up to three sexual partners at a time. No condoms were used and ARV therapy was not available. The results show a drastic increase in HIV prevalence in the first two years from the initial 6% to 57%, quickly affecting the entire sexually active population by the fourth year. By the end of the 10th year, 39% had died from AIDS related illnesses (Figure 10).

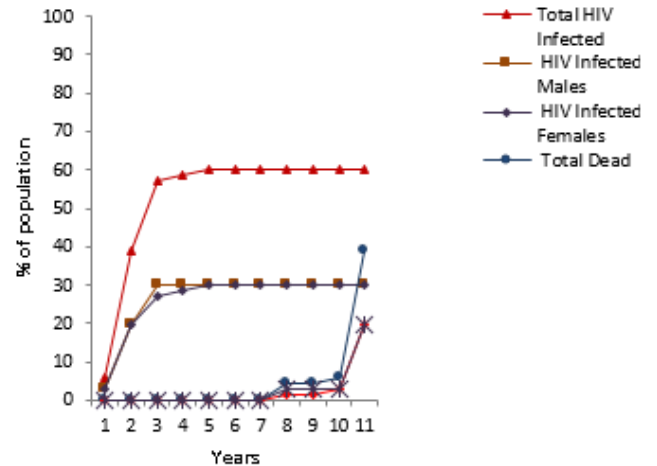


Figure 10: Results Of The Experiment With Multiple Partner Relationships, No Condom Use And No ARV

Experiment 8: Multiple Partner Relationships, 50% Condom Use And No ARV

The eighth experiment was where individuals had up to three sexual partners at a time. Condoms were used 50% of the time during interactions, and ARV therapy was not available. The results show a dramatic increase in HIV prevalence from the initial 6% to 55%, in the first two years, quickly affecting the entire sexually active population by the eighth year. By the end of the 10th year, 12% had died from AIDS (Figure 11).

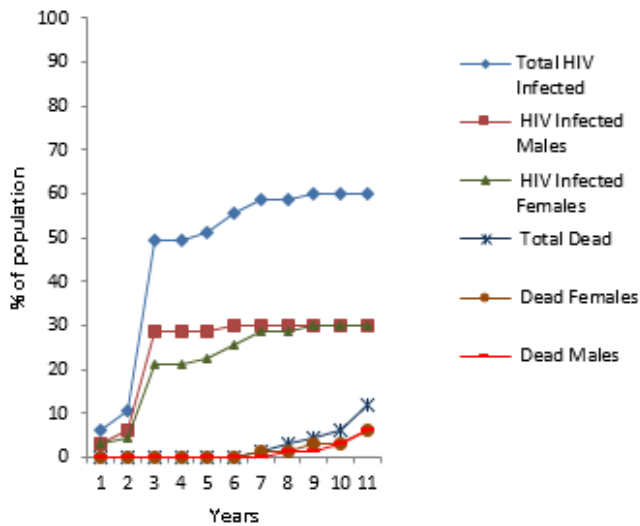


Figure 11: Results Of The Experiment with Multiple Partner Relationships, 50% Condom Use And No ARV

Experiment 9 : Multiple Partner Relationships, 90% Condom Use And No ARV

In the ninth experiment, individuals had up to three sexual partners at a time. Condoms were used 90% of the time during interactions, and ARV therapy was not available. The results show a small increase in HIV prevalence from the initial 6% to 9% in the first two years, increasing to 16% by the end of the fifth year, and 31% by the tenth year. There was a 2% AIDS related mortality recorded in the first five years and up to 6% had died from AIDS by the end of the tenth year (Figure 12).

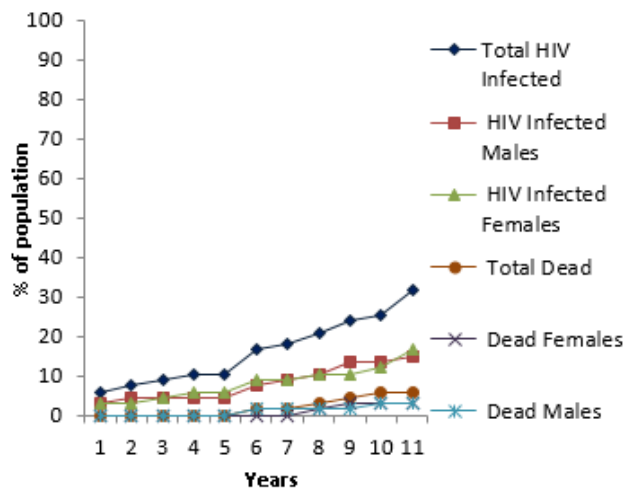


Figure 12: Results Of The Experiment With Multiple Partner Relationships, 90% Condom Use And No ARV

