Mathematical Modeling of the HIV-AIDS Epidemic

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Abstract

A simple subset of an epidemic population model for HIV-AIDS can be split into the following: Susceptible, HIV-Infected, AIDS-infected, and Removed subsets (SHAR). We consider that the rate at which susceptible people become infected is proportional to the number of encounters between susceptible and infected individuals, which is proportional to the product of the two populations. A non-linear model is developed and its solution is produced with an Excel numerical approach using difference equations. Some solutions also are produced using MAPLE (CAS). Further research analysis, refining the model and qualitative analysis is the goal of this research.

Subject Areas

Mathematical Analysis

Keywords

Epidemics, Susceptible, HIV Infected, AIDS Infected, Removed and Cured Continuous Dynamical Systems, Discrete Dynamical Systems

1. Introduction and History

HIV Cause:

Human Immunodeficiency Virus is a virus that attacks the immune system of humans. It will develop into AIDS, or Acquired Immune Deficiency Syndrome. There is not cure for HIV-AIDS disease yet, but it is possible to control the virus with medication and avoid its spread.

Where the HIV-AIDS virus came from: HIV-AIDS virus has its origins in African monkeys and apes, HIV started as a disease affecting them. Later, the virus changed and was able to infect humans. A 2014 study suggests that the disease crossed over to humans more than a century ago, became endemic in 1920s Congo, and then traveled to Haiti in the 1960s and to the United States

later. The disease became widespread in the West in the 1980s (see [1] [2] [3]).

White blood cells are our body's protection against any infection including HIV virus. This virus invades a certain kind of white blood cell, the CD4-positive T cell, and creates damages on the cell. The virus then makes copies of itself and spreads throughout the host body, infecting more T cells. Over time, healthy T cells go into decline while HIV-infected cells increase and weaken the immune system and evolve to AIDS.

A mathematical model for HIV infection had begun to be developed in the late 1980 using SIS and SIR models. These models have since been used to describe many other human virus infections, such as Hepatitis B and C, influenza, etc. [4]. Recently a mathematical model is proposed for the dynamics of HIV/AIDS with incorporation of weak CD4$^+$T cells in which assumed in several categories: uninfected CD4$^+$T cells, infected CD4$^+$T cells, and virus [5].

Before we attempt to model the HIV-AIDS Epidemic, it is natural for us to first gain some insight as to what we are going to be studying. Let us first look at where the disease came 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 HIV) 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. HIV stands for Human Immuno-Deficiency Virus. Unlike some other viruses, the human body cannot 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 T-cells that the body cannot fight off infections and disease. If HIV goes left untreated, it can lead to a more severe disease known as AIDS. AIDS stands for Acquired Immuno-Deficiency Syndrome. AIDS is the final stage of the HIV infection, and not everyone has HIV advances to this stage. AIDS is the stage of infection that the immune system, as the result of so much damage, causes the body to become vulnerable to opportunistic infections. When the number of your CD4 cells falls below 200 cells per cubic millimeter of blood (200 cells/cubic mm), the body has AIDS. People with AIDS need medical treatment to prevent death (see [6] [7]).

2. The Statement of the Problem

HIV and AIDS have been around for about 100 years, far longer than scientists have expected. People who do not have any of these two terminal diseases are very susceptible if they have contact with an HIV infected person. While it is not difficult to produce differential equations that are adequate to model this epidemic, as some exist already, it is always beneficial to add new perspectives and

ideas on this epidemic. However, upon further exploration of this epidemic, we find that there exists no graphical representation of these two diseases. In this research, we will attempt to model the prevalence of contracting HIV or contracting AIDS over time. In this paper, we will show the representations of three separate experiments using Microsoft Excel and two separate experiments using Maple (CAS); after this research is represented, we will then show you one more experiment using Excel and three more using Maple, but in these particular experiments we will institute a new variable, a cure. The purpose of these representations is to try to predict the spread of the disease over a given period.

3. Terms

We are going to use specific letters to label our subsets of the population. In this paper, we shall use:

S: Susceptible, those people who are currently unaffected by either virus but may become infected.

H: HIV Infected, those people infected with the HIV virus.

A: AIDS Infected, those people infected with the AIDS virus.

R: Removed, those people isolated, cured, or permanently immune to the HIV and AIDS virus.

4. Assumptions

Before we start representing our data using different experiments, we must first institute postulates so our research and data has a particular framework to follow.

Assumption 1: We have a closed population, which means that no one enters, no one leaves, no one is born, and no one dies; so basically, the people that the population starts with are the exact same people that the population ends with.

