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Computation, Modeling, and Simulation of HIV-AIDS Epidemics with Vaccination

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Abstract

The principles of the HIV-AIDS epidemics are established based on the subpopulation 1) Susceptible; 2) HIV-infected; 3) AIDS-infected; 4) Immunized. The immunized subset of the population in this paper is the total individuals who were infected and cured or immunized by vaccination. The immunized group can be identified by removing individuals from the susceptible group. A general mathematical model is developed for HIV-AIDS epidemics with Vaccination to understand the spread of the virus throughout the population. Particularly we use numerical simulation with some values of parameters to predict the number of infected individuals during a certain period in a population and the effect of vaccine to reduce infected group and increase the number of immunized individuals. Further, we expand the research to special cases with no vaccinations. A special case is when the removal subset of the population is empty, or there is no recovery in this epidemic. We also can consider the total infected number is equal to the sum of the HIV infected and the number of AIDS infected. As a result, one can reduce four-stage HIV-AIDS investigation to a three-stage of SIR. With this introduction and modification, the numerical simulation can be developed the Monte Carlo simulation method in SIR case to verify the Validity of the HIV-AIDS model.

Keywords

Epidemics of "SHAR", $s(t)$: Susceptible, $h(t)$: HIV Infected, $a(t)$: Aids, $r(t)$: Removed, Antibody, HIV-Vaccine

1. Introduction

It is very important to present a mathematical description of a natural disaster like HIV-AIDS epidemics. To forecast the spread of any disease, one can use a deterministic approach or use stochastic modeling.

In the deterministic model, the use of the method of differential equations and Monte Carlo simulation is also a powerful approach for prediction of the epidemics (see [1]).

We postulated all related assumptions and defined all parameters involved in this epidemics process. The mathematical model presented in this investigation is a nonlinear ODE (ordinary differential equation) that can predict the progress of the infected population or epidemics throughout time (see [2]).

To solve a nonlinear system of ODE, one can choose a numerical, graphical, or analytical approach.

The basic concept of mathematical modeling in epidemiology is the variety of subsets of the population and their fundamental interactions. Simple subsets of the epidemic population model for HIV-AIDS are: Susceptible, HIV-Infected, AIDS-infected, and Removed subsets for which we used $s(t)$, $h(t)$, $a(t)$, and $r(t)$.

Our simulation, using numerical and graphical approaches will be demonstrated with imposed conditions or choices of parameters. Initially, one HIV infected individual can transmit the virus to the entire susceptible population and can infect the entire population.

In the simplest epidemic model, it is usually assumed that the population is partitioned into $s(t)$ = "susceptible", $I(t)$ = " infected", and $r(t)$ = "removed or recovered" which is called the SRI model (see [3] and [4]).

We will consider the vaccination factor for modeling this epidemic. A reasonable function for removing the immune individuals who are not susceptible to the virus will be denoted by $r(t)$. The nonlinear system will be a system of four ODE equations. Further research analysis, refining the model and qualitative analysis is the goal of this research.

1) HIV stands for human immunodeficiency virus. If left untreated HIV can lead to the disease AIDS (acquired immunodeficiency syndrome). Unlike some other viruses, the human body can't get rid of HIV completely. So once you have HIV, you have it for life. HIV attacks the body's immune system, specifically the CD4 cells (T cells) which help the immune system fight off infections. If left untreated, HIV reduces the number of CD4 cells (T cells) in the body, making the person more likely to get infections or infection-related cancers. Over time, HIV can destroy so many of these cells that the body cannot fight off infections and disease. These opportunistic infections or cancers take advantage of a very weak immune system and signal that the person has AIDS, the last state of HIV infection. No effective cure for HIV currently exists, but with proper treatment and medical care, HIV can be controlled. The medicine used to treat HIV is called antiretroviral therapy or ART. If taken the right way, every day, this medicine can dramatically prolong the lives of many people with HIV, keep them healthy, and greatly lower their chance of transmitting the virus to others. Today, a person who is diagnosed with HIV, treated before the disease is far advanced, and stays on treatment can live nearly as long as someone who does not have HIV.

2) AIDS stands for acquired immunodeficiency syndrome. AIDS is the final stage of HIV infection, and not everyone who has HIV advances to this stage.

AIDS is the stage of infection that occurs when the immune system is badly damaged, and one becomes vulnerable to opportunistic infections. When the number of your CD4 cells falls below 200 cells per cubic millimeters of blood (200 cells/mm^3), you are considered to have progressed to AIDS. The CD4 count of an uninfected adult/adolescent who is generally in good health ranges from 500 cells/mm^3 to 1600 cells/mm^3. You can also be diagnosed with AIDS if you develop one or more opportunistic infections, regardless of your CD4 count. Without treatment, people who are diagnosed with AIDS typically survive about 3 years. Once, someone has a dangerous opportunistic illness, life expectancy without treatment falls to about 1 year. People with AIDS need medical treatment to prevent death (see [5] [6] [7]).

3) Where AIDS-HIV Come From?

Scientists identified a type of chimpanzee in Central Africa as the source of HIV infection in humans. They believe that the chimpanzee version of the immunodeficiency virus (called simian immunodeficiency virus, or SIV) most likely was transmitted to humans and mutated into HIV when humans hunted these chimpanzees for meat and encountered their infected blood. Studies show that HIV may have jumped from apes to humans as far back as the late 1800s. Over decades, the virus slowly spread across Africa and later into other parts of the world. We know that the virus has existed in the United States since at least the mid- to late 1970s.