Experiment 10 : Multiple Partner Relationships, With ARV And No Condom Use

In this experiment, individuals had up to 3 sexual partners at a time. No condoms were used during sexual interactions, but ARV was available for those infected individuals whose CD4 T cell count fell below 200cells/ μ l. The results show a drastic increase in HIV prevalence from the initial 6% to 52% by the end of the second year, reaching 58% by the end of the fifth year, and completely covering the entire sexually active population by the end of the eighth year. A total of 50% were on ARV therapy by the end of the tenth year. There were no recorded AIDS related deaths (Figure 13).

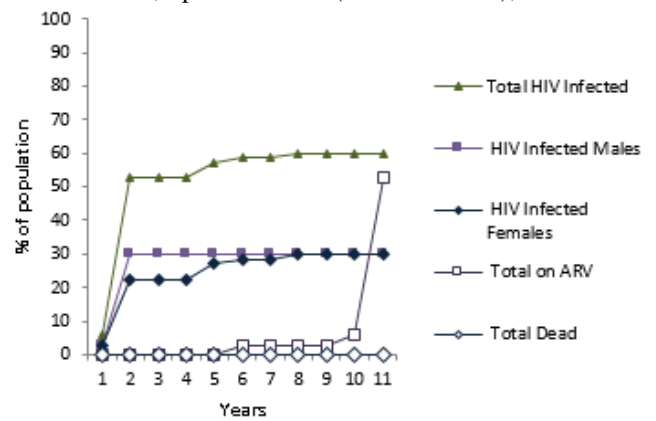


Figure 13: Results Of The Experiment With Multiple Partner Relationships, With ARV And No Condom Use

Experiment 11 : Multiple Partner Relationships, With ARV And 50% Condom Use

In the eleventh experiment, individuals had up to 3 sexual partners at a time. Condoms were used 50% of the time during sexual interactions and ARV was given to all those infected individuals whose CD4-Tcell count fell below 200 cells/ μ l. The results show that HIV prevalence reached 52% by the end of the second year from the initial 6%. 58% of the population was infected by the end of the fifth year and the entire sexually active population was infected by the end of the eighth year. There were no AIDS related deaths recorded and 49% of the population was on ARV therapy by the end of the 10th year (Figure 14).

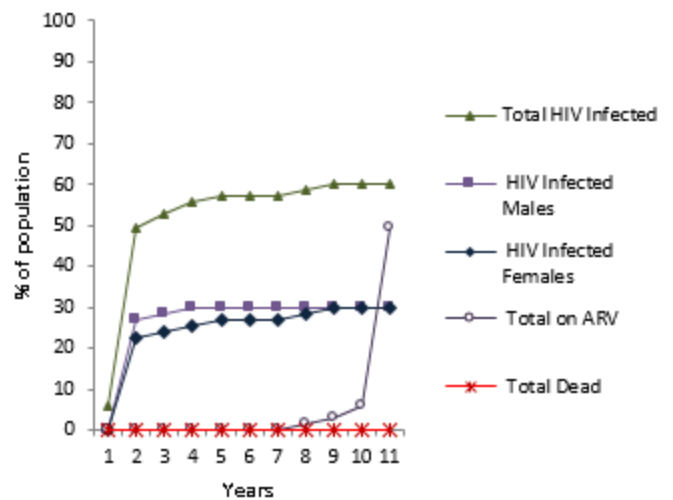


Figure 14: Results Of The Experiment With Multiple Partner Relationships, With ARV And 50% Condom Use

Experiment 12 : Multiple Partner Relationships, With ARV And 90% Condom Use

In this experiment, individuals have up to 3 sexual partners at a time. Condoms were used 90% of the time and ARV therapy was given as needed. The results show that during the first 2 years, HIV prevalence increased from the initial 6% to 9%. By the end of the fifth year, prevalence had reached 13%, and eventually 33% by the end of the tenth year. There was no recorded AIDS related mortality and 7% of the population was on ARV therapy (Figure 14).

