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Dynamics of a HIV Epidemic Model

Nguyen Huu Khanh

Abstract— We study a non-linear mathematical model for the transmission of HIV disease. The model is represented by a system of differential equations depending on parameters. We divide the population into three subclasses: uninfected cells, infected cells and free virus particles. A factor deciding the spread of virus is the basic reproduction number R_0. We found that if $R_0 < 1$ then the disease goes extinct, whereas if $R_0 > 1$ then the disease remains. This phenomenon is explained by a transcritical bifurcation. A numerical investigation for the model is carried by the software Mathematica and AUTO.

Index Terms— Bifurcation, free disease equilibrium, endemic disease equilibrium, basic reproductive ratio, transcritical bifurcation, transmission, virus.

1 INTRODUCTION

HIV is primarily a sexual transmitted disease, its spread reflects the social pattern of human sexual relationships. Since it was discovered in 1981, HIV has become one of the leading causes of death of people in countries. HIV has killed an estimated 25 million individuals world wide [2, 7, 14].

One of the most important concerns about any infectious disease is its ability to invade a population. The dynamics between virus infections and the immune system involve many different components and are multifactorial. The understanding of the long-time behaviour of this disease will help us to find whether this epidemics will die out or stay in the population and to design strategies of fighting them.

Mathematical models and computer simulations have become useful in analyzing the spread and control of infectious diseases. They build and test theories that are involved with complex biological systems related disease, getting quantitative conjectures, determining dynamical parameters due to change and estimating parameters from data.

Various approaches for studying epidemiology of HIV have been developed in recent years [1, 2, 3, 8, 9, 11, 13]. Many epidemiological models have a free disease equilibrium (FDE) at which the population remains in the absence of disease. These models usually have a threshold parameter, known as the basic reproduction number, R_0, such that if $R_0 < 1$, then the FDE is locally asymptotically stable, and the disease cannot invade the population, but if $R_0 > 1$, then the FDE is unstable and an epidemic is expected.

In this paper, we study a HIV endemic model as mentioned in [13]. The model is given by a system of three dimensional ordinary differential equations depending to parameters. The population size is divided into three subclasses, that are uninfected cells, infected cells and free virus particles. We assume that the environment is homogeneous.

• *Nguyen Huu Khanh is working at Department of Mathematics, College of Natural Science, Can Tho University, Viet Nam.*
E-mail: nhkhanh@ctu.edu.vn

Our emphasis lies on obtaining a mathematical understanding of the dynamics and bifurcation of the model. We analyze the stability of equilibria and exhibit phase portraits for competition dynamics. We show that the factor that govern the dynamics of the model is the basic reproductive number R_0. Transcritical bifurcation is useful to explain the exchange of stability of equilibria. Obtained results explain the transmission of disease in the HIV model. Numerical method is used to investigate behaviour of the model.

2 THE STUCTURE OF THE MODEL

The endemic model of HIV consists of three variables: the population size of uninfected cells x, infected cells y and free virus particles v.

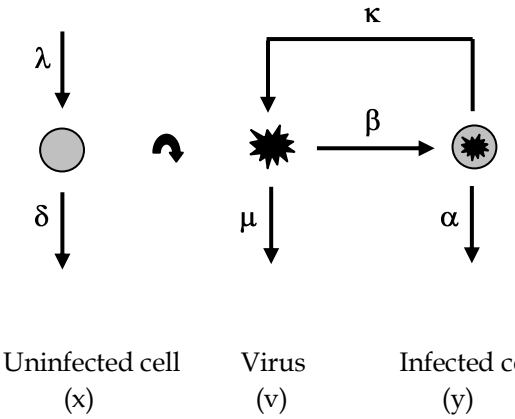

Fig 1. Flow diagram of the HIV endemic model

Free virus particles infect uninfected cells at a rate proportional to the product of their abundances, βxv. The rate β describes the impact of this process, including the rate at which virus particles find uninfected cells, the rate of virus entry, and the rate and probability of successful infection. Infected cells produce free virus at a rate κ. Infected cells die at a rate α, and free virus particles are removed from the system at a rate μ. One can see that the average life-time of an infected cell is $1/\alpha$,

whereas the average life-time of a free virus particles is $1/\mu$. The total amount of virus particles produced from one infected cell is κ/α. Uninfected cells are produced at a constant λ, and die at a rate δ. The average life-time of an uninfected cell is $1/\delta$.

