Analysis of a mathematical model of transmission dynamics of HIV/AIDS with saturated incidence rate

Olopade I Adesola[1,*], Ajao S. Oladele[2], Mohammed I. Temilade[3], Iorhen S. Felix[4] and Philemon E. Musa[5]

[1,4,5]Department of Mathematics and Statistics, Federal University Wukari, PMB 1020, Wukari, Taraba State, Nigeria
[2]Department of Mathematics and Computer Science, Elizade University, Ilara−mokin, Ondo State. Nigeria
[3]Department of Mathematics and Social Sciences, Osun State Polytechnic Iree, Nigeria

ABSTRACT

In this study, a mathematical model for the HIV/AIDS epidemic is developed and analyzed to gain insight into the current and past states of HIV/AIDS and other epidemiological features that cause the progression from HIV to full-blown AIDS. The existence and uniqueness of the model show that the solutions exist and are unique. The basic reproduction number is the average number of new secondary infections generated by a single infected individual during the infectious period, which is established using the next-generation matrix method. The analysis shows that the disease-free equilibrium is locally asymptotically stable whenever the threshold quantity is less than unity, i.e., $R_0 < 1$, and is otherwise epidemic. The sensitivity of parameters with respect to the basic reproduction number shows that parameters with a positive index will increase the basic reproduction number; for example, the effective contact rate must not exceed 0.39 to avoid an endemic stage. Numerical analysis of the work shows the importance of the memory term; it also indicates that control measures targeted at the history of any disease and immunity boosts should be adopted to prevent HIV from leading to full-blown AIDS.

Keywords: HIV/AIDS; Treatment; Effective reproduction number; Equilibrium points and stability; Sensitivity; Numerical simulation.
DOI: https://dx.doi.org/10.4314/ejst.v17i2.3

INTRODUCTION

Human immunodeficiency Virus (HIV) is a virus that targets the body's immune system, particularly the CD4-positive cells, which are vital for fighting diseases and infections (Huo *et al*., 2016; Global Fact Sheet, 2020). Acquired Immunodeficiency Syndrome (AIDS) poses a significant risk to a substantial portion of the global population, impacting not only individuals infected with the virus but also their families and friends (Gelaw *et al*., 2019). Global HIV estimates have been compiled by the Joint World Health Organization (WHO) and the United Nations Program on HIV/AIDS (UNAIDS) since the late 1980s. The identification of the first AIDS patient occurred in 1981, marking the beginning of the classification of AIDS as a global pandemic (Udoy *et al*., 2015). The initial stages of HIV infection are characterized by symptoms such as flu-like signs, night sweats, cough, weight loss, headaches, diarrhea, sunburn-like rash, body aches, joint pain, and tonsillitis. In these early phases, the virus has a higher viral load in the bloodstream, making the spread of HIV infections more efficient throughout the

* Corresponding author: isaac.olopade@fuwukari.edu.ng

body. HIV is transmitted through various body fluids (blood, tears, urine, saliva, etc.) and can infect uninfected individuals (Endalamaw *et al*., 2019). CD4-positive cells are crucial for fighting infections and play a significant role in modifying the immune system. Any disruption or reduction in the functionality of these CD4-positive cells can have wide-ranging consequences, leading to the impairment of the immune system's functioning. The retention time of these lymphocytes is critical for maintaining a healthy immune response (Endalamaw *et al*., 2019). Many researchers have worked on the dynamic spread of HIV/AIDS using various assumptions.

Adewale *et al*. (2016) presented and analyzed five nonlinear differential compartmental models to gain a deeper understanding of the parameters influencing the dynamic spread of HIV in society. The study involved numerical simulations to assess the effects of various parameters on the dynamic spread of the disease. The effective contact rate and the presence of fast progressors emerged as the primary key parameters that significantly influenced the dynamic spread of HIV in the community.

Bushnaq *et al*. (2018) conducted a study focused on the existence theory of an HIV-1 infection model. They employed arbitrary fractional order derivatives without a singular kernel type. Their research delved into the stability and persistence of HIV/AIDS within the framework of biomechanics, considering the impact of memory and fractional differentiation.

Toro *et al*. (2020) developed a mathematical model consisting of equations that depict the population dynamics of CD4-positive T-cell immunological activation. This model resulted in a two-dimensional integro-differential system, which was subsequently transformed into a system comprising three ordinary differential equations.

The study by Tigabu *et al*. (2021) focuses on a deterministic HIV/AIDS model tailored to the challenges faced in Ethiopia, particularly concerning undiagnosed infectious individuals. Qualitative aspects of the model, such as equilibrium points and stability, were examined, highlighting the significance of the effective reproductive number (R_e). Additionally, an optimal control problem was formulated, integrating prevention, screening, and treatment as control variables. Numerical investigations revealed the efficacy of combined optimal control strategies in reducing the prevalence of HIV/AIDS and alleviating associated costs.

A mathematical model for the transmission of HIV/AIDS with early treatment was developed and analyzed by Akinwumi *et al*. (2021). They determined the basic reproduction number, which represents the average number of new secondary infections generated by a single infected individual during the infectious period. The analysis indicated that the disease-free equilibrium is both locally and globally asymptotically stable when the threshold quantity is less than one. Numerical analysis demonstrated that early treatment of latently infected individuals reduces the dynamic progression to full-blown AIDS. The results also revealed that substances boosting immunity increase red

blood cells, and sensitivity analysis of the basic reproduction number concerning parameters indicated that the effective contact rate should not exceed 0.3 to prevent the endemic stage.

Ajao *et al*. (2023) introduced a mathematical model to investigate the transmission dynamics of HIV in Nigeria, addressing a unique aspect by partitioning detected individuals into those receiving treatment and those not accessing treatment. This consideration, which has been absent in recent literature, adds depth to the understanding of HIV dynamics. The study's findings emphasize the pivotal role played by the fraction of detected individuals receiving treatment, affecting the population of latently infected individuals and the AIDS class. The treatment's impact is highlighted as it hinders the progression of individuals into the AIDS class. Researchers have developed various variations of the HIV/AIDS model, and some of these are outlined in other reports (Adewale *et al*., 2015a; Olopade *et al*., 2016; Sanna, 2021, 2022; Hamou *et al*., 2023).

