The Australian Journal of Mathematical Analysis and Applications

AJMAA

Volume 16, Issue 1, Article 17, pp. 1-11, 2019

DYNAMICAL ANALYSIS OF HIV/AIDS EPIDEMIC MODEL WITH TWO LATENT STAGES, VERTICAL TRANSMISSION AND TREATMENT

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Received 30 November, 2018; accepted 13 April, 2019; published 4 June, 2019.

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ABSTRACT. We discuss about dynamical analysis of HIV/AIDS epidemic model with two latent stages, vertical transmission and treatment. In this model, the spreading of HIV occurs through both horizontal and vertical transmission. There is also treatment for individual who has been HIV infected. The latent stage is divided into slow and fast latent stage based on the immune condition which varies for each individual. Dynamical analysis result shows that the model has two equilibrium points: the disease-free equilibrium point and the endemic equilibrium point. The existence and global stability of equilibrium points depend on the basic reproduction number R_0. When $R_0 < 1$, only the disease-free equilibrium point exists. If $R_0 > 1$, there are two equilibrium points, which are the disease-free equilibrium point and the endemic equilibrium point. Based on the result of stability analysis, the disease-free equilibrium point is globally asymptotically stable if $R_0 < 1$, while if $R_0 > 1$ and $p = q$, the endemic equilibrium point will be globally asymptotically stable. In the end, we show some numerical simulations to support the analytical result.

Key words and phrases: HIV/AIDS model; Two latent stages; Vertical transmission; Treatment.

2000 *Mathematics Subject Classification.* Primary 46C05, 46C99. Secondary 26D15, 26D10.

ISSN (electronic): 1449-5910

This research is supported by Hibah Peneliti Pemula (HPP 2018), LPPM, University of Brawijaya with contract number DIPA-042.012.400919/2018.

1. INTRODUCTION

Human Immune deficiency Virus (HIV) is virus that cause a disease in human immune system called AIDS (Acquired Immune Deficiency Syndrome). AIDS developed into a global pandemic since it was first identified as a disease in 1981. The spreading of HIV occurred through horizontal transmission, e.g., blood transfusion, contaminated equipment in blood transfusion, sexual intercourse [1]. Beside that, HIV also spread through vertical transmission from infected mother to her baby during pregnancy, the birth of her baby, or breastfeeding [2, 3].

There is no medical cure for HIV/AIDS. However, there are some options, such as prevention (avoid the direct and indirect contact with the virus) and understanding the spread of the virus. This understanding also can be obtained from mathematical models; this represents the HIV / AIDS model. Many researchers have worked on development of the HIV/AIDS model. The first one was introduced by May and Anderson [4] in 1986.

The progression rate of HIV to AIDS depends on the condition of immune system. The latent period for the individual that has good immune system may be longer than the individual with an immune system in a worse condition. One of the factors that can reduce the immune condition is chronic disease, e.g., TBC and diabetes. Based on this consideration, at 2013, Huo and Feng [1] constructed and analysed the global stability of HIV/AIDS epidemic model with different latent stages (slow latent and fast latent stages) and treatment.

As the third biggest method of HIV's infection, vertical transmission should also be considered in HIV/AIDS models. Smith et al. [2] discussed about SEIR epidemic model with vertical transmission. Mahato et al., [3] proposed a mathematical model SEIA with vertical transmission of AIDS epidemic. Even though there is still no medicine that can cure this disease, the treatment is very important step to reduce the number of infected individuals. Cai et al. [5] and Huo et al. [6] discussed about HIV/AIDS model with treatment.

This research focuses on HIV/AIDS epidemic model with two latent stages, vertical transmission and treatment. These are all the factors that are considered in spreading of HIV in other models. We construct the model under some assumptions and then perform dynamical analysis of the model: find the equilibrium points, find the basic reproduction number, analyse the existence of the equilibrium points, and analyse the stability of the equilibrium points. Lastly, we do some numerical simulations to support the analytical result that we have obtained.