In accordance with the previous assumptions, the model is given by the following differential equations

$$\begin{aligned} \frac{dx}{dt} &= \lambda - \delta x - \beta x v, \\ \frac{dy}{dt} &= \beta x v - \alpha y, \\ \frac{dv}{dt} &= \kappa y - \mu v. \end{aligned} \qquad (1)$$

We assume that parameters α, β, δ, λ, κ and μ are positive.

The system (1) is a system of nonlinear differential equation. To study the dynamics of this system, we consider the linearization at equilibria.

3 Analysis of the Model

3.1 Invariant set

We establish the invariant set of the system (1) that is the first quadrant

$$D = \{(x(t), y(t), v(t)) : x(t) \geq 0,\ y(t) \geq 0,\ v(t) \geq 0\}.$$

This means that the solution of the system is still in D for $t > 0$. Hence, for the rest of the paper we only focus on system (1) restricted to D.

3.2 Equilibria

To find equilibria, we set the right-hand side of the system (1) equal to zero. There are two equilibria in the (x, y, v) space:

1) The free disease equilibrium $E_0(\lambda/\delta, 0, 0)$.

2) The endemic disease equilibrium $E_1(x^*, y^*, z^*)$, where

$$x^* = \frac{\alpha\mu}{\beta\kappa}, \quad y^* = \frac{\beta\kappa\lambda - \alpha\delta\mu}{\alpha\beta\kappa}, \quad v^* = \frac{\beta\kappa\lambda - \alpha\delta\mu}{\alpha\beta\sigma}. \qquad (2)$$

The equilibrium E_0 always exists, while E_1 only exists for $\beta\kappa\lambda > \alpha\delta\mu$.

3.3 The basic reproductive ratio

The dynamics of the HIV model is decided by the basic reproductive ratio R_0, which is defined as the number of newly infected cells that arise from any one cell when almost all cells are uninfected. We found that

$$R_0 = \frac{\beta\lambda\kappa}{\alpha\delta\mu}. \qquad (3)$$

As $R_0 < 1$, the system has an unique equilibrium E_0 and it is stable. For $R_0 > 0$, the system has two equilibria E_0 and E_1, where E_0 is unstable and E_1 is stable.

In the next section, we will show that for $R_0 < 1$ the transmission is extinct whereas for $R_0 > 1$ the virus still remain.

We consider two cases to illustrate the characteristics of the basic reproductive ratio R_0.

*** Case $R_0 < 1$**

Choosing $\alpha = 1$, $\beta = 2$, $\delta = 7$, $\lambda = 0.5$, $\kappa = 2$, $\mu = 0.45$, we have $R_0 = 0.634921 < 1$. With the initial condition x(0) = 0.09, y(0) = 0.025, v(0) = 0.035, one can see the infected cell component $y(t) \to 0$ and the free virus component $v(t) \to 0$ as $t \to \infty$. This means that the epidemics will die out (see Fig 2).

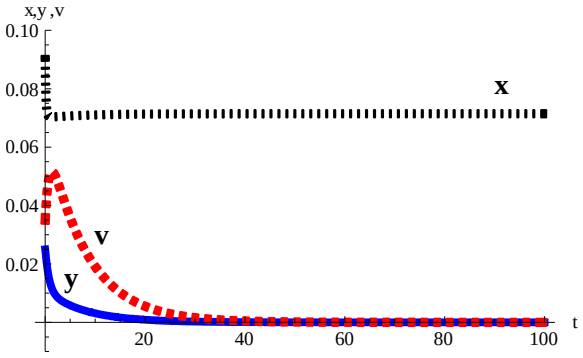

Fig 2. Time series of x, y and v for $R_0 < 1$.