In contemporary literature, a considerable portion has tended to overlook the historical aspect when utilizing mathematical epidemic models for HIV/AIDS. What sets this study apart is its focus on the "memory term," integrating information on both the current and past states of the disease. This addition enhances the model's capability to consider the historical context, thereby offering a more thorough and insightful approach to the analysis of epidemics. In this study, we modified the work done by Akinwumi *et al*. (2021) by incorporating the non-linear saturated function $\beta SI/(1+\alpha I)$, where I is the information term that reflects the past and present state of the disease, i.e., HIV/AIDS. Therefore, a five-compartmental mathematical model for the study of the HIV/AIDS epidemic with a memory term is presented and analyzed to gain insight into the current and past states of HIV/AIDS and other epidemiological features that cause the progression from HIV to full-blown AIDS.

The paper follows the following structure: Section 2 outlines the methodology, encompassing the design and formulation of the model, along with its analysis. Section 3 is devoted to presenting the results and engaging in a subsequent discussion of those findings. The paper is wrapped up with Section 4, which serves as the conclusion.

MODEL FORMULATIONS

The population size $N(t)$ of humans is sub–divided into five (5) classes of individuals who are Susceptible $S(t)$, Latently infected $L(t)$, Infected $I(t)$, Treated $T(t)$ and Aids $A(t)$, So that;

$$\left(N(t) = S(t) + L(t) + I(t) + T(t) + A(t)\right) \quad (1)$$

The susceptible population is increased by the recruitment of individuals into the population (either by birth or immigration) at the rate (Λ). The population decreases by the ratio of the newly infected individuals that move to the latently infected class with

information term at the rate $\left(\frac{1}{1+\alpha I}\right)$.The population also decreases by natural death at the rate μ . Thus;

$$\frac{dS}{dt} = \Lambda - \frac{\beta SI}{1+\alpha I} - \mu S \tag{2}$$

The ratio of the population of the latently infected class consists of newly infected individuals with the memory term at the rate $\left(\frac{1}{1+\alpha I}\right)$, following a contact with the infected human/object at the rate β. The population decreases due to progression to infectious class at the rate κ, natural and disease-induced death at the rate (μandδ), respectively, also decreases due to early treatment at the rate (σ_1).The population is assumed to be later increased by the help of an immunity boost from the treated compartment whenever the CD4 counts rise above 50%. Thus;

$$\frac{dL}{dt} = \frac{\beta SI}{1+\alpha I} - (\kappa + \mu + \delta + \sigma_1)L + \theta T \tag{3}$$

The population of infected individual increases by progression from latently infected individual due to lack of treatment or treatment failure at the rate (κ) the population decreases due to treatment (at the rate σ_2), natural death at the rate μ and disease-induced death at the rate δ . Thus;

$$\frac{dI}{dt} = \kappa L - (\mu + \sigma_2 + \delta)I \tag{4}$$

The population of the treated individuals increases by the treatments of those that are latently and fully infected by HIV at the rate (σ_1 and σ_2). The population decreases due to natural death at the rate μ , death due to the disease at the rate δ , treatment failure due to drug resistance or inadequate dosing at the rate ω and the immunity boosted after treatment and CD4 count rises above 50% at the rate θ . Then,

$$\frac{dT}{dt} = \sigma_1 L + \sigma_2 I - (\mu + \delta + \omega + \theta)T \tag{5}$$

Full-blown AIDS compartment increases by treated individuals that failed treatment due to one medical reason or the other at the rate α The acquire immuno-deficiency syndrome individuals suffer natural death and death due to the disease at the rate(μ and δ) respectively. Hence;

$$\frac{dA}{dt} = \omega T - (\mu + \delta)A \tag{6}$$

In summary, the system of the model as follows:

$$\begin{aligned}
\frac{dS}{dt} &= \Lambda - \frac{\beta SI}{1+\alpha I} - \mu S \\
\frac{dL}{dt} &= \frac{\beta SI}{1+\alpha I} - (\kappa + \mu + \delta + \sigma_1)L + \theta T \\
\frac{dI}{dt} &= \kappa L - (\mu + \sigma_2 + \delta)I \\
\frac{dT}{dt} &= \sigma_1 L + \sigma_2 I - (\mu + \delta + \omega + \theta)T \\
\frac{dA}{dt} &= \omega T - (\mu + \delta)A
\end{aligned} \tag{7}$$

Table1. Description of parameters with values

Parameter	Descriptions	Values	Source
Λ	Recruitment Rate	25	Varied
β	Contact Rate	0.35	Sanna (2021).
μ	Natural Death Rate	0.07	https://www.worldometers.info./aids/
δ	Disease Death Rate	0.016	https://www.unaids.org./en
ω	Treatment Failure	0.01	Varied
θ	Immunity Boost	0.10	Varied
κ	Progression Rate	0.07	Saha (2019)
σ_1	Latently Treatment	0.20	Varied
σ_2	Infected Treatment	0.25	Varied
α	Information Term	1	Varied

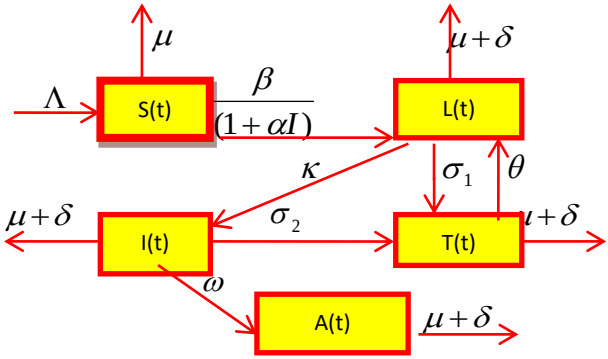

Figure 1. Flow chat of the SLITA model

For the simplicity, we rewrite equation (7) as follows:

$$\begin{aligned}
\frac{dS}{dt} &= \Lambda - \frac{\beta SI}{1+\alpha I} - \mu S \\
\frac{dL}{dt} &= \frac{\beta SI}{1+\alpha I} - K_1 L + \theta T \\
\frac{dI}{dt} &= \kappa L - K_2 I \\
\frac{dT}{dt} &= \sigma_1 L + \sigma_2 I - K_3 T \\
\frac{dA}{dt} &= \omega T - K_4 A
\end{aligned} \tag{8}$$

where; $K_1 = (\kappa + \mu + \delta + \sigma_1)$, $K_2 = (\mu + \sigma_2 + \delta)$, $K_3 = (\mu + \delta + \omega + \theta)$ and $K_4 = (\mu + \delta)$

Model analysis

The analysis of the model is conducted here, aiming to establish and investigate the threshold necessary for the persistence of HIV/AIDS.