In a recent investigation, a mathematical model of HIV-AIDS developed without considering the vaccination factor when the vaccination of HIV-AIDS did not exist (see [8]). This paper was produced during the COVID-19 pandemic when the vaccination became important and possible. In this model using vaccination factor in developing the model, computation, and simulation we observe that the cured subpopulation and immunized individuals together create a larger set of removed subpopulation.

2. Basic Assumptions for (SHAR) Model

Each population develops and evolves through two important basic principles, variations and natural selection. The principle of evolution causes some characteristics in a diverse environment and genetic changes. The HIV-AIDS epidemics is not an exception, and it follows the rule of evolution. For developing a model, we subdivide the population into the following characteristics that can be observed in a subset of a population.

1) Infective (I): A person in the population who has the disease and can spread it to another individual who is not yet exposed to HIV-aids virus.

2) Susceptible (S): Person who does not have the symptoms of the disease but, can be infected by exposure to the virus from the infective.

3) Exposed to Virus: Individual did not develop the symptoms of HIV but is contaminated and carrying the virus through the infected environment.

4) Infected Person: Infected individual who tested positive and is a potentially

infectious contact which spreads the disease to a susceptible person.

5) Latently Infected (L): Those currently exposed and tested positive but may not be certain to yet be capable of transmitting the disease to others.

6) Immunized Person: is a person who developed antibodies through recovery or by Vaccination. Individuals who developed immune system fight against the virus naturally or by vaccination.

7) Removed (R): Those who have had the disease and are dead or have recovered and are permanently immunized or isolated until death, recovery, or permanent immunity occurs (Figure 1).

Principles and the dynamics of the subpopulations: The epidemic model is based on the following Susceptible (s), Infected (I), and Removed (r) subpopulation called (SIR) is well known and developed extensively. In addition, we will use $E(t)$ for individuals exposed to the virus, $L(t)$ for latency, and $V(t)$ for the population vaccinated at time t.

Assuming these subsets are mutually disjoint subsets of the population, then:

Assumption 1: The population during the time of study remains approximately constant and has mutually exclusive subgroups such that

$$P = s(t) + E(t) + L(t) + h(t) + a(t) + r(t) \tag{2.1}$$

We are assuming in HIV-AIDS model both $L(t)$ and $E(t)$ are zero. Of course, in corona virus case this is not true.

Assumption 2: The susceptible population is negatively proportional to the contacts with the HIV infected and the AIDS infected sub-populations.

Assumption 3: Vaccination during the epidemic reduces the susceptible and converts to the immunized individuals.

Using these assumptions there exist positive constants k, l, and m_1, such that

$$\frac{\mathrm{d}s}{\mathrm{d}t} = -k \cdot h(t)s(t) - l \cdot a(t)s(t) - m_1 s(t) \tag{2.2}$$

The following is the definition of the parameters used in Equation (2.2):

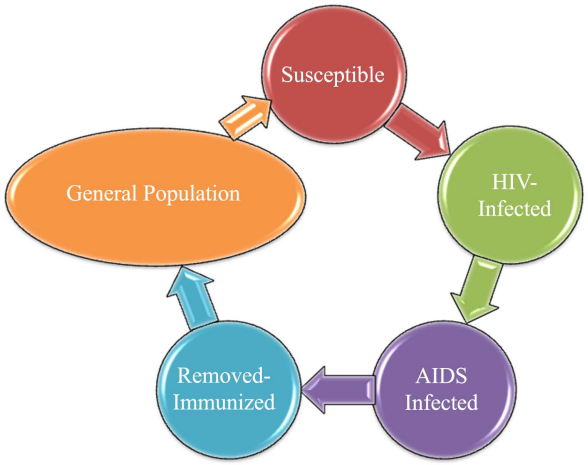


Figure 1. This is a diagram showing the subpopulations s(t)-susceptible, HIV-infected-h(t), AIDS infected subset-a(t), and immunized group or removed-r(t).

$$\begin{cases} k = \text{transmision rate from Susceptible to HIV} \\ l = \text{transmission rate from Susceptible to AIDS} \\ m_1 = \text{rate chaging susceptible to recovere} \end{cases}$$

Assumption 4: The rate of change in the HIV infected population $h(t)$ is positively proportional to the number of contacts with the susceptible.

Assumption 5: The rate of change of HIV infection will be reduced by some factors in transforming to AIDS and by some factors in converting to the immune group.

$$\frac{\mathrm{d}h}{\mathrm{d}t} = k \cdot h(t)s(t) + l \cdot a(t)s(t) - n \cdot h(t) - m_2 h(t) \tag{2.3}$$

Two new parameters in this equation are defined:

$$\begin{cases} n = \text{transmision rate from HIV to AIDS caused by virus mutation} \\ m_2 = \text{rate chaging of HIV to recovere by vaccination} \end{cases}$$

By taking the derivative of the relation (2.1) we can find the rate of change for AIDS infection.

$$\frac{\mathrm{d}a}{\mathrm{d}t} = -\frac{\mathrm{d}s}{\mathrm{d}t} - \frac{\mathrm{d}h}{\mathrm{d}t} - \frac{\mathrm{d}r}{\mathrm{d}t} \tag{2.4}$$