Postulate 2: There is a positive integer P such that:

$$s(t) + h(t) + a(t) + r(t) = P \text{, for all } t$$

Assumption 3: No one is permanently immune to the disease, and once a person has contracted HIV or AIDS, they can no longer be cured. The removal rate is so small that we can assume that $r(t) = 0$ which gives us the following:

$$s(t) + h(t) + a(t) = P \tag{3.1}$$

Assumption 4: The rate of change of the susceptible population is negatively proportional to the rate of contact between the susceptible population with the HIV infected population, minus the rate of contact between the susceptible population, and AIDS infected population giving us the following equation:

$$\frac{ds}{dt} = -\frac{dh(t)}{dt} - \frac{da(t)}{dt} = -\alpha h(t) \cdot s(t) - \beta a(t) \cdot s(t) \tag{4.1}$$

where the constant β is the AIDS infection rate and the constant α is the HIV infection rate. Notice that $s'(t)$ is always negative (or possibly zero), since the number of people who have not yet caught the disease can only decrease with

5. Computation of HIV and AIDS Epidemics

Assumption 5: The rate of change of those infected with the HIV virus is proportional to the rate of contact between the HIV infected population and the AIDS infected population with those susceptible to the disease, which gives us the following equation:

$$\frac{\mathrm{d}s}{\mathrm{d}t} = s'(t) = -\alpha h(t) \cdot s(t) - \beta a(t) \cdot s(t) \tag{5.1}$$

and

$$\frac{\mathrm{d}h}{\mathrm{d}t} = h'(t) = \delta_1 \cdot h(t) \cdot s(t) + \delta_2 \cdot a(t) \cdot s(t) = \left[\delta_1 \cdot h(t) + \delta_2 \cdot a(t)\right] \cdot s(t) \tag{5.2}$$

where the constant δ is the constant infection rate of HIV for $\mathrm{d}h/\mathrm{d}t$. Notice that $h'(t)$ always increases since the number of people who have the HIV virus will increase as those infected with the HIV virus and those infected with the AIDS virus interact with the susceptible population.

Now, as we scrutinize the previous axioms we can conclude that the rate of change of the AIDS population is negatively proportional to the rate of change of the susceptible population minus the rate of change of the HIV infected population, which gives us the following equation:

$$\begin{aligned}
\frac{\mathrm{d}a}{\mathrm{d}t} &= -\frac{\mathrm{d}s}{\mathrm{d}t} - \frac{\mathrm{d}h}{\mathrm{d}t} \\
&= -\left[-\beta a(t) \cdot s(t) - \alpha h(t) \cdot s(t)\right] - \delta_1 h(t) \cdot s(t) - \delta_2 a(t) \cdot s(t) \\
&= h(t) \cdot s(t)\left[\alpha - \delta_1\right] + a(t) \cdot s(t)\left[\beta - \delta_2\right]
\end{aligned} \tag{5.3}$$

6. Developing the System of Nonlinear Model

If we assume that the epidemic started in a community with P people with a positive number of HIV infected people and a positive number of AIDS infected people with $s_0 = P - a_0 - h_0$ susceptible, then we can produce the following system of differential equations by utilizing Equations (5.1), (5.2), and (5.3):

However, in order to produce a table and a graph that can approximate the prevalence and graph that can approximate the prevalence and outbreak of the epidemics over time we must first create a system of discrete difference equations from the continuous systems of differential Equation (6.1).

$$\begin{cases}
\dfrac{\mathrm{d}s}{\mathrm{d}t} = -\alpha \cdot h(t)s(t) - \beta \cdot a(t)s(t) = -\langle s(t), s(t)\rangle \cdot \langle \alpha \cdot h(t), \beta \cdot a(t)\rangle \\[2mm]
\dfrac{\mathrm{d}h}{\mathrm{d}t} = \delta_1 \cdot h(t)s(t) + \delta_2 \cdot a(t)s(t) = \langle s(t), s(t)\rangle \cdot \langle \delta_1 \cdot h(t), \delta_2 \cdot a(t)\rangle \\[2mm]
\dfrac{\mathrm{d}a(t)}{\mathrm{d}t} = m \cdot s(t)h(t) + n \cdot s(t)a(t) = \langle s(t), s(t)\rangle \cdot \langle m \cdot h(t), n \cdot a(t)\rangle
\end{cases} \tag{6.1}$$

where $m = \alpha - \delta_1$ and $n = \beta - \delta_2$. In a special case when two contagious factors delta are the same the system (6.1) will be

$$\begin{cases} \dfrac{\mathrm{d}s}{\mathrm{d}t} = -\alpha \cdot h(t)s(t) - \beta \cdot a(t)s(t) \\ \dfrac{\mathrm{d}h}{\mathrm{d}t} = \delta \left[h(t) + a(t) \right]s(t) \\ \dfrac{\mathrm{d}a(t)}{\mathrm{d}t} = m \cdot s(t)h(t) + n \cdot s(t)a(t) \end{cases} \tag{6.2}$$

Let us assume that the initial conditions are given at time $t = 0$,

$$s(0) = s_0,\ h(0) = h_0,\ r(0) = r_0\ \text{and}\ s(0) = a_0 \tag{6.3}$$

There will be many different approaches to use this differential equations model. We will use a numerical computation approach to observe the behavior of the solution to this nonlinear system.