The invariant region

Theorem 1: The closed set $D = \left\{ (S, L, I, T, A) \in R_+^5 : N \le \frac{\Lambda}{\mu} \right\}$ is positively- invariant with non-negative initial values in R_+^5

Proof: Consider the feasible region D as defined above, then the rate of change of the total population with $\delta = 0$ is given by;

$$\frac{dN}{dt} = \Lambda - \mu N \tag{9}$$

It follows that $\frac{dN}{dt} \le \Lambda - \mu N$.

Hence, if $N(0) \le \frac{\Lambda}{\mu_1}$, then $N(t) \le \frac{\Lambda}{\mu_1}$. Therefore, all solutions of the model with initial values in D remain in D for all time t > 0 and this implies that D is positively invariant and the model is deemed both epidemiologically meaningful and mathematically well-posed.

Disease-free equilibrium point

The disease-free equilibrium point of equation (7) is obtained by setting $\frac{dS}{dt} = \frac{dL}{dt} = \frac{dI}{dt} = \frac{dT}{dt} = \frac{dA}{dt} = 0$

Since there is no infection, i.e., $L = I = T = A = 0$

Hence, the disease free-equilibrium point of equation (7) is given by

$$\varepsilon_0 = (S, L, I, T, A) = \left(\frac{\Lambda}{\mu}, 0, 0, 0, 0 \right)$$

Existence of endemic equilibrium

Here we analyze the condition for the existence of equilibrium for which the HIV/AIDS disease is endemic in the population. We consider the model equation (8)
where $\mathcal{E}_0^* = (S^*, L^*.I^*, T^*, A^*)$ are the endemic equilibrium points.
Hence,

$$S^{**} = \frac{\Lambda - A\beta}{\mu} \tag{10}$$

$$L^{**} = \frac{AK_2\mu R_0}{\Lambda\kappa} \tag{11}$$

$$I^{**} = \frac{A\mu R_0}{\kappa} \tag{12}$$

$$T^{**} = \frac{A(\sigma_2\kappa + \sigma_1 K_2)R_0}{\Lambda\kappa K_3} \tag{13}$$

$$A^{**} = \frac{A\omega(\sigma_2\kappa + \sigma_1 K_2)R_0}{\Lambda\kappa K_3} \tag{14}$$

Effective reproduction number

The effective reproduction number is the number of secondary cases of infection generated from a single infection (Adewale *et al*. 2015b, 2015c; Olopade *et al*., 2017, 2021a, 2021b, 2022; Musibau *et al*., 2022). We obtained this using next-generation matrix method. The matrices F (new infection terms) and V (other transferring terms) are given as:
Given the matrices F and V below,

$$\text{F}=\begin{bmatrix} 0 & \frac{\beta\Lambda}{\mu} & 0 & 0 \\ 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 \end{bmatrix} \tag{15}$$

$$\text{V}=\begin{bmatrix} K_1 & 0 & -\theta & 0 \\ -\kappa & K_2 & 0 & 0 \\ -\sigma_1 & -\sigma_2 & K_3 & 0 \\ 0 & 0 & -\omega & K_4 \end{bmatrix} \tag{16}$$

$$V^{-1}=\begin{bmatrix} -\frac{K_2K_3}{\kappa\theta\sigma_2+\theta K_2\sigma_1-K_1K_2K_3} & -\frac{\theta\sigma_2}{\kappa\theta\sigma_2+\theta K_2\sigma_1-K_1K_2K_3} & -\frac{\kappa K_2}{\kappa\theta\sigma_2+\theta K_2\sigma_1-K_1K_2K_3} & 0 \\ -\frac{\kappa\sigma_2+K_2\sigma_1}{\kappa\theta\sigma_2+\theta K_2\sigma_1-K_1K_2K_3} & \frac{\theta\sigma_1-K_1K_3}{\kappa\theta\sigma_2+\theta K_2\sigma_1-K_1K_2K_3} & -\frac{\kappa\theta}{\kappa\theta\sigma_2+\theta K_2\sigma_1-K_1K_2K_3} & 0 \\ -\frac{\kappa\sigma_2+K_2\sigma_1}{\kappa\theta\sigma_2+\theta K_2\sigma_1-K_1K_2K_3} & -\frac{\sigma_2K_1}{\kappa\theta\sigma_2+\theta K_2\sigma_1-K_1K_2K_3} & -\frac{\kappa\theta}{\kappa\theta\sigma_2+\theta K_2\sigma_1-K_1K_2K_3} & 0 \\ -\frac{\alpha(\kappa\sigma_2+K_2\sigma_1)}{(\kappa\theta\sigma_2+\theta K_2\sigma_1-K_1K_2K_3)K_4} & -\frac{\alpha K_1\sigma_2}{(\kappa\theta\sigma_2+\theta K_2\sigma_1-K_1K_2K_3)K_4} & -\frac{\alpha K_2K_1}{(\kappa\theta\sigma_2+\theta K_2\sigma_1-K_1K_2K_3)K_4} & \frac{1}{K_4} \end{bmatrix}$$

$$F.V^{-1}=\begin{bmatrix} \frac{\beta\Lambda\kappa K_3}{\mu(\kappa\theta\sigma_2+\theta K_2\sigma_1-K_1K_2K_3)} & \frac{\beta\Lambda(\theta\sigma_1-K_1K_3}{\mu(\kappa\theta\sigma_2+\theta K_2\sigma_1-K_1K_2K_3)} & \frac{\beta\Lambda\kappa\theta}{\mu(\kappa\theta\sigma_2+\theta K_2\sigma_1-K_1K_2K_3)} & 0 \\ 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 \end{bmatrix}$$

$$\rho\left(F.V^{-1}\right)=\begin{bmatrix} 0 \\ 0 \\ 0 \\ -\frac{\beta\Lambda\kappa K_3}{\mu(\kappa\theta\sigma_2+\theta K_2\sigma_1-K_1K_2K_3)} \end{bmatrix}$$

$$R_0=-\frac{\beta\Lambda\kappa K_3}{\mu(\kappa\theta\sigma_2+\theta K_2\sigma_1-K_1K_2K_3)}$$

The threshold quantity R_0 is the effective reproduction number of the model equation above, which is the average number of new case of an infection caused by one typical infected HIV/AIDS in a population of susceptible.

