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An SIA Model of HIV Transmission in Ghana

Stephen Eduafo

Department of Mathematics
Kwame Nkrumah University of Science and Technology
Kumasi-Ghana

Isaac Kwasi Adu

Department of Mathematics
Valley View University, Techiman Campus
P.O. Box 183 B/A-Ghana

Francis Tabi Oduro

Department of Mathematics
Kwame Nkrumah University of Science and Technology
Kumasi-Ghana

Isaac Owusu Darko

Department of Mathematics
Valley View University, Techiman Campus
P.O. Box 183 B/A-Ghana

Abstract

We seek to discuss how the transmission of HIV infection, and hence AIDS disease, depends on various biological and social factors, which may be different within and between the different population groups.
In this paper an SIA compartment model of the transmission dynamics of HIV/AIDS is developed using Ghana Data. The resulting system of three non-linear differential equations was analyzed in respect of stability of the three equilibrium points namely the disease free which was found to be locally asymptotically stable and two endemic equilibrium points which were found to be

stable. Further analysis to determine the conditions for the breakout of epidemic were done using the basic reproductive number of the infection. It was found that the rate of transition from HIV infected to AIDS relative to the rate of transition from susceptible to HIV infected state would need to be increased in order to effectively control the spread of the disease.

Keywords: SIA model, Stability analysis, Equilibrium points, Reproductive Number, Mathematical model

1 Introduction

The human immunodeficiency virus (HIV) is a lentivirus which attacks the immune system [1] [2]. Lentiviruses belong to a larger group of viruses known as retroviruses that causes acquired immunodeficiency syndrome (AIDS), a condition in human beings in which the immune system begins to fail, leading to life threatening opportunistic infections[3].
The name 'lentivirus' literally means 'slow virus' because they take such a long time to produce any adverse effects in the body[3].
The severity of the infection can be minimized by the administration of the Antiretroviral drugs (ARD) to the infected person which only slows the sero-conversion period.
Mathematical methods have been one of the potent mechanisms that have been use over decades to address issues on the behavior and transmission of HIV/AIDS.
One of the basic procedures for modeling HIV is the Compartmental model, in which the total population is divided into three groups (variables), a susceptible population, the population with the HIV infection and the population which are infected and show symptoms of AIDS.
The SIR model is used in epidemiology to compute the number of people in the different population group and also to predict the number of people needing medical attention during an epidemic.

2 Methodology

Mathematical models have played an important role in the study of diseases and their behavior at each epidemiologically relevant class. Mathematical models are commonly known to have two distinct roles: to predict and to facilitate understanding.
Deterministic models is one of the best understood models which are normally expressed in terms of differential equations aside the stochastic models.

2.1 Model Parameters and Assumptions

We formulate an HIV/AIDS model by considering the population of individuals in the different groups or stages. At time t, there are $S(t)$ human susceptibles, $I(t)$ infectives who are the infected and infectious individuals that

have not yet developed AIDS symptoms, $A(t)$ AIDS patients who are infected and with AIDS symptoms and $R(t)$ are individuals who die of the AIDS. Susceptibles have sexual contacts at a rate ζ with a probability of transmission at one sexual encounter denoted by ρ. A proportion of these sexual contacts are with infectives. Let us assume there is a constant immigration rate λ of susceptible into a population of size N. We assume that susceptibles die naturally at a rate μ. We also assume AIDS patients also die a natural death at a rate μ. In addition we assume uniform mixing with the different population groups and also sexual contacts within susceptibles do not result in any transmission and thus do not feature in the model. Also, sexual contacts within infectives which give rise to issues about the role of re-infections are ignored.

2.2 Derivation of Equations for the SIA Model

We generate the system of nonlinear differential equations with the help of the flow diagram which shows the direction of flow of the disease.

2.1.1 A Flow Diagram of the Disease as Modeled by the System Below:

Presented below is a flow diagram that represents the SIA epidemic model for HIV/AIDS based on which we generate our systems of nonlinear differential equation.