Assumption 6: The rate of change in removable set of the epidemic is proportional to the vaccine contribution to the immune group from susceptible, HIV, and AIDS groups.

$$\frac{\mathrm{d}r(t)}{\mathrm{d}t} = m_1 s(t) + m_2 \cdot h(t) + m \cdot a(t) \tag{2.5}$$

We can combine (2.4) and (2.5) to find $\frac{\mathrm{d}a}{\mathrm{d}t}$. As a result:

$$\frac{\mathrm{d}a(t)}{\mathrm{d}t} = n \cdot h(t) - m \cdot a(t) \tag{2.6}$$

Given a function $h(t)$, the relation (2.6) will be a first order linear differential equation.

To summarize the result, we will have a system of the following nonlinear differential equations:

$$\begin{cases} \frac{\mathrm{d}s}{\mathrm{d}t} = -k \cdot h(t)s(t) - l \cdot a(t)s(t) - m_1 s(t) \\ \frac{\mathrm{d}h}{\mathrm{d}t} = k \cdot h(t)s(t) + l \cdot a(t)s(t) - n \cdot h(t) - m_2 h(t) \\ \frac{\mathrm{d}r(t)}{\mathrm{d}t} = m_1 s(t) + m_2 \cdot h(t) + m \cdot a(t) \\ \frac{\mathrm{d}a(t)}{\mathrm{d}t} = n \cdot h(t) - m \cdot a(t) \end{cases} \tag{2.7}$$

with the initial conditions: $s(0) = s_0, h(0) = h_0, a(0) = a_0, r(0) = r_0$. We can use the technology of MAPLE (CAS) to demonstrate the solution.

3. Solution of the Nonlinear System by Numerical Computation

Solving the nonlinear system (2.7) using an analytical approach to analyze the behavior of the system is a challenge. In this presentation, we will try to use a computational approach to simulate the behavior of the solution of the nonlinear system. There is much research work that focuses on susceptibility, infection, and removed the (SIR) using a variety of computational tools like MAPLE and Sage (see [9]). The model (2.7) is a four-stage model representing susceptible, HIV, AIDS, with Removed of (SHAR) model.

In the first stage, we present MAPLE code to show the numerical and graphical results.

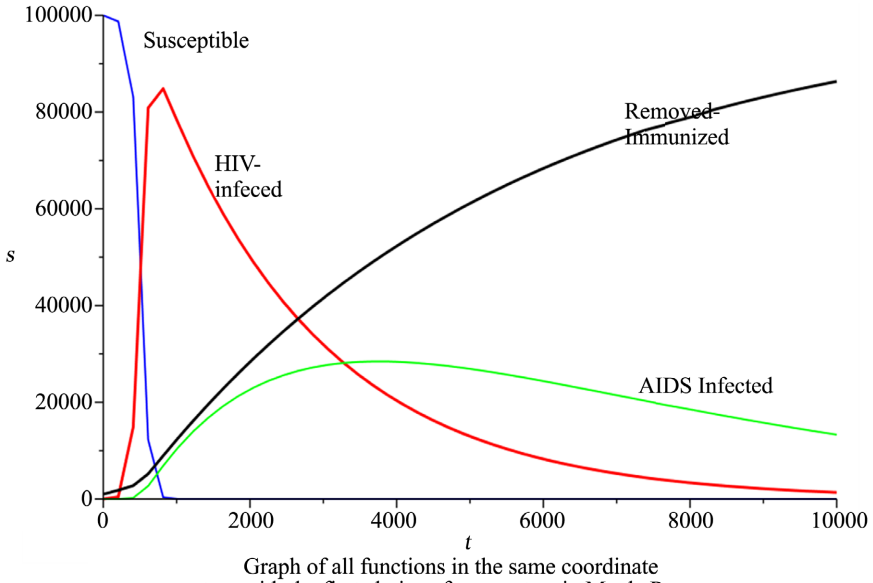
In **Figure 2**, the first result of the graphs of all $s(t)$, $h(t)$, $a(t)$, and $r(t)$ are in the same coordinate system.

We can run the Maple numerical solution for the nonlinear system (2.7) with different initial conditions and different values of parameters:

> display([ps2, ph2, pa2, pr2]) (**Figure 3**).

4. Numerical Approximation by Computer Algebra (Maple)

We can take advantage of the discrete system of (2.7) to view the solution forecast for the epidemics. Consider an index $j = 0,1,2,\cdots,N$ counting the step by step calculation for a unit time interval $\Delta t = t(j+1) - t(j)$. The equivalent system will be the following discrete difference equations:



Graph of all functions in the same coordinate system with the first choice of parameters in Maple Program

Figure 2. The numerical solution with the given parameter values, for the system (2.7) demonstrates that the initial susceptible $s(0)$ = 10,000 will approach to zero, the initial hiv and aides infected $h(0)$ = 1, $a(0)$ = 0 and a rise to maximum and decrease to annihilated, The removed sub population that immunized due to the epidemic will be increasing in longer period of *time.*

