Stability analysis of host dynamics for hiv

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Abstract: The phenomenon of disease modeling can be easily accomplished through mathematical framework. In this paper the transmission of disease in human is represented mathematically as a nonlinear system. We think about the components of the Human Immunodeficiency Virus (HIV) among the beginning periods of illness. Throughout this paper we have determined those logical representation of a three-compartmental HIV demonstrate for their stability evaluation. We tend to likewise explore the stimulating behavior of the model and acquire those Steady states for the disease-free and the endemic agreement. The framework can be evaluated by reproduction number R₀. We additionally clarify the numerical recreation and their outcomes.

1. Introduction
The anatomy need been viewed as for various period, furthermore likewise the information assembled as such incorporates mind boggling sub-atomic level instruments that check those routes over which inside which a endemic Might infect cells and reproduce [1].this information might be obliged to create medicines for maladies beginning starting with liver infection of the human immunodeficiency infection (HIV) and obtained immunodeficiency syndrome (AIDS)[2]. An seeing of the development of parts of these relations crosswise over a timescale from claiming therapeutic connectedness permits the formation from claiming higher medicine routes. Throughout this paper we need aid setting off will ponder the three-component model for HIV. We are going to investigation the contamination around person mankind's group victimisation this system for differential equations, examine those following Progress of the model, and recreate those natures for results. In general HIV infection while not the composition of anti-retroviral medical aid (ART) is delineated by variety of different phases [3-4].Inside the promptly phases from claiming HIV infection, critical intense contamination provides for enormous requisition for virions partner degree individual’s blood alternately tissue. At the point when numerous weeks, seasonal influenza like manifestations vanish and furthermore the irresistible specialist thickness at that point decreases rapidly among numerous days. This compares on a move inside the sum about cytotoxic T lymphocytes and furthermore the ulterior look of hostile to HIV antibodies inside the blood. In this paper we have specified three-compartmental HIV model Furthermore inspected their dependability in infection spare of endemic harmony focuses. [5-6].
2. Mathematical modelling of hiv infection

In this way an essential model of HIV disease just incorporates uninfected target cells, P, infected cells Q and Virus particle F and the objective cells are thought to be made at steady rate s, to depart this life at rate $\eta$ per cell, and $\gamma_1$ is the rate of CD4+ T cells become contaminated with infection. $\gamma_2$ is the rate of infected cells become active. This creates profitably contaminated cells Q, which are vanished at rate k, bigger than $\eta$, to reproduce thriving development in reduction the infected cell duration. Free infections are created by contaminated cells at steady rate m per cell, and Clearance rate $\phi$ [7-8].

The differential equations describing this framework are:

$$\frac{dP}{dt} = s - \eta P - \gamma_1 FP$$

$$\frac{dQ}{dt} = \gamma_2 FP - kQ$$

$$\frac{dF}{dt} = mQ - \gamma_1 FP - \phi F$$

(1)

3. Analysis of the model

3.1 Disease free equilibrium and the reproduction number

The model has a disease free equilibrium given by $E_0 = \left( \frac{S}{\eta}, 0, 0 \right)$

The fundamental proliferation number of framework (1) will be acquired by the next generation matrix method. The related non negative network $F$, for the new contamination terms and the non singular matrix $V$, for the rest of the exchange terms are given separately by

$$F(E_0) = \begin{pmatrix} \frac{\gamma_2 S}{\eta} & 0 \\ 0 & 0 \end{pmatrix} \quad \text{and} \quad V(E_0) = \begin{pmatrix} 0 & k \\ \gamma_1 P + \phi & -m \end{pmatrix}$$

The basic reproduction number $R_0$ is calculated by the matrix $FV^{-1}$.

$$R_0 = \frac{\gamma_2 sm}{k(\gamma_1 s + \eta \phi)}$$

3.2 Local stability of the disease free equilibrium

**Corollary 3.2.1:** The disease free equilibrium $E_0$ is locally asymptotically stable for $R_0 < 1$ and Unstable otherwise.

**Corollary 3.2.2:** The endemic equilibrium $E_1$ of the system (1) is locally asymptotically stable in for $R_0 > 1$. 

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The Jacobian matrix corresponding to system (1) about $E_0$ is obtained as follows.

$$J(E_0) = \begin{bmatrix}
-\eta & 0 & -\frac{\gamma_1 s}{\eta} \\
0 & -k & \frac{\gamma_2 s}{\eta} \\
0 & m & -\left(\frac{\gamma_1 s}{\eta} + \phi\right)
\end{bmatrix}$$

The characteristic equation is given by

$$\lambda^3 + c_1 \lambda^2 + c_2 \lambda + c_3 = 0 \quad (2)$$

Where

$$c_1 = \eta + k + \frac{\gamma_1 s}{\eta} + \phi$$

$$c_2 = \frac{k\gamma_1 s}{\eta} + k\phi + \gamma_1 s + \eta\phi + \eta k - \frac{m\gamma_2 s}{\eta}$$

$$c_3 = k\gamma_1 s + k\eta\phi - m\gamma_2 s$$

By Routh Hurwitz criteria, we see that all roots of (2) have negative real parts therefore the disease free equilibrium $E_0$ is locally asymptotically stable when $R_0 < 1$ and is unstable if $R_0 > 1$.