2. MATHEMATICAL MODEL

In HIV/AIDS epidemic model with two latent stages, vertical transmission and treatment, the population is divided into 5 sub population: Susceptible (S), Slow Latent (I_1), Fast Latent (I_2), Symptomatic (J) and AIDS (A) subpopulation. Susceptible S consist of individual that susceptible of the disease, Slow Latent I_1 consist of individual in latent period / asymptomatic stage and never have the chronic disease before, Fast latent I_2 consist of individual in latent period / asymptomatic stage and have the chronic disease before, Symptomatic J consist of individual in Symptomatic stage / infected individual, and AIDS A subpopulation consist of individual that its HIV has been developing progress into AIDS. The model is constructed under the assumptions:

- The spread of HIV virus is caused by horizontal and vertical transmission. Horizontal transmission through interaction between susceptible individuals with individuals in fast latent stage and symptomatic stage, while vertical transmission from mother in fast latent stage.
- Babies born from infected mother are assumed to be directly infected with HIV. Therefore, they will enter directly into Symptomatic stage (J)

- Some susceptible individuals have other chronic diseases (TBC, diabetes) that can reduce the capacity of the immune system.
- The treatment for infected individual can make the individual condition better
- The number of babies that are infected (from vertical transmission process) is less than the number of individual that have died because of AIDS ($\gamma I_2 < \alpha A$).

The model can be written as the system of differential equations:

$$\begin{aligned}
\frac{dS}{dt} &= \Lambda - \gamma I_2 - (\beta_1 I_2 S + \beta_2 J S) - \mu S, \\
\frac{dI_1}{dt} &= p\beta_1 I_2 S + q\beta_2 J S + \xi_1 J - b_1 I_1, \\
\frac{dI_2}{dt} &= (1-p)\beta_1 I_2 S + (1-q)\beta_2 J S + \varepsilon I_1 + \xi_2 J - b_2 I_2, \\
\frac{dJ}{dt} &= b_5 I_2 - b_3 J, \\
\frac{dA}{dt} &= p_2 J - b_4 A,
\end{aligned}$$

with $b_1 = \varepsilon + \mu, b_2 = p_1 + \mu, b_3 = \xi_1 + \xi_2 + p_2 + \mu, b_4 = \mu + \alpha, b_5 = p_1 + \gamma$ and the parameters used in the model are described in Table 1.
The feasible domain Ω be defined as

$$\Omega = \{S(t), I_1(t), I_2(t), J(t), A(t) \in R_+^5, S(t) + I_1(t) + I_2(t) + J(t) + A(t) \leq \frac{\Lambda}{\mu}\},$$

with $S(0) \geq 0, I_1(0) \geq 0, I_2(0) \geq 0, J(0) \geq 0, A(0) \geq 0$ as initial condition.

The compartment diagram that represent this model can be depicted in Figure 1.

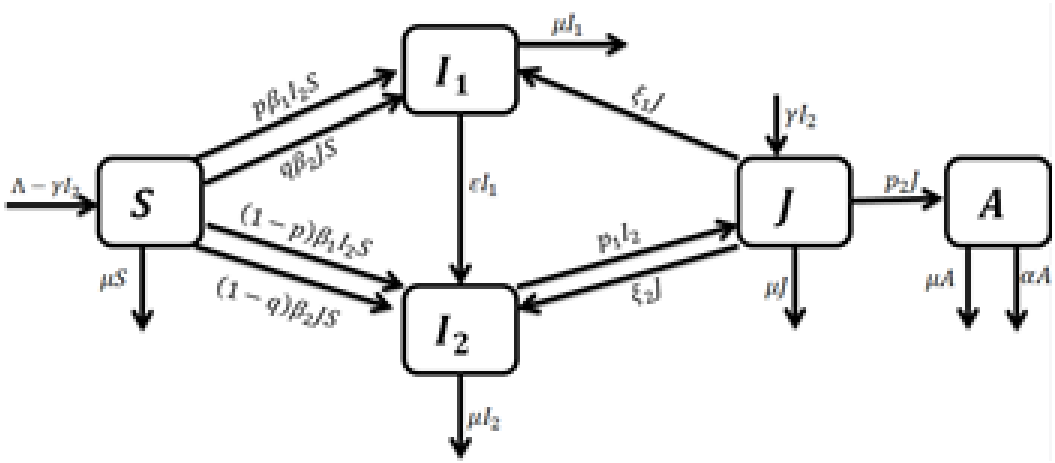

Figure 1: The compartment diagram of HIV/AIDS epidemic model with two latent stages, vertical transmission and treatment