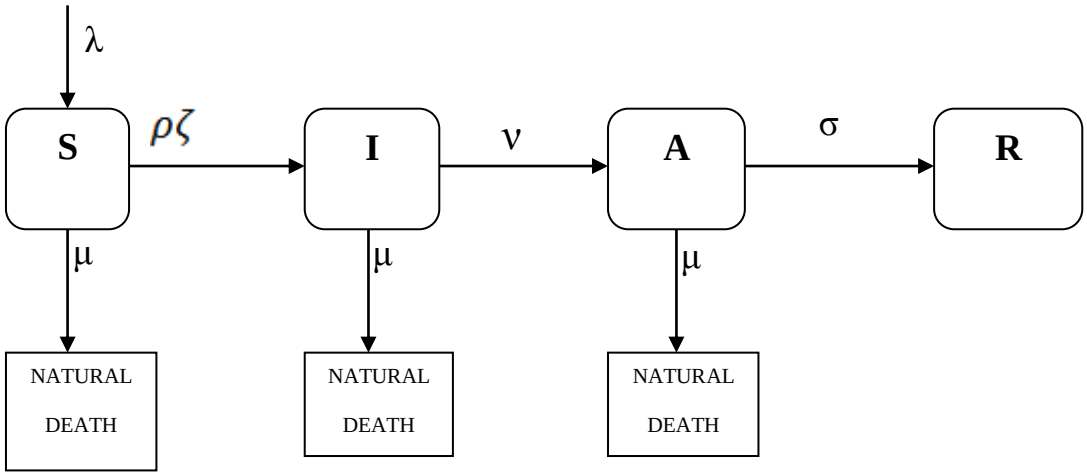

Fig.2.1: A flow diagram of the disease as modeled by the system of equations.

2.1.2 Model Equations

The first set of dependent variable counts people in the groups, each as a function of time:

$S = S(t)$, is the number of susceptible individuals,

$I = I(t)$, is the number of infected individuals, and

$A = A(t)$, is the number of AIDS patients.

From the descriptions and assumptions on the dynamics of the epidemic made above, the following are the model equations.

$$\frac{dS}{dt} = \lambda - \mu S - \rho\zeta S \qquad (3.0)$$

$$\frac{dI}{dt} = \rho\zeta S - \mu I - \upsilon I \qquad (3.1)$$

$$\frac{dA}{dt} = \upsilon I - \mu A - \sigma A \qquad (3.2)$$

Where N is the total size of the population and $\rho = \eta I/N$. Thus, S, I, A are all bounded above by N.
The mathematical formulation of the epidemic problem is completed given initial conditions such as

$$S(0) = S_0 > 0, I(0) = I_0 > 0, A(0) = A_0 > 0$$

2.2 Stability of Fixed Point of the Nonlinear SIA Epidemic Equations

2.2.1 Steady State Equilibrium

Because of the biological meaning of the components $(S(t), I(t), A(t))$, we focus on the model in the first octant of $\mathbb{R}^3$.we first consider the existence of equilibrium of system $(3.0) - (3.3)$. For any value of parameters, model $(3.0) - (3.3)$ always has a disease-free equilibrium $E_0 = (N, 0, 0)$.
In equation $(3.0) - (3.3)$, if at $t = 0$, the system without any infected individual is assumed to receive an individual with the HIV virus either by birth or immigration. We have initially $S = N, I = 0, \text{and } A = 0$ and the disease-free equilibrium point is determined as

$$(S, I, A) \longrightarrow (N, 0, 0).$$

When the epidemic starts, the system $(3.0) - (3.3)$ evolves to a steady state when

$$\frac{dS}{dt} = \frac{dI}{dt} = \frac{dA}{dt} = 0$$

Since

$$N = S(t) + I(t) + A(t)$$

$$\frac{dN}{dt} = \lambda - \mu S - \mu I - \mu A - \sigma A$$

$$= \lambda - \mu N - \sigma A$$

It implies that
Solving for the various population groups, S, I, A we get

$$S^* = \frac{(\upsilon+\mu)N^*}{\eta\zeta} \qquad I^* = \frac{(\sigma+\mu)(\lambda-\mu N^*)}{\sigma\upsilon} \qquad A^* = \frac{(\lambda-\mu N^*)}{\sigma}$$

$$(S^*, I^*, A^*) = \left(\frac{(\upsilon+\mu)N^*}{\eta\zeta}, \frac{(\sigma+\mu)(\lambda-\mu N^*)}{\sigma\upsilon}, \frac{(\lambda-\mu N^*)}{\sigma}\right)$$

