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Mathematical Study on Co-infection of Diabetes Mellitus and HIV

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Abstract:*In this paper we formulate a mathematical modelbased on the dynamics of Diabetes Mellitus and HIV(AIDS). The co-infection model has a locally asymptotically stable disease-free equilibrium (DFE) whenever, the basic reproduction number ($\mathcal{R}_0$) that is a certain epidemiological threshold, is less than unity. It is also shown, using a Lyapunov function and Lasalle Invariance Principle, that the DFE of the co-infection model is globally –asymptotically stable (GAS) whenever $\mathcal{R}_0 < 1$. If $\mathcal{R}_0 > 1$ then the model has locally-asymptotically stable endemic equilibrium point (EEP). Numerical simulation suggest that the reduction of the effective contact rate of HIV and increase in the treatment rate can reduce the disease burden of co-infection.*
Keywords*: Equilibrium, Local and Global stability, Endemic Equilibrium.*

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I. Introduction

Diabetes mellitus (DM) which is commonly known as diabetes and is a group of metabolic diseases in which there are high blood sugar levels over a prolonged period. If it is left untreated then many complications can arise for diabetes. Such acute complications are diabetic ketoacidosis and nonketotic hyperosmolar coma. Cardiovascular disease, chronic kidney disease, stroke, foot ulcers and eye damages are serious long-term complications[2]. Diabetes is causedwhenever the cells of the body do not respond properly to the insulin produced orwhenever the pancreasdoes not produce enough insulin.

The human immunodeficiency virus (HIV) is a lentivirus which causes HIV infection and over time acquired immunodeficiency syndrome (AIDS)[1]. Mostly, HIV is a sexually transmitted infection and this infection is occurred by contact with or transfer of blood,semen, pre-ejaculate, and vaginal fluids. HIV can transmit from an infected mother to her infant during pregnancy, during childbirth by exposure to hervaginal fluid orblood, and through breast milk[4]. In the human immune system, helper T cells (specifically $CD4^+$T cells), dendrite cells and macrophages are infected by HIV. HIV infection can lessen the number of $CD4^+$T cells through pyroptosis of abortively infected T cells, apoptosis of uninfected bystander cells, viral killing of infected cells, and killing of infected $CD4^+$T cells by $CD8^+$ cytotoxic lymphocytes that identify infected cells. When $CD4^+$T cell numbers decrease below a critical level, cell-mediated immunity is lost, and the body becomes more susceptible to opportunistic infections, leading to the development of AIDS[4].

The combination of Diabetes Mellitus and HIV infection creates a collision of two chronic conditions. HIV infected patients are twice as likely to develop diabetes mellitus compared with HIV uninfected individuals.The study of co-infection of HIV and diabetes mellitus has been of great interest due to its universal threat to humanity, which drives to use mathematical modelling to acquire knowledge about their transmission dynamics and from which we can identify effective control strategies.By studying some model[8,10,11], a mathematical model is formulated based on co-infection of HIV and diabetes mellitus. In section II the model is formulated and analyzed (for the stability of the disease-free equilibrium and endemic equilibrium) in section III,IV,V and VI and in section VIInumerical simulations are carried out

II. Formulation of Model

The total sexually-active population at time t, denoted by $N(t)$, is subdivided into ten mutually-exclusive compartments, namely susceptible $(S(t))$, individuals who are HIV positive$(H(t))$, individuals having AIDS $(A(t))$, individuals having diabetes mellitus without complications $(D(t))$, individuals having diabetes mellitus with complications $(C(t))$, individuals having diabetes mellitus with and without complications, who are taking treatments $(A(t))$, individuals who are HIV positive and having diabetes mellitus without complications $(D_H(t))$, individuals who are HIV positive and having diabetes mellitus with complications $(C_H(t))$, individuals who are HIV positive and having diabetes mellitus with and without

complications and are taking treatments $(T_H(t))$, individuals in the AIDS class having diabetes $(A_D(t))$. So that the total population at time t is denoted by, N(t), where,

$N(t) = S(t) + H(t) + A(t) + D(t) + C(t) + T(t) + D_H(t) + C_H(t) + T_H(t) + A_D(t).$

The susceptible population is increased by the recruitment of individuals (assumed susceptible)at a rate π, into the population. Let γ denote the incidence of diabetes mellitus. Susceptible individuals acquire HIV at a rateλ_H , where, $\lambda_H = \frac{\beta(H+\eta A)}{N}$; $\eta > 1$. Where $\lambda_H$is the force of infection for HIV, β is the transmission rate for HIV and the parameter $\eta(\eta > 1)$ indicates that an individuals with AIDS is more infectious than an individual having HIV positive.

