Journal of Mathematical Extension
Vol. 11, No. 2, (2017), 19-31
ISSN: 1735-8299
URL: http://www.ijmex.com

Dynamic Analysis of a Mathematical Model for HIV and Hepatitis C Virus Co-Infection

M. Zerehpoush*
University of Tabriz

H. Kheiri
University of Tabriz

Abstract. Hepatitis C is the leading cause of death among individuals infected with human. Here, we present a deterministic model for HCV and HIV infections transmission and use the model to assess the potential impact of antiviral therapy. The model is based on the Susceptible-Infective-Removed-Susceptible (SIRS) compartmental structure with chronic primary infection and possibility of reinfection. Important epidemiologic thresholds such as the basic and control reproduction numbers and a measure of treatment impact are derived. We find that if the control reproduction number is greater than unity, there is a locally unstable infection-free equilibrium and a unique, globally asymptotically stable endemic equilibrium. If the control reproduction number is less than unity, the infection-free equilibrium is globally asymptotically stable.

AMS Subject Classification: 92B05; 92D25; 92D30
Keywords and Phrases: Dynamical systems, Epidemiological models, HIV/AIDS, Reproduction number, Stability

1. Introduction

we propose a class of HIV infection models incorporating both HIV positive (only individuals not yet showing AIDS) and direct HIV positive to HIV posi-

Received: April 2016; Accepted: Jonuary 2017
*Corresponding author

tive transmission. According to recent studies, the direct HIV positive to HIV positive transfer of HIV is a significantly more efficient mode of retroviral dissemination. Infection with hepatitis C virus (HCV) is a major global public health problem. According to the Word Health Organization (WHO) statistics, 3-4 million people are infected every year and the number of people currently infected with HCV worldwide is approximately 130-150 million [10]. However, the study of infectious disease co-epidemics is critical to understanding how the diseases are related, and how prevention and treatment efforts can be most effective. Mathematical models can provide insight into the complicated infection dynamics, and into effective control measures. Most mathematical epidemic models evaluate a single disease [8, 11], although a growing number of studies have considered co-epidemics [7, 13]. Mathematical studies of co-infection models are not very common. On the other hand, the huge public health burden inflicted by HIV and HCV necessitates the use of mathematical modeling to gain insights into their transmission dynamics and to determine effective control strategies. Co-infection with HIV has been associated with a more rapid progression of liver disease as well as a higher prevalence of cirrhosis [1, 6, 12, 16, 17]. The paper is organized as follows; In Section 2, we present an HCV/HIV model that allows for the incorporation of both infections. In Section 3, the basic reproduction numbers of each infectious disease and the overall reproduction number for the full system are computed. Furthermore, we study the existence of equilibria and their stabilities. Section 4 is devoted to discussing the results of our analysis using selected numerical solutions.

2. Model Formulation

Based on the individuals epidemiological status, the total population N has been subdivided into the following classes or subgroups: Susceptible individuals to both diseases $S(t)$, HIV positive-only individuals not yet showing HIV symptoms $J_h(t)$, $I_h(t)$ represent positive-only individuals not yet showing HIV that cannot produce virions but are ready to do so once they are activated by their recall antigens. individuals infected just with hepatitis C $I_c(t)$, AIDS patients not yet on antiretroviral therapy $A_h(t)$, AIDS patients on antiretroviral therapy $A_t(t)$. We consider HIV positive not yet showing AIDS symptoms dually infected with HCV in two classes called $I_{hc}(t)$ and $J_{hc}(t)$, AIDS patients not yet on antiretroviral therapy dually infected with HCV $A_{hc}(t)$, AIDS patients on antiretroviral therapy dually infected with HCV $A_{tc}(t)$. AIDS patients in this model are assumed to be sexually inactive study. Thus, the total population size is given by