2.2.2 Linearization of Equation

In this section we investigate the behavior of the flow near equilibrium solutions using the linearization technique and connect it to the Hartman-Grobman theorem, which relates a nonlinear system to the corresponding linear one near the equilibrium.
The Jacobian matrix for the SIA model is therefore given by:

$$J = \begin{pmatrix} -\frac{\eta\zeta I}{N} - \mu & -\frac{\eta\zeta S}{N} & 0 \\ \frac{\eta\zeta I}{N} & \frac{\eta\zeta S}{N} - (\upsilon+\mu) & 0 \\ 0 & \upsilon & -(\sigma+\mu) \end{pmatrix}$$

$$\text{Where} \qquad \rho = \eta I/N$$

Solving for the eigenvalues of the Jacobian matrix at the disease free equilibrium point, we get

$$T = -\mu, -(\sigma + \mu) \; and \; \eta\zeta - (\upsilon + \mu)$$

Solving for the eigenvalues of the Jacobian matrix at the non zero endemic equilibrium point, we get:

$$T = -(\sigma + \mu),$$

and

$$\frac{-(\mu\sigma\upsilon N^* + \eta\zeta(\sigma+\mu)(\lambda - \mu N^*))}{2\sigma\upsilon N^*}$$

$$\pm \sqrt{\left(\frac{(\mu\sigma\upsilon N^* + \eta\zeta(\sigma+\mu)(\lambda - \mu N^*))}{2\sigma\upsilon N^*}\right)^2 - \frac{\eta\zeta(\mu+\upsilon)(\sigma+\mu)(\lambda-\mu N^*)}{\sigma\upsilon N^*}}$$

Where T is our eigenvalue.

2.3 Reproductive Number

The reproductive number defines the direction of the disease. This can be written mathematically as:

$$R_0 = T^* * (infectious\ period) + 1$$

$$infectious\ period = \frac{1}{Rate\ of\ change}$$

and T^* *is the dominant eigenvalue.*

2.3.1 Calculations

Now, we want to find the reproductive number for this model first with a simple method. In this method for finding R_0, we survey to have increase and decrease of infectives, therefore we have:

if

$$\frac{dI}{dt} > 0$$

then

$$\frac{\eta\zeta S}{N(\mu+\upsilon)} > 1 \qquad \text{but at t} = 0, \text{S} \approx \text{N}$$

$$\Rightarrow$$

$$\frac{\eta\zeta}{(\mu+\upsilon)} > 1$$

If we take

$$R_0 = \frac{\eta\zeta}{(\mu+\upsilon)}$$

Therefore: $\frac{dI}{dt} > 0$, we have$R_0 > 1$.

Also if $\frac{dI}{dt} < 0$ we will get $R_0 < 1$ by similar computation as we did in the above calculation.

3 Model Analysis and Discussion

We realized that at the non-endemic equilibrium point, the state of the system can be estimated in either of two ways, that is the system experiences a nodal sink provided $\eta\zeta < (\upsilon + \mu)$ and hence the system will be in a state of total stability and this explains that either there is no body in the population infected with the HIV/AIDS disease or there are some infective in the population but the disease spread are completely under control.
Now if $\eta\zeta > (\upsilon + \mu)$, then the system will now have a saddle point.

From the result of our eigenvalues, the state of the system at the non-zero endemic equilibrium point can also be estimated in either of two ways:
Considering the case where $\lambda > \mu N^*$ for all the cases below, Then if:

$$\left(\frac{(\mu\sigma\upsilon N^* + \eta\zeta(\sigma+\mu)(\lambda-\mu N^*))}{2\sigma\upsilon N^*}\right)^2 - \frac{\eta\zeta(\mu+\upsilon)(\sigma+\mu)(\lambda-\mu N^*)}{\sigma\upsilon N^*} < 0$$

Then the eigenvalues T_2 *and* T_3, are complex conjugate, this goes to explain the fact that in this case the system will have a spiral sink at $\lambda > \mu N^*$ since

$T_1, T_2\ and\ T_3$ have a negative real part.

That means the system have a certain form of oscillatory behavior at equilibrium while its solution still moves to stable direction.
In other words, the system behaves in a damped oscillatory manner with a certain period determined by the parameters since it has a spiral sink.