In addition to analytical analysis, we may use the computer algebra and programming methodology to simulate the model parameters.

7. Discrete Form of HIV-AIDS Model

To study the outbreak of the HIV-AIDS epidemic over time, we must first create a system of discrete difference equations from the continuous system of differential equations shown above.

At the partition points on the t axis for $j = 1, 2, 3, \cdots$, the discrete difference equations are as follows:

$$\begin{cases} s[j] = -s[j-1] - \alpha h[j-1] \cdot s[j-1] - \beta a[j-1] \cdot s[j-1] \\ h[j] = h[j-1] + \delta \left(h[j-1] + a[j-1] \right) \cdot s[j-1] \\ a[j] = a[j-1] + s[j-1] \cdot h[j-1](\alpha - \delta) + a[j-1]s[j-1](\beta - \delta) \end{cases} \tag{7.1}$$

In the following experiment, we will use the spreadsheet computation method to show some numerical solution to the system. The system (7.1) can be solved by the method of discrete approximation, using the four initial conditions given in (6.3) and six other parameters involved in this model.

7.1. Initial Conditions

In our research, we conducted three separate experiments utilizing Microsoft Excel. Each experiment has its own parameters that are unique to that particular experiment. However, each experiment using Excel will have the same following initial conditions:

$N = 25000$ people, $s(0) = s_0 = 24650$ people, $h(0) = h_0 = 250$ people, $a(0) = s_0 = 100$ people, $r(0) = r_0 = 0$ people, and $s(t) + h(t) + a(t) = P$ for all $t \geq 0$.

7.2. Parameters for Excel Experiment (1)

Assume that $\alpha = 0.000012$, this means 12 out of every 100 thousand people with no disease may contract HIV. Let $\beta = 0.00000003$. This means 3 out of every 100 million people with no disease contract AIDS. Also assume $\delta = 0.000005$. This means the constant rate of infection for HIV is 5 out of every 1 million people.

7.3. Interpretation of the First Observation

In this special experiment, we notice, with the parameters we used, that the susceptible population, $s(t)$, decreases over the 20-unit time-period. We can see from Table 1 that the susceptible population starts at 24,650 people and decreases

Table 1. This is a discrete computation for $S(t)$, $H(t)$, and $A(t)$.

n	S(n)	H(n)	A(n)	S(n+1)	H(n+1)	A(n+1)
0	24,650	250	100	23,910	293	131
1	23,910	293	131	23,069	344	164
2	23,069	344	164	22,117	402	201
3	22,117	402	201	21,049	469	241
4	21,049	469	241	19,864	544	285
5	19,864	544	285	18,567	626	333
6	18,567	626	333	17,171	715	383
7	17,171	715	383	15,697	810	437
8	15,697	810	437	14,172	907	492
9	14,172	907	492	12,628	1007	547
10	12,628	1007	547	11,103	1105	602
11	11,103	1105	602	9631	1199	654
12	9631	1199	654	8244	1289	704
13	8244	1289	704	6969	1371	749
14	6969	1371	749	5823	1445	790
15	5823	1445	790	4813	1510	826
16	4813	1510	826	3941	1566	857
17	3941	1566	857	3200	1614	884
18	3200	1614	884	2580	1654	906
19	2580	1654	906	2068	1687	924
20	2068	1687	924	1650	1714	939
21	1650	1714	939	1310	1736	951
22	1310	1736	951	1037	1753	961
23	1037	1753	961	819	1767	969
24	819	1767	969	645	1778	975
25	645	1778	975	508	1787	980
26	508	1787	980	399	1794	984
27	399	1794	984	313	1800	987
28	313	1800	987	245	1804	989
29	245	1804	989	192	1808	991
30	192	1808	991	150	1810	992
31	150	1810	992	118	1813	994
32	118	1813	994	92	1814	995
33	92	1814	995	72	1815	995
34	72	1815	995	56	1816	996
35	56	1816	996	44	1817	996
36	44	1817	996	34	1818	997
37	34	1818	997	27	1818	997
38	27	1818	997	21	1819	997
39	21	1819	997	16	1819	997
40	16	1819	997	13	1819	997

Table 1: Selected parameters-alpha = 0.000012, beta = 0.00000003, delta = 0.000005, N = 25,000. Figure 1: S(0) = 24,650, H(0) = 250, A(0) = 100, R(0) = 0.

