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A Simulation of an Sir Mathematical Model of HIV Transmission Dynamics Using the Classical Euler's Method.

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Abstract:

In this paper we establish a numerical solution to the classical SIR mathematical model of HIV transmission dynamics using the traditional Euler's method. We will discuss the mathematics behind the model and various tools for judging effectiveness of policies and control methods. We will complete the paper with a computer simulation of the model equations using the model parameters. From the result, the epidemic can be controlled within a finite time.

Introduction:

One of the most basic procedures in the modeling of diseases is to use a compartmental model, in which the population is divided into different groups. The SIR Model is used in epidemiology to compute the amount of susceptible, infected, and removed/recovered people in a population. It is also used to explain the change in the number of people needing medical attention during an epidemic. It is important to note that this model does not work with all diseases. For the classical SIR HIV model to be appropriate, once a person has been infected with the disease, they would remain infected and later die of disease of or off natural death. This is true because presently there is no known medical cure for HIV. The so called Antiretroviral

Drugs (ARD) only burst the immune systems of the infected paper against secondary infections. Though, the ARD slow the sero-conversion period because they produce T-cells which are the inducer/helper cells and this increases the CD4+ counts.

1.1. Assumptions

The SIR Model is used in epidemiology to compute the amount of susceptible, infected, removed people in a population. This model is an appropriate one to use under the following assumptions [5]:

1) The population is fixed.

2) The only way a person can leave the susceptible group is to become infected.

The only way a person can leave the infected group is to be placed under Antiretroviral Therapy (ART).

3) Age, sex, social status, and race do not affect the probability of being infected.

4) There is no inherited immunity.

5) The member of the population mix homogeneously (have the same interactions with one another to the same degree).

2.1. SIR Formulas

The model starts with some basic notations:

S(t) is the number of susceptible individuals at time t

I(t) s the number of infected individuals at time t

R(t) is the number of removed individuals at time t

N is the total population size.

The assumptions lead us to a set of differential equations.

$$\frac{dS}{dt} = -\beta S(t) I(t) \quad (1)$$

$$\frac{dI}{dt} = (\beta S(t) - k) I(t) \quad (2)$$

$$\frac{dR}{dt} = kI(t) \quad (3)$$

where k is the removed rate (with greater or equal to zero), α is the probability of becoming infected, λ is the number of people infected person comes in contact with in each period of time on average, β is the average number of transmissions from an infected person in a time period (with β greater or equal to zero), and

$$N(t) = S(t)+I(t)+R(t) \quad (4)$$

From these equations [1,5], we can discover how the different groups will act as $t \to \infty$

We can see from equation (1), that the susceptible group will decrease over time and approach zero. From equation (3), we know that the removed group increase and will approach N over time. How the infected group behaves is more complicated. We start by taking the integral of equations (3) from 0 to t, which gives us

$$\int_0^t \frac{dR}{dt} dt = k \int_0^t I(t) dt R(t)$$

$$R(t) = k \int_0^t I(t) dt \quad (5)$$

We then manipulate equation (4) to get

R(t)=N(t)-S(t)-I(t)
(6)

By combining equations (5) and (6) we get

$$k\int_0^t I(t)dt = R(t) = N(t) - S(t) - I(t)$$
(7)

When we take the integral from zero to infinity of right hand side i.e. $k\int_0^t I(t)dt$, that this integral is less than infinity, since the amount of people in a group must be finite. By combining this integral with equation (7), we get that as t goes to infinity

$$I(t) \to N(t) - S(\infty) - k\int_0^\infty I(s)ds$$

Since S(∞) goes to zero, and $k\int_0^t I(t)dt$, which is equal to R(∞) , goes to zero. Thus as t goes to infinity I(t)→0 as given by [5].

The rate of change of the infected group is not always negative or zero as it is in the susceptible group, nor is strictly positive or zero like the removed group. Whether the rate of change is positive or negative depends on k and S(t). We can see from equation (2) when βS(t) is less than k then the rate of change for the infected group is negative. If βS(t) is greater than k then the rate of change for the infected group is positive. Finally, if βS(t) is equal to k, then the rate of change for the infected group is zero.

By applying Euler's method of systems, we can solve the differential equations. The solutions to the differential equations are:

$$S_{n+1} = S_n - \beta S_n I_n \Delta t \quad (8)$$
$$I_{n+1} = I_n(1 + \beta S_n - k)\Delta t \quad (9)$$
$$R_{n+1} = R_n + kI_n\Delta t \quad (10), \qquad \Delta t = 1$$

where , Sn+1, In+1 and Rn+1 are the number of susceptible, infected and removed people at time (n+1). Δt is a small change in time or time steps, and will be equal to one from now on.[6] It is important to note, that researchers and health officials first collect data on who is in what group at a given period of time. The amount of people in a group does not come from equations (8), (9), and (10). These equations are primarily used to calculate β and k.