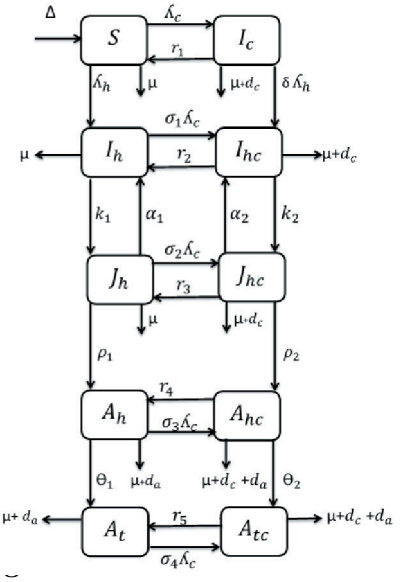
$$\begin{aligned} N(t) &= S(t) + I_h(t) + I_c(t) + J_h(t) + A_h(t) + A_t(t) \\ &+ I_{hc}(t) + J_{hc}(t) + A_{hc}(t) + A_{tc}(t). \end{aligned} \tag{1}$$

Suppose that Λ is constant recruitment rate. Furthermore, natural mortality rate, μ, is assumed to be constant in all classes. The forces of infection associated with HCV or HIV infection denoted by λ_c, λ_h, respectively, have the form

$$\lambda_h(t) = \frac{\beta_h[I_h(t) + \phi I_{hc}(t)]}{N(t)}, \qquad \lambda_c(t) = \frac{\beta_c[I_c(t) + \eta I_{hc}(t)]}{N(t)}. \tag{2}$$

Parameters β_c and β_h denotes the probability of getting infected with either HCV or HIV, respectively. The parameter $\eta > 1$ and $\phi > 1$ captures the assumed increased probability for individuals dually infected with HCV and HIV to infect their partners. Susceptible individuals are infected with HIV and HCV at rates λ_h and λ_c, respectively.

Once an individual have been infected with HCV, they enter the class I_c. Individuals in I_c move back into the susceptible class following treatment at a rate r_1, since previous infection does not confer immunity. Susceptible infected with HIV enters symptomless HIV class I_h move in to class J_h at a rate k, people in class J_h where they progress to the AIDS class A_h at a rate ρ. Individuals in the AIDS stage J_h are detected and put on treatment at rate θ to enter the class A_t. HIV infected individuals not yet in the AIDS stage of disease progression, I_h are infected with HCV at rates $\sigma\lambda_c$ to enter thc class, J_h are infected with HCV at rates $\sigma\lambda_c$ to enter J_{hc} class. It is worth noting that $\sigma > 1$ is the modification parameter accounting for the increased risk of getting HCV infection for someone already infected with HIV (since most co-infections potentially promote transmission and faster progression to AIDS). HCV infected individuals $(I_c; I_{hc}; J_{hc}; A_{hc}; A_{tc})$ have an additional HCV induced death rate d_c. Individuals in the AIDS stages of disease progression $(A_h; A_t; A_{hc}; A_{tc})$ have an additional AIDS-induced death rate d_a. HCV only infected individuals I_c are infected with HIV at a rate $\sigma\lambda(\sigma > 1)$ to move into the class I_{hc}. Here, $\delta > 1$ accounts for the increased susceptibility to HIV infection for HCV infected people, since HCV exerts a cofactor effect, leading to accelerated decline in immune function and increased vulnerability to other infections. Individuals in I_{hc} enter J_{hc} at a rate k, People in J_{hc} progress to their respective AIDS stage A_{hc} at a rate ρ. AIDS patients dually infected with HCV are detected and put on antiretroviral therapy at a rate θ_2 to get into A_{tc} class. Dually infected people in the classes I_{hc}, A_{hc} and A_{tc} are treated for HCV at rates r_2, r_3, r_4 and r_5 to move back into the classes I_h, J_h, A_h and A_t, respectively.