Combining all the assumptions mentioned above, the model becomes:

$$\frac{dS}{dt} = \pi - (\lambda_H + \mu + \gamma)S,$$
$$\frac{dH}{dt} = \lambda_H S - (\mu + \omega)H,$$
$$\frac{dA}{dt} = \omega H - (\mu + \delta_3)A,$$
$$\frac{dD}{dt} = \gamma S - (\mu + \sigma + \tau_D)D - \lambda_H D,$$
$$\frac{dC}{dt} = \sigma D - (\nu + \mu + \delta_1 + \tau_C)C - \lambda_H C,$$
$$\frac{dT}{dt} = \tau_D D + \tau_C C - (\mu + \lambda_H)T, \quad (1)$$
$$\frac{dD_H}{dt} = \lambda_H D - (\mu + \sigma_H + \tau_{DH} + \sigma_D)D_H,$$
$$\frac{dT_H}{dt} = \tau_{DH} D_H + \lambda_H T + \tau_{CH} C_H - (\mu + \sigma_T)T_H,$$
$$\frac{dC_H}{dt} = \lambda_H C + \sigma_H D_H - (\nu_H + \mu + \delta_2 + \tau_{CH} + \sigma_C)C_H,$$
$$\frac{dA_D}{dt} = \sigma_D D_H + \sigma_T T_H + \sigma_C C_H - (\mu + \delta_4)A_D.$$

Parameters of the above model are mentioned in table 1.

III. Disease-Free Equilibrium Points

For a disease model, in the absence of infection or disease, its steady-state solutions are called disease-free equilibrium (DFE) point, E_0. The model (1) has a DFE,which is given by

$$E_0 = (S, H, A, D, C, T, D_H, C_H, T_H, A_D) = \left(\frac{\pi}{\mu}, 0, 0, 0, 0, 0, 0, 0, 0, 0\right)$$

IV. Local Stability of the Disease-free equilibrium

To establish the local stability ofdisease-free equilibrium, we first calculate the basic reproduction number that depends on the associated non-negative matrix F, for the new infection terms, and the non-singular M-matrix, V, for the remaining transfer terms, are givenby,

$$F = \begin{bmatrix} \frac{\beta S}{N} & \frac{\beta\eta S}{N} & 0 & 0 & 0 & 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 \\ \frac{-\beta D}{N} & \frac{-\beta\eta D}{N} & 0 & 0 & 0 & 0 & 0 & 0 & 0 \\ \frac{-\beta C}{N} & \frac{-\beta\eta C}{N} & 0 & 0 & 0 & 0 & 0 & 0 & 0 \\ \frac{-\beta T}{N} & \frac{-\beta\eta T}{N} & 0 & 0 & 0 & 0 & 0 & 0 & 0 \\ \frac{\beta D}{N} & \frac{\beta\eta D}{N} & 0 & 0 & 0 & 0 & 0 & 0 & 0 \\ \frac{\beta T}{N} & \frac{\beta\eta T}{N} & 0 & 0 & 0 & 0 & 0 & 0 & 0 \\ \frac{\beta C}{N} & \frac{\beta\eta C}{N} & 0 & 0 & 0 & 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 \end{bmatrix}, V = \begin{bmatrix} k_1 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 \\ -\omega & k_2 & 0 & 0 & 0 & 0 & 0 & 0 & 0 \\ 0 & 0 & k_3 & 0 & 0 & 0 & 0 & 0 & 0 \\ 0 & 0 & -\sigma & k_4 & 0 & 0 & 0 & 0 & 0 \\ 0 & 0 & -\tau_D & -\tau_C & \mu & 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 & 0 & k_5 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 & 0 & -\tau_{DH} & k_6 & -\tau_{CH} & 0 \\ 0 & 0 & 0 & 0 & 0 & -\sigma_H & 0 & k_7 & 0 \\ 0 & 0 & 0 & 0 & 0 & -\sigma_D & -\sigma_T & -\sigma_C & k_8 \end{bmatrix}$$

where , $k_1 = \mu + \omega, k_2 = \mu + \delta_3, k_3 = \mu + \sigma + \tau_D, k_4 = \mu + \upsilon + \delta_1 + \tau_C,$

$k_5 = \mu + \sigma_H + \tau_{DH} + \sigma_D, k_6 = \mu + \sigma_T, k_7 = \nu_H + \mu + \delta_2 + \tau_{CH} + \sigma_C, k_8 = \mu + \delta_4$

The associated basic reproduction number, $R_0 = \rho(FV^{-1})$. Here ρ is the spectral radius of the matrix FV^{-1}.We get$R_0 = \frac{\beta S(\eta\omega + k_2)}{Nk_1k_2}$. In a completely susceptible human population, the average number of secondary cases which is generated by a single infected individual, is measured bythe threshold quantity ${R_0}^5$.