The removed group includes people who receive drugs and those who used a preventive measure (like the condom). We can therefore replace equation (3), with one equation for people who received ARD and one equation for those who used the condom. To do this we actually start by splitting the removed rate k, into two removed rates. These rates are kD (the removed rate for those who received ARD) and kc (the removed rate for those that used the condom). We now can replace the rate of change for the removed group. In its place, we have two equations, one for drugs (Dt) and the other for condom (Ct).[4] Specifically,

$$\frac{dD}{dt} = k_D I(t)$$
$$\frac{dC}{dt} = k_C I(t)$$

Using Euler's method for systems, the solutions to the above equations become

$$D_{n+1} = D_n + (1-k)I(t)\Delta t$$
$$C_{n+1} = C_n + kI(t)\Delta t$$

where Dn+1 and Cn+1 are the number of people that received ARD and used the condom respectively, at time (n+1) .

Again, we will have Δt be equal to one.

2.2. Basic Reproductive Ratio

An important part of modeling diseases is the Basic Reproductive Ratio, denoted as R0. The Basic Reproductive Ratio is important since it tells us if a population is at risk from a disease. R0 is affected by the infection and removal rates, i.e. β,k and is obtained by $R_0 = \frac{\beta}{k} S_0$. When R0 >1, the occurrence of the disease will increase. When R0<1 the occurrence of the disease will decrease and the disease will eventually be eliminated. When R0=1, the disease occurrence will be constant.[3, 5]

The Basic Reproductive Ratio also helps us predict who will not become infected at all. This is done by looking how the SIR model behaves as t→∞. Mathematicians

Kermack and McKendrick came up with the equation $S_\infty = \exp((1-S_\infty)R_0)$, where S∞ is the amount of people who will always remain in the susceptible group.[8]

Members are recruited into S-class through natural birth (b) and we assume is proportional to the natural population N. Death is explicit and occur in all compartments, there is an additional disease induced death rates in the I and R compartments denoted by a0 and a1 respectively. Now, if we incorporate these parameters into our governing model equations, we would have a new set of equations representing this situation. Equations 1-3 become thus:

$$\frac{dS}{dt} = bN - (\beta + \mu)S(t) \qquad (11)$$
$$\frac{dI}{dt} = \beta S(t) - (k + \mu + a_0)I(t) \qquad (12)$$
$$\frac{dR}{dt} = kI(t) - (\mu + a_1)R(t) \qquad (13)$$

Integrating both sides of (13) we have thus,

$$k\int_0^t [I(t) - (\mu + a_1)]ds = R(t)$$
$$= N(t) - S(t) - I(t)$$
$$= (1-b)N(t) + \mu S(t) + (k + \mu + a_0)$$

Appling Euler's method of systems of equations, we have;

$$S_{n+1} = S_n + bN - (\beta + \mu)S_n \qquad (8)$$

$$I_{n+1} = I_n + \beta S_n - (k + \mu + a_0)I_n \qquad (9)$$

$$R_{n+1} = R_n + kI_n - (\mu + a_1)R_n \qquad (10), \quad \Delta t = 1$$

3. Stability analysis of the free equilibrium states

We will establish the stability of free equilibrium states using Routh-Hurwitz stability condition. The equilibrium points are

$$E_0 = (\frac{bN}{\beta+\mu}, 0, 0)$$

The Jacobian matrix associated with the systems of equations above is given as

$$J_{E_0} = \begin{bmatrix} -\mu & -\frac{\beta\mu}{\beta+\mu} & 0 \\ 0 & \frac{\beta\mu}{\beta+\mu} - (k+\mu+a_0) & 0 \\ 0 & k & -(\mu+a_0) \end{bmatrix}$$

$$\det(J_{E_0}) = \left[\frac{\beta\mu}{\beta+\mu} - (k+\mu+a_0)\right]\left[-(\mu+a_0)\right]$$

$$= (k+\mu+a_0)(\mu+a_0) - (\mu+a_0)\frac{\beta\mu}{\beta+\mu}$$

$$= (\mu+a_0)\left[(k+\mu+a_0) - \frac{\beta\mu}{\beta+\mu}\right] < 0$$

$$If \quad (k+\mu+a_0) < \frac{\beta\mu}{\beta+\mu}$$

$$trace(J_{E_0}) = \left[\frac{\beta\mu}{\beta+\mu} - (k+3\mu+2a_0)\right] > 0$$

$$If \quad \frac{\beta\mu}{\beta+\mu} > (k+3\mu+2a_0)$$

By Routh-Hurwitz stability conditions, the disease is locally asymptotically stable under these two conditions.

3.1 Numerical Simulation of the Difference Equations

In this section, a computer based program is developed and used to generate the data using the difference equations equivalent to the differentials equations in (11-13). We fix some of the parameters and vary some of the key interest parameters and these will enable us to see whether or not the derived difference equations have biological meaning. With the computer simulation we see physically what is happening through the graphs and should be able to conclude whether or not the stability of free equilibrium states established in the previous section is correct or not.