Table 1. Parameters of The Model

Parameter	Description
Λ	Recruitment rate of the population
β_1	Transmission coefficient of I_2
β_2	Transmission coefficient of J
p	Fraction of S being infected by I_2 and entering I_1
q	Fraction of S being infected by J and entering I_1
ε	Progression rate I_1 to I_2
p_1	Progression rate I_2 to J
p_2	Progression rate J to A
ξ_1	Treatment rate from J to I_1
ξ_2	Treatment rate from J to I_2
γ	Vertical transmission rate
μ	Natural death rate
α	The disease-related death rate

3. EQUILIBRIUM POINTS AND BASIC REPRODUCTION NUMBER

We find the equilibrium point by using the definition of equilibrium point [7], we set

$$\frac{dS}{dt} = \frac{dI_1}{dt} = \frac{dI_2}{dt} = \frac{dJ}{dt} = \frac{dA}{dt} = 0.$$

We find that the model has two equilibrium points,

(1) The disease-free equilibrium point

$$E^0 = (S^0, I_1^0, I_2^0, J^0, A^0) = (\frac{\Lambda}{\mu}, 0, 0, 0, 0).$$

The disease-free equilibrium point always exist.

(2) The endemic equilibrium point

$$E^* = (S^*, I_1^*, I_2^*, J^*, A^*),$$

with

$$S^* = \frac{\Lambda - \gamma(\frac{b_3 J^*}{b_5})}{\beta_1 \frac{b_3}{b_5} J^* + \beta_2 J^* + \mu},$$

$$I_1^* = \frac{J}{b_1}\left(\left(p\beta_1 \frac{b_3}{b_5} + q\beta_2\right)\left(\frac{\Lambda b_5 - \gamma b_3 J^*}{\beta_1 b_3 J^* + \beta_2 J^* b_5 + \mu b_5}\right) + \xi_1\right),$$

$$I_2^* = \frac{b_3}{b_5} J^*,$$

$$J^* = \frac{b_5 I_2^*}{b_3},$$

$$A^* = \frac{p_2}{b_4} J^*.$$

Basic reproduction number R_0 is the important number in epidemic model. It represent the number of new infected individual because of infection that occurred in the population [8]. Basic reproduction number can show whether the spread of HIV/AIDS has occurred in a population or not. We use Next Generation Matrix [9] to approximate the basic reproduction number R_0. Let $\mathbf{x} = (I_1, I_2, J, A)$, from the model, we have $\frac{d\mathbf{x}}{dt} = F(\mathbf{x}) - V(\mathbf{x})$,

with

$$F(\mathbf{x}) = \begin{bmatrix} p\beta_1 I_2 S + q\beta_2 JS \\ (1-p)\beta_1 I_2 S + (1-q)\beta_2 JS \\ 0 \\ 0 \end{bmatrix}, \; V(\mathbf{x}) = \begin{bmatrix} b_1 I_1 - \xi_1 J \\ b_2 I_2 - (\epsilon I_1 + \xi_2 J) \\ b_3 J - b_5 I_2 \\ b_4 A - p_2 J \end{bmatrix},$$

The Jacobian matrix for F and V at disease-free equilibrium point E^0,

$$F(E^0) = \begin{bmatrix} 0 & p\beta_1\frac{\Lambda}{\mu} & q\beta_2\frac{\Lambda}{\mu} & 0 \\ 0 & (1-p)\beta_1\frac{\Lambda}{\mu} & (1-q)\beta_2\frac{\Lambda}{\mu} & 0 \\ 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 \end{bmatrix}, \; V(E^0) = \begin{bmatrix} b_1 & 0 & -\xi_1 & 0 \\ -\epsilon & b_2 & -\xi_2 & 0 \\ 0 & -b_5 & b_3 & 0 \\ 0 & 0 & -p_2 & b_4 \end{bmatrix}.$$

Basic reproduction number can be approximated as spectral radius of FV^{-1} matrix, which is the biggest modulus of eigen values of FV^{-1} matrix. We obtain,

$$R_0 = \frac{(\beta_1 b_3((1-p)b_1 + p\epsilon) + \beta_2 b_5(q\epsilon + (1-q)b_1)\frac{\Lambda}{\mu}}{b_1 b_2 b_3 - b_5(b_1\xi_2 + \xi_1\epsilon)}.$$

Basic reproduction number R_0 must be positive. Therefore, it is required that

$$b_1 b_2 b_3 > b_5(b_1\xi_2 + \xi_1\epsilon).$$

To know the existence of the endemic equilibrium point, we can rewritten the endemic equilibrium point in term of R_0 then we get that the endemic equilibrium point exists if $R_0 > 1$.