Lemma 1[3]**:** The Disease-free equilibrium (DFE), E_0 of the model (1), is Locally-asymptotically stable (LAS) if $R_0 < 1$ and unstable if $R_0 > 1$.

V. Global Stability of the Disease-free equilibrium

Before to prove the global stability of DFE, we consider the region,

$$\psi = \{(S, H, A, D, C, T, D_H, C_H, T_H, A_D) \in \mathbb{R}_+^{10} : S + H + A + D + C + T + D_H + C_H + T_H + A_D \leq \frac{\pi}{\mu}\}$$

Theorem 1: If $R_0 < 1$ then the DFE, E_0, of the model (1), is globally asymptotically stable (GAS) in ψ.

Proof: Consider the Lyapunov function, $\mathcal{F} = f_1 H + f_2 A$, where $f_1 = \frac{\eta\omega + k_2}{\eta k_1}$, $f_2 = 1$, with Lyapunov derivative (where dot represents differentiation with respect to t) ,

$$\dot{\mathcal{F}} = f_1\dot{H} + f_2\dot{A} = \frac{\eta\omega + k_2}{\eta k_1}\left[\frac{\beta S(H + \eta A)}{N} - Hk_1\right] + \omega H - Ak_2 = \frac{Hk_2}{\eta}(R_0 - 1) + Ak_2(R_0 - 1)$$

As all the model parameters are nonnegative, it follows that $\dot{\mathcal{F}} < 0 \; if \; R_0 < 1$ with $\dot{\mathcal{F}} = 0$ if and only if H=A=0 and $R_0 = 1$.It follows from the LaSalle's Invariance Principle[6],that, whenever $R_0 < 1$, every solution to the equations of the model (1), with initial conditions in ψ approaches E_0 as $t \to \infty$,

VI. Existence and Local Stability of Endemic Equilibrium point:

To determine the conditions for the existence of the endemic equilibria of the model (1), denoted by $E_1 = (S^{**}, H^{**}, A^{**}, D^{**}, C^{**}, T^{**}, {D_H}^{**}, {T_H}^{**}, {C_H}^{**}, {A_D}^{**})$**,**the equations in the model (1) are solved in terms of the associated forces of infection at steady-state, namely

${\lambda_H}^{**} = \frac{\beta(H^{**} + \eta A^{**})}{N^{**}}$ (2)

We get the following expressions of the modelfor the state variables:

$$H^{**} = \frac{{\lambda_H}^{**} S^{**}}{k_1},$$

$$A^{**} = \frac{{\lambda_H}^{**} S^{**}\omega}{k_1 k_2},$$

$$D^{**} = \frac{\gamma S^{**}}{{\lambda_H}^{**} + k_3},$$

$$C^{**} = \frac{\sigma\gamma S^{**}}{({\lambda_H}^{**} + k_3)({\lambda_H}^{**} + k_4)},$$

$$T^{**} = \frac{\gamma S^{**}[\tau_D({\lambda_H}^{**} + k_4) + \sigma\tau_C]}{({\lambda_H}^{**} + k_3)({\lambda_H}^{**} + k_4)(\mu + {\lambda_H}^{**})},$$

${D_H}^{**} = \frac{\gamma S^{**}{\lambda_H}^{**}}{({\lambda_H}^{**} + k_3)k_5}$,(3)

$${C_H}^{**} = \frac{\gamma S^{**}{\lambda_H}^{**}[\sigma k_5 + \sigma_H({\lambda_H}^{**} + k_4)]}{({\lambda_H}^{**} + k_4)({\lambda_H}^{**} + k_3)k_5 k_7},$$

$${T_H}^{**} = \frac{\gamma S^{**}{\lambda_H}^{**}}{k_5 k_6 k_7({\lambda_H}^{**} + k_3)({\lambda_H}^{**} + k_4)(\mu + {\lambda_H}^{**})}[k_7({\lambda_H}^{**} + k_4)(\mu + {\lambda_H}^{**})\tau_{DH} + k_5 k_7(\tau_D({\lambda_H}^{**} + k_4)k_5 k_7 + \sigma\tau_C) + \tau_{CH}(\mu + {\lambda_H}^{**})(\sigma k_5 + \sigma_H({\lambda_H}^{**} + k_4))],$$

$${A_D}^{**} = \frac{\gamma S^{**}{\lambda_H}^{**}}{k_5 k_6 k_7 k_8({\lambda_H}^{**} + k_3)({\lambda_H}^{**} + k_4)(\mu + {\lambda_H}^{**})}[({\lambda_H}^{**} + k_4)(\mu + {\lambda_H}^{**})(k_6\sigma_C\sigma_H + \sigma_T k_7\tau_{DH} + k_6 k_7\sigma_D + \sigma_T\sigma_H\tau_{CH}) + ({\lambda_H}^{**} + k_4)\sigma_T\tau_D k_5 k_7 + \sigma k_5(\mu + {\lambda_H}^{**})(k_6\sigma_C + \sigma_T\tau_{CH})].$$