First we consider k=0 and β=0.5,

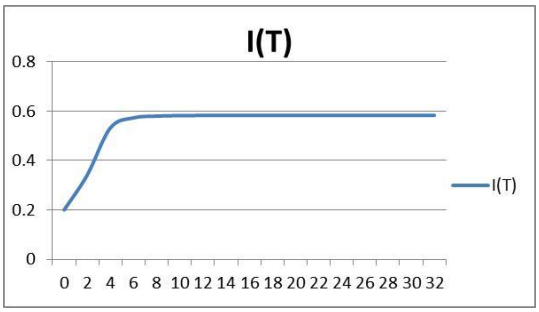

Figure 4.1: A graph showing the rate of infective when k=0 and β=0.5.

From the graph we observe that the rate of infective increases over time this is because k=0 (means no intervention) and β=0.5 (means, high incidence rate). That is, when there is no intervention in a population with high incidence rate, the epidemic would persist.

Now, we consider a situation when k=0.7 and β=0.1,

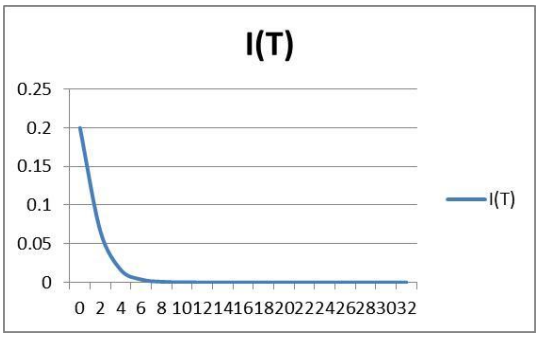

Figure 4.2 Rate of infective for k=0.7 and β=0.1

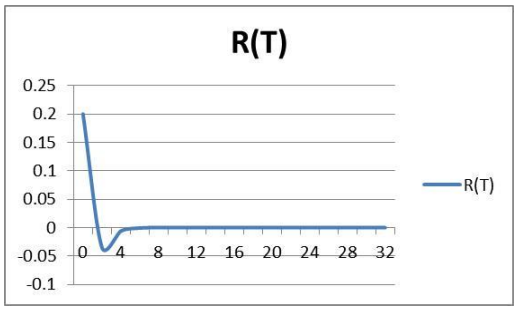

Figure 4.3: Treatment rate when k=0.7 and β=0.1

From the two graphs, we can see that when there is high treatment rate (k=0.7) and low incidence rate (β=0.1), the rates of infected and removed classes approach zero over a finite time.

Conclusion:

We have seen in the above section, the result for computer simulations of the model equations using the model parameters which confirmed that our output is consistent and can be applied in solving real world situations. We have seen also from figures 4.1, 4.2 and 4.3 that with our model and the conditions imposed, the deadly scourge can be totally eradicated. Hence, this research work confirmed that ART and condom could be useful methods for the control and eradication of HIV/AIDS in this our generation so that our children may have HIV free generation. The stability analysis is based on the use of the basic reproduction number called R0 that is we use the idea of Diekmann by using the next generation operator method. The model is found to be locally asymptotically stable under the given conditions that mean the disease can be controlled under such conditions. In fact we can eradicate the deadly scourge if this model is critically implemented.

Mathematicians and medical experts should intensify efforts at finding a cure for AIDS. The research emphasis on the one and only one cure of AIDS that is, "totals abstinence from unprotected sex and mutual fidelity". Therefore we conclude with the following recommendations:

- We recommend that government and other agencies should co-opt mathematicians in their HIV/AIDS programmes.
- Mathematical models like ours should be applied in solving HIV/AIDS problems.
- Government, NGOs and individuals should fund and encourage mathematical researches for HIV/AIDS
- The national response to the HIV/AIDS epidemic must be strengthened and expanded to ensure balance in interventions between urban and rural areas, as well as in intervention strategies – Prevention, Treatment and Care for people living with HIV/AIDS.
- Definite intervention should be designed to target people with primary and secondary level education especially using mass media campaigns that they will be responsive to.
- The extent of adoption and implementation of HIV/AIDS education curricula should be assessed and strengthened in order to reduce the prevalence among people with primary and secondary level education that is in school.
- Emphasis should continue to focus on the youth to ensure a sustained downward trend in new infections.
- There should be increased efforts to expand quality comprehensive HIV/AIDS prevention, treatment, care and support services.

• In view of the large number of AIDS orphans with its attendant burden, comprehensive care and support programmes should be packaged and adequately delivered on sustainable basis.

• Focused research in sites/states with consistently low and high prevalence would facilitate the identification of possible factors for appropriate intervention strategies.

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