*** Case $R_0 > 1$**

Choosing $\alpha = 1.2$, $\beta = 1.5$, $\delta = 5.5$, $\lambda = 1.85$, $\kappa = 2$, $\mu = 0.75$, we have $R_0 = 1.12121 > 1$. With the initial condition x(0) = 0.2, y(0) = 0.025, v(0) = 0.5, one can see the infected cell component $y(t) \to 0.751$ and the free virus component $v(t) \to 0.4325$ as $t \to \infty$. This means that the epidemics still remain (see Fig 3).

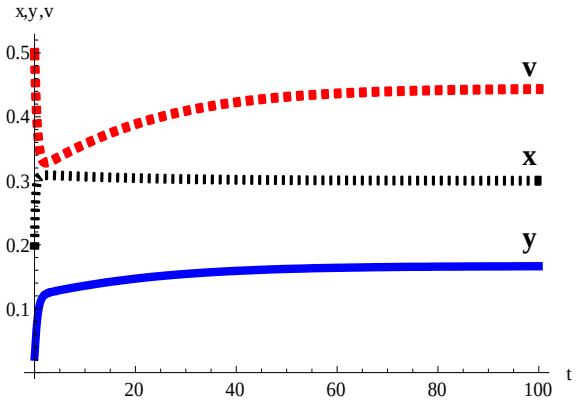

Fig 3. Time series of x, y and v for $R_0 > 1$.

4 Stability of Equilibria

The local stability for equilibria is determined by the Jacobian matrix of the system (1), which is

$$J=\begin{pmatrix} -\delta-\beta v & 0 & -\beta x \\ \beta v & -\alpha & \beta x \\ 0 & \kappa & -\mu \end{pmatrix}.$$

4.1 The free disease equilibrium E_0

The free disease equilibrium $E_0(\lambda/\delta, 0, 0)$ always exists for $\lambda > 0$ and $\delta > 0$.

Theorem 1. *The free disease equilibrium* E_0 *is locally asymptotically stalble for* $R_0 < 1$ *and unstable for* $R_0 > 1$.

Proof. The Jacobian matrix at E_0 is given by

$$J_0=\begin{pmatrix} -\delta & 0 & -\dfrac{\beta\lambda}{\delta} \\ 0 & -\alpha & \dfrac{\beta\lambda}{\delta} \\ 0 & \kappa & -\mu \end{pmatrix}.$$

The eigenvalues are obtained by solving the characteristic equation $\det(J_0 - \lambda I) = 0$ due to Mathematica. We get the following eigenvalues:

$$\lambda_1 = -\delta,$$
$$\lambda_2 = \frac{1}{2}\left[-(\alpha+\mu)\sqrt{\delta} - \sqrt{\alpha^2\delta + 4\beta\kappa\lambda - 2\alpha\delta\mu + \delta\mu^2}\right],$$
$$\lambda_3 = \frac{1}{2}\left[-(\alpha+\mu)\sqrt{\delta} + \sqrt{\alpha^2\delta + 4\beta\kappa\lambda - 2\alpha\delta\mu + \delta\mu^2}\right].$$

We see that $\lambda_1 < 0$, $\lambda_2 < 0$. When $R_0 < 1$, we have $\beta\lambda\kappa < \alpha\delta\mu$ and

$$\lambda_3 = (\alpha+\mu)\sqrt{\delta} > \sqrt{\alpha^2\delta + 4\beta\kappa\lambda - 2\alpha\delta\mu + \delta\mu^2}\ .$$

This implies $\lambda_3 < 0$. Therefore, E_0 is stable.

Similarly, if $R_0 > 1$ then $\beta\lambda\kappa > \alpha\delta\mu$. It leads to $\lambda_3 > 0$ and E_0 is unstable.

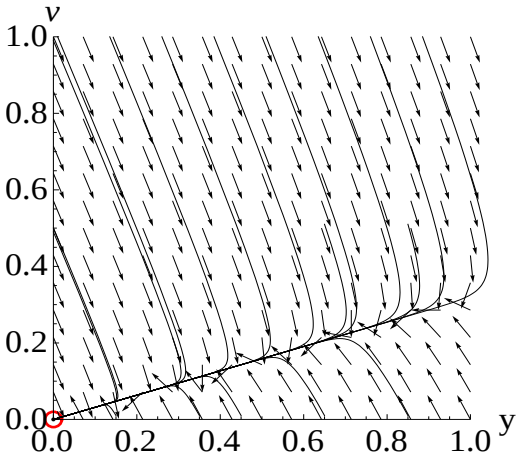

Fig 4. Phase trajectories of the system (1) near E_0 on the (y, v) plane. The circle stands for E_0.