The parameters k_1 and k_2 represent the rate at which HIV Latent-infected individuals and Latent-infected individuals dually infected with HCV move to HIV-positive class and HIV-positive class dually infected with HCV, respectively. The parameters α_1 and α_2 are the transmission rate of J_h and J_{hc} classes to I_h and I_{hc} classes. The population is assumed to be uniform and homogeneously mixing. The structure of the model is presented in Fig. 1. Motivated by Bhunu and Mushayabasa in [3], our HCV/HIV model is given by the following systems of ten ordinary differential equations:

$$
\begin{aligned}
\dot{S}(t) &= \Lambda - (\lambda_c + \lambda_h + \mu)S + r_1 I_c,\\
\dot{I}_c(t) &= \lambda_c S - (\mu + d_c + r_1 + \delta\lambda_h)I_c,\\
\dot{I}_h(t) &= \lambda_h S + r_2 I_{hc} - (\mu + \sigma_1\lambda_c + k_1)I_h + \alpha_1 J_h,\\
\dot{J}_h(t) &= k_1 I_h + r_3 J_{hc} - (\mu + \alpha_1 + \rho_1 + \sigma_2\lambda_c)J_h,\\
\dot{A}_h(t) &= \rho_1 J_h + r_4 A_{hc} - (\mu + d_a + \theta_1 + \sigma_3\lambda_c)A_h,\\
\dot{A}_t(t) &= \theta_1 A_h + r_5 A_{tc} - (\mu + d_a + \sigma_4\lambda_c)A_t,\\
\dot{I}_{hc}(t) &= \delta\lambda_h I_c + \sigma_1\lambda_c I_h - (\mu + d_c + r_2 + k_2) + \alpha_2 J_{hc},\\
\dot{J}_{hc}(t) &= \sigma_2\lambda_c J_h - (\mu + d_c + r_3 + \rho_2 + \alpha_2)J_{hc} + k_2 I_{hc},\\
\dot{A}_{hc}(t) &= \rho_2 J_{hc} + \sigma_3\lambda_c A_h - (\mu + d_a + d_c + \theta_2 + r_4)A_{hc},\\
\dot{A}_{tc}(t) &= \theta_2 A_{hc} + \sigma_4\lambda_c A_t - (\mu + d_a + d_c + r_5)A_{tc}.
\end{aligned}
\tag{3}
$$

3. Model Properties

In this section, we study the basic properties of the solutions of system (3), which are for the proofs of stability.

3.1 Invariant region

The following Lemmas show that the solution of system (3), remains bounded (and hence exists for all time) and is nonnegative for all $t > 0$.

Lemma 3.1.1. *The region* Ω *defined by*

$$\Omega = \Big\{S, I_c, I_h, J_h, A_h, A_t, I_{hc}, J_{hc}, A_{hc}, A_{tc} \in R_+^{10} : N \leqslant \frac{\Lambda}{\mu}\Big\},$$

is positively invariant and attracting with respect to model (3).

Proof. Let $(S, I_c, I_h, J_h, A_h, A_t, I_{hc}, J_{hc}, A_{hc}, A_{tc}) \in R_+$ be any solution of system (3) with given nonnegative initial condition

$$(S(0), I_c(0), I_h(0), J_h(0), A_h(0), A_t(0), I_{hc}(0), J_{hc}(0), A_{hc}(0), A_{tc}(0)).$$

Since

$$\begin{aligned} \dot{N}(t) &= \dot{S}(t) + \dot{I}_h(t) + \dot{J}_h(t) + \dot{I}_c(t) + \dot{A}_h(t) \\ &+ \dot{A}_t(t) + \dot{I_{hc}}(t) + \dot{J_{hc}}(t) + \dot{A_{hc}}(t) + \dot{A_{tc}}(t), \end{aligned}$$

in the absence of infection, the system reduces to

$$N(t) = S(t) \Longrightarrow \dot{N}(t) = \dot{S}(t) = \Lambda - \mu S.$$

Applying the Birkhoff-Rota's (1982) theorem on differential inequality into last equation, it becomes:

$$\dot{N}(t) \leqslant \Lambda - \mu S, \tag{4}$$

integrating (4) and applying initial conditions, we obtain

$$N(t) \leqslant \frac{\Lambda}{\mu} - N_0 e^{-\mu t}. \tag{5}$$

As $t \longrightarrow \infty$, the inequality (5), becomes $0 \leqslant N(t) \leqslant \frac{\Lambda}{\mu}$ which implies that $N(t) \longrightarrow \frac{\Lambda}{\mu}$. Hence, the feasible solution set of system (3) enters in the region

$$\Omega = \Big\{S(t), I_c(t), I_h(t), J_h(t), A_t(t), I_{hc}(t), J_{hc}(t), A_{hc}(t), A_{tc} \in R_+ : N \leqslant \frac{\Lambda}{\mu}\Big\} \tag{6}$$