Thus using (3) in (2) we get:$a(\lambda_H^{**})^4 + b(\lambda_H^{**})^3 + c(\lambda_H^{**})^2 + d\lambda_H^{**} + e = 0$ (4)

where, a=$\omega k_5 k_6 k_7 k_8 + k_2 k_5 k_6 k_7 k_8$, (5)

$b = \gamma k_1 k_2 k_6 k_7 k_8 + k_2 k_4 k_5 k_6 k_7 k_8 + \gamma k_1 k_2 k_7 k_8\tau_{DH} + \gamma k_1 k_2 k_6\sigma_C\sigma_H + \mu\omega k_5 k_6 k_7 k_8 + \mu k_2 k_5 k_6 k_7 k_8 + \gamma k_1 k_2 k_6 k_7\sigma_D + k_1 k_2 k_5 k_6 k_7 k_8 + \omega k_4 k_5 k_6 k_7 k_8 + \gamma k_1 k_2 k_6 k_8\sigma_H + \gamma k_1 k_2 k_8\sigma_H\tau_{CH} + \gamma k_1 k_2\sigma_H\sigma_T\tau_{CH} + \omega k_3 k_5 k_6 k_7 k_8 + k_2 k_3 k_5 k_6 k_7 k_8 + \gamma k_1 k_2 k_7\sigma_T\tau_{DH} - k_5 k_6 k_7 k_8\beta(\eta\omega + k_2)$

$c =$

$\gamma\sigma k_1 k_2 k_5 k_6 k_8 + \gamma\mu k_1 k_2 k_7 k_8 + \gamma k_1 k_2 k_4 k_6 k_7 k_8 + \gamma k_1 k_2 k_5 k_6 k_7 k_8 + \mu k_1 k_2 k_5 k_6 k_7 k_8 + \mu\omega k_3 k_5 k_6 k_7 k_8 + \mu k_2 k_3 k_5 k_6 k_7 k_8 + k_2 k_3 k_1 k_5 k_6 k_7 k_8 + \mu\omega k_4 k_5 k_6 k_7 k_8 + \mu k_2 k_4 k_5 k_6 k_7 k_8 + k_1 k_2 k_4 k_5 k_6 k_7 k_8 +$

$\omega k_3k_4k_5k_6k_7k_8 + k_2k_3k_4k_5k_6k_7k_8 + \gamma\sigma\sigma_C k_1k_2k_5k_6 + \gamma k_1k_2k_6k_7\mu\sigma_D + \gamma k_1k_2k_4k_6k_7\sigma_D +$
$\gamma k_1k_2k_4k_6k_8\sigma_H + \gamma\mu k_1k_2k_6k_8\sigma_H + \gamma\mu k_1k_2k_6\sigma_C\sigma_H + \gamma k_1k_2k_4k_6\sigma_C\sigma_H + \gamma\mu k_1k_2k_7k_8\tau_D + \gamma k_4k_1k_2k_7k_8\tau_D +$
$\gamma\mu k_1k_2k_7\sigma_T\tau_D + \gamma k_4k_1k_2k_7\sigma_T\tau_D + \gamma\sigma k_1k_2k_5\tau_C k_8 + \gamma\sigma_H\mu k_1k_2k_8\tau_C + \gamma\sigma_H k_4k_1k_2k_8\tau_C + \gamma\sigma k_1k_2k_5\tau_C\sigma_T +$
$\gamma k_1k_2\tau_C\sigma_T\sigma_H(\mu + k_4) + \gamma k_1k_2k_5k_7\tau_D(\sigma_T + k_8) - k_5k_6k_7k_8\beta(\eta\omega + k_2)(\mu + k_3k_4$