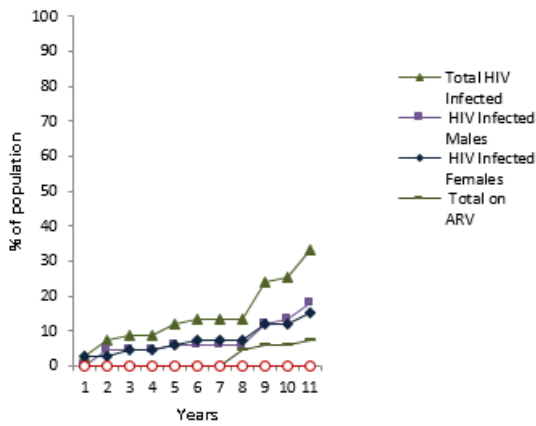


Figure 15: Results Of The Experiment With Multiple Partner Relationships, With ARV and 90% Condom Use

The results presented above are raw data that is produced from running the experiments. No mathematical analysis has been applied. The results obtained from this model are consistent with epidemiological nature of the spread of HIV as affected by different factors. The graphs presented below are a comparison of different experiments using this model to illustrate this consistency.

Comparison Of Single Partner And Multiple Partner Relationships.

Figure 16 shows a comparison of the spread of HIV related to differences in the number of sexual partners individuals had relationships with at a time.

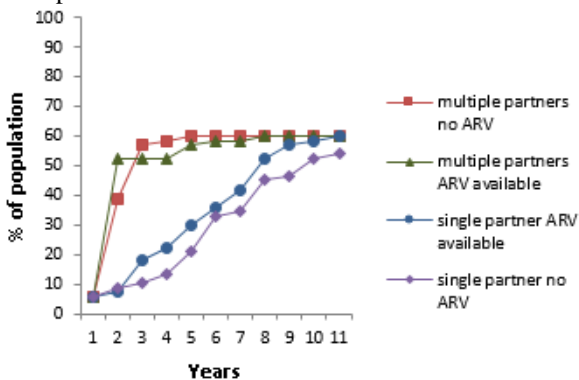


Figure 16: Comparison Of The Spread Of HIV With Varying Number Of Partners And No Condom Use.

The results show that multiple partner relationships are a great driver of the infection rate. Where individuals maintained single partner relationships the spread of HIV was not as drastic as where individuals had multiple partners even without the use of condoms. It took no more than 3 years in the multiple partner relationship experiment, for HIV prevalence to reach 50% of the population whilst it took up to 9 years for prevalence to reach 50% in the single partner relationship experiment. This is consistent with, and supports the campaign for sticking to one partner. In the experiments, over the ten year run period, individuals may change partners any number of times. Without the use of condoms, HIV is spread through the population because of the partner exchange.

Condom Use and Spread of HIV

Consistently high use of condoms has been promoted as the most effective way of controlling the spread of HIV. The results

consistently show a slow spread of HIV when condoms are used successfully 90% of the time in both multiple partner relationships and single partner relationships. These results are consistent with the findings that condoms are a very effective way of controlling the spread of HIV.

The graph below shows trends related to the high use of condoms in both single partner relationships and multiple partner relationships.

ARV Therapy and Spread of HIV

The successful use of ARV treatment has been found to reduce the infectivity of infected individuals by reducing their viral load to undetectable traces. However this has not been promoted as an effective way of controlling the spread of the virus.

Another comparison with the graph below, which was generated this proposed model, shows relatively similar trends related to high risk behaviour of not practicing safe sex by consistently using condoms during sexual interactions.

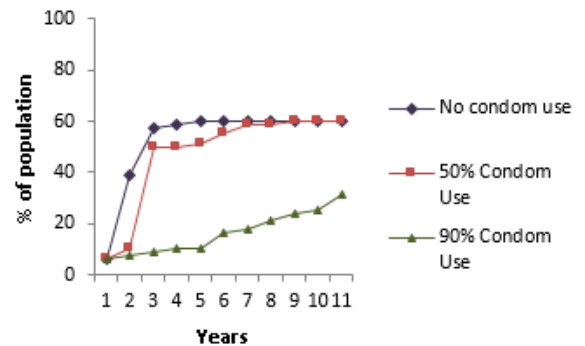


Figure 17: Comparison of the spread of HIV in relation to risky behaviour of no or inconsistent condom use vs safer behaviour of consistently using a condom most or all the time.

The EPP graph shows a sharp increase in HIV prevalence within a space of 2 years between the 3rd and 5th year of the epidemic, whereas this project's model shows a similar increase in prevalence between the first and second year of the epidemic, both for high risk populations.