Thus for all $t > 0$, every solution of system (3) with initial conditions in remains there and the solutions of system equation (3) are always positive. □

Lemma 3.1.2. *All solutions of system (3) are bounded.*

Proof. Using system (3) we have $\dot{N} \leqslant \Lambda - \mu N$. Assume that $N(t) \leqslant M$ for all $t \geqslant 0$ where $M = \frac{\Lambda}{\mu} + \varepsilon$, $\varepsilon > 0$. Solutions to the equation $\dot{M} = \Lambda - \mu M$ are monotone increasing and bounded by $\frac{\Lambda}{\mu}$ if $M(0) < \frac{\Lambda}{\mu}$. They are monotone decreasing and bounded above if $M(0) \geqslant \frac{\Lambda}{\mu}$. Since $\dot{N} \leqslant \dot{M}$, the claim follows. □

3.2 Positivity

Lemma 3.2.1. *The equations preserve positivity of solutions.*

Proof. We need to show that for all $t > 0$, the solutions of system (3) are always positive. From the second equation of model system (3), we have:

$$\dot{I}_c(t) = \lambda_c S - (\mu + d_c + r_1 + \delta\lambda_h) I_c, \tag{7}$$

Since $\lambda_c S > 0$, then

$$\frac{dI_c(t)}{dt} \geqslant -(\mu + d_c + r_1 + \delta\lambda_h) I_c. \tag{8}$$

integrating with respect t, yields

$$I_c(t) \geqslant I_{0c}(t) e^{-(\mu + d_c + r_1 + \delta\lambda_h)}. \tag{9}$$

The right side of the inequality (9) is always positive, hence I_c is positive for all $t > 0$.
Using Birkhoff-Rota's (1982) theorem, the second equation can be solved for I_{hc} as follows

$$\frac{dI_{hc}}{dt} \geqslant -(\mu + d_c + r_2 + \rho) I_c. \tag{10}$$

Integrating with respect to t yields

$$I_{hc} \geqslant I_{0hc}(t) e^{-(\mu + r_2 + \rho + d_c)}. \tag{11}$$

Here again, it is clear that the right side of the last inequality in (11) is always positive, hence I_{hc} is positive for all $t \geqslant 0$. From above results, we can conclude that whenever $t \geqslant 0$, the solutions of the system (3) are positive. □

3.3 Infection-free equilibrium and reproduction numbers.

The model (3) has a disease-free equilibrium given by

$$\varepsilon_0 = (S^*, I_c^*, I_h^*, J_h^*, A_h^*, A_t^*, I_{hc}^*, J_{hc}^*, A_{hc}^*, A_{tc}^*) = (\frac{\Lambda}{\mu}, 0, 0, 0, 0, 0, 0, 0, 0, 0) \quad (12)$$

A commonly used measures of the severity of an epidemic is the basic reproduction number R_{hc}. It is defined as the expected number of new infections generated by a single infected person during his/her entire period of infectiousness when introduced in a completely susceptible population. However, in the proposed model, infectious individuals can be in one of the nine classes $I_c, I_h, J_h, A_c, A_t, I_{hc}, J_{hc}, A_{hc}, A_{tc}$ and the expected number of secondary infections depend on the class. By the next generation method, the Jacobian for systems (3) for the new infections and transfer from one compartment to another is given by:

$$F = \begin{pmatrix} \beta_c & 0 \\ 0 & \beta_h \end{pmatrix}, \qquad V = \begin{pmatrix} \mu + d_c + r_1 & 0 \\ 0 & \mu + k_1 - \alpha_1 \end{pmatrix},$$