4. GLOBAL STABILITY ANALYSIS

(1) Global Stability of Disease-Free Equilibrium Point

Theorem 4.1. *The Disease-Free Equilibrium Point is globally asymptotically stable if* $R_0 < 1$.

Proof. We use comparison theorem [10] to analyse the global stability of disease-free equilibrium. Write the rate of change of I_1, I_2, J, A in matrix form,

$$\begin{aligned} \begin{bmatrix} I_1' \\ I_2' \\ J' \\ A' \end{bmatrix} &= \begin{bmatrix} -b_1 & p\beta_1 S & q\beta_2 S + \xi_1 & 0 \\ \varepsilon & (1-p)\beta_1 S - b_2 & (1-q)\beta_2 S + \xi_2 & 0 \\ 0 & b_5 & -b_3 & 0 \\ 0 & 0 & p_2 & -b_4 \end{bmatrix} \begin{bmatrix} I_1 \\ I_2 \\ J \\ A \end{bmatrix} \\ &= (F-V)\begin{bmatrix} I_1 \\ I_2 \\ J \\ A \end{bmatrix} - (1 - S\frac{\Lambda}{\mu})F \begin{bmatrix} I_1 \\ I_2 \\ J \\ A \end{bmatrix} \\ &\leq (F-V)\begin{bmatrix} I_1 \\ I_2 \\ J \\ A \end{bmatrix}. \end{aligned}$$

Based on Lemma related with Next Generation Matrix in [9], all eigen values of (FV^{-1}) matrix have negative real part. Furthermore, the disease-free equilibrium will be locally asymptotically stable when $R_0 < 1$. Hence, when $R_0 < 1$,

$(I_1, I_2, J, A) \to (0, 0, 0, 0)$ for $t \to \infty$.

Then we have $S \to \dfrac{\Lambda}{\mu}$ because $S(t) + I_1(t) + I_2(t) + J(t) + A(t) \leq \dfrac{\Lambda}{\mu}$ (the feasible domain Ω) and $(I_1, I_2, J, A) \to (0, 0, 0, 0)$.

Here we can write $(S, I_1, I_2, J, A) \to (\dfrac{\Lambda}{\mu}, 0, 0, 0, 0)$ for $t \to \infty$ when $R_0 < 1$. We conclude that when $R_0 < 1$, the disease-free equilibrium point will be globally asymptotically stable. This conclude the proof of Theorem 4.1. ∎

(2) Global Stability of Endemic Equilibrium Point

Theorem 4.2. *The Endemic Equilibrium Point is globally asymptotically stable if* $R_0 > 1$ *and* $p = q$.

Proof. In order to show the global stability of endemic equilibrium point, we use Lyapunov function that be used in Li et al. [11]

$$\begin{aligned} & L(S, I_1, I_2, J, A) \\ = \ & (S - S^* - S^* ln\frac{S}{S^*}) + B(I_1 - I_1^* - I_1^* ln\frac{I_1}{I_1^*}) + C(I_2 - I_2^* - I_2^* ln\frac{I_2}{I_2^*}) + D(J - J^* - J^* ln\frac{J}{J^*}), \end{aligned}$$

with $B, C, D > 0$ such that $L'(S, I_1, I_2, J, A) < 0$ in $\Omega = \{(S, I_1, I_2, J, A) | S, I_1, I_2, J, A > 0\}$. To know whether the Lyapunov function is weak Lyapunov function or strong Lyapunov function, we observe some conditions in the Definition of weak and strong Lyapunov function that explained in Alligood et al. [12],