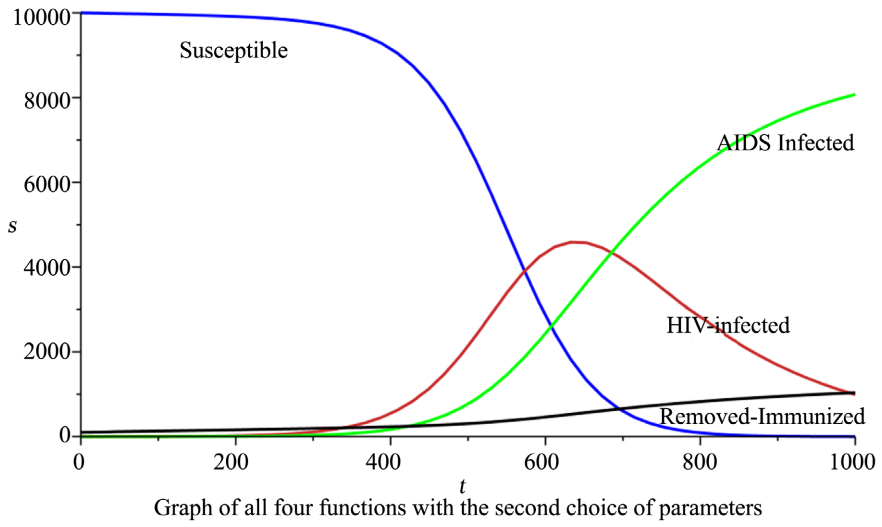


Figure 3. A similar solution is demonstrated with the following parameters. $k = 0.000008$, $l = 0.000007$, $m = 0.0002$, $n = 0.00025$, $m_1 = 0.00004$, $m_2 = 0.0002$.

$$\begin{cases} s[j] = s[j-1] - k*s[j-1]*h[j-1] - l*s[j-1]*a[j-1] - m_1*s[j-1] \\ h[j] = h[j-1] + k*h[j-1]*s[j-1] + l*h[j-1]*a[j-1] - (n+m_2)h[j-1] \\ a[j] = a[j-1] + n*s[j-1] - m*a[j-1] \\ r[j] = r[j-1] + m_1*s[j-1] + m_2*h[j-1] + m*a[j-1] \end{cases} \tag{4.1}$$

with initial conditions: $s[0] = s_0, h[0] = h_0, a[0] = a_0, r[0] = r_0$.

To compare the variations between every two graphs and the output of the discrete system, we depicted the following graph of curve A for susceptible, curve B for HIV infection, curve C for aids infection, and curve D for removed immunized set.

Please see **Figure 4** for MAPLE code to solve these nonlinear difference equations.

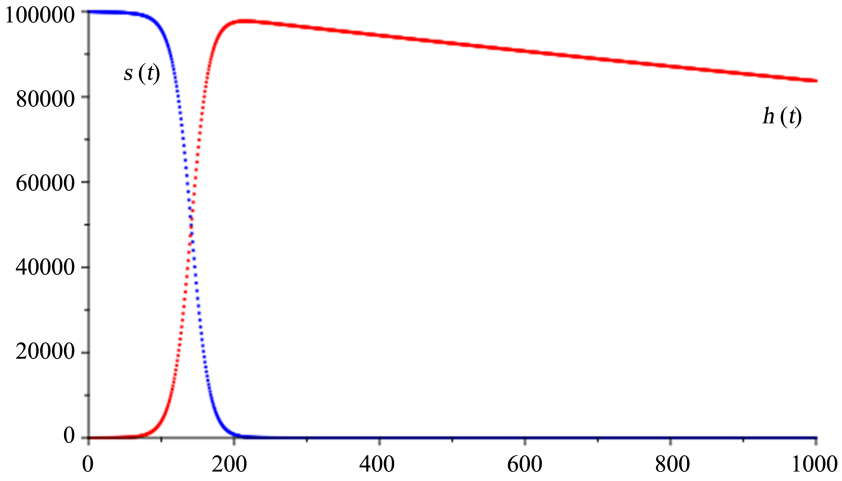
5. Numerical Approximation by Excel Spreadsheet

The method of discrete computation of the nonlinear system (Section 4.) is good to visualize the behavior graphically throughout a longer time. It is important to know the numerical values to forecast the epidemics in a city or country. The spreadsheet can produce the number of infected individuals in every time-period.

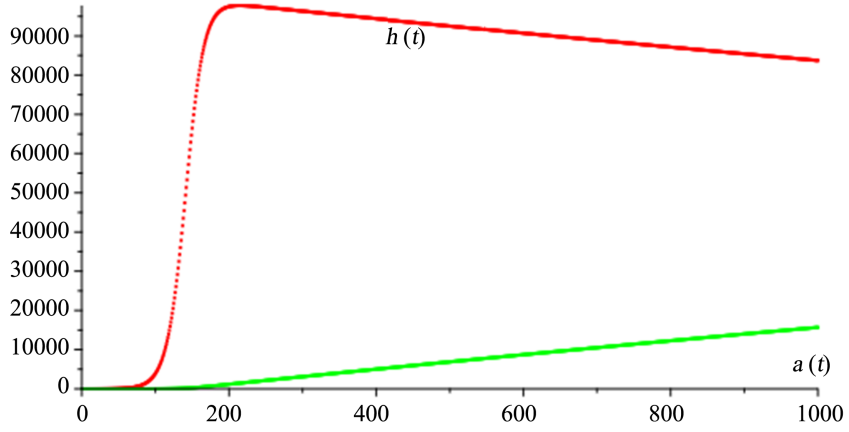
Notice that the last three columns are auxiliary columns to help us to move the computations from one time-period to the next (see [10]) (**Figure 5** and **Table 1**).