By the next generation matrix method, we have

$$FV^{-1} = \begin{pmatrix} \frac{\beta_c}{\mu + r_1 + d_c} & 0 \\ 0 & \frac{\beta_h}{\mu + k_1 - \alpha_1} \end{pmatrix}.$$

From which we obtain the eigenvalues

$$R_c = \frac{\beta_c}{\mu + r_1 + d_c}, \qquad R_h = \frac{\beta_h}{\mu + k_1 - \alpha_1}. \quad (13)$$

R_0 is equal to the spectral radius of the matrix FV^{-1}:

$$\mathcal{R}_0 = max\{R_c, R_h\} = max\{\frac{\beta_c}{\mu + r_1 + d_c}, \frac{\beta_h}{\mu + k_1 - \alpha_1}\}. \quad (14)$$

A threshold condition for endemicity is given by $R_0 = 1$: the disease dies out if $R_0 < 1$, and becomes endemic if $R_0 > 1$. Thus we conclude with the following theorem and follows from Theorem 2 of [14].

Theorem 3.3.1. *If ε_0 is a DFE of the model (3), then ε_0 is locally asymptotically stable if $R_0 < 1$, but unstable if $R_0 > 1$.*

4. The Existence and Stability Analysis of Endemic Equilibrium Point (EEP)

This is a case when there is infection in the study population. To explore the existence of endemic equilibrium, we set the right hand side of system (3) to zero and solve it.

HCV-only Equilibrium

This occurs when $I_h = A_h = A_t = I_{hc} = A_{hc} = A_{tc} = 0$ and is given by

$\varepsilon_c^* = (S_c^*, I_c^*, 0, 0, 0, 0, 0, 0, 0, 0)$

from (3), with ε_c^*,

$$\Lambda - (\lambda_c + \mu)S_c^* + r_1 I_c^* = 0, \tag{15}$$

$$\lambda_c S_c^* - (\mu + d_c + r_1 + \delta\lambda_h)I_c^* = 0. \tag{16}$$

From (14),

$$\mu + r_1 + d_c = \frac{\beta_c}{R_c}, \tag{17}$$

with applying (17) in (16), we get

$$\lambda_c S_c^* - \frac{\beta_c I_c^*}{R_c} = 0 \Longrightarrow I_c^* = \frac{S_c^* R_c \lambda_c}{\beta_c}. \tag{18}$$

From (18), with $\lambda_c(t) = \frac{\beta_c[I_c^*(t)]}{N(t)}$,

$$I_c^* = S_c^*(R_c - 1). \tag{19}$$

In the same way we can show that $S_c^* = \beta_c[1 - \frac{1}{R_c}]$.

Using the next generation method, the reproductive number for system (3) is given by:

$$R_{c_h} = \frac{\beta_h[A(R_c - 1) + R_c(\mu + d_c + r_2 + \rho)]}{R_c[\beta_c\sigma(\mu + d_c + \rho)(R_c - 1) + R_c(\mu + d_c + r_2 + \rho)]} \tag{20}$$

where $A = (\delta R_c(r_2 + (\rho + \mu)\phi) + \phi\sigma\beta_c[\delta(R_c - 1) + 1])$.

In order to derive an expression for the region of stability of the boundary equilibrium ε_c^*, we measure the capacity of HIV to invade and persist in a population where HCV is endemic.

5. HIV-Only Submodel

Consider the HIV-only submodel (obtained by setting $I_c = I_{hc} = J_{hc} = A_{hc} = A_{tc} = 0$) in system (2.3), so that we have

$$\begin{aligned}
\dot{S}(t) &= \Lambda - (\lambda_c + \lambda_h + \mu)S, \\
\dot{I}_h(t) &= \lambda_h S - (\mu + k_1 - \alpha_1)I_h, \\
\dot{J}_h(t) &= k_1 I_h - (\mu + \alpha_1 + \rho_1)J_h, \\
\dot{A}_h(t) &= \rho_1 J_h - (\mu + \theta + d_a)A_h, \\
\dot{A}_t(t) &= \theta_1 A_h - (\mu + d_a)A_t,
\end{aligned} \tag{21}$$