(1) $L(E^*) = 0$
It is clear that $L(E^*) = 0$.
(2) $L(E) > 0, \forall E \neq E^*$ in W with W is some neighborhood of E^*
It is clear that $L(E) > 0, \forall E \neq E^*$ in W
(3) $L'(E) \leq 0, \forall E$ in W (weak Lyapunov function) or $L'(E) < 0, \forall E \neq E^*$ in W (strong Lyapunov function)
Based on the chain rule, we get the derivation of L,

$$\begin{aligned} L' &= (1 - \frac{S^*}{S})S' + B(1 - \frac{I_1^*}{I_1}I_1' + C(1 - \frac{I_2^*}{I_2})I_2' + D(1 - \frac{J^*}{J})J' \\ &= (1 - \frac{S^*}{S})(\Lambda - \gamma I_2 - (\beta_1 I_2 S + \beta_2 JS) - \mu S) + B(1 - \frac{I_1^*}{I_1}(p\beta_1 I_2 S + q\beta_2 JS + \xi_1 J - b_1 I_1) \\ &\quad + C(1 - \frac{I_2^*}{I_2})((1-p)\beta_1 I_2 S + (1-q)\beta_2 JS + \varepsilon I_1 + \xi_2 J - b_2 I_2) + D(1 - \frac{J^*}{J})(b_5 I_2 - b_3 J). \end{aligned}$$

Then, by using

$$\begin{aligned} \Lambda &= \gamma I_2^* + (\beta_1 I_2^* S^* + \beta_2 J^* S^*) + \mu S^*, \\ b_1 &= \frac{p\beta_1 I_2^* S^* + q\beta_2 J^* S^* + \xi_1 J^*}{I_1^*}, \\ b_2 &= \frac{(1-p)\beta_1 I_2^* S^* + (1-q)\beta_2 J^* S^* + \varepsilon I_1^* + \xi_2 J^*}{I_2^*}, \\ b_3 &= \frac{b_5 I_2^*}{J^*}, \end{aligned}$$

we obtain

$$\begin{aligned}L' &= (1-\frac{S^*}{S})(\gamma I_2^* + (\beta_1 I_2^* S^* + \beta_2 J^* S^*) + \mu S^* - \gamma I_2 - (\beta_1 I_2 S + \beta_2 J S) - \mu S)\\ &+ B(1-\frac{I_1^*}{I_1}(p\beta_1 I_2 S + q\beta_2 J S + \xi_1 J - (\frac{p\beta_1 I_2^* S^* + q\beta_2 J^* S^* + \xi_1 J^*}{I_1^*})I_1)\\ &+ C(1-\frac{I_2^*}{I_2})((1-p)\beta_1 I_2 S + (1-q)\beta_2 J S + \varepsilon I_1 + \xi_2 J\\ &- (\frac{(1-p)\beta_1 I_2^* S^* + (1-q)\beta_2 J^* S^* + \varepsilon I_1^* + \xi_2 J^*}{I_2^*})I_2)\\ &+ D(1-\frac{J^*}{J})(b_5 I_2 - (\frac{b_5 I_2^*}{J^*})J).\end{aligned}$$

Let $\frac{S}{S^*} = x, \frac{I_1}{I_1^*} = y, \frac{I_2}{I_2^*} = z, \frac{J}{J^*} = u$, then we have

$$\begin{aligned}L' &= (1-\frac{1}{x})(\gamma I_2^* + (\beta_1 I_2^* S^* + \beta_2 J^* S^*) + \mu S^* - \gamma z I_2^* - (\beta_1 z I_2^* x S^* + \beta_2 u J^* x S^*) - \mu x S^*)\\ &+ B(1-\frac{1}{y})(p\beta_1 z I_2^* x S^* + q\beta_2 u J^* x S^* + \xi_1 u J^* - (\frac{p\beta_1 I_2^* S^* + q\beta_2 J^* S^* + \xi_1 J^*}{I_1^*})y I_1^*)\\ &+ C(1-\frac{1}{z})((1-p)\beta_1 z I_2^* x S^* + (1-q)\beta_2 u J^* x S^* + \varepsilon y I_1^* + \xi_2 u J^*\\ &- (\frac{(1-p)\beta_1 I_2^* S^* + (1-q)\beta_2 J^* S^* + \varepsilon I_1^* + \xi_2 J^*}{I_2^*})z I_2^*)\\ &+ D(1-\frac{1}{u})(b_5 z I_2^* - (\frac{b_5 I_2^*}{J^*})u J^*),\end{aligned}$$