6. HIV-AIDS Modeling without Vaccinations

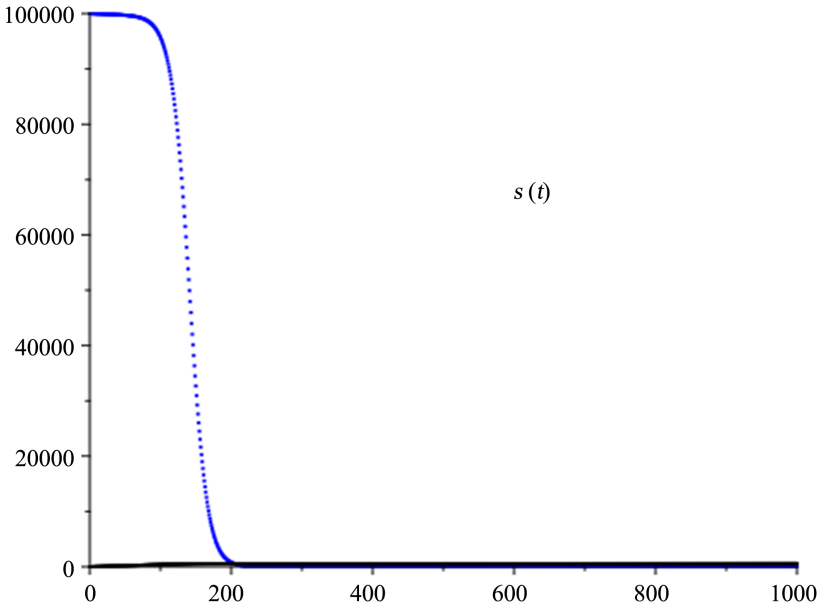
Assume that during the studying of the spread of the Virus, no vaccination exists. We are wondering what is going to happen in the population.



Variation of susceptible $s(t)$ Vs. HIV population $h(t)$



Variation of HIV $h(t)$ Vs. AIDs population $a(t)$



Variation of susceptible $s(t)$ with respect to recovered popul ati on $r(t)$

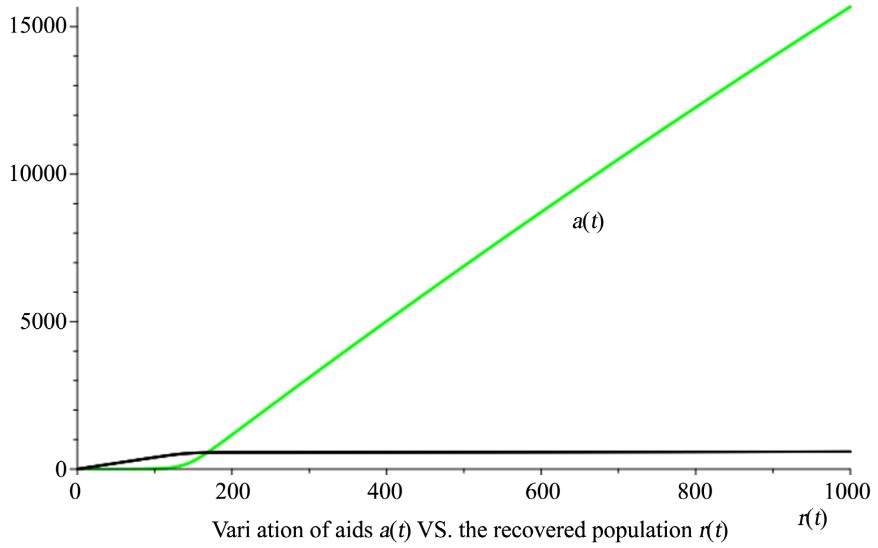


Figure 4. This is a demonstration of the variations of susceptible, HIV-AIDS and recovered two by two for comparison.