HCV-free endemic equilibrium given by

$$\begin{aligned}
S_h^* &= \frac{\Lambda(\mu + k_1 + d_a)(\mu + d_a + \rho_1)}{\mu(\mu + k_1 + d_a)(\mu + d_a + \rho_1) + A} \\
I_h^* &= \frac{(\mu + d_a)(\mu + \rho_1 + \alpha_1)B\Lambda(\mu + k_1 + d_a)}{((\mu + k_1) - \frac{\alpha_1 k_1}{\mu + \alpha_1 + \rho_1})\mu(\mu + k_1 + d_a)(\mu + d_a + \rho_1) + A} \\
J_h^* &= \frac{k_1(\mu + d_a)[(\mu + k_1)(R_h - 1) + \frac{\alpha_1 k_1}{\mu + \alpha_1 + \rho_1}]\Lambda(\mu + k_1 + d_a)}{((\mu + k_1) - \frac{\alpha_1 k_1}{\mu + \alpha_1 + \rho_1})\mu(\mu + k_1 + d_a)(\mu + d_a + \rho_1) + A} \\
A_h^* &= \frac{\rho_1 k_1(\mu + d_a)B\Lambda(\mu + k_1 + d_a)}{(\mu + \theta_1 + d_a)((\mu + k_1) - \frac{\alpha_1 k_1}{\mu + \alpha_1 + \rho_1})C + A} \\
A_t^* &= \frac{\theta_1 \rho_1 k_1(\mu + d_a)B\Lambda(\mu + k_1 + d_a)}{(\mu + d_a)(\mu + \theta_1 + d_a)((\mu + k_1) - \frac{\alpha_1 k_1}{\mu + \alpha_1 + \rho_1})C + A}
\end{aligned}$$

where

$$\begin{aligned}
A &= (\mu + d_a)(\mu + \alpha_1 + \rho_1)[((\mu + k_{1)}(R_h - 1)) + \frac{\alpha_1 k_1}{\mu + \alpha_1 + \rho_1}] \\
B &= [(\mu + k_1)(R_h - 1) + \frac{\alpha_1 k_1}{\mu + \alpha_1 + \rho_1}] \\
C &= \mu(\mu + k_1 + d_a)(\mu + d_a + \rho_1)
\end{aligned}$$

Now we explore the potential of HCV to invade a population in which HIV is already endemic ($R_h > 1$). This requires us to find the invasion reproduction number of model system (3) around ε_h^*, which is given by

$$\begin{aligned}
R_{h_c} = \; & \frac{\delta\eta\beta_c}{R_h n}\Big(\frac{\beta_c(\mu + d_a)(\mu + \rho + \alpha_1)(\mu + k + d_a)(R_h + 1) + mnR_h}{mgR_h + \delta\beta_h(\mu + d_a)(\mu + \rho + \alpha_1)(\mu + k + d_a)(R_h - 1)} \\
& + \frac{(\mu + d_a)(\mu + \rho + \alpha_1)(\mu + k + d_a)(R_h - 1)}{m}\Big).
\end{aligned}$$

where

$$\begin{aligned} m &= (\mu + d_a + k_1)(\mu + d_a + \rho_1), \\ n &= (\mu + r_2 + k_2 + d_c - \alpha_2), \\ g &= (\mu + d_c + r_1). \end{aligned}$$

This formalism permits the derivation of a threshold condition for coexistence, now equivalent to a threshold condition for HIV endemicity in a population where HCV is at equilibrium, $R_{h_c} = 1$: only HIV persists for $R_{h_c} < 1$, while for $R_{h_c} > 1$ HCV can invade a population where HIV state are fixed, that is, to say coexistence is possible.