$$\begin{aligned}L' &= -\mu S^* \frac{(1-x)^2}{x} + (1 - z - \frac{1}{x} + \frac{z}{x})\gamma I_2^* + (1-\frac{1}{x})[\beta_1 I_2^* S^*(1-xz) + \beta_2 J^* S^*(1-xu)]\\ &+ B(1-\frac{1}{y})[p\beta_1 I_2^* S^*(xz-y) + q\beta_2 J^* S^*(xu-y) + \xi_1 J^*(u-y)]\\ &+ C(1-\frac{1}{z})[(1-p)\beta_1 I_2^* S^*(xz-z) + (1-q)\beta_2 J^* S^*(xu-z) + \varepsilon I_1^*(y-z) + \xi_2 J^*(u-z)]\\ &+ D(1-\frac{1}{u})[b_5 I_2^*(z-u)].\end{aligned}$$

Simplify L' such that we get some coefficients with positive variables and vanish the coefficients so that we obtain B, C and D,

$$B = \frac{\varepsilon}{\varepsilon p + b_1(1-p)}, C = \frac{b_1}{\varepsilon p + b_1(1-p)}, D = \frac{b_1 b_2}{b_5(\varepsilon p + b_1(1-p))} - \frac{\beta_1 S^* + \gamma}{b_5},$$

with $p = q$. Substitute B,C, D into L', we get

$$\begin{aligned}
L' = &-\mu S^* \frac{(1-x)^2}{x} + \frac{b_1}{\varepsilon p + b_1(1-p)}(1-p)\beta_1 I_2^* S^*(2 - x - \frac{1}{x}) \\
&+ \frac{b_1}{\varepsilon p + b_1(1-p)}\xi_2 J^*(2 - \frac{u}{z} - \frac{z}{u}) + \frac{b_1}{\varepsilon p + b_1(1-p)}(1-q)\beta_2 J^* S^*(3 - \frac{1}{x} - \frac{xu}{z} - \frac{z}{u}) \\
&+ \frac{\varepsilon}{\varepsilon p + b_1(1-p)} p\beta_1 I_2^* S^*(3 - \frac{1}{x} - \frac{xz}{y} - \frac{y}{z}) \\
&+ \frac{\varepsilon}{\varepsilon p + b_1(1-p)} q\beta_2 J^* S^*(4 - \frac{1}{x} - \frac{xu}{y} - \frac{y}{z} - \frac{z}{u}) \\
&+ \frac{\varepsilon}{\varepsilon p + b_1(1-p)}\xi_1 J^*(3 - \frac{y}{z} - \frac{z}{u} - \frac{u}{y}).
\end{aligned}$$

By using the Theorem in Peter [13], that the arithmetical mean is greater than or equal to the geometrical mean, we get $2 \geq x - \frac{1}{x}; 2 \geq \frac{u}{z} - \frac{z}{u}; 3 \geq \frac{1}{x} - \frac{xz}{y} - \frac{y}{z}; 3 \geq \frac{1}{x} - \frac{xz}{y} - \frac{y}{z}; 4 \geq \frac{1}{x} - \frac{xu}{y} - \frac{y}{z} - \frac{z}{u}; 3 \geq \frac{y}{z} - \frac{z}{u} - \frac{u}{y}$ and the equal sign will be at $\{S^*, I_1^*, I_2^*, J^*\}$, then we can conclude that $L'(E) < 0, \forall E \neq E^*$ in W, (Lyapunov function is strong Lyapunov function). Therefore, when $R_0 > 1$ and $p = q$, the endemic equilibrium point is globally asymptotically stable. This conclude the proof of Theorem 4.2. ∎

The stability of endemic equilibrium point if $R_0 > 1$ and $p \neq q$ will be illustrated numerically in numerical simulation.

5. NUMERICAL SIMULATIONS

To support the analytical results, we show three numerical simulations: Simulation 1 to illustrate the stability of disease-free equilibrium point when $R_0 < 1$, Simulation 2 to illustrate the stability of endemic equilibrium point when $R_0 > 1$ and $p = q$ and Simulation 3 to illustrate the stability of endemic equilibrium point when $R_0 > 1$ and $p \neq q$.