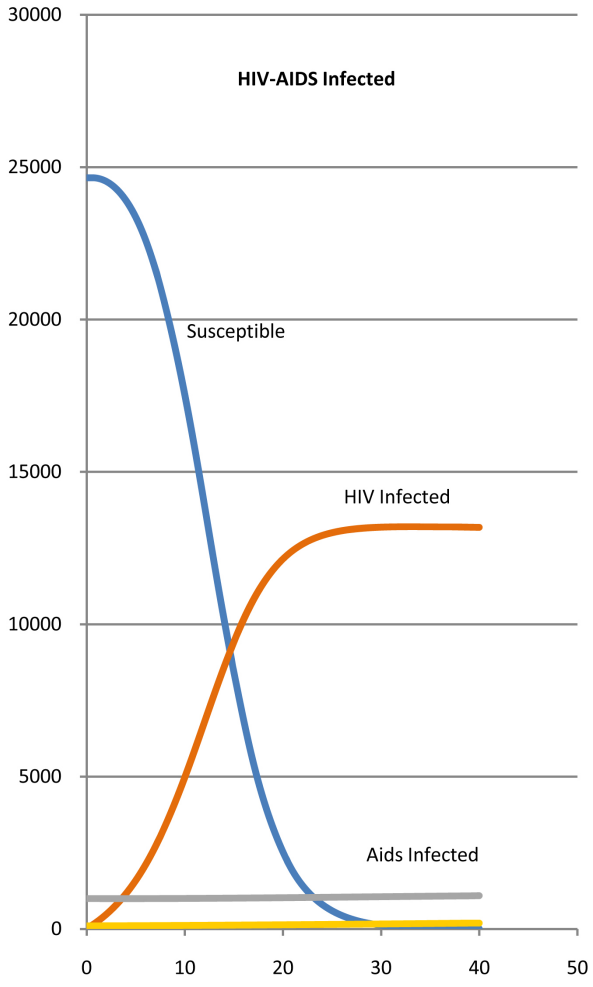


Figure 5. The susceptible population is diminishing; the HIV reaches to the highest level, and the AIDS and recovered population is demonstrate to be approximately constant.

Table 1. The numerical prediction for $s(j)$, $h(j)$, $a(j)$, and $r(i)$ when $j = 1\ldots$ 40-time interval (day), with the given parameters are computed.

Numerical Computation for HIV-AIDS Modeling with Recovery (Vaccination) using Excel spreadsheet								
n	$s(n)$	$h(n)$	$a(n)$	$r(n)$	$s(n+1)$	$h(n+1)$	$a(n+1)$	$r(n+1)$
0	24,650	10	1000	100	24,643	222	1000	101
1	24,643	222	1000	101	24,531	477	1000	102
2	24,531	477	1000	102	24,295	785	1001	104
3	24,295	785	1001	104	23,911	1154	1001	105
4	23,911	1154	1001	105	23,357	1591	1001	106
5	23,357	1591	1001	106	22,612	2105	1001	108
6	22,612	2105	1001	108	21,658	2701	1002	109
7	21,658	2701	1002	109	20,486	3382	1003	111
8	20,486	3382	1003	111	19,098	4144	1003	113
9	19,098	4144	1003	113	17,514	4977	1004	114
10	17,514	4977	1004	114	15,769	5866	1006	116
11	15,769	5866	1006	116	13,918	6784	1007	118
12	13,918	6784	1007	118	12,028	7703	1009	121
13	12,028	7703	1009	121	10,174	8590	1011	123
14	10,174	8590	1011	123	8425	9416	1013	125
15	8425	9416	1013	125	6838	10,159	1015	127
16	6838	10,159	1015	127	5448	10,804	1018	130
17	5448	10,804	1018	130	4270	11,346	1021	133
18	4270	11,346	1021	133	3301	11,790	1023	135
19	3301	11,790	1023	135	2522	12,144	1026	138
20	2522	12,144	1026	138	1909	12,421	1029	141
21	1909	12,421	1029	141	1435	12,634	1032	143
22	1435	12,634	1032	143	1072	12,795	1036	146
23	1072	12,795	1036	146	798	12,915	1039	149
24	798	12,915	1039	149	592	13,004	1042	152
25	592	13,004	1042	152	438	13,069	1045	155
26	438	13,069	1045	155	323	13,115	1049	158
27	323	13,115	1049	158	238	13,148	1052	160
28	238	13,148	1052	160	176	13,171	1055	163
29	176	13,171	1055	163	129	13,187	1058	166
30	129	13,187	1058	166	95	13,196	1062	169

Continued

31	95	13,196	1062	169	70	13,202	1065	172
32	70	13,202	1065	172	52	13,204	1068	175
33	52	13,204	1068	175	38	13,205	1072	177
34	38	13,205	1072	177	28	13,203	1075	180
35	28	13,203	1075	180	21	13,201	1078	183
36	21	13,201	1078	183	15	13,197	1082	186
37	15	13,197	1082	186	11	13,193	1085	189
38	11	13,193	1085	189	8	13,189	1088	192
39	8	13,189	1088	192	6	13,184	1091	195
40	6	13,184	1091	195	4	13,179	1095	197

k=	0.0002
l=	0.00000005
m_1	0.0004
n_1=	0.00025
m_2=	0.0002
n_2=	0.025

In this case we are actually assuming that $m_2 = m_1 = m = 0$, and the system (2.7) will be reduced to the following:

$$\begin{cases} \dfrac{\mathrm{d}s}{\mathrm{d}t} = -k \cdot h(t)s(t) - l \cdot a(t)s(t) \\ \dfrac{\mathrm{d}h}{\mathrm{d}t} = k \cdot h(t)s(t) + l \cdot a(t)s(t) - n * h(t) \\ \dfrac{\mathrm{d}r(t)}{\mathrm{d}t} = 0 \\ \dfrac{\mathrm{d}a(t)}{\mathrm{d}t} = n \cdot h(t) \end{cases} \tag{5.1}$$

The third equation implies that $r(t) = r_0$ is a constant. When there is no immunity in the population system the removal number is zero.

7. Special Case When the HIV-AIDS Model System Does Not Have Removable Subset ($r(t) = 0$)

The Epidemic Model with zero removed individuals, that is when $r(t) = 0$ will be in the following form.

$$\begin{cases} \dfrac{\mathrm{d}s}{\mathrm{d}t} = -k \cdot h(t)s(t) - l \cdot a(t)s(t) \\ \dfrac{\mathrm{d}h}{\mathrm{d}t} = k \cdot h(t)s(t) + l \cdot a(t)s(t) \\ \dfrac{\mathrm{d}a(t)}{\mathrm{d}t} = n \cdot h(t) - m \cdot a(t) \end{cases}$$

This model was developed in [11].