Theorem 5.1. *This endemic equilibrium ε_h^* exists and is unique if and only if $R_h > 1$ and $R_{h_c} < 1$.*

Proof. See [4]. □

6. Numerical Simulations

In this section, we use numerical illustrations to asses the effects of HCV treatment and antiretroviral therapy and the demographic impact of the epidemic.

Table 1: Variables and parameters for viral spread

Parameter	Value (range)	Source
Λ	50000	[?]
μ	$0.02yr^{-1}$	[?]
$\beta_c(t)$	$0.015 - 0.90yr^{-1}$	[?]
$\beta_h(t)$	$0.011 - 0.95yr^{-1}$	[?]
$(r_1, r_2, r_3, r_4, r_5)$	$0.30yr^{-1}$	[?]
$(\sigma_1, \sigma_2, \sigma_3, \sigma_4)$	$0.30yr^{-1}$	[?]
(θ_1, θ_2)	$0.33yr^{-1}$	[?]
ϕ_1	1.02	[?]
ϕ_2	1.05	[?]
ρ_1	0.5	Assume
d_a	$0.333yr^{-1}$	[?]
d_c	$0.25yr^{-1}$	[?]
δ	1.0001	[?]
η	1.0002	[?]
k_1	0.4	Assume
α_1	0.009	Assume

The parameters that we use for numerical simulations of the model system (3) are given in Table 1. We use a fourth order RungeKutta numerical scheme coded in matlab programming language for the numerical simulations of model system (3).

We assume $S_0 = 4000000, I_{c0} = 10, I_{h0} = 10, J_{c0} = 10, J_{h0} = 10, A_{h0} = 10, A_{t0} = 10, I_{hc0} = 1, A_{hc0} = 1$ and $A_{tc0} = 1$ be the initial population proportions of individuals in each compartment at the start of the epidemic.

In the presence of antiretroviral therapy for people in the AIDS stage and HCV treatment, susceptibles decline to their corresponding asymptotic state as noted in Fig. 2 and the HIV only infected people increase to their corresponding asymptotic state (see Fig. 3), and we assume $S_0 = 4000000, I_{c0} = 2000, I_{h0} = 200, J_{c0} = 200, J_{h0} = 20000, A_{h0} = 10000, A_{t0} = 100, I_{hc0} = 1, A_{hc0} = 10000$ and $A_{tc0} = 1$ be the initial population proportions of individuals in each compartment at the start of the epidemic (see Fig. 4 and Fig. 5).

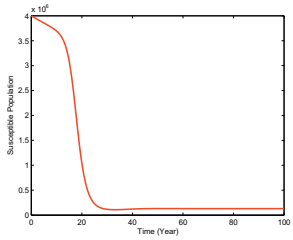


Figure 2

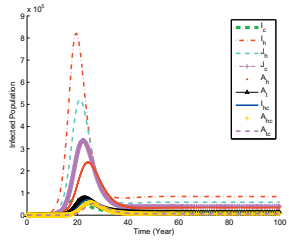


Figure 3

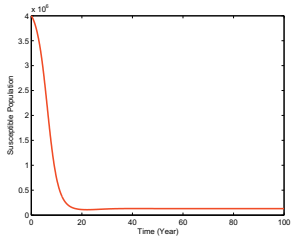


Figure 4

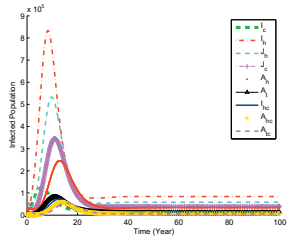


Figure 5

7. Conclusion

In this paper we have discussed the asymptotic behaviour of antiretroviral therapy for AIDS cases and HCV treatment model with a time delay due to

the long incubation period of the disease. We have established the conditions under which the equilibria for the model are locally and globally stable. The dynamics behavior of the ODE treatment proposed model can be determined by its basic reproduction number R_0, i.e., If R_0 is less than unitythere is a unique infection free equilibrium which is globally asymptotically stable. If R_0 greater than unity, the disease persists and the unique endemic equilibrium is globally asymptotically stable.

References

[1] R. M. Anderson and R. M. May, *Infectious Disease of Humans : Dynamics and Control*, Semin. Liver, 1992.