$d = \gamma\mu k_1k_2k_6k_8(\sigma k_5 + k_4k_7 + k_5k_7) + k_1k_2k_5k_6k_7k_8(\gamma\sigma + \mu k_3 + \gamma k_4 + \mu k_4) +$
$k_3k_4k_5k_6k_7k_8(\mu\omega + \mu k_2 + k_1k_2) + \gamma\mu k_1k_2k_6(\sigma k_5\sigma_C + k_4k_7\sigma_D + k_4k_8\sigma_H + k_4\sigma_C\sigma_H)$
$+ \gamma\mu k_1k_2k_8(k_4k_7\tau_D + \tau_C\sigma_H + k_4\tau_C\sigma_H) + \gamma\mu k_1k_2\tau_C\sigma_T(k_5\sigma + k_4\sigma_H)$
$+ \gamma k_1k_2k_5k_7(\sigma k_8\tau_C + \sigma\sigma_T\tau_C + k_4k_8\tau_D + k_6k_8\tau_D + k_4\sigma_T\tau_D) - k_5k_6k_7k_8\beta(\eta\omega + k_2)(\mu k_3$
$+ \mu k_4 + k_3k_4)$

e=$k_1k_2k_5k_6k_7k_8(\gamma\mu\sigma + \gamma\mu k_4 + \mu k_3k_4 + \gamma\sigma\tau_C + \gamma k_4\tau_D)$-$\mu k_3k_4k_5k_6k_7k_8\beta(\eta\omega + k_2)$

From (5) it follows that a>0 (since all the model parameters are non-negative).By applying the Descartes rule of signs[12] on the equation (4), we get the following result.

Theorem 2: The model (1) has:(i)a unique endemic equilibrium if b,c,d>0 and e<0, (ii) a unique endemic equilibrium if b,c >0 and d, e<0, (iii) a unique endemic equilibrium if b>0 and c,d,e<0, (iv) a unique endemic equilibrium if b,c,d,e<0, (v)two endemic equilibrium if b,c,e>0 and d<0, (vi) two endemic equilibrium if b,d,e>0 and c<0, (vii) two endemic equilibrium if b,e>0 and c,d<0, (viii) two endemic equilibrium if b<0 and c,d,e>0, (ix) two endemic equilibrium if b,c<0 and d,e>0, (x) two endemic equilibrium if b,c,d<0 and e>0, (xi) three endemic equilibrium if b,d>0 and c,e<0, (xii) three endemic equilibrium if c,d>0 and b,e<0, (xiii) three endemic equilibrium if b,c,e<0 and d>0, (xvi) three endemic equilibrium if b,d,e<0 and c>0, (xv) four endemic equilibrium if b,d<0 and c,e>0.

The local stability of endemic equilibrium point, E_1, of the model (1) is consider for the special case where we use $N = N^{**}$, and $S = N^{**} - H - A - D - C - T - D_H - T_H - C_H - A_D$ in (2).

Theorem 3: Whenever $R_0 > 1$,the endemic equilibrium, E_1, of the reduced basic model (6) is Locally-asymptotically stable.

Proof: The proof of theorem is based on using a Krasnoselskii sub-linearity trick[7]. Using $N = N^{**}$, and $S = N^{**} - H - A - D - C - T - D_H - T_H - C_H - A_D$ in the system (1) we get nonlinear system of equations. Now linearizing that system around the endemic equilibrium, E_1, we get

$$\frac{dH}{dt} = (-a_1 - k_1 + a_2)H + (-a_1 + \eta a_2)A - a_1(D + C + T + D_H + T_H + C_H + A_D)$$
$$\frac{dA}{dt} = \omega H - k_2 A,$$
$$\frac{dD}{dt} = a_3 - k_3 D - a_1 D,$$
$$\frac{dC}{dt} = \sigma D - k_4 C - a_1 C,$$
$$\frac{dT}{dt} = \tau_D D + \tau_C C - (\mu + a_1)T,$$
$$\frac{dD_H}{dt} = a_1 D - k_5 D_H, \quad (6)$$
$$\frac{dT_H}{dt} = \tau_{DH} D_H + a_1 T + \tau_{CH} C_H - k_6 T_H,$$
$$\frac{dC_H}{dt} = a_1 C + \sigma_H D_H - k_7 C_H,$$
$$\frac{dA_D}{dt} = \sigma_D D_H + \sigma_T T_H + \sigma_C C_H - k_8 A_D.$$

Where,$a_1 = \frac{\beta(H+\eta A)}{N^{**}}$, $a_2 = \frac{\beta(N^{**}-H-A-D-C-T-D_H-T_H-C_H-A_D)}{N^{**}}$,