to about 16,074 people over the 20-year span. If we look at the HIV infected population, $h(t)$, in **Figure 1** we notice that the population increases to slightly above 5000 people. Looking back at **Table 1** we notice that the HIV Infected population increases from 250 people to about 5759 people over the 20-year span. If we take a moment to look at the AIDS Infected population, $a(t)$, in **Figure 1**, we will notice that the AIDS-Infected population increased but seems to increase at about half the rate as the HIV Infected population. In **Table 1**, we see that the AIDS population increases from 100 people to about 3168 people. From the given parameters that we used in this first experiment on Microsoft Excel, we can see that this special epidemic spread over the 20-unit time period, but it did not completely exterminate the population. Since we assumed that there would be no cure in this special experiment, we can conclude that, if we extended the time-period, the susceptible population would eventually converge to 0 as the HIV and AIDS infected population converge to their maximums (see [9] [10]).

7.4. Parameters for Excel Experiment (2)

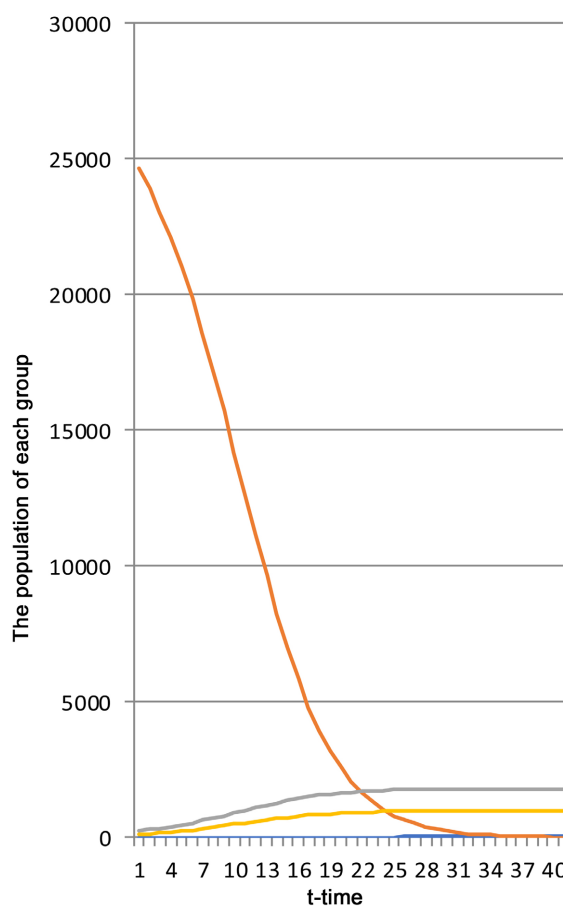Assume that $\alpha = 0.00002$. This means that 2 out of every 100 thousand people

Figure 1. Graph of $S(t)$-Susceptible blue, $H(t)$-HIV Red, and $A(t)$-Aids Green.

with no disease contract HIV. Let $\beta = 0.00000005$. This means 5 out of every 100 million people with no disease contract AIDS. Also assume $\delta = 0.0000085$. This means the constant rate of infection for HIV is 85 out of every 1 million people.

7.5. Observation of the Computation for the Experiment (2)

In this particular experiment, we notice, with the parameters we used, that the susceptible population, $s(t)$, decreases very dramatically over the 20-time period. We can see from Table 2 that the susceptible population decreases radically over

Table 2. Susceptible. HIV-Aids population.

n	S(n)	H(n)	A(n)	S(n+1)	H(n+1)	A(n+1)		
0	24,650	250	100	24,527	332	150	alfa	0.00002
1	24,527	332	150	24,364	444	213	beta	0.00000005
2	24,364	444	213	24,147	597	293	delta	0.0000085
3	24,147	597	293	23,858	801	399	n	0.00025
4	23,858	801	399	23,476	1073	538	m1	0.00004
5	23,476	1073	538	22,971	1433	721	m2	0.00002
6	22,971	1433	721	22,312	1903	960		
7	22,312	1903	960	21,462	2511	1267		
8	21,462	2511	1267	20,383	3281	1657		
9	20,383	3281	1657	19,043	4238	2141		
10	19,043	4238	2141	17,427	5393	2724		
11	17,427	5393	2724	15,545	6738	3404		
12	15,545	6738	3404	13,448	8237	4162		
13	13,448	8237	4162	11,229	9822	4962		
14	11,229	9822	4962	9021	11,400	5760		
15	9021	11,400	5760	6961	12,872	6504		
16	6961	12,872	6504	5167	14,154	7151		
17	5167	14,154	7151	3702	15,201	7680		
18	3702	15,201	7680	2575	16,006	8087		
19	2575	16,006	8087	1750	16,596	8385		
20	1750	16,596	8385	1168	17,012	8595		
21	1168	17,012	8595	770	17,296	8739		
22	770	17,296	8739	504	17,487	8835		
23	504	17,487	8835	327	17,613	8899		
24	327	17,613	8899	212	17,695	8941		
25	212	17,695	8941	137	17,749	8968		
26	137	17,749	8968	88	17,784	8985		
27	88	17,784	8985	57	17,806	8997		