Also if

$$\left(\frac{(\mu\sigma\upsilon N^* + \eta\zeta(\sigma+\mu)(\lambda-\mu N^*))}{2\sigma\upsilon N^*}\right)^2 - \frac{\eta\zeta(\mu+\upsilon)(\sigma+\mu)(\lambda-\mu N^*)}{\sigma\upsilon N^*} > 0$$

Then we will get two real eigenvalues, $T_2\ and\ T_3$. This goes to explain the fact that the system will be a nodal sink at $T_2 < 0\ and\ T_3 < 0$ but the system will experience a saddle point at either $T_2 > 0\ or\ T_3 > 0\ or\ both$ for $\lambda > \mu N^*$seeing $T_1 < 0$.
This means the system moves to stable direction if and only if the two distinct real values are both negative else the system experiences a state of instability.
If:

$$\left(\frac{(\mu\sigma\upsilon N^* + \eta\zeta(\sigma+\mu)(\lambda-\mu N^*))}{2\sigma\upsilon N^*}\right)^2 - \frac{\eta\zeta(\mu+\upsilon)(\sigma+\mu)(\lambda-\mu N^*)}{\sigma\upsilon N^*} = 0,$$

Then

$$T = \frac{-(\mu\sigma\upsilon N^* + \eta\zeta(\sigma+\mu)(\lambda-\mu N^*))}{2\sigma\upsilon N^*}$$

This implies that at the case where $\lambda > \mu N^*$,we will get one repeated eigenvalues, T which is negative hence a nodal sink is established.
Considering the case where the discriminant is equal to zero. This measures a stable system since the eigenvalues of the Jacobian matrix have a negative real value and one repeated value hence a nodal sink is established.

Also:
Considering the case where $\lambda < \mu N^*$ for all the cases below, Then if:

$$\left(\frac{(\mu\sigma\upsilon N^* + \eta\zeta(\sigma+\mu)(\lambda-\mu N^*))}{2\sigma\upsilon N^*}\right)^2 - \frac{\eta\zeta(\mu+\upsilon)(\sigma+\mu)(\lambda-\mu N^*)}{\sigma\upsilon N^*} < 0$$

Then the eigenvalues T_2 *and* T_3, are complex conjugate, this goes to explain the fact that in this case the system will have a saddle point at $\lambda < \mu N^*$ since $T_1 < 0$ *while* T_2 *and* T_3 both have a positive real part.

Also if:

$$\left(\frac{\left(\mu\sigma\upsilon N^* + \eta\zeta(\sigma+\mu)(\lambda-\mu N^*)\right)}{2\sigma\upsilon N^*}\right)^2 - \frac{\eta\zeta(\mu+\upsilon)(\sigma+\mu)(\lambda-\mu N^*)}{\sigma\upsilon N^*} > 0$$

Then we will get two real eigenvalues, T_2 *and* T_3. This goes to explain the fact that the system will be a saddle point at either $T_2 > 0$ *or* $T_3 > 0$ *or both* for $\lambda < \mu N^*$ seeing that $T_1 < 0$.
If:

$$\left(\frac{\left(\mu\sigma\upsilon N^* + \eta\zeta(\sigma+\mu)(\lambda-\mu N^*)\right)}{2\sigma\upsilon N^*}\right)^2 - \frac{\eta\zeta(\mu+\upsilon)(\sigma+\mu)(\lambda-\mu N^*)}{\sigma\upsilon N^*} = 0,$$

Then

$$T_2, T_3 = \frac{-\left(\mu\sigma\upsilon N^* + \eta\zeta(\sigma+\mu)(\lambda-\mu N^*)\right)}{2\sigma\upsilon N^*}$$

This implies that at the case where $\lambda < \mu N^*$, we will get one repeated eigenvalue, T which are positive hence a saddle point is established.

4 Conclusion

We have investigated the transmission dynamics of an SIA epidemic model with positive immigration. We have also characterized the equilibrium and thresholds and shown how they are affected by the immigration profile.
After a series of analysis made with respect to the various models, we realize in conclusion that in almost all the cases where $\lambda > \mu N^*$, the system realized a total stability but in all the cases where $\lambda < \mu N^*$ the system is always unstable.
We are also able to establish that in situations where net transmission rates is very small as compared to the rate of progression to AIDS, the system experience stability. Hence increasing the birth rate (immigration rate), increasing AIDS progression rate relative to the net transmission rate and Minimizing net Transmission for almost all cases may eradicate HIV/AIDS, but would give long incubation period for AIDS since from our assumption $\upsilon \gg \mu$.

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