### 3.3 Stability of Endemic Equilibrium

**Theorem 3.3.1**

The Endemic equilibrium is locally asymptotically stable iff the following conditions are satisfied.

$$d_1 > 0, d_2 > 0, d_3 > 0, d_1 d_2 - d_3 > 0$$

Endemic Equilibrium $E_1 = (P^*, Q^*, F^*)$ the Jacobian matrix is

$$J(E_1) = \begin{bmatrix}
-(\eta + \gamma_1 F^*) & 0 & -\gamma_1 P^* \\
\gamma_2 F^* & -k & \gamma_2 P^* \\
-\gamma_1 F^* & m & -(\phi + \gamma_1 P^*)
\end{bmatrix}$$

The characteristic equation is given by

$$\lambda^3 + d_1 \lambda^2 + d_2 \lambda + d_3 = 0$$

$$d_1 = \eta + \gamma_1 F^* + k + \phi + \gamma_1 P^*$$

$$d_2 = k(\phi + \gamma_1 P^* + \eta + \gamma_1 F^*) + (\eta + \gamma_1 F^*)(\phi + \gamma_1 P^*) - \gamma_1 F^* P^* - m\gamma_2 P^*$$

$$d_3 = (\eta + \gamma_1 F^*)(k\phi + k\gamma_1 P^* - m\gamma_2 P^*) + \gamma_1 \gamma_2 P^* mF^* - k\gamma_1^2 P^* F^*$$
By using the above theorem I, we have the result that the endemic equilibrium $E_1$ is locally asymptotically stable. This implies that when $R_0 > 1$.

4. Numerical results & discussion

The framework (1) is recreated for different arrangement of parameters and initial values satisfying the state of neighborhood asymptotic steadiness of equilibria $E_0$ and $E_1$ [9-11]. Figure 1 shows the stability of the disease free harmony $E_0$ for the parameter esteems $s = 10$, $k=0.1$, $\gamma_1 = 0.0024$, $\gamma_2 = 0.003$, $\varphi = 2.6$, $\eta = 0.02$, $m = 0.24$ and $P(0) = 300, Q(0) = 10, F(0) = 10$ for this arrangement of parameter esteems reproduction number is evaluated as $R_0 = 0.9474$. Figure 2 shows the stability of the endemic harmony side of the point $E_1$ for the parameter values $s = 10, k=0.1, \gamma_1 = 0.0024$, $\gamma_2 = 0.008$, $\varphi = 2.6$, $\eta = 0.02$, $m = 0.24$ and $P(0) = 300, Q(0) = 10, F(0) = 10$ for this arrangement of parameter esteems reproduction number is evaluated as $R_0 = 2.5263$. Figure 3 the stability of the endemic harmony side of the point $E_1$ for the parameter values $s = 10, k=0.1, \gamma_1 = 0.0024$, $\gamma_2 = 0.014$, $\varphi = 2.6$, $\eta = 0.02$, $m = 0.24$ and $P(0) = 300, Q(0) = 10, F(0) = 10$ for this arrangement of parameter esteems reproduction number is evaluated as $R_0 = 4.4211$.

Fig.1. The stability of the disease free harmony $E_0$ for the parameter esteems $s = 10, k=0.1, \gamma_1 = 0.0024$, $\gamma_2 = 0.003$, $\varphi = 2.6$, $\eta = 0.02$, $m = 0.24$ and $P(0) = 300, Q(0) = 10, F(0) = 10$. 

![Graph of disease stability](image-url)
Fig. 2. The stability of the endemic harmony side of the point $E_1$ for the parameter values $s = 10, k = 0.1, \gamma_1 = 0.0024, \gamma_2 = 0.008, \varphi = 2.6, \eta = 0.02, m = 0.24$ and $P(0) = 300, Q(0) = 10, F(0) = 10$.

Fig. 3. The stability of the endemic harmony side of the point $E_1$ for the parameter values $s = 10, k = 0.1, \gamma_1 = 0.0024, \gamma_2 = 0.014, \varphi = 2.6, \eta = 0.02, m = 0.24$ and $P(0) = 300, Q(0) = 10, F(0) = 10$.

5. Conclusion
The essential of Mathematical analysis of infectious agent dynamics has managed to variety of vital insights concerning the dynamics and pathological process of HIV infection. During this paper, a non-
linear mathematical model is constructed. Stabilities of the two equilibrium square measure investigated by determining the corresponding characteristic equations. The disease free and endemic harmony focuses were acquired and evaluated their dependable qualities. The disease free equilibrium purpose $E_0$ is shown locally asymptotically stable when $R_0 < 1$ and is unstable for $R_0 > 1$. Finally we revealed that the model includes a distinctive endemic equilibrium purpose $E_1$ that is locally asymptotically stable when $R_0 > 1$.

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