Table 2: This is a model for HIV-AIDS with no vaccination or removed subset of the population: $r(t) = 0$.

the given time period and drops well below 5000 people. If we look at **Figure 2**, we can see that the susceptible population starts at 24,650 people and decreases to about 2977 people over the 20-year span. If we take a look over at the HIV infected population, $h(t)$, in **Figure 2** we notice that the population increases substantially, near 15,000 over the 20-year span. Looking back at **Figure 2** we notice that the HIV Infected population increases from 250 people to about 14,348 people over the 20-year span. If we take a look at the AIDS Infected population, $a(t)$, in **Figure 2**, we notice that the AIDS Infected population also increased a great deal, just as the HIV Infected population did, but we can still notice that the HIV population increased a lot more than the AIDS population. If we look at **Figure 2**, we see that the AIDS population increases from 100 people to about 7675 people. From the given parameters we used in this second experiment on Microsoft Excel, we can see that this particular epidemic spread very quickly over 20 years, and it seems to put a big dent in the susceptible population, dropping it to under 5000 people. Since, as before, we assumed that there would be no cure in this particular experiment, we can conclude that, if we extended the time period, the susceptible population would probably decrease to zero within the next few years, and the HIV and AIDS population would reach their maximums rather quickly.
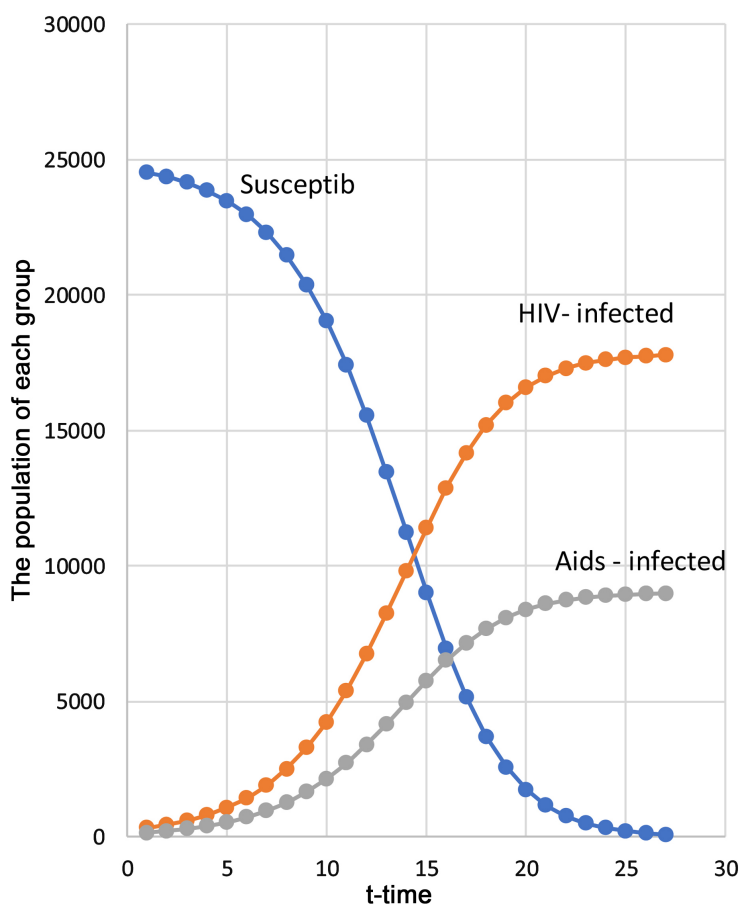

Figure 2. Portrait of susceptible, HIV, and Aids infection.

7.6. Analytical Attempt to Find the Exact Solution

In the following nonlinear model, we consider distinct parameters coefficients and demonstrate that all other known models, then we will study some of the special cases of this general form.

$$\begin{cases} \dfrac{\mathrm{d}s}{\mathrm{d}t} = -\alpha \cdot h(t)s(t) - \beta \cdot a(t)s(t) \\[2mm] \dfrac{\mathrm{d}h}{\mathrm{d}t} = \delta_1 \cdot h(t)s(t) + \delta_2 \cdot a(t)s(t) \\[2mm] \dfrac{\mathrm{d}a(t)}{\mathrm{d}t} = m \cdot s(t)h(t) + n \cdot s(t)a(t) \end{cases} \tag{7.3}$$

Note that $m = \alpha - \delta_1$ and $n = \beta - \delta_2$. The system (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.