8. Special Case of SHAR Modeling

If the parameters in the system (2.7) are selected such that:

$$m_1 = m_2 = n = m = 0$$

Then, we will reduce the system to SIR model

$$\begin{cases} \dfrac{\mathrm{d}s}{\mathrm{d}t} = -k \cdot h(t)s(t) - l \cdot a(t)s(t) \\ \dfrac{\mathrm{d}h}{\mathrm{d}t} = k \cdot h(t)s(t) + l \cdot a(t)s(t) \\ \dfrac{\mathrm{d}r(t)}{\mathrm{d}t} = 0 \\ \dfrac{\mathrm{d}a(t)}{\mathrm{d}t} = 0 \end{cases} \tag{6.1}$$

According to the new nonlinear system we have only two subsets, susceptible and HIV infected. That is

$$\begin{cases} s(t) + h(t) = \text{constant} = P \\ r(t) = \text{constant} = r(0) \\ a(t) = \text{constant} = a(0) \end{cases} \tag{6.2}$$

In a particular case when the initial AIDS infection is considered zero then two systems of Equations (5.1) and (5.2) will be the SIR model.

The SIR model is a simple model, due to Kermack and McKendrick (see [2]), of an epidemic of an infectious disease in a large population [9].

According to SIR model, we need to redefine the total infection as the sum of the HIV and AIDS infections. That is $h(t) + a(t) = I(t)$ and the accumulated rate of contagion factor between healthy susceptible individuals and infected group is denoted by beta.

$S'(t) = -\beta I(t) \cdot S(t)$ for all non-negative t.

Axiom 3: Assume that the latency period, which is negligibly short, that is:

$L(t) = 0$ for all t.

Axiom 4: Assume that there is no removal from the population, that is the population of removed remains at zero. $r(t) = 0$ for all t.

Axiom 5: Assume that the initial population is $I(0) = I_0$.

9. Analytical Attempt to Find the Exact Solution

$$\begin{cases} \dfrac{\mathrm{d}s}{\mathrm{d}t} = -\alpha \cdot h(t)s(t) - \beta \cdot a(t)s(t) \\ \dfrac{\mathrm{d}h}{\mathrm{d}t} = \delta_1 \cdot h(t)s(t) + \delta_2 \cdot a(t)s(t) \\ \dfrac{\mathrm{d}a(t)}{\mathrm{d}t} = m \cdot s(t)h(t) + n \cdot s(t)a(t) \end{cases} \tag{6.3}$$

where $m = \alpha - \delta_1$ and $n = \beta - \delta_2$. Thus, systems (6.1) and (6.3) are equivalent.

Two subsets of the populations HIV infected, and AIDS infected in general have different rates of transmitting the disease. That is all parameters in (6.1) to (6.3) are not equal and the nonlinear systems can be solved by numerical approximation and demonstrate the general behavior of the system using the technology of computer algebra system (CAS) or spreadsheet.

But for simplicity in checking the validity of the model, we may assume that the susceptible group can be infected at equal rates by mixing with the subsets of the big population. That is, consider

$$\alpha = \beta, \delta_1 = \delta_2 \text{ and } m = n \tag{6.4}$$

We can add another condition: $h(t) + a(t) = I(t)$ to (6.4), then the system (6.3) will change to,

$$\begin{cases} \dfrac{\mathrm{d}s}{\mathrm{d}t} = -\beta\left[h(t)+a(t)\right]s(t) \\ \dfrac{\mathrm{d}h}{\mathrm{d}t} = \delta\left[h(t)+a(t)\right]s(t) \\ \dfrac{\mathrm{d}a(t)}{\mathrm{d}t} = m\cdot\left[h(t)+a(t)\right]s(t) \end{cases} \tag{6.5}$$

Or, equivalently

$$\begin{cases} \dfrac{\mathrm{d}s}{\mathrm{d}t} = -\beta\cdot I(t)\cdot s(t) \\ \dfrac{\mathrm{d}h}{\mathrm{d}t} = \delta\cdot I(t)\cdot s(t) \\ \dfrac{\mathrm{d}a(t)}{\mathrm{d}t} = m\cdot I(t)\cdot s(t) \end{cases} \tag{6.6}$$

Adding the second and the third equation in (6.6) we will get

$$\frac{\mathrm{d}I(t)}{\mathrm{d}t} = h'(t)+a'(t) = (\delta+m)I(t)s(t).$$

With no removal function, using $s(t) = P - I(t)$ and $k = (\delta + m)$, we can produce the following set of SIR differential equations that can be solved by separation of variables.

$$\frac{\mathrm{d}I(t)}{\mathrm{d}t} = M\cdot I(t)s(t) \quad \text{or} \quad \begin{cases} \dfrac{\mathrm{d}I(t)}{I(N-I)} = k\mathrm{d}t \\ I(t) = I(0) \end{cases} \tag{6.7}$$

The well-known solution of Equation (6.7) can be described by

$$I(t) = \frac{N\cdot I(0)}{I(0)+\left(N-I(0)\right)\cdot \mathrm{e}^{-Nkt}} = \frac{N}{1+\left(\dfrac{N}{I_0}-1\right)\cdot \mathrm{e}^{-Nkt}} \tag{6.8}$$

This result shows that the total HIV plus AIDS infection over the time interval [0, t] can be calculated (see [11] and [12]).