Remark 1. For $R_0 < 1$, if $u(t) = (x(t), y(t), v(t))$ is a solution of the system (1) near to $E_0(\lambda/\delta, 0, 0)$ then $u(t) \to E_0$ as $t \to \infty$. Therefore, $u(t) \to 0$ and $v(t) \to 0$ as $t \to \infty$. This means that the epidemics will die out.

4.2 The endemic disease equilibrium E_1

For $R_0 > 1$, from (2) we can see the endemic disease equilibrium $E_1(x^*, y^*, z^*)$ has positive coordinates. Therefore, E_1 is belonging to the invariant set D.

Theorem 2. *The endemic disease equilibrium* E_1 *is only existed and locally asymptotically stable for* $R_0 > 1$.

Proof. The Jacobian matrix evalued at E_0 is given by

$$J_1=\begin{pmatrix} -\delta-\beta v^* & 0 & -\beta x^* \\ \beta v^* & -\alpha & \beta x^* \\ 0 & \kappa & -\mu \end{pmatrix},$$

where x^*, y^* and v^* are given by (2).

Solving the characteristic equation $\det(J_1 - \lambda I) = 0$ by Mathematica, we obtain the following eigenvalues:

$$\bar{\lambda}_1 = -\mu\ < 0,$$
$$\bar{\lambda}_2 = -\frac{\alpha^2\mu + \beta\kappa\lambda + \sqrt{\alpha^4\mu^2 + 4\alpha^3\mu^3\delta - 2\alpha^2\mu\beta\kappa\lambda + \beta^2\kappa^2\lambda^2}}{2\alpha\mu},$$
$$\bar{\lambda}_3 = \frac{-\alpha^2\mu - \beta\kappa\lambda + \sqrt{\alpha^4\mu^2 + 4\alpha^3\mu^3\delta - 2\alpha^2\mu\beta\kappa\lambda + \beta^2\kappa^2\lambda^2}}{2\alpha\mu}.$$

It is easy to see that $\bar{\lambda}_1 < 0$, $\bar{\lambda}_2 < 0$. For $R_0 > 1$, we have $\beta\lambda\kappa > \alpha\delta\mu$ and

$$\alpha^2\mu + \beta\kappa\lambda > \sqrt{\alpha^4\mu^2 + 4\alpha^3\mu^3\delta - 2\alpha^2\mu\beta\kappa\lambda + \beta^2\kappa^2\lambda^2}$$

This implies $\bar{\lambda}_3 < 0$. Therefore, E_1 is stable.

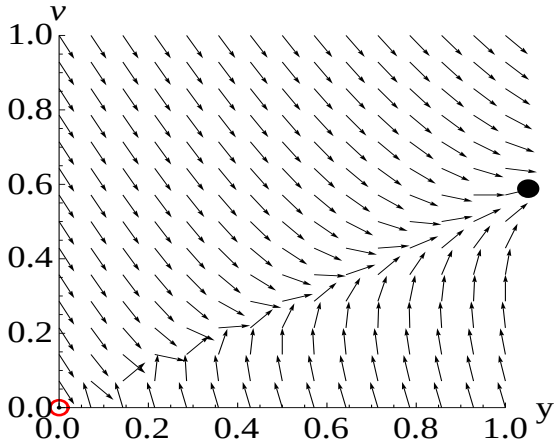

Fig 5. Phase trajectories of the system (1) on the (y, v) plane. The circle stands for E_0 and the solid circle is for E_1.

Remark 2. For $R_0 > 1$, if $u(t) = (x(t), y(t), v(t))$ is a solution of the system (1) near to $E_1(x^*, y^*, z^*)$, where x^*, y^*, z^* are given by (2), then $u(t) \to E_1$ as $t \to \infty$. Therefore, $u(t) \to x^* > 0$ and $v(t) \to y^* > 0$ as $t \to \infty$. This shows that the transmission remains.