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

$$\alpha = \beta, \ \delta_1 = \delta_2 \ \text{and} \ m = n \tag{7.4}$$

We can add another condition: $h(t) + a(t) = I(t)$, to (6.4) then, the system (7.3) will change,

$$\begin{cases} \dfrac{\mathrm{d}s}{\mathrm{d}t} = -\beta \big[h(t) + a(t) \big] s(t) \\[2mm] \dfrac{\mathrm{d}h}{\mathrm{d}t} = \delta \big[h(t) + a(t) \big] s(t) \\[2mm] \dfrac{\mathrm{d}a(t)}{\mathrm{d}t} = m \cdot \big[h(t) + a(t) \big] s(t) \end{cases} \tag{7.5}$$

Or, equivalently

$$\begin{cases} \dfrac{\mathrm{d}s}{\mathrm{d}t} = -\beta \cdot I(t) \cdot s(t) \\[2mm] \dfrac{\mathrm{d}h}{\mathrm{d}t} = \delta \cdot I(t) \cdot s(t) \\[2mm] \dfrac{\mathrm{d}a(t)}{\mathrm{d}t} = m \cdot I(t) \cdot s(t) \end{cases} \tag{7.6}$$

Adding the second and the third equation in (7.6) 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 $s(t) = N - I(t)$ and $k = \delta + m$, we can produce the following SIR differential equations that can be solved by separation of variables.

$$\frac{dI(t)}{dt} = M \cdot I(t)s(t) \ \text{ or } \ \begin{cases} \dfrac{dI(t)}{I(N-I)} = k dt \\ I(t) = I(0) \end{cases} \tag{7.7}$$

The well-known solution of Equation (6.7) is

$$I(t) = \frac{N \cdot I(0)}{I(0) + (N - I(0)) \cdot e^{-Nkt}} = \frac{N}{1 + \left(\dfrac{N}{I_0} N - 1\right) \cdot e^{-Nkt}} \tag{7.8}$$

This result shows that the total HIV plus AIDS infection over the time interval $[0, t]$ can be calculated.

8. Maple Computation for Epidemic Experiment (1)

Now we want to represent the same data using different parameters and a different software. For this, we utilized Maple Software (CAS). Maple is a computer algebra system, is a symbolic and numeric computing environment as well as a multi-paradigm programming language.

The nonlinear model (6.2) is constructed based on the assumption that the subpopulation of AIDS infected individuals is coming from the interactions between susceptible and HIV, not directly from HIV. To refine this model, we can assume:

Assumption 6: During the time-period of this study, we are assuming a certain constant proportion p of the HIV infected individual will develop AIDS.

$$\begin{cases} \dfrac{ds}{dt} = -\alpha \cdot h(t)s(t) - \beta \cdot a(t)s(t) \\ \dfrac{dh}{dt} = \delta \big[h(t) + a(t) \big] s(t) \\ \dfrac{da(t)}{dt} = (\alpha - \delta) \cdot s(t)h(t) + (\beta - \delta) \cdot s(t)a(t) + p \cdot h(t) \end{cases} \tag{8.1}$$

Notice that in the Maple code (**Figure 3**), we replaced all Greek letters in this system by k, l, m, and n for convenience.

8.1. Results (Maple Experiment 1)

Maple Software has its own spreadsheet, but it is more convenient to create a table like the one produced on Microsoft Excel and Maple can produce much more interesting graphical results. If we look above at the coding for the software,

```
>restart:
>with(plots):
> eq1 := diff(s(t),t) = -k*h(t)*s(t)-l*a(t)*s(t):
> eq2 := diff(h(t),t) =n*s(t)*a(t) +m*s(t)*h(t):
> eq3 := diff(a(t),t) = (l-n)*s(t)*a(t)+(k-m)*(s(t)*h(t))+p*h(t):
> s0 := 1000: h0:=1: a0:=0:
> soln1 := dsolve(eval({eq1, eq2, eq3, s(0)=s0, h(0)=h0, a(0)=a0},
{k=.0008, l=0.00007, m=.0002,n=.0025,p=.0004}), {s(t), h(t), a(t)},
numeric);
```

Figure 3. This is the updated code for Maple, you can see the three same equations, along with slightly modified initial conditions and new parameters for the rates of change.

we notice that the parameters are not Greek letters, but instead, are English letters. The reason for this is that it is easier to input English letters into the software rather than inputting Greek letters to represent the rates of change. However, this does not mean that the graphs are wrong. If we take a moment to look at **Figure 4(a)**, we can see that the susceptible population dramatically decreases to 0 extremely quickly. Within 20 years, the susceptible population diminishes to zero. If we look at **Figure 4(b)**, we can see that the HIV Infected population, which only started with one person, converged to its peak very quickly and then plateaued once it reached its maximum value. Just as with the susceptible population, the HIV Infected population peaked in about a 20-year span of time. If we move over to **Figure 4(c)** we notice that the AIDS Infected population also increased very rapidly in the first 20 years. However, unlike the susceptible and HIV population, the AIDS population does not seem to plateau after the first 20 years of time. If we look closely at the graphs, we can see that after the first two decades of time, the AIDS population still increased by about 20 people over the next 80 years of time. This could be a result of some people form the HIV infected population not taking care of themselves, which allows their number of T-cells to drop drastically causing them to succumb to the AIDS virus (see [10] [11]).