Local stability of disease-free equilibrium

Theorem 2: The disease-free equilibrium is locally asymptotically stable (LAS) if $R_0< 1$ and unstable if $R_0>1$.

Proof: To determine the local stability of E_0, the Jacobian matrix below is computed corresponding to disease-free equilibrium $\mathcal{E}_0$. Considering the stability of the disease-free equilibrium at $\left(\frac{\Lambda}{\mu},0,0,0,0\right)$ equation (8)

$$J_1(\mathcal{E}_0)=\begin{bmatrix} -\mu & 0 & \frac{-\beta\Lambda}{\mu} & 0 & 0 \\ 0 & -K_1 & \frac{\beta\Lambda}{\mu} & \theta & 0 \\ 0 & \kappa & -K_2 & 0 & 0 \\ 0 & \sigma_1 & \sigma_2 & -K_3 & 0 \\ 0 & 0 & 0 & \alpha & -K_4 \end{bmatrix} \qquad (17)$$

Since the first and the fifth column of the equation (17) have only the diagonal term that forms the first two negative eigen values, i.e., $-\mu$ and $-K_4$, hence, the remaining sub-matrix is given

by
$$J_2(\varepsilon_0)=\begin{bmatrix} -K_1-\lambda & \frac{\beta\Lambda}{\mu} & \theta \\ \kappa & -K_2-\lambda & 0 \\ \sigma_1 & \sigma_2 & -K_3-\lambda \end{bmatrix}=0 \quad (18)$$

The characteristics equation of the matrix (18) is given below;
$$A_3\lambda^3+A_2\lambda^2+A_1\lambda+A_0=0 \quad (19)$$
Where
$$A_3=1$$
$$A_2=K_3+K_2+K_1$$
$$A_1=\frac{\mu\theta\sigma_1-\mu K_1K_2-\mu K_1K_3-\mu K_2K_3+\Lambda\beta\kappa}{\mu}$$
$$A_0=\frac{\sigma_2\kappa\theta\mu+\sigma_1\theta\mu K_2-\mu K_1K_2K_3+\Lambda\beta\kappa K_3}{\mu}$$

From A_0;
$$\frac{\Lambda\beta\kappa K_3}{\mu}+(\sigma_2\kappa\theta+\sigma_1\theta K_2-K_1K_2K_3)>0$$
$$\frac{\Lambda\beta\kappa K_3}{\mu}>-(\sigma_2\kappa\theta+\sigma_1\theta K_2-K_1K_2K_3) \quad (20)$$
$$\frac{-\Lambda\beta\kappa K_3}{\mu(\sigma_2\kappa\theta+\sigma_1\theta K_2-K_1K_2K_3)}<1$$

Therefore,
$R_0<1$.

According to Routh Hurwitz criterion, which states that all the roots of the polynomial will have negative real parts if and only if all the coefficients $A_i(i=0,1,2,3)$ are positive and the matrices $T_i(i=0,1,2,3)$ are all positive. Clearly $A_3>0, A_2>0, A_1>0$ and $A_0>0$ if $R_0>1$ Also, the Hurwitz matrix T_i is all positive which are given below;

$$T_1=A_2>0,\ T_2=\begin{bmatrix} A_2 & A_3 \\ A_0 & A_1 \end{bmatrix}>0,\ T_3=\begin{bmatrix} A_2 & A_3 & 0 \\ A_0 & A_1 & A_2 \\ 0 & 0 & A_0 \end{bmatrix}>0$$

Therefore, all the eigen-values of the matrix (17) are negative which shows that the disease-free equilibrium is locally asymptotically stable.

Global stability of the disease-free equilibrium

Theorem 2: The disease-free equilibrium of model (8) is globally asymptotically stable if $R_o<1$.

Proof: We use comparison theorem to prove the global stability (Lakshmikantham *et al.*, 1989). The rate of change of variables representing the infected components of equation (8) can be re-written as;

$$\begin{pmatrix} \frac{dL}{dt} \\ \frac{dI}{dt} \\ \frac{dT}{dt} \\ \frac{dA}{dt} \end{pmatrix} = (F-V)\begin{pmatrix} L \\ I \\ T \\ A \end{pmatrix} - F_i \begin{pmatrix} L \\ I \\ T \\ A \end{pmatrix} \tag{21}$$

Where;

$$\begin{pmatrix} \frac{dL}{dt} \\ \frac{dI}{dt} \\ \frac{dT}{dt} \\ \frac{dA}{dt} \end{pmatrix} = (F-V)\begin{pmatrix} \beta S-\kappa-\mu-\delta-\sigma_1-\theta \\ \kappa-\mu-\sigma_2-\delta \\ \sigma_1+\sigma_2-\mu-\delta-\alpha-\theta \\ \alpha-\mu-\delta \end{pmatrix} - F_i \begin{pmatrix} L \\ I \\ T \\ A \end{pmatrix} \tag{22}$$

Then,

$$\begin{pmatrix} \frac{dL}{dt} \\ \frac{dI}{dt} \\ \frac{dT}{dt} \\ \frac{dA}{dt} \end{pmatrix} (F-V)\begin{pmatrix} \beta S-\kappa-\mu-\delta-\sigma_1-\theta \\ \kappa-\mu-\sigma_2-\delta \\ \sigma_1+\sigma_2-\mu-\delta-\omega-\theta \\ \omega-\mu-\delta \end{pmatrix} \tag{23}$$

The matrix F – Vhas eigenvalues with negative real parts, indicating stability for the linearized differential inequality system described above. Therefore, according to the comparison theorem, it can be inferred that $E_h = I_h = J_h = I_R = 0, \rightarrow (0,0,0,0,0)$ as $t \rightarrow \infty$. Substituting $E_h = I_h = J_h = I_R = 0$ into (8) we have that $S(t) \rightarrow S(0)$ as $t \rightarrow \infty$. Therefore, a positive invariant region exists, leading to the global asymptotic stability of the disease-free equilibrium whenever $R_0 < 1$ (Adewale *et al.*, 2015a).

Theorem 4: Let $\varepsilon*$ be the unique positive equilibrium point of the system (7), If $R_0 > 1$, then endemic equilibrium $\varepsilon*$ of the system (7) is globally asymptotically stable.