$a_3 = \gamma[N^{**} - H - A - D - C - T - D_H - T_H - C_H - A_D]$

It follows that the Jacobian of the system (6),at $E_1$is given by

$$J(E_1) = \begin{bmatrix} -a_1 - k_1 + a_2 & -a_1 + a_2\eta & -a_1 & -a_1 & -a_1 & -a_1 & -a_1 & -a_1 & -a_1 \\ \omega & -k_2 & 0 & 0 & 0 & 0 & 0 & 0 & 0 \\ 0 & 0 & -k_3 - a_1 & 0 & 0 & 0 & 0 & 0 & 0 \\ 0 & 0 & \sigma & -k_4 - a_1 & 0 & 0 & 0 & 0 & 0 \\ 0 & 0 & \tau_D & \tau_C & -\mu - a_1 & 0 & 0 & 0 & 0 \\ 0 & 0 & a_1 & 0 & 0 & -k_5 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 & a_1 & \tau_{DH} & -k_6 & \tau_{CH} & 0 \\ 0 & 0 & 0 & a_1 & 0 & \sigma_H & 0 & -k_7 & 0 \\ 0 & 0 & 0 & 0 & 0 & \sigma_D & \sigma_T & \sigma_C & -k_8 \end{bmatrix}$$

Assume that the system (6) has solution of the form

$\bar{Z}(t) = \bar{Z}_0 e^{\theta t}$, (7)

With$\bar{Z}_0 = (Z_1, Z_2, Z_3, Z_4, Z_5, Z_6, Z_7, Z_8, Z_9)$, $\theta Z_i \in \mathbb{C}(i = 1,2,3, \ldots,9)$. Substituting (7) into (6), we get

$$\begin{aligned}
&Z_1[1 + F_1(\theta)] + \Gamma = (M\bar{Z})_1 ,\\
&Z_2[1 + F_2(\theta)] = (M\bar{Z})_2 ,\\
&Z_3[1 + F_3(\theta)] = (M\bar{Z})_3 ,\\
&Z_4[1 + F_4(\theta)] = (M\bar{Z})_4 ,\\
&Z_5[1 + F_5(\theta)] = (M\bar{Z})_5 ,\\
&Z_6[1 + F_6(\theta)] = (M\bar{Z})_6 ,\\
&Z_7[1 + F_7(\theta)] = (M\bar{Z})_7 ,\\
&Z_8[1 + F_8(\theta)] = (M\bar{Z})_8 ,\\
&Z_9[1 + F_9(\theta)] = (M\bar{Z})_9 .
\end{aligned} \qquad (8)$$

where,$F_1 = \left[\frac{\theta+a_1-a_2}{k_1} + \frac{a_1\omega}{k_1(\theta+k_2)} - \frac{\eta\omega a_2}{k_1(\theta+k_2)}\right]$, $F_2 = \frac{\theta}{k_2}$, $F_3 = \frac{\theta+a_1}{k_3}$, $F_4 = \frac{\theta+a_1}{k_4}$, $F_5 = \frac{\theta+a_1}{\mu}$, $F_6 = \frac{\theta}{k_5}$, $F_7 = \frac{\theta}{k_6}$, $F_8 = \frac{\theta}{k_7}$, $F_9 = \frac{\theta}{k_8}$

with $M = \begin{bmatrix}
0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0\\
\frac{\omega}{k_2} & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0\\
0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0\\
0 & 0 & \frac{\sigma}{k_4} & 0 & 0 & 0 & 0 & 0 & 0\\
0 & 0 & \frac{\tau_D}{\mu} & \frac{\tau_C}{\mu} & 0 & 0 & 0 & 0 & 0\\
0 & 0 & \frac{a_1}{k_5} & 0 & 0 & 0 & 0 & 0 & 0\\
0 & 0 & 0 & 0 & \frac{a_1}{k_6} & \frac{\tau_{DH}}{k_6} & 0 & \frac{\tau_{CH}}{k_6} & 0\\
0 & 0 & 0 & \frac{a_1}{k_7} & 0 & \frac{\sigma_H}{k_7} & 0 & 0 & 0\\
0 & 0 & 0 & 0 & 0 & \frac{\sigma_D}{k_8} & \frac{\sigma_T}{k_8} & \frac{\sigma_C}{k_8} & 0
\end{bmatrix}$

Here,$M(\bar{Z})_i$, (with i=1,2,3,4,5,6,7,8,9) denotes the ith co-ordinate of the vaector $M(\bar{\boldsymbol{Z}})$. Here, the matrix M is non-negative, and the equilibrium E_1 satisfies$E_1 = ME_1$ and the coordinates of E_1 are all positive. Therefore if $\bar{\boldsymbol{Z}}$ is a solution of equation (8), then there exists a minimal positivereal number , s, such that $|\bar{\boldsymbol{Z}}| \leq sE_1$, where , $|\bar{\boldsymbol{Z}}| = (|Z|_1, |Z|_2, |Z|_3, |Z|_4, |Z|_5, |Z|_6, |Z|_7, |Z|_8, |Z|_9)$, where $|.|$ is a norm in $\mathbb{C}$.we have to show that $Re\theta < 0$. We assume $Re\theta \geq 0$. At first we consider $\theta = 0$. The determinant of this system corresponds to that of the Jacobian of system (6) at E_1, which is given by

