Available online www.jsaer.com

***Journal of Scientific and Engineering Research*, 2017, 4(9):111-121**

Research Article

ISSN: 2394-2630
CODEN(USA): JSERBR

Deterministic and Stochastic Models to Simulate the Effects of Antiretroviral Therapy (ART) and Counseling on HIV/AIDS Transmission Dynamics in a Heterosexual Population

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Abstract HIV/AIDS has been a global dreadful infection/disease. The advent of ART and counseling, as intervention measures, has brought about a remarkable achievement in the control of HIV/AIDS. In this paper, we constructed a stochastic differential equation model from a deterministic model and simulated both to study the effects of antiretroviral therapy and counseling on HIV/AIDS transmission dynamics in a heterosexual population. The objective is to compare the solutions of both models. Numerical simulations, considering the number of sex partners, the proportion of individuals on ART and the transmission probability for individuals on ART as control parameters, were carried out. Numerical results demonstrate that the noise inherent in the stochastic model can cause the disease to be eliminated in situations where the deterministic model predicts persistence. Furthermore, the numerical results reveal that reducing the transmission probability and the number of sex partners, and increasing the proportion of people receiving treatment can steer the sample paths of the stochastic model and the trajectory of the deterministic model to the disease-free equilibrium state. The findings in this study recommend that effective ART and counseling are crucial for the control of HIV/AIDS.

Keywords HIV/AIDS, antiretroviral therapy, deterministic model, stochastic model, stochastic differential equations, Wiener process and numerical simulation

1. Introduction

The human immune-deficiency virus (HIV) together with the associated acquired immune deficiency syndrome (AIDS) is still a global threat [1-2].

The basic routes of HIV transmission between persons are well understood. The major routes are sexual (heterosexual and homosexual) and mother- to-child [2-3].

Several intervention methods are available. These range from sex abstinence, use of condoms, education and use of antiretroviral drugs and counseling.

As pointed out in Williams *et al* [2], the development of antiretroviral drugs to treat HIV has been a singular scientific achievement. Between 1995 and 2009 an estimated 14.4 million life-years has been gained globally among adults on ART but the rate of new infections is unacceptably high and still exceeds the number of people starting ART each year.

As presented in casels *et al* [3], ART reduces viral load and the probability of transmission. It also reduces HIV/AIDS