Both models show that even with reduced risk factors, the spread of HIV is still evident. These similarities show that our model has some credibility and with future development may actually function for prediction of future epidemics based on behaviour trends. It can actually model the human ecosystem sufficiently to produce reliable results of trends in the spread of such epidemics as HIV.

IX. CONCLUSION

The results observed and presented in this research project are consistent with the epidemiological nature relating to factors that influence the spread of HIV such as sexual behaviour and condom use. By changing parameters related to sexual behaviour, such as patterns of condom use, and number of partners per individual, the model was able to play out different scenarios.

The results obtained show a high increase in HIV prevalence in a short space of time where condom use was inconsistent or low, and number of partners was high. Lower increase in HIV prevalence was observed where condom use was consistently high, i.e. 90% or higher, even where multiple partner relationships prevailed. There was no significant difference

observed as a result of reducing the number partners to one where condom use was consistently high. This is consistent with the fact that high condom use is the most effective method of controlling the spread of HIV.

Inclusion of anti-retroviral therapy to the experiments proved effective only as a means of reducing the number of AIDS related deaths. The results show no significant difference in the spread of HIV as a result of the introduction of ARV treatment where multiple partner relationships were prevalent and condoms were not used most of the time. Only a small difference in the spread of HIV was observed as a result of ARV treatment where single partner relationships prevailed. This is consistent with the fact that ARV medications are only effective as means of controlling or minimising the devastating effect of the disease on the individuals, but not as a means of controlling the spread of HIV in the population.

The lowest increase in the prevalence of HIV was observed where single partner relationships, high condom use and ARV therapy were applied. The results show that a combination of all the intervention strategies is the most effective means of controlling the overall devastation that the HIV pandemic brings to communities. That is, the practice of safe sex through condom use and sticking to one partner, and the provision of ARV treatment, together, promises a reduction in infection rate and AIDS related deaths.

This model is capable of simulating even larger populations and where more processing power is required, additional computers can be added to the cluster of resources without any modification to the coding of the model itself. Hosts only need to be identified in the start-up parameters.

Limitations of this model are related to the fact that it was designed as a closed ecosystem model and therefore does not account for other none AIDS related mortality and introduction of new entrants into the heterosexually active population. The model also does not account for other modes of transmission of HIV.

However, within the scope of this project, the model has clearly demonstrated the ability to use distributed object oriented approach on a high performance cluster in the ecological modelling of the spread of HIV.

X. FUTURE WORK

There are more factors that influence the overall effect of the spread of HIV than what is outlined in this research. Some of these factors are outside the scope of this research project and can be developed in future as further enhancements.

- 6.1.1 The model did not include the introduction of new entrants, nor did it include other deaths that are not HIV related. This area was beyond the scope of this research project as the model was designed and developed as a closed ecosystem specifically for the observation of the spread of HIV under different circumstances.
- 6.1.2 The model did not include the effect of Sexually Transmitted Infections on the spread of HIV as had been proposed. This is due to the fact that there are no published details of the level to which STIs increase the

risk of HIV transmission, and possibly due to the limitation of time to do further research on this topic.

- 6.1.3 The model did not implement the effect of opportunistic infections such as tuberculosis, malaria, pneumonia and others, on the rapid progression of infected individuals from HIV infection to AIDS. There is no clear indication of the type of people who develop these deadly opportunistic infections, other than for the fact that their CD4+ count has to be very low for some of these infections to progress, or that they have been exposed to such infections in their living environments. The occurrence of these opportunistic infections would affect the eligibility of a person to receive ARV therapy. For this factor to be included in such a model, a thorough research into the occurrence of opportunistic infections has to be done to deduce the factors that influence their occurrence.
- 6.1.4 The model did not consider the socio-economic background of individuals that may otherwise affect their general health and exposure to other factors that may weaken their immune systems even in the absence of HIV, possibly rendering them highly vulnerable to HIV infection, and opportunistic infections.
- 6.1.5 The model did not account for ARV defaulters that may result in resistant HIV strains that do not respond to ARV treatment. However, there are different combinations of anti-retroviral medications that are used to address resistant occurrences. Exploration of the different strains was beyond the scope of this project.