8.2. Maple (Experiment 2)

We knew that showing this epidemic only one time with the Maple software was not going to be adequate, so we restarted the Maple code and repeated the experiment using slightly modified initial conditions that you will notice in the updated code below. Also, just as we did with the Microsoft Excel experiments, we utilized new parameters for the rates of change within each separate equation.

The nonlinear model (6.2) it was constructed based on the assumption that the subpopulation of AIDS infected individuals is quarantined, and there is no
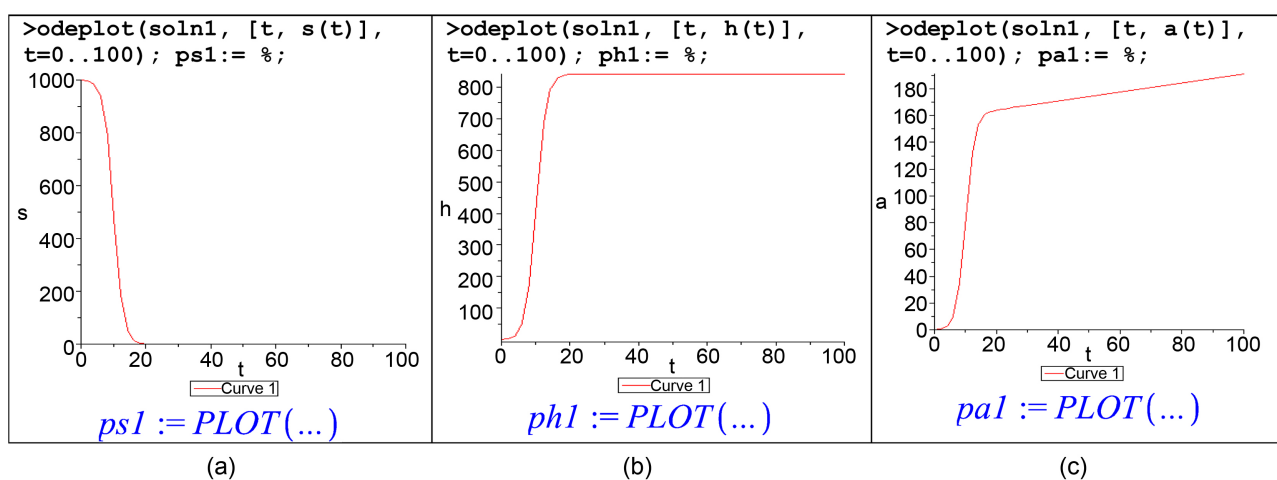

Figure 4. This is the code for Maple, you can see the three equations, along with initial conditions and parameters for the rates of change. (a) With this rate of fast virus transmission the susceptible population $s(t)$ tends to zero. (b) The HIV epidemic converging to the highest level. (c) This graph shows that the AIDS population increasing fast.

interaction between susceptible and AIDs infected individuals.

To refine this model, we can assume:

Assumption 6: During the time-period of this study, we are assuming that a certain constant proportion p of the HIV infected individuals will develop AIDS.

Let us run the MAPLE code with different initial conditions and different values of parameters (**Figure 5**).

8.3. Results for Maple Experiment (2)

The new parameters and initial conditions produced the graphs shown above. If we take a moment to look at **Figure 6(a)**, we can see the susceptible population dramatically decrease to 0 over a long period of time. Within 200 years, the susceptible population completely vanishes. Just as in experiment 1, the susceptible population goes to 0, but this time it took 200 years, not 20. If we look at **Figure 6(b)**, we can see that the HIV Infected population, which only started with 1 person, shows little to no change at first, then it rapidly increases dramatically after about 75 years of dormancy. If we look closer at the susceptible population

```
>restart:
>with(plots):
> eq1 := diff(s(t),t) = -k*h(t)*s(t)-l*a(t)*s(t):
> eq2 := diff(h(t),t) =n*s(t)*a(t) +m*s(t)*h(t):
> eq3 := diff(a(t),t) = (l-n)*s(t)*a(t)+(k-m)*(s(t)*h(t))+p*h(t):
> s0 := 10000: h0:=1: a0:=0:
> soln2 := dsolve(eval({eq1, eq2, eq3, s(0)=s0, h(0)=h0, a(0)=a0},
{k=.0008, l=0.00007, m=.0002,n=.0025,p=.0004}), {s(t), h(t), a(t)},
numeric);
```