The parameter that be used in Simulation 1, Simulation 2 and Simulation 3 can be shown in Table 2.

Table 2. Parameters for Each Simulation

Parameter	Simulation 1	Simulation 2	Simulation 3
Λ	0.545	0.545	0.545
β_1	0.0001	0.0001	0.0001
β_2	0.0006	0.006	0.006
p_1	0.01	0.01	0.01
p_2	1.73	0.03	0.03
ε	0.002	0.002	0.002
α	0.01	0.01	0.01
μ	0.01	0.01	0.01
p	0.9	0.9	0.9
q	0.8	0.9	0.8
ξ_1	0.8	0.02	0.02
ξ_2	0.9	0.0019	0.0019
γ	0.005	0.005	0.005

(1) Simulation 1 : Stability E^0 for $R_0 = 0.1313 < 1$

In this case, only the disease-free equilibrium point exists. The numerical result of simulation 1 is depicted in Figure 2. As time increase, the initial value converge to E^o. We can say that when $R_0 < 1$ no infection occurs in the population. Therefore, the disease-free equilibrium point is globally asymptotically stable. This conclusion support the analytical result that we have obtained.

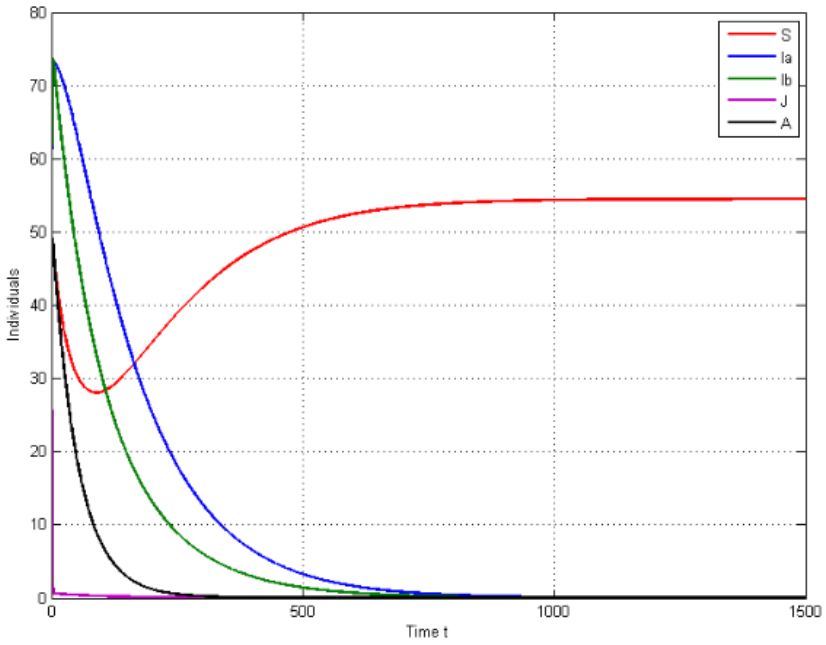

Figure 2: Stability E^0 for $R_0 = 0.1313 < 1$

(2) Simulation 2 : Stability E^* for $R_0 = 1.303 > 1$ and $p = q$

In Simulation 2, the disease-free equilibrium point and endemic equilibrium point exist. From Figure 3, we can conclude that the infections occurred in that population. The initial value converge to E^* which is the endemic equilibrium point. Therefore, we get the same result with the analytical result, when $R_0 > 1$ and $p = q$ the endemic equilibrium point is globally asymptotically stable.

(3) Simulation 3 : Stability E^* for $R_0 = 1.4828 > 1$ and $p \neq q$

The result of simulation 3 is almost the same as simulation 2. Figure 4 shows that when $R_0 > 1$ and $p \neq q$, the infection still occurred in that population and the initial condition converge to endemic equilibrium point. If $R_0 > 1$ and $p \neq q$, the numerical result shows that the endemic equilibrium point is globally asymptotically stable.