Proof: Using theorem 5 and 6, consider;

Theorem 5: (Dulac's Criterion)

Consider the following general nonlinear autonomous system

$$x(t) = f(x), x \in E \tag{24}$$

Let $f = C^1(E)$where E is a simple connected region in R^n. If there exists a function $H \in C^1(E)$ such that $\nabla.(H.f)$is not identically zero and does not change sign in E, the system (7) has no close orbit lying entirely in E. if A is an annular region contained in E on which $\nabla.(H.f)$ does not change sign, then there is at most one limit cycle of the system (7) in A.

Theorem 6: (The Poincare-Bendixson Theorem)

Suppose that $f \in C^1(E)$

Where E is an open subset of R^n and that the system (7) has a trajectory Γ contained in a compact subset f of E. Assume that the system (7) has only one unique equilibrium point x_0 in f, then one of the following possibilities holds.

(1) $w(\Gamma)$ is the equilibrium point x

(2) $w(\Gamma)$ is a periodic orbit

(3) $w(\Gamma)$ is a graphic

$H(S,L,I,T,A) = \frac{1}{SLITA}$, $S>0, L>0, I>0, T>0$ and $A>0$,

Then,

$$\nabla.(H.f) = \frac{\partial}{\partial S}(H.f_1) + \frac{\partial}{\partial L}(H.f_2) + \frac{\partial}{\partial I}(H.f_3)\frac{\partial}{\partial T} + (H.f_4) + \frac{\partial}{\partial A}(H.f_5) \quad (25)$$

$$= -\frac{\Lambda}{(S)^2 LITA} - \frac{1}{(1+\alpha I)(L)^2 TA} - \frac{\theta}{S(L)^2 IA} - \frac{\kappa}{S(I)^2 TA} \quad (26)$$
$$- \frac{\sigma_1}{SI(T)^2 A} - \frac{\sigma_2}{SL(T)^2 A} - \frac{\omega}{SLI(A)^2}$$

$$= -\left[\frac{\Lambda}{(S)^2 LITA} + \frac{1}{(1+\alpha I)(L)^2 TA} + \frac{\theta}{S(L)^2 IA} + \frac{\kappa}{S(I)^2 TA} + \frac{\sigma_1}{SI(T)^2 A} + \frac{\sigma_2}{SL(T)^2 A} + \frac{\omega}{SLI(A)^2}\right] < 0 \quad (27)$$

Consequently, as per Dulac's criterion, a closed orbit exists in the first quadrant, implying that the endemic equilibrium is globally asymptotically stable.

Sensitivity analysis

Sensitivity analysis investigates the relations between the parameters of a model and its threshold quantity basic reproduction number R_o, which determines the spread/eradication of a disease in a community at a particular time (Adesola *et al.*, 2024; Olopade *et al.*, 2024). Sensitivity Analysis has been used for different parameterization tasks of models of biological systems, such as finding necessary parameters for research prioritization, identifying less influenced parameters or parameters clustering.

Sensitivity analysis of the model is determined by the partial derivatives of the basic reproduction number to its parameters;

$$"P": X_P{}^{R_0} = \frac{\partial R_0}{\partial P} \times \frac{P}{R_0} \quad (28)$$

The sensitivity expressions for the parameters in the basic reproduction number are displayed below:

For β,

$$\frac{\partial R_0}{\partial \beta} = \frac{\Lambda \kappa K_3}{\mu(\sigma_2 \kappa\theta + \sigma_1 \theta K_2 - K_1 K_2 K_3)}$$

$$\frac{\beta}{R_0} = -\frac{\mu(\sigma_2 \kappa\theta + \sigma_1 \theta K_2 - K_1 K_2 K_3)}{\Lambda \kappa K_3}$$

$$\frac{\partial R_0}{\partial \beta} \times \frac{\beta}{R_0} = 1$$

For Λ,

$$\frac{\partial R_0}{\partial \Lambda} = \frac{\beta \kappa K_3}{\mu(\sigma_2 \kappa\theta + \sigma_1 \theta K_2 - K_1 K_2 K_3)}$$

$$\frac{\Lambda}{R_0} = -\frac{\mu(\sigma_2 \kappa\theta + \sigma_1 \theta K_2 - K_1 K_2 K_3)}{\beta \kappa K_3}$$

$$\frac{\partial R_0}{\partial \Lambda} \times \frac{\Lambda}{R_0} = 1$$

We apply the same methodology to analyze other parameters in a similar manner. Using the data in Table 1, we obtained the following sensitivity values. The results of the sensitivity indices of R_0 are as shown in the Table 2 below:

Table 2.Values and signs of sensitivity index (S. I) for R_0

Parameter	**S. I.**	**Sensitivity values**
R_0	Positive	0.9162098083
Λ	Positive	1.00000000
β	Positive	1.00000000
μ	Negative	-0.742533291
δ	Negative	-0.1697218951
ω	Positive	0.0288512858
θ	Positive	0.2770380345
κ	Positive	0.8090170006
σ_1	Negative	-0.4308055914
σ_2	Negative	-0.7141361289

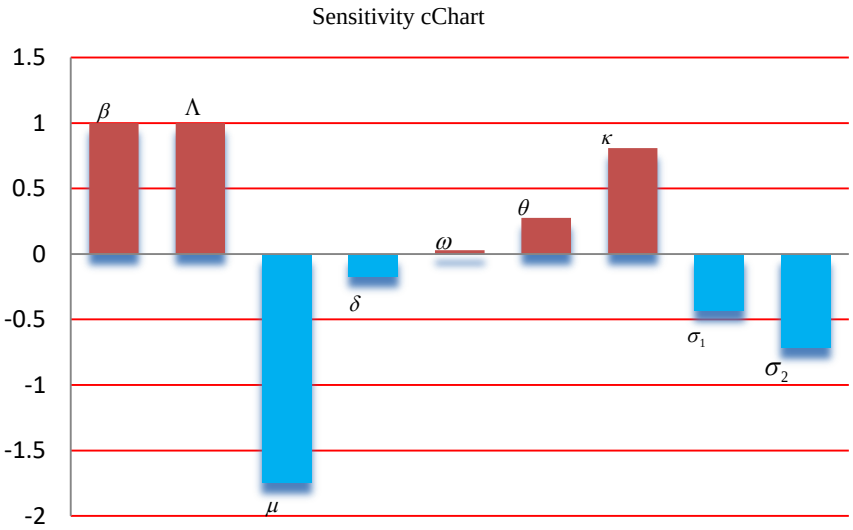

Figure 2. The graph of sensitivity analysis

Numerical simulations

To authenticate the theoretical calculations of the model, the numerical simulations of the model (8) are carried out by differential transformation method, using a set of parameter values given in Table 1.

