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HIV is transmitted primarily via unprotected sexual intercourse which may include anal or even oral sex, contaminated blood transfusions, hypodemic needles and from mother to child transmission during pregnancies delivery or breast feeding. (William N. R and Steven B. (2007)). Some bodily fluids such as saliva and tears do not transmit HIV (CDC (2003)). Prevention is primarily through safe sex and needle exchange program is a key strategy to control the spread of the disease. There is no known cure or vaccines for AIDS for now, however HAART can reduce or slow the course of the disease and may lead to normal life expectancy. Since it was first recognized in 1981 by Centre for Disease Control and Prevention (CDC), AIDS has caused over 34 million deaths as of 2010 (CDC (2011)). As of 2010, approximately 36 million people are living with HIV/AIDS globally (UNAID (2010)). AIDS is now a global pandemic in the 21st century.

Numerous deterministic and stochastic models since mid 1980s have been developed to describe the immune system and its interaction with HIV. Stochastic models aims to account for the early events in the disease when there are few infected cells and small number of virus. Nowak et al (1996) investigated the effects of variability among vital strains, this and other works have been commented on critically by Stillianakis, N. I. et al (1994).

Most models appearing in literature have been deterministic in nature, such as Mclean and Nowak (1992), Frost and Mclean (1994), Kirschner and Webb (1997) and Wein et al (1998) models. These models try to reflect the dynamical change in mean cell populations. These models typically consider the dynamics of the $CD_{4}$ cells. Laterly infected cells and virus population, as well as effects of drug therapy.

In this article, we develop and analyze a SIR model to study the dynamics of HIV/AIDS infections within the human immune system by the considering the stability and the basics reproduction number. The immune system is a collection of cells and organs that work together synergistically. The T-cells are the subsets of white blood cells, which includes the $CD_{4}^{+}$ T cells (helper cells that signal when invaders enter) $CD_{8} T-cells$ (killer T-cells, which produce antibodies to kill invaders). The virus HIV target the $CD_{4}^{+}$ T cells not to send strong signal for the $CD_{8} T-cells$ to produce the antibodies. This cause immunodeficiency (stage of AIDS).

1. INTRODUCTION

Human Immunodeficiency Virus (HIV) is a virus that attacks the immune system of human beings and renders it weak to infection. HIV can progress to Acquired Immune Deficiency Syndrome (AIDS) once the number of T-cells in the immune system have been significantly reduced (UNAIDS 2007). During the initial infection, a person may experience a brief period of influenza like illness. This is usually followed by a prolonged period without symptoms. As the illness progresses, it interferes more and more with the immune system thereby making the person much more likely to get infections such as opportunistic infections and tumor that do not usually affect people who have working immune systems.

HIV/AIDS mathematical models. Furthermore, we developed a model to confirm the endemcity of the disease by using the basic reproduction number $R_{0}$ as a basis.

Keywords Terms - Reproduction, Epidemiology, HIV, Mathematical Modeling, Virus, Model

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In this article, we develop and analyze a SIR model to study the dynamics of HIV/AIDS infections within the human immune system by the considering the stability and the basics reproduction number. The immune system is a collection of cells and organs that work together synergistically. The T-cells are the subsets of white blood cells, which includes the $CD_{4}^{+}$ T cells (helper cells that signal when invaders enter) $CD_{8} T-cells$ (killer T-cells, which produce antibodies to kill invaders). The virus HIV target the $CD_{4}^{+}$ T cells not to send strong signal for the $CD_{8} T-cells$ to produce the antibodies. This cause immunodeficiency (stage of AIDS).

2. MODEL FORMULATION

We assume that the population are homogeneously mixed and the interaction within the population is a mass action type, cells once infected start producing virus. Furthermore, we ignore the latency period and there is a constant migration of susceptible into the population of size $N$ (t) infected cells which produces same number of virus particles.

Abstract - In this article, we survey the stability analysis and the basic reproduction number ($R_{0}$) that are significant concepts for the development of HIV/AIDS mathematical models. Furthermore, we developed a model to confirm the endemcity of the disease by using the basic reproduction number $R_{0}$ as a basis.