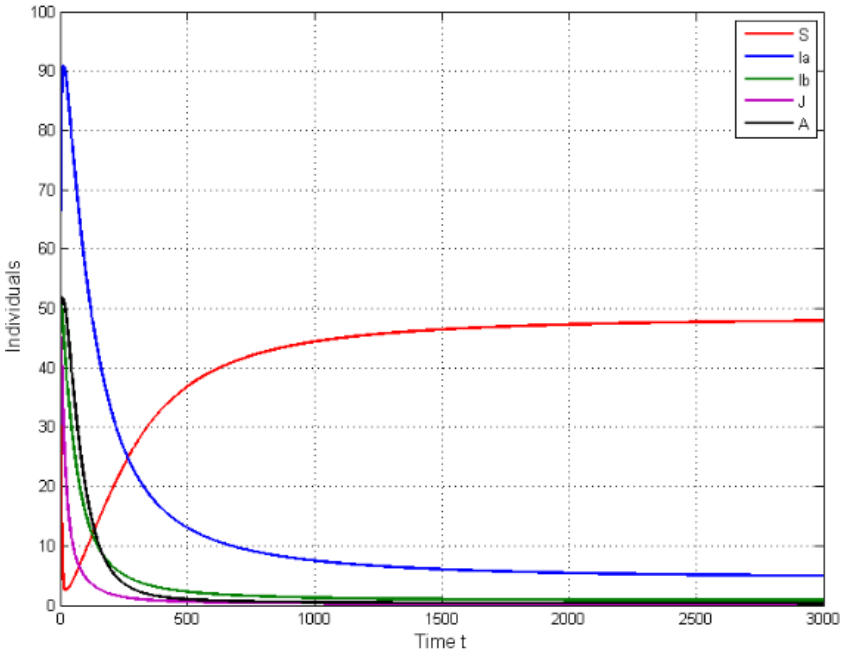

Figure 3: Stability E^* for $R_0 = 1.303 > 1$ and $p = q$

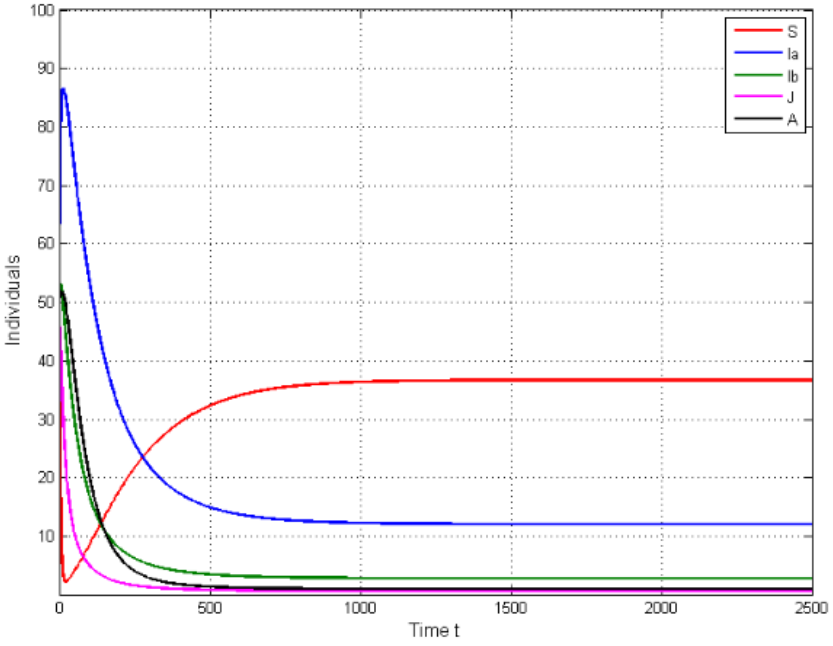

Figure 4: Stability E^* for $R_0 = 1.4828 > 1$ and $p \neq q$

6. CONCLUSION

We can conclude some results about HIV/AIDS model with two latent stages, vertical transmission and treatment. The model has two equilibrium points, which are the disease-free and the endemic equilibrium points. The existence and stability of equilibrium points depend on R_0. If $R_0 < 1$, there is one equilibrium point which is exist, namely the disease-free equilibrium point. If $R_0 > 1$, there are two equilibrium points, which are the disease-free and the endemic equilibrium points. Based on stability analysis result, we obtained that the disease-free equilibrium point will be globally asymptotically stable if $R_0 < 1$, while the endemic equilibrium point will be globally asymptotically stable if $R_0 > 1$ and $p = q$. The numerical simulations support the analytical results.

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