10. Mathematical Modeling of Simple (SIR = SHAR)

When a model has only the three stages of Susceptible, Infected, and Removed

subsets of the population, then a well-known differential equation model will be in the following from. With the assumption:

$R(t) = 0$, the differential equation of the epidemic will be

$$\begin{cases} \dfrac{\mathrm{d}S}{\mathrm{d}t} = -\beta S(t)\cdot I(t) \\ \dfrac{\mathrm{d}I}{\mathrm{d}t} = \beta S(t) I(t) \\ S(t) + I(t) = P \end{cases} \tag{7.1}$$

where, $I(0) = I_0$ and $S(0) = P - I_0$.

In our HIV-AIDS model one can use the Monte-Carlo method by the simple assumption

$$I(t) = h(t) + a(t) \tag{7.2}$$

After a substitution $S(t) = P - I(t)$ in the second equation of (7.1), we can solve a first order differential equation:

$$\frac{\mathrm{d}I}{\mathrm{d}t} = \beta I(t)\cdot\left(P - I(t)\right),\ \ I(0) = I_0 \tag{7.3}$$

using separation of variables.

The solution to this differential equation is in the following form:

$$I(t) = \frac{P\cdot I_0}{1 + \left(P - I_0\right)\mathrm{e}^{-\beta P t}} \tag{7.4}$$

This function can be rearranged to

$$I(t) = \frac{P\cdot I_0}{I_0 + \left(\dfrac{P}{I_0} - 1\right)\mathrm{e}^{-\beta P t}} \tag{7.5}$$

where the constant number B is defined, $B = \dfrac{P}{I_0} - 1$.

If we define M as a mixing factor and C a contagious factor, then we can assume the coefficient of proportionality will be: $\beta = MC/P$. Thus, the new version of (5.7) will be

$$I(t) = \frac{P\cdot I_0}{I_0 + B\mathrm{e}^{-MCt}} = \frac{P\left(h_0 + a_0\right)}{h_0 + a_0 + B\mathrm{e}^{-MCt}} \tag{7.6}$$

where, $I(t) = h(t) + a(t)$ (see [11] [13]).

11. Conclusions and Path to the Future

We presented HIV-AIDS model in this paper, which is described by nonlinear systems of differential equation of four unknowns. The data produced for prediction of the epidemics is justified in mathematical language. We used computer algebra MAPLE (CAS) and numerical computation of both continuous and discrete dynamical systems.

1) Further development is necessary to analyze the parameters for regularity

and stability of the system.

2) There is a similarity in the spread of the HIV epidemic and Corona Virus. This model can be used for COVID-19 pandemic.

3) Developing Monte Carlo simulation for SHAR model was presented in this article. Here is an introduction to applying a computer simulation for HIV-Aids epidemics.

We would like to show how the Monte Carlo simulations can be used to conduct experiments. This extremely valuable application of Monte Carlo Simulation will be illustrated for epidemics caused by HIV-AIDS virus.

In the simulation we assume the following:

1) A disease strikes a community (city, state, or country) with a population P.

2) The disease is of sufficiently long duration so that no cures occur during the time-period studied.

3) A person is infected by HIV virus and is immediately contagious for the duration of the epidemic.

4) If a sick person and a susceptible person come into contact, then there is a 100 * C percent chance that the susceptible person will become infected (We call C the contagion factor for the epidemic).

5) Each susceptible person makes M contacts per day with other persons (not necessarily all distinct) chosen randomly from the population (M is the mixing factor).

6) The epidemic begins with one sick person (randomly chosen), and we study the spread of disease for T days.

Input: the input will be the following parameters.

P—population on the city or community;

C—contagion factor of the HIV-AIDS virus;

M—average mixing factor of individual;

I—initial number of infected people;

T—The time-period of study.

Output: The number of people infected each day to see the spread of the disease in the community.

The computer uses a random number generator to pick a number using.

RANDOMIZE to generate different random numbers at different times.

RND represent a particular random number.

INT(10 RND) to generate random positive integer 1, 2, 3, …, 9.

INT(P * RND) + 1 generates one of the integers 1, 2, 3, …, p, that is, the "name" of some person in the population.

Using the model in this paper can be helpful to implement a project for Monte Carlo Simulation leading to the following stages:

1) Write a computer program to run N times and calculate the mean and standard deviation of the output.

2) a) Rewrite the program to calculate the output of the epidemic using the exact solution to the differential equation.

$$I(t)=\frac{P}{1+B\mathrm{e}^{-MCt}},\ P(t_0)=P_0,\ I(t_0)=I_0$$

The solution to the differential equation is where $B=\frac{P_0}{I_0}-1$.

b) Modify the basic program so that in addition to printing D and S each day, the program also prints the number of sick persons predicted by the differential equation model.

c) Run the program with $P=1000$, $C=0.1$, $M=5$, $I=10$, $T=15$.

d) Plot both points from the computer simulation and the points determined by the differential equation model (for further study see [14] [15]).

Conflicts of Interest

The author declares no conflicts of interest regarding the publication of this paper.

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