Figure 5. This is the updated code for Maple, you can see the same three equations, along with slightly modified initial conditions and new parameters for the rates of change.
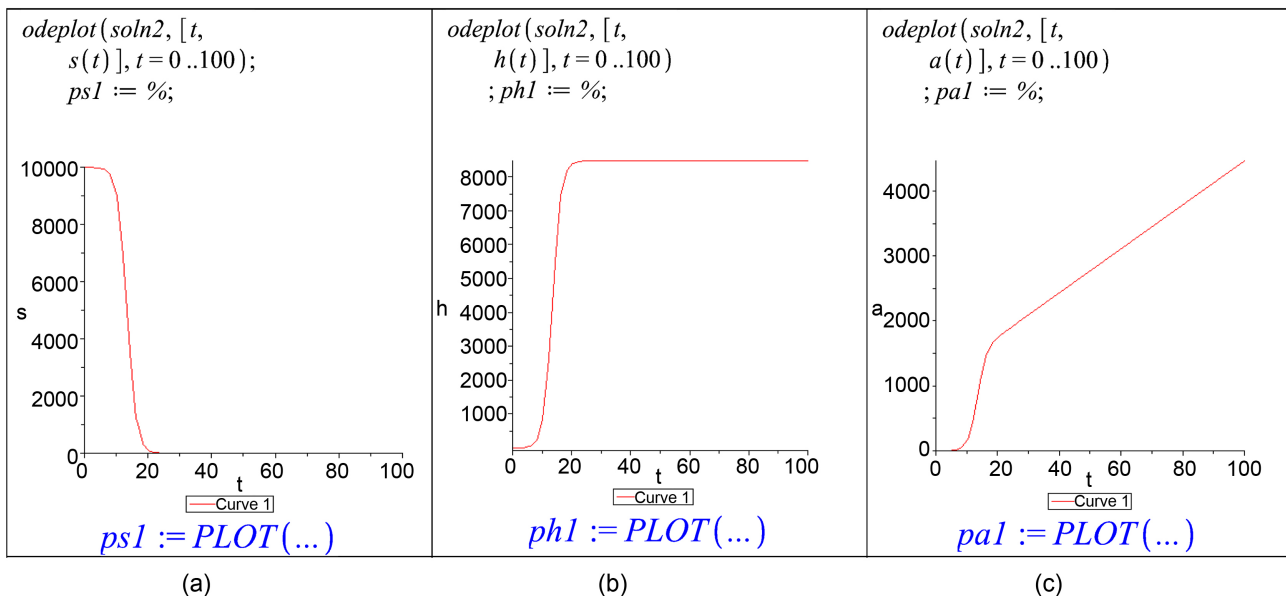

Figure 6. This is the updated code for Maple, you can see the three same equations, along with slightly modified initial conditions and new parameters for the rates of change. (a) With the new parameters the susceptible population still decreases rapidly over time. (b) The HIV population show little change at first, then rapidly increases after 75 years. (c) The AIDS population increases rapidly and converges at its peak.

and the HIV population, we notice that their graphs almost look like reflections of each other. If we move over to Figure 6(c) we notice that the AIDS Infected population also increased very rapidly but only after about 150 years. As we can see upon further inspection of Figure 6(c), we notice that the AIDS population increases very rapidly and converges to its maximum very quickly. It is safe to say that our parameters are far from perfect, and it is quite difficult to produce rates of change that go hand in hand with those produced by Mother Nature. Upon scrutinizing and analyzing our data, we visualize where our experiment can be modified and greatly improved. Further improvement of the maple code is the goal.

9. Conclusions

It is very important to present a mathematical description of a natural phenomenon like HIV/AIDS epidemic.

We postulated all related assumptions and defined all parameters involved. The mathematical model presented in this investigation is a nonlinear ODE (ordinary differential equation). To solve a nonlinear system of ODE, one can choose either 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. A simple subset of the epidemic population model for HIV-AIDS is: Susceptible, HIV-Infected, AIDS-infected, and Removed subsets that we used $S(t)$, $H(t)$, $A(t)$, and $R(t)$.

Our numerical and graphical approaches demonstrate that with some certain conditions or choices of parameters, one HIV infected individual can transmit the virus to the entire susceptible population and can infect the entire population.

We did not consider the vaccination factor for modeling this epidemic model in the first few experiments. 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 (see reference [12]).

Once we added the removed population, we can see that it can play a role in determining the outcome of each unique, separate population that we focused on.

As we sit down and analyze our experiments and our results, we can conclude that an epidemic such as this one can play out in a few different ways. This why we reproduced several different scenarios including one where there is a cure and one where there is not. We know that some of our parameters are not exact, but the point of this research was to show several different possibilities. The end goal of our research is to improve the Maple code and produce more accurate results.

Conflicts of Interest

The authors declare no conflicts of interest.

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