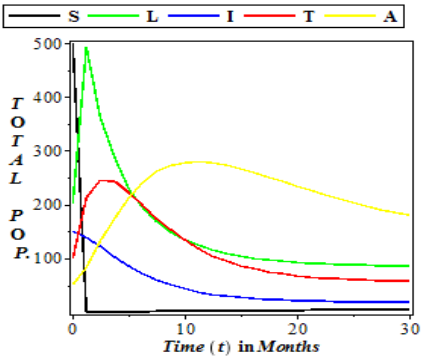

Figure 3. Total population of SEITA with $\alpha = 0$

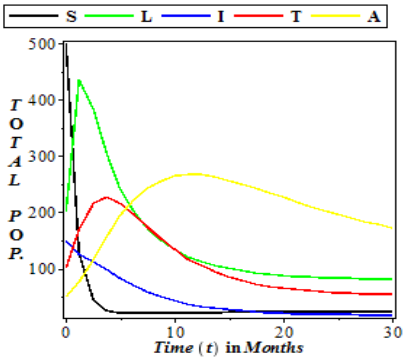

Figure. 4. Total population of SEITA with $\alpha = 0.3$

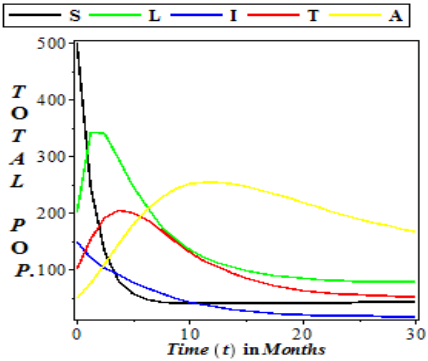

Figure 5. Total population of SEITA with $\alpha = 0.6$

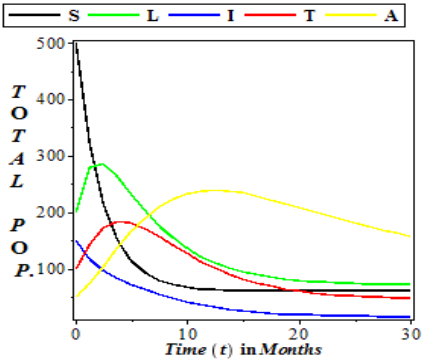

Figure 6. Total population of SEITA with $\alpha = 1.0$

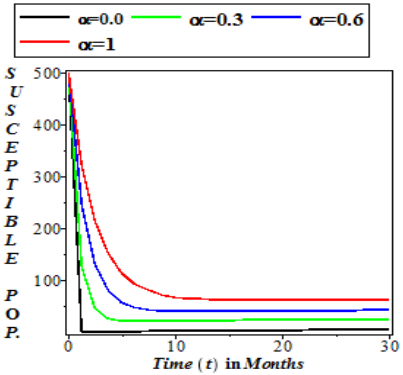

Figure 7. Total population of susceptible individuals with $\alpha = 0.0, 0.3, 0.6 \& 1$

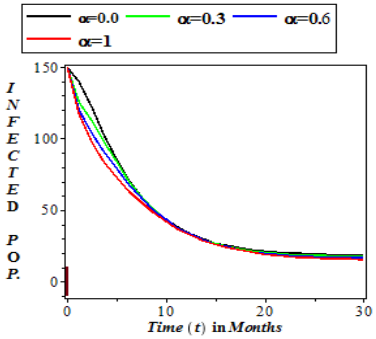

Figure 8. Total population of infected individuals with $\alpha = 0.0, 0.3, 0.6 \& 1$

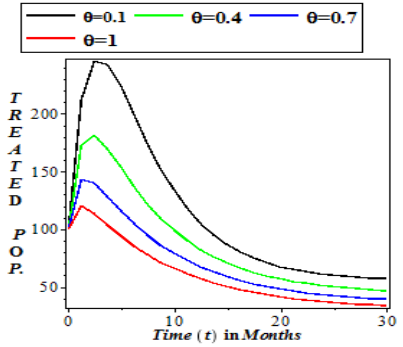

Figure 9. Total population of treated individuals with $\theta = 0.1, 0.4, 0.7 \& 1$

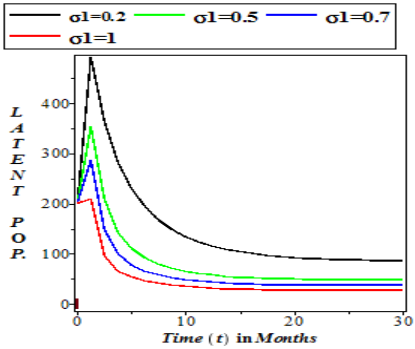

Figure 10. Total population of latently infected individuals with $\sigma_1 = 0.1, 0.4, 0.7 \& 1$

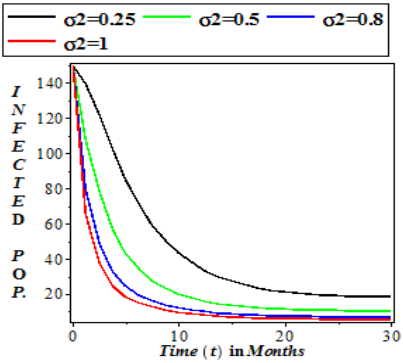

Figure 11. Total population of aids individuals with $\sigma_2 = 0.25, 0.5, 0.8 \& 1$

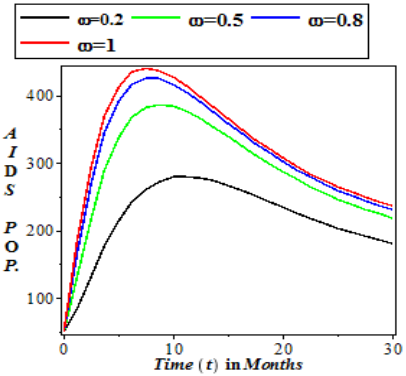

Figure 12. Total population of AIDS individuals with $\omega = 0.2, 0.5, 0.8 \& 1$