Keywords Terms - Reproduction, Epidemiology, HIV, Mathematical Modeling, Virus, Model
Let \( x(t), y(t) \) and \( z(t) \) denote the number of susceptible, infectious and those that have developed acute AIDS (i.e. AIDS patient).

We assume a natural death throughout the population at the rate \( \mu \).

The schematic diagram of the disease on which we base our model is as follows:

\[
\begin{align*}
\pi & \rightarrow X(t) \rightarrow Y(t) \rightarrow Z(t) \\
\mu & \downarrow \quad \mu & \downarrow \quad \psi & \\
& = x' = \beta x y - \gamma y - \mu x \quad \ldots (2.2) \\
& = y' = \gamma y - \mu x - dz \quad \ldots (2.3) \\
& = z' = \gamma y - \mu x - dz \quad \ldots (2.3)
\end{align*}
\]

- \( \pi \) = Recruitment of susceptible into the population
- \( \mu \) = Natural death rate
- \( d \) = Death rate of infected cells which also includes the possibility of death by bursting of the cell, hence \( d \geq \mu \)
- \( \beta \) = Rate at which susceptible becomes infected with the virus
- \( \gamma \) = The rate at which infectious moves to full blown AIDS

The total population at time \( t \) is given by
\[
N(t) = x(t) + y(t) + z(t).
\]

Thus \( x = X \), \( y = Y \), \( z = Z \), this leads to a normalized system;
\[
\pi - \beta x y - \mu x = 0 \quad \ldots (2.4)
\]
\[
\beta x y - (\gamma + \mu)y = 0 \quad \ldots (2.5)
\]
\[
\gamma y - (\mu + d)z = 0 \quad \ldots (2.6)
\]

where \( x + y + z = 1 \) and \( x(t) > 0 \), \( y(0) > 0 \), \( z(0) > 0 \) \( \forall \ t \geq 0 \)

The continuity of equation (2.4) – (2.6) indicate that the model is well posed for \( N > 0 \). 

3. MODEL ANALYSIS

3.1 Existence of disease-free equilibrium state \( E_1 \)

At the disease free equilibrium state, we have absence of infection. Thus, all the infected classes will be zero and the entire population will comprises of only susceptible individuals.

Theorem 1: A disease free equilibrium state of the model exist at the point.
\[
\left( x^*, y^*, z^* \right) = \left( \frac{\pi}{\mu}, 0, 0 \right).
\]

Proof: At equilibrium, the rate of change of each variable is equal to zero.
\[
i.e. \quad \frac{dx}{dt}^0 = \frac{dy}{dt}^0 = \frac{dz}{dt}^0 = 0 \quad \ldots (3.1)
\]
from equation (2.5)
\[
\gamma y^* - (\mu + d)z^* = 0 \quad \ldots (3.2)
\]
\[
\Rightarrow y^* = 0 \text{ or} \quad \ldots (3.3)
\]
\[
\beta x^* - (\gamma + \mu) = 0 \quad \ldots (3.4)
\]
Substitute (3.3) in (2.6)
\[
\Rightarrow z^* = 0 \quad \ldots (3.5)
\]
Substitute (3.3) and (3.5) into (2.6)
\[
\pi - \beta x^* y^* - \mu x^* = 0
\]
\[
\Rightarrow \pi - \mu (x) = 0
\]
\[
x^* = \frac{\pi}{\mu} \quad \ldots (3.6)
\]
\[
\Rightarrow x^* = \frac{\pi}{\mu}, \quad y^* = 0, \quad z^* = 0
\]
\[
\left( x^*, y^*, z^* \right) = \left( \frac{\pi}{\mu}, 0, 0 \right)
\]
Hence the disease free-equilibrium state exist.

3.2 Existence of Endemic Disease Equilibrium State

At the endemic equilibrium state the disease is present. Therefore the susceptible, infectious and the removed classes are not anyway equal to zero.
Theorem II: An endemic equilibrium state of the model exist at the points

\[(x, y, z) = \left( \frac{\gamma + \mu}{\beta}, \frac{\mu \gamma + \mu^2 + \pi \beta}{\beta(\gamma + \mu)}, \frac{\mu \gamma + \mu^2 + \pi \beta}{\beta(\gamma + \mu)} \right)\]

Proof: Since at the equilibrium state of the endemic case, the disease is present, then;

\[
\frac{ds}{dt} = \frac{dI}{dt} = \frac{dR}{dt} = (x_0, y_0, z_0)
\]