$$\begin{aligned}
\Delta &= (-k_3 - a_1)(-k_4 - a_1)(-\mu - a_1)k_5k_6k_7k_8(-\eta\omega a_2 + \omega a_1 + a_1k_2 - a_2k_2 + k_1k_2)\\
&= -(k_3 + a_1)(k_4 + a_1)(\mu + a_1)k_5k_6k_7k_8[a_1(\omega + k_2) + k_1k_2(1 - R_0)]
\end{aligned}$$

since parameters of the model are non-negative ,then $\Delta \neq 0$,whenever $a_1(\omega + k_2) \neq k_1k_2(1 - R_0)$.Therefore the system has a trivial solution $\bar{\boldsymbol{Z}}$**=0** , (corresponds to the DFE, E_0). Now we consider $\theta \neq 0$ and and assume that$Re\theta > 0$. In this case $|1 + F_i(\theta)| > 1$ for i=1,2,….,9 and we define $F(\theta) = \min\{|1 + F_i(\theta)|, i = 1,2, \ldots,9\}$ then $F(\theta) > 1$. Here, $\frac{s}{F(\theta)} < s$. Here, s is the minimal positive real number such that $|\bar{Z}| \leq sE_1$, so $|\bar{Z}| > \frac{s}{F(\theta)}E_1$ and we obtain the inequality, $F(\theta)Z \leq MZ \leq s(ME_1) \leq sE_1$, which follows that $Z \leq \frac{s}{F(\theta)}E_1$, which is a contradiction.Therefore, $Re\theta < 0$ and this provesfor $\mathcal{R}_0 > 1$ the EE, E_1, is locally asymptotically stable.

Table 1. Description of the parameters of the model

Parameter	Description
π	Recruitment rate of humans
γ	Incidence rate of Diabetes Mellitus
β	Effective contact rate
σ	Transfer rate between $D(t)$ and $C(t)$
η	Modification parameter
σ_H	Transfer rate between$D_H(t)$ and $C_H(t)$
σ_D	Transfer rate between$D_H(t)$ and $A_D(t)$
σ_C	Transfer rate between$C_H(t)$ and $A_D(t)$
σ_T	Transfer rate between$T_H(t)$ and $A_D(t)$
ν	Disable rate
ν_H	Disable rate
τ_D	Transfer rate between $D(t)$ and $T(t)$

τ_{DH}	Transfer rate between $D_H(t)$ and$T_H(t)$

Table 1. Description of the parameters of the model(continued)

τ_C	Transfer rate between $C(t)$ and $T(t)$
τ_{CH}	Transfer rate between $C_H(t)$ and$T_H(t)$
μ	Natural mortality rate
ω	Transfer rate between $H(t)$ and$A(t)$
δ_1	Disease induced mortality rate due to complication
δ_2	Disease induced mortality rate due to co-infection
δ_3	Disease induced mortality rate due to HIV
δ_4	Disease induced mortality rate due to co-infection

VII. Numerical Simulations and Discussions:

The model (1) is simulated, using the different parameter values. From figure (1), it is monitored that, if the effective contact rate (β), decreases and the treatment rates $(\tau_D, \tau_C, \tau_{DH}, \tau_{CH})$ increases then the total number of infected human population decreases rapidly $(R_0 < 1)$. Figure (2) and (3)indicates that if the rate β, the effective contact rate increases and the rateμ, the natural mortality rate decreases, then the total number of infected human population increases rapidly $(R_0 > 1)$. Figure(4) presents a contour plot of R_0 as a function of effective contact rate (β) and modification parameter (η) which depicts that if the rate β and η increases then the burden of the disease increases and if the rate β and η decreases then the burden of the disease decreases.

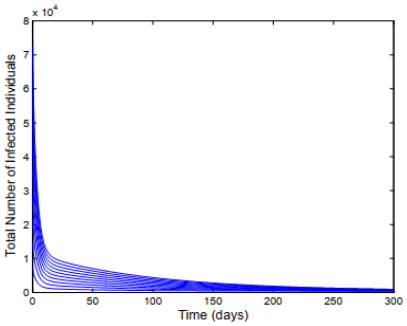

Figure 1: Graph of the model (1) showing the total number of infected human population as a function of time, where $\beta = 0.19, \tau_D = 0.7\ , \tau_C = 0.76, \tau_{DH} = 0.8, \tau_{CH} = 0.7, R_0 = 0.6571.$