RESULTS AND DISCUSSION

We present and analyze five (5) compartmental mathematical models that incorporate memory terms to better understand the dynamics of the HIV/AIDS epidemic. These models offer insights into both current and past states of HIV/AIDS, as well as other epidemiological features contributing to the progression from HIV to full-blown AIDS. This aspect, which has not been explored in existing literature, provides a comprehensive framework for studying the complexities of the disease transmission and progression. We analyzed the effective reproduction number R_0 which determines whether the disease dies off or spread, the result shows that the disease dies off whenever R_0 is less than unity i.e. $R_0<1$ but spreads when $R_0>1$. Sensitivity analysis of basic reproduction number R_0concerning parameters shows the parameters that need to be checked by medical practitioners/health policy makers, parameters with positive index such as effective contact rate increases the basic reproduction number and must not exceed 0.39 to avoid endemic stage. The numerical analysis of the model shows the dynamical behavior of the epidemiological parameters used in the formulation of the model (8).This paper conducts sensitivity analysis to demonstrate the effects of the memory term, treatment rate, and other epidemiological parameters associated with the basic reproduction number.

Table 2 discloses the sensitivity index rate of the effective reproduction number (R_o), which gauges the average number of new secondary infected individuals generated by a single infected individual during the infectious period. The table critically indicates that R_o is less than one ($R_o< 1$), i.e., $R_0 = 0.9162098083$, signifying that the disease is locally asymptotically stable and can be controlled. Furthermore, the recruitment rate into the population is deemed satisfactory, given its positive value $(\Lambda = 1)$. The negative value of the death rate ($\mu = -1.742533291$) suggests that HIV/AIDS can be controlled in society,

leading to a significant reduction in the rate of individuals infected by HIV. The HIV/AIDS-induced death rate, also negative ($\delta = -0.1697218951$), implies that the mortality of those infected by HIV in society would contribute to the reduction of the dynamic spread of HIV. Examining both treatment rates for latent and infected individual classes (σ_1=-0.4308055914 and $\sigma_2 = -0.7141361289$), it becomes evident that the treatments can effectively reduce the viral load in HIV patients, thereby mitigating the progression to full-blown AIDS. Additionally, the positive index of the progression rate (σ) suggests that the progression from latent HIV to active HIV can lead to full-blown AIDS if proper measures are not taken. Figure 2 represents the bar chart of Table 2.Figures 3 to 6 illustrate the impact of increasing the memory term ($i.e.\ \alpha = 0,0.3,0.6,1.0$) on each compartmental class in the total population of the model (Susceptible S, Latent L, Infected I, Treated T, and AIDS A). Each graph was generated using MAPLE 18 through Runge-Kutta's fourth-order method. The total population was plotted against time (t) in months, with variations in the memory term. The memory term provides information about any disease.

In Figure 3, where $(\alpha = 0)$ means there is no information or awareness of HIV in society, the graph reveals that the population of the latent class was very high, while the susceptible class was low to the point of insignificance. As α increases in Figures 4 and 5, i.e. $\alpha = 0.3$, 0.6 respectively, there is little awareness of the disease in the society, resulting in a gradual reduction in the population of the latent class and a small increment in the susceptible class within a short period. In Figure 6, where α is greater, i.e., $\alpha = 1$, indicating awareness of the disease, there is an increase in the susceptible class while the latent population decreases within a relatively short period. Furthermore, Figures 7 and 8 indicate that the memory term is directly proportional to the susceptible class and inversely proportional to the infected class. Consequently, when society is informed about the HIV/AIDS disease, its transmission rate is significantly reduced.

Figure 9 visually illustrates a notable trend: an augmentation in immunity boost corresponds to a decrease in the number of viral load in the HIV host. This suggests that a strengthened immune system serves as a preventive force within the individual's body, acting to reduce the likelihood of HIV infection. The figure provides a clear representation of the positive impact of enhanced immunity in mitigating the HIV leading to full blown-AIDS, emphasizing the critical role of immune strength in individual resistance to HIV.

Figures 10 and 11 offer additional confirmation that prompt initiation of treatment is imperative in the event of an HIV outbreak in society. These graphs underscore the importance of timely intervention, showing that the treatment rate exhibits an inverse relationship with both the latent and infected classes, respectively. The findings emphasize that a higher treatment rate corresponds to a reduction in the populations of latent and infected individuals. This highlights the critical role of swift treatment

initiation in mitigating the impact of an HIV outbreak and curbing the progression of the disease within the affected population.

Figure 12 visually depicts the consequences of treatment failure, showcasing a notable rise in the full-blown AIDS compartment. This illustration provides a visual representation of how the failure of treatment contributes to an escalation in the population affected by advanced stages of AIDS. The figure serves as a valuable tool for understanding the dynamics and implications of treatment shortcomings in the context of disease progression within the model or study.

CONCLUSION

In conclusion, this study has illuminated the transmission dynamics of HIV/AIDS with a saturated incidence rate and underscored specific epidemiological features. However, it is crucial to acknowledge the limitations of the research. Firstly, the model employed in this study may oversimplify the intricate dynamics of real-world HIV/AIDS transmission, failing to consider factors such as varying transmission rates, population mobility, and socio-economic factors. Additionally, the findings may be constrained by the assumptions and parameters utilized in the model, which might not accurately capture the complexity of HIV/AIDS dynamics across all populations. Moreover, while the study highlights the significant impact of information terms and treatment rates on susceptible, infected, and latent infected populations, it is essential to recognize that additional factors, including access to healthcare, stigma, and cultural beliefs, also exert considerable influence on the spread and management of HIV/AIDS. Therefore, while the study implies that HIV/AIDS transmission can be mitigated by considering memory terms and treatment rates, policymakers and stakeholders must adopt a holistic approach to HIV/AIDS prevention and control. This approach should encompass not only medical interventions but also address socio-economic disparities, promote education and awareness, and combat stigma and discrimination. In light of these considerations, it is incumbent upon government officials and lawmakers to adopt proactive measures to control the spread of HIV/AIDS. This entails implementing evidence-based policies and interventions that address the multifaceted nature of the epidemic and prioritize the needs of affected communities.