From equations (2.1), (2.2) and (2.3) we have,

\[
\pi - \beta xy - \mu x = 0 \quad \ldots (3.7)
\]

\[
\beta xy - (\gamma + \mu)y = 0 \quad \ldots (3.8)
\]

\[
\gamma - (\mu + \delta)z = 0 \quad \ldots (3.9)
\]

From (3.9)

\[
\gamma - (\mu + \delta)z = 0
\]

\[
\Rightarrow \gamma = (\mu + \delta)z
\]

\[
y = \left( \frac{\mu + \delta}{\gamma} \right)z \quad \ldots (3.10)
\]

Substituting (3.10) in (3.7) we have

\[
\pi - \frac{\beta(\mu + \delta)}{\gamma} \cdot z - \mu x = 0 \quad \ldots (3.11)
\]

Substituting (3.10) in (3.8)

\[
\Rightarrow \beta x - (\gamma + \mu) \left( \frac{\mu + \delta}{\gamma} \right) z = 0 \quad \ldots (3.12)
\]

From (3.12)

\[
\beta \mu x - (\gamma + \mu) \mu \varepsilon + \beta x \varepsilon \times - (\gamma + \mu) \varepsilon = 0
\]

\[
\beta(\mu + \delta) x - (\gamma \mu + \gamma \delta + \mu \delta + \mu^2) z = 0
\]

\[\Rightarrow z \left[ \beta (\mu + \delta) x - (\mu + \delta)(\mu + \gamma) \right] = 0
\]

\[\Rightarrow z = 0 \text{ or }
\]

\[
\beta(\mu + \delta) x - (\mu + \delta)(\mu + \gamma) = 0
\]

\[\Rightarrow x = \left( \frac{\mu + \gamma}{\beta(\mu + \delta)} \right)
\]

\[\Rightarrow x = \frac{\mu + \gamma}{\beta} \quad \ldots (3.13)
\]

Substituting (3.13) in (3.7)

\[
\pi - (\beta y + \mu) \left( \frac{\mu + \gamma}{\beta} \right) = 0
\]

\[\Rightarrow \pi \beta - \left( (\beta y + \beta \gamma) y + \mu \gamma + \mu^2 \right) = 0
\]

\[\Rightarrow (\beta y + \beta \gamma) y = \mu \gamma + \mu^2 - \pi \beta
\]

\[y = \frac{\pi \beta - \mu \gamma - \mu^2}{\beta(\gamma + \mu)} \quad \ldots (3.14)
\]

From equation (3.10)

\[
z = \frac{\gamma y}{\mu + \delta}
\]

Substituting from (3.14)

\[
z = \gamma \left( \frac{\pi \beta - \mu \gamma - \mu^2}{\beta(\gamma + \mu)} \right) \frac{y}{\mu + \delta}
\]

\[\Rightarrow z = \frac{\pi \beta - \mu \gamma - \mu^2}{\beta(\gamma + \mu)(\mu + \delta)} \quad \ldots (3.15)
\]

Therefore at the endemic state, we have

\[
x = \frac{\gamma + \mu}{\beta}
\]

\[y = \frac{\mu \gamma + \mu^2 + \pi \beta}{\beta(\gamma + \mu)} \quad \ldots (3.17)
\]

\[z = \frac{\mu \gamma + \mu^2 + \pi \beta}{\beta(\gamma + \mu)(\mu + \delta)} \quad \ldots (3.16)
\]

which indicates that the disease is endemic in the population, the susceptible, infection and the removed cases are seriously affected.

3. Effective Basic Reproduction Number \( R_0 \)

The basic reproduction number represent the average number of secondary cases generated by an infected individual if introduced into the susceptible population with no immunity to the disease in the absence of intervention to control the infections.