REFERENCES

- [1] AIDS Committee of the Actuarial Society of South Africa. "ASSA2003 AIDS and Demographic Models: User Guide." November 2005.
- [2] Chakraborty, Hrishikesh; Sen, Pranab K., Helms, Ronald W., Vernazza, Pietro L., Fiscus, Susan A., Eron, Joseph J., Patterson, Bruce K., Coombs, Robert W., Krieger, John N., and Cohen, Myron S. "Viral Burden In Genital Secretions Determines Male-To-Female Sexual Transmission Of HIV-1: A Probabilistic Empiric Model." AIDS. 15(5):621-627, March 30, 2001.
- [3] Corley C.D., Brown L. and Mikler A.R. "Generating Social Networks of Intimate Contacts for the Study of Public Healths Intervention Strategies." BIBE 2007. 1235-1239.
- [4] Coulouris G., Dollimore J., and Kindberg T. "Distributed Systems: Concepts and Design.." 4th Edition. Addison Wesley. 2005.
- [5] Hanley B. "An Object Simulation Model For Modeling Hypothetical Disease Epidemics – EpiFlex." Theoretical Biology and Medical Modelling. 2006; 3: 32.
- [6] Hoffmann C., Rockstroh J. K. and Kamps B. S. "HIV Medicine 2006." Flying Publisher. 2006.
- [7] Johnson L. F. and Dorrington R. E. "Modelling the demographic impact of HIV/AIDS in South Africa And The Likely Impact Of Interventions." Demographic Research. June 2006; 14: 541-574.
- [8] Merelli Emanuela, Armano Giuliano, Cannata Nicola, Corradini Flavio, d'Inverno Mark, Doms Andreas, Lord Phillip W., Martin Andrew, Milanesi Luciano, Möller Steffen, Schroeder Michael, and Luck Michael. "Agents in Bioinformatics, Computational and Systems Biology." Briefings in Bioinformatics 8(1): 45-59 (2007)
- [9] Merli M. G., and Hertog S. "Modelling the Course of the HIV/AIDS Epidemic in China: An Application of a Bio-Behavioral Macrosimulation Model of the Spread of HIV/AIDS." Population Studies, vol. 60, Issue 1, March 2006. 1-22.

- [10] Ministry of Health. Department of HIV/AIDS Prevention and Care. "2005 Botswana Second Generation HIV/AIDS Surveillance: Technical Report." 2005.
- [11] National Aids Coordinating Agency (NACA). "Botswana 2003 Second Generation HIV/AIDS Surveillance: A Technical Report." November 2003.
- [12] Salomon J. A. and Murray C. J. L. "Modeling HIV/AIDS epidemics in sub-Saharan Africa using sero-prevalence data from antenatal clinics." Bulletin of world Health Organization, 2001, 79(7), 596-607.
- [13] Seloilwe E. S. "Factors That Influence The Spread Of HIV/AIDS Among Students Of The University Of Botswana." Journal of The Association Of Nurses In AIDS Care. Vol. 16. No.3. May/June 2005. 3-10.
- [14] Silvert William. "Object Oriented Ecosystem Modelling." Ecological Modelling, 68(1993) 91-118
- [15] Teweldemedhin E., Marwala T. and Mueller C. "Object-based Modelling: A case Study in HIV Epidemic." Proceedings of the Fourth International Conference on Hybrid Intelligent Systems. HIS 2004: 154-159.
- [16] UNAIDS Best Practice Collection. "Consultation on STD Intervention for Preventing HIV: What is the Evidence?" Geneva, Switzerland. May 2000.
- [17] UNAIDS Reference Group on Estimates, Models and Projections. "Estimating and Projecting National HIV/AIDS Epidemics: The models and methodology of the UNAIDS/WHO approach to estimating and projecting national HIV/AIDS epidemics." January 2003.
- [18] UNAIDS. "Improving parameter estimation, projection methods, uncertainty estimation, and epidemic classification. Report of a meeting of the UNAIDS Reference Group on Estimates, Modelling and Projections." Prague Czech Republic, November 29th – December 1st 2006.
- [19] UNAIDS. 2006 Report on Global AIDS Epidemic. May 2006.
- [20] Van Der Ploeg C. P. B., Vliet C.V., Vlas S.J.D., Achola J.O.N., Fransen L., Oortmarssen G.J.V. and Habbema J.D.F. "STDSIM: A Microsimulation Model for Decision Support in STD Control." Interfaces 28: 3 May-June 1998 (pp.84-100).
- [21] Venkatachalam S. and Mikler A.R. "An Infetious Disease Outbreak Simulator Based on the Cellular Automata Paradigm." IICS 2004. 198-211.
- [22] http://www.pipelinedrugs.com/biotechnology_encyclopedia/500px-Hiv-timecourse.png