CONFLICT OF INTEREST

We would like to declare that there are no conflicts of interest to report for any of the authors involved in this research.

REFERENCES

Adesola, O.I., Oloruntoyin, S.S., Emmanuel, P.M., Temilade, M.I., Adeyemi, A.G., Oladele, A.S., Mamman, A.U and Kareem, A.A. (2024). Mathematical modelling and analyzing the dynamics of condom efficacy and compliance in the spread of HIV/AIDS. *Asian Research Journal of Current Science* **6**(1): 54–65.

Adewale, S.O., Olopade, I.A., Ajao, S.O and Adeniran, G.A. (2015a). Mathematical analysis of diarrhea in the presence of vaccine. *International Journal of Scientific and Engineering Research* **6**(12): 396–404.

Adewale, S.O., Olopade, I.A., Adeniran, G.A., Mohammed, I.T and Ajao, S.O. (2015b). Mathematical analysis of effects of isolation on ebola transmission dynamics. *Research Journali's Journal of Mathematics* **2**(2): 1–20.

Adewale, S.O., Olopade, I.A., Ajao, S.O and Mohammed, I.T. (2016). Mathematical analysis of sensitive parameters on the dynamical spread of HIV. *International Journal of Innovative Research in Science, Engineering and Technology* **5**(5): 2624–2635.

Ajao, S.O., Olopade, I.A., Akinwumi, T.O., Adewale, S.O and Adesanya, A.O. (2023). Understanding the transmission dynamics and control of HIV infection: A mathematical model approach. *Journal of the Nigerian Society of Physical Sciences* **5**(2): 1389.

Akinwumi, T.O., Olopade, I.A., Adesanya, A.O and Alabi, M.O. (2021). A mathematical model for the transmission of HIV/AIDS with early treatment. *Journal of Advances in Mathematics and Computer Science* **36**(5): 35–51.

Bushnaq, S., Shah, K and Zaman, G. (2018).Existence theory of HIV- 1 infection model by using arbitrary order derivative of without singular kernel type. *Journal of Mathematical Analysis* **9**(1): 16–28.

Endalamaw, A., Ambachew, S., Geremew, D and Habtewold, T.D. (2019). HIV infection and unknown HIV status among tuberculosis patients in Ethiopia: A systematic review and meta-analysis. *International Journal of Tuberculosis and Lung Diseases* **23**(2):187–94.

Gelaw, Y.A., Williams, G., Soares, R.J., Gilks, C.F and Assefa, Y. (2019). HIV prevalence among tuberculosis patients in Sub-Saharan Africa: Asystematic review and meta-analysis. *AIDS Behavior* **23**(6): 1561–1575.

Global HIV & AIDS statistics — 2020 fact sheet.

Hamou, A.A., Azroul, E., Bouda, S and Guedd, M. (2023). Mathematical modelling of HIV transmission in a heterosexual population: incorporating memory conservation. https://www.researchgate.net/publication/371179334_

https://www.unaids.org./enhttps://www.worldometers.info./aids/

Huo, H.F., Chen, R and Wang, X.Y. (2016). Modelling and stability of HIV/AIDS epidemic model with treatment. *Applied Mathematical Model* **40**: 6550–6559

Lakshmikantham, V., Leela, S and Martynyuk, A.A. (1989).Stability analysis of non-linear system. Marcel Dekker, Inc; New York and Basel.

Musibau, A.O., Muritala, A.A., Isaac, A.O., Adelani, O.A and Akeem, O.Y. (2022). Mathematical analysis of sensitive parameters due to dynamic transmission of Ebola virus disease. *Comprehensive Research and Reviews in Multidisciplinary Studies* **01**(01): 001–016.

Olopade, I.A., Adewale, S.O, Mohammed, I.T, Ajao, S.O and Oyedemi, O.T. (2016). Mathematical analysis of the role of detection in the dynamical spread of HIV-TB co-infection. *Journal of Advances in Mathematics* **11**(10): 5715–5740.

Olopade, I.A., Adesanya, A.O and Mohammed, I.T. (2017). Mathematical analysis of the global dynamics of an SVEIR epidemic model with herd immunity. *International Journal of Science and Engineering Investigations* **6**(69): 141–148.

Olopade, I.A., Adesanya, A.O and Akinwumi, T.O. (2021a). Mathematical transmission of SEIR epidemic model with natural immunity. *Asian Journal of Pure and Applied Mathematics* **3**(1):19–29.

Olopade, I.A., Adewale, S.O., Muhammed, I.T., Adeniran, G.A., Ajao, S.O and Ogunsola, A.W. (2021b). Effect of effective contact tracing in curtaining the spread of Covid-19. *Asian Journal of Research in Biosciences* **3**(2): 118–134.

Olopade, I.A., Ajao, S.O., Adeniran, G.A., Adamu, A.K., Adewale, S.O and Aderele, O.R. (2022). Mathematical transmission of tuberculosis (TB) with detection of infected undetected. *Asian Journal of Research in Medicine and Medical Sciences* **4**(1): 100–119.

Olopade, I.A., Akinola, E.I., Philemon, M.E., Mohammed, I.T., Ajao, S.O., Sangoniyi, S.O and Adeniran, G.A. (2024). Modeling the mathematical transmission of a pneumonia epidemic model with awareness. *Journal of Applied Science Environment Management* **28**(2): 403–413.

Saha, S and Samanta, G.P. (2019). Modelling and optimal control of HIV/AIDS prevention through PrEP and limited treatment. *Physica A: Statistical Mechanics and its Applications* **516:** 280–307.

Sanna, M.S. (2021). Memory and media coverage effects on an HIV/AIDS epidemic model with treatment. *Journal of Computational and Applied Mathematics* **385**(1): 113203.

Tigabu, K.A., Emile, F.D.G and Stella, M. (2021). Mathematical modeling of HIV/AIDS with optimal control: a case study in Ethiopia. *Results in Physics* **26**(6): 104263

Toro Zapata, H.D., Trujillo Salazar, C.A and Carranza Moyonga., E.M. (2020). Mathematical model describing HIV infection with time- delayed CD4T-cell activation. *Processes* **8**(7): 782. https://doi.org/10.3390/pr 8070782.

Udoy, S.B. (2015). Mathematical study of HIV and HSV-2 co-infection. *American Journal of Mathematics and Statistics* **5**(1): 15–23.