[2] Y. Benhamou, M. Bochet, V. Di Martino, F. Charlotte, F. Azria, A. Coutellier, M. Vidaud, F. Bricaire, P. Opolon, C. Katlama, and T. Poynard, Liver fibrosis progres-sion in immunodeficiency virus and hepatitis C virus coinfection patients, *The Multivirc Group, Hepatology*, 30 (1999), 1054-1058.

[3] C. P. Bhunu, W. Garira, and G. Magombedze, Mathematical analysis of a two strain HIV/AIDS model with antiretroviral treatment, *Acta Biotheor.,* 57 (2009), 361-381.

[4] C. P. Bhunu and S. Mushayabasa, Modelling the transmission dynamics of HIV/AIDS and hepatitis C virus co-infection, *HIV & AIDS Reviw,* 12 (2013), 37-42.

[5] G. Birkhoff and G. C. Rota, *Ordinary differential equations*, Ginn (1982).

[6] J. Garcia-Samaniego, V. Soriano, J. Castilla, R. Bravo, A. Moreno, J. Carbo, A.Iniguez, J. Gonzalez, and F. Minoz, Influence of hepatitis C virus genotypes and HIV infection on histological severity of chronic hepatitis C, The Hepatitis/HIV Spanish Study Group, *Am. J. Gastroenterol,* 92 (1997), 1130-1134.

[7] W. O. Kermack and A. G. Mckendrick, A contribution to the mathematical theory of epidemics, *Proc Roy Soc.,* 5 (2003).

[8] Z. Mukandavire, A. B. Gumel, W. Garira, and J. M. Tchuenche, Mathematical Analysis of a Model for HIV-Malaria co-Infection, *Math. Biosci. Eng.,* 6 (2) (2009), 333-362.

[9] A. Monforte, A. Cozzi-Lepri, A. Castagna, A. Antinori, A. De Luca, C. Mussini, S. L. Caputo, M. Arlotti, G. Magnani, G. Pellizzer, F. Maggiolo, and M. Puoti, Icona Foundation Study Group. Risk of developing specific AIDS-defining illnesses in patients coinfected with HIV and hepatitis C virus with or withoutliver cirrhosis, *Clin. Infect. Dis.,* 49 (4) (2009), 612-622.

[10] L. Perko, *Differential equation and dynamical system*, New York, Springer-Verlag (1991).

[11] R. Romeo, M.G. Rumi, M.F. Donato, M.A. Cargnel, P. Vigano, M. Mondelli, B.Cesana, M. Colombo, Hepatitis C is more severe in drug users with human immunodeficiency virus infection, *J. Viral Hepat.*, 7 (2000), 297-301.

[12] O. Sharomi, C. N. Podder, A. B. Gumel, and B. Song, Mathematical analysis of the transmission dynamics of HIV/TB co-infection in the presence of treatment, *Math. Biosci. Engnr.,* 5 (2008).

[13] H. H. Thein, Q. Yi, G.J. Dore, M.D. Krahn, Natural history of hepatitis C virusinfection in HIV infected individuals and the impact of HIV in the era of highly active antiretroviral therapy, *A meta-analysis, AIDS.,* 22 (2008), 1979-1991.

[14] P. Van Den Driesche, J. Watmough, *Reproduction numbers and subthresholdendemic equilibria for the compartmental models of disease transmission*, Math. Biosci., 180 (2002), 29-48.

[15] H. Zylberberg, S. Pol, Reciprocal interactions between human immunodeficiency virus and hepatitis C virus infections, *Clin. Infect. Dis.,* 23 (1996), 1117-1126.

Morteza Zerehpoush
Faculty of Mathematical Sceinces
Graduate master science Mathematics
Author's Affiliation
Tabriz, Iran
Email: mortza.zerehpoush@gmail.com

Hossein Kheiri
Faculty of Mathematical Sceinces
Professor of Applied Mathematics
Author's Affiliation
Tabriz, Iran
Email: kheirihossein@yahoo.com