5 BIFURCATION ANALYSIS

In this section we study the change of solution of the system (1) as parameters vary. The change of dynamical feature of the system is called bifurcation. In order to explain bifurcation of the system we assume that the equilibrium E_1 exists for $R_0 < 1$, although this is untrue. The software package AUTO is useful tool to detect bifurcation points.

The free disease equilibrium E_0 always exists. As $R_0 > 1$, it is unstable. When $R_0 < 1$, it is stable, and this is correspondent to the transmission die out. The disease virus equilibrium E_1 only exists for $R_0 > 1$. It is stable and this case corresponds to the epidemics still remain. Transcritical bifurcation occurs as $R_0 = 1$. At this value, E_0 loses its stability (the eigenvalue λ_3 moves from negative to positive) and change from stable to unstable. For $R_0 > 1$, E_1 go from unstable to stable. Two equilibria exchange their stability. This bifurcation explains the meaning of the basic reproductive ratio R_0 that decide the epidemics die out or remain.

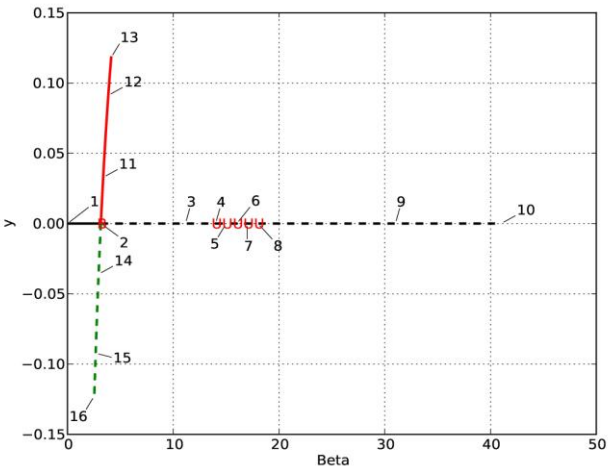

Fig 6. Bifurcation duagram of the HIV model in the (β, y) plane

By using the software package AUTO [3], one can detect the transcritical bifurcation of the equilibria E_0 and E_1. Fixing the following parameters $\alpha = 1$, $\delta = 7.0$, $\gamma = 0.1$, $\lambda = 0.5$, $\kappa = 2.0$, $\mu = 0.45$ and let β varies. We note that β is important parameter that cause the infection of virus on cells. Continue from the free disease equilibrium E_0 with $x = 0.0714286$, $y = 0$ and $v = 0$, AUTO detects a transcitical bifurcation occurs at value $\beta = 3.1499$ that correspond to $R_0 = 1$. At this value, two equilibria exchange their stability.

Figure 6 shows the bifurcation diagram of the HIV model computed by AUTO. The horizontal axes stands for the parameter β and the vertical axes is for values of y. The line contains solutions 1, 2, ..., 10 is the line of the free disease equilibria and the line consists of solutions 13, 12, 11, 2, 14, 15 and 16 is the line of the endemic disease equilibria. The dashed line is unstable and the solid line is stable. The transcritical bifurcation occurs at the solution 2.

6 CONCLUSION

A model for the infection of HIV was constructed and analyzed. We examine the potential effects of the proximate determinants of HIV transmission dynamics alone and in combination. There are two equilibrium points for this model, first, E_0 occurs when all the cells are not infected and there is no contaminated process. This point is called a disease-free equilibrium point. Second, E_1 occurs when there are HIV-infected cells and contaminated process. Several parameters affect on x(t), y(t), and v(t). One of important parameters is the rate β that relating to infection of virus on uninfected cells. The basic reproductive ratio R_0 is the factor that governs the transmission of disease. By governing suitable parameters, one can let $R_0 < 1$ and the disease will die out. The theory of dynamical system shows that a transcritical bifurcation occurs for $R_0 = 1$. The software Mathematica and AUTO is used to describe the dynamics of the model. This model reflects many stability properties of more complicated models.

ACKNOWLEDGMENT

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