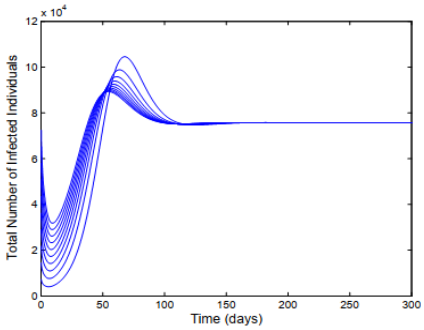

Figure 2 : Graph of the model (1) showing the total number of infected human population as a function of time, where $\beta = 0.21, R_0 = 1.7796.$

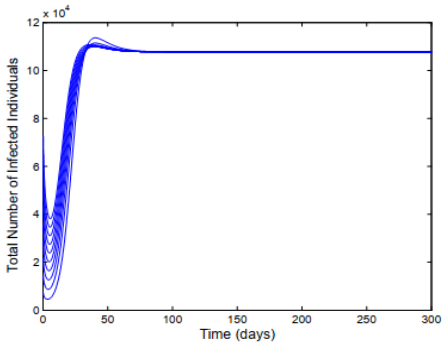

Figure 3: Graph of the model (1) showing the total number of infected human population as a function of time, where $\beta = 0.3, \mu = \frac{1}{30}, R_0 = 3.7813.$

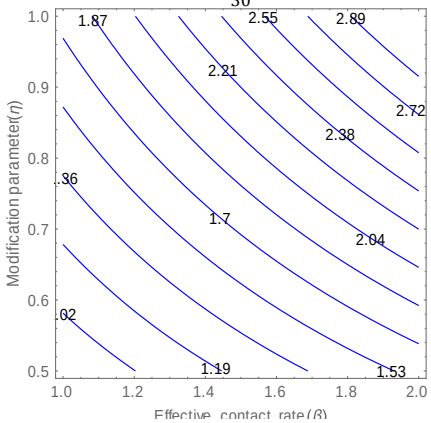

Figure 4: Graph of the model (1) showing a contour plot of R_0 as a function of effective contact rate (β) and modification parameter (η)

VIII. Conclusions

In summary the main findings of this paper are itemized below

I. The disease-free equilibrium, E_0, is locally asymptotically stable when the basic reproduction number,$\mathcal{R}_0$, is less than unity.
II. The disease-free equilibrium, E_0, is globally asymptotically stable when $\mathcal{R}_0 < 1$
III. The endemic equilibrium, E_1, is locally asymptotically stable when$\mathcal{R}_0 > 1$
IV. Reduction of the effective contact rate β of HIV can lessen the disease burden.
V. Increase in the treatment rate $(\tau_D, \tau_C, \tau_{DH}, \tau_{CH})$ can lessen the disease burden of co-infection

References

[1]. Weiss R A (May 1993). 'How does HIV cause AIDS?'. Science. 260(5112):1273-9. Bibcode:1993Sci…260.1273W.doi:10.1126/science. 8493571. PMID 8493571.
[2]. Diabetes Fact sheet N^{0}312. WHO. October 2013. Archived from the original on 26 August 2013. Retrieved 25 March 2014.
[3]. Chandra (2009). Transmission Dynamics of a two sex Model for Herpes Simplex Virus Type-2. Canadian Applied Mathematics Quarterly , Vol-17, Number-2.
[4]. Belfour Henry H.. Herpes group viruses and HIV infection. The PRN note Book.
[5]. Anderson and May (1991). Infectious Diseases of Humans: Dynamics and Control. Oxford University, London/NewYork, 1991.
[6]. LaSalle J. P. (1976). The stability of dynamical systems. Regional Conference Series in Applied Mathematics. SIAM. Philadelphia.
[7]. Safi. M. A Thesis Paper on Mathematical Analysis of The Role of Quarantine and Isolation in Epidemiology.
[8]. Sarah et al (2011). Stability analysis of an HIV/AIDS Epidemic model with Screening. International Mathematical Forum, vol.6, 2011, no.66,3251-3273.
[9]. Sharomi O., C. N. Podder, A. B. Gumel, E. H. Elbasha and J. Watmough (2007). Role of incidence Function in vaccine-induced backward bifurcation in some HIV models. Bull. Math. Biol.210:436-463.
[10]. Boutayeb A., EH Twizell, K Achouayb and A Chetouani (2004). A mathematical model for the burden of diabetes and its complications. BioMedical Engineering Online, doi:10.1186/1475-925X-3-20.
[11]. SharomiO., C. N.Podder, A. B.Gumel(2008).Mathematical Analysis of the Transmission Dynamics of HIV\TB Coinfection in the Presence of Treatment. Mathematical Biosciences and Engineering, volume 5,number 1.
[12]. Safi Muhammad A., Dessalegn Y. Melesse(2013). Dynamics Analysis of a Multi-strain Cholera Model with an Imperfect Vaccine. Bull Math Biol (2013)75:1104-11.

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