If \( R_0 \) is less than 1, the infected individual produces less than are newly infected individual over the course of the infection period, therefore the disease will dies out at along run. Conversely if \( R_0 > 1 \) each infected individual produces an average more than one new infection, the infection will be
able to spread in a population. A large value of \( R_0 \) indicate
that the disease can turn to an epidemic case over long run.
Heesterbeek and Dietz (1996) using the technique introduced
by Dickman and Heesterbeek (2000) and subsequently
proofed by Vanden and Watmough (2005). We obtained the
basic reproduction number \( R_0 \) of the our models which is the
spectral radius \( \ell \) of the next generation matrix \( K \).

\[ R_0 = \ell k \]

where \( k = FV^{-1} \)

\[ R_0 = \ell (FV^{-1}) \]

\[ F = \begin{pmatrix} \beta x & 0 \\ 0 & 0 \end{pmatrix} \]

\[ V = \begin{pmatrix} 0 & 0 \\ \gamma & 0 \end{pmatrix} \]

\[ V^{-1} = \begin{pmatrix} k & 0 \\ 0 & k_2 \end{pmatrix} \]

based on the equations in the SIR model analyzed above

\[ V = V^{-1} - \sum^+ \]

\[ V = \begin{pmatrix} k & 0 \\ \gamma & k_2 \end{pmatrix} \]

\[ V^{-1} = \frac{1}{k_1k_2} \begin{pmatrix} k_2 & 0 \\ \gamma & k_1 \end{pmatrix} \]

\[ = \begin{pmatrix} \frac{1}{k_1} & 0 \\ \gamma & \frac{1}{k_2} \end{pmatrix} \quad \ldots \ (3.18) \]

\[ FV^{-1} = \begin{pmatrix} \beta x & 0 \\ 0 & 0 \end{pmatrix} \begin{pmatrix} \frac{1}{k_1} & 0 \\ \gamma & \frac{1}{k_2} \end{pmatrix} \]

\[ = \begin{pmatrix} \frac{\beta x}{k_1} & 0 \\ 0 & 0 \end{pmatrix} \quad \ldots \ (3.19) \]

We now seek for the highest dominant eigen values

\[ \ell (FV^{-1}) = \begin{pmatrix} \frac{\beta x}{k} & 0 \\ 0 & -\lambda \end{pmatrix} \quad \ldots \ (3.20) \]

\[ \Rightarrow \left( \frac{\beta x}{k} - \lambda \right) (\lambda) = 0 \]

\[ \Rightarrow \lambda = 0 \quad \ldots \ (3.21) \]

or \( \lambda = \frac{\beta x}{k} \quad \ldots \ (3.22) \)

since the value of \( x = \frac{\pi}{\mu} \), this implies that

\[ \frac{\beta x}{k} = \frac{\beta x}{\mu k_1} = R_0 \]

\[ \ldots \ (3.23) \]

\( R_0 \) is the basic reproduction number

4. Local Stability of Disease Free Equilibrium (DFE) State

From equation (3.7), (3.8) and (3.9), we have the Jacobian matrix

\[ \begin{pmatrix} \beta x - \mu & -\beta x & 0 \\ \beta y & \beta x - (\gamma + \mu) & 0 \\ 0 & \gamma & \mu + \delta \end{pmatrix} \quad (3.24) \]

For local stability of DFE state, we have \( (x^*, y^*, z^*) = (\mu, 0, 0) = \left( \frac{\pi}{\mu}, 0, 0 \right) \) linearization of the equation, gives the Jacobian matrix

\[ J(E_z) = \begin{pmatrix} -\mu & \frac{\beta x}{\mu} & 0 \\ 0 & \frac{\beta x}{\mu} - (\gamma + \mu) & 0 \\ 0 & \gamma & -(\mu + \delta) \end{pmatrix} \quad \ldots (3.25) \]

we set \( \gamma + \mu = k_1 \) and \( \mu + \delta = k_2 \) without loss of

generality we have

\[ J(E_z) = \begin{pmatrix} -\mu & -\frac{\beta x}{\mu} & 0 \\ 0 & \frac{\beta x}{\mu} - k_1 & 0 \\ 0 & \gamma & -k_2 \end{pmatrix} \quad (3.26) \]
\[
\begin{vmatrix}
- \mu - \lambda_1 & - \frac{\beta \pi}{\mu} & 0 \\
0 & \frac{\beta \pi}{\mu} - k_1 - \lambda_2 & 0 \\
0 & \gamma & - k_2 - \lambda_3 \\
\end{vmatrix}
\]

\[J(E_s) = \left(- \mu - \lambda_1 \right) \left( \frac{\beta \pi}{\mu} - k_1 - \lambda_2 \right) (- k_2 - \lambda_3) = 0\]

If \(- \mu - \lambda_1 = 0 \Rightarrow \lambda_1 = - \mu < 0\)

If \(\lambda_3 - k_2 = 0 \Rightarrow \lambda_3 = - k_2 < 0\)

and if \(\frac{\beta \pi}{\mu} - k_1 - \lambda_2 \Rightarrow \lambda_2 = \frac{\beta \pi}{\mu} - k_1\)

for \(\lambda_2\) to be less than zero

\[\Rightarrow \frac{\beta \pi}{\mu} - k_1 < 0\]

\[\Rightarrow \frac{\beta \pi}{\mu} < k_1 \quad \ldots \ldots (3.27)\]

\[\frac{\beta \pi}{\mu} < k_1 \quad \frac{\mu}{k_1} < 1, \quad \lambda_3 < 0, \quad \text{where} \quad R_0 = \frac{\beta \pi}{k_1 \mu}\]

This indicates that the DFE is locally asymptotically stable if

\[\frac{\beta \pi}{\mu k_1} < 1 \ldots \]

\[\frac{\beta \pi}{\mu k_1} < 1 \text{ then DFE is locally asymptotically stable.}\]

Theorem (III): The disease free equilibrium \(E_s\) of the model is locally asymptotically stable (LAS) if \(R_0 < 1\).

Prof: see e.g Kumour (2012)

(3.5) Local Stability of Endemic Equilibrium State

From the linearization of our model used above, we have the Jacobian matrix as

\[
\begin{vmatrix}
- (\beta y + \mu) - \beta x & 0 \\
\beta y & \beta x - (\gamma + \mu) & 0 \\
0 & \gamma & - (\mu + \delta) \\
\end{vmatrix}
\]

\[J(E_{ss}) = \begin{vmatrix}
- (\beta y + \mu) - \lambda_1 - \beta x & 0 \\
\beta y & \beta x - (r + \mu) - \lambda_2 & 0 \\
0 & \gamma & - (\mu + \delta) - \lambda_3 \\
\end{vmatrix}\]

we set

\[\frac{\beta y + \mu}{\beta x} = A\]

\[\beta x - (r + \mu) - \lambda_2 = B\]

\[\lambda_3 + \lambda_2 + \lambda_3 = C\]

without loss of generality, therefore

\[\begin{vmatrix}
-A - \lambda & - \beta x & 0 \\
\beta y & - \beta - \lambda & 0 \\
0 & \gamma & - c - \lambda \\
\end{vmatrix} = 0\]

\[\begin{vmatrix}
-(A + \lambda_1) & - \beta x & 0 \\
\beta y & -(\beta + \lambda_2) & 0 \\
0 & \gamma & -(C + \lambda_3) \\
\end{vmatrix} = 0\]

\[\begin{vmatrix}
(A + \lambda_1) \{B + \lambda_2\} \{C + \lambda_3\} - \beta_1 \beta_2 (C + \lambda_3) = 0 \\
(A + \lambda_1) (B + B \lambda_3 + C \lambda_2 + \lambda_2 \lambda_3) - \beta_1 \beta_2 C - \beta_1 \lambda_2 \lambda_2 = 0 \\
\end{vmatrix}\]

We set \(\lambda_1 = \lambda_2 = \lambda_3 = \lambda\)

\[ABC + A(B + C)\lambda + A\lambda^2 + BC\lambda + (B + C)\lambda^2 + \lambda^3 + \beta_1 \beta_2 C + \beta_1 \lambda_2 \lambda_2 + \lambda \lambda_3\lambda_3 = 0\]

\[\Rightarrow (A + \lambda_1) (B + B \lambda_3 + C \lambda_2 + \lambda_2 \lambda_3) = 0\]

From equation (3.28) we discovered that \(\lambda > 0\) indicating that \(\lambda_1 > 0, \lambda_2 > 0, \lambda_3 > 0\) which indicates the disease is endemic in the population.

Conclusion

From our investigation, we observed that the disease free equilibrium (DFE) is locally asymptotically stable for our model when the basic reproduction number of \(R_0\) is \(R_0 < 1\) and when \(R_0 > 1\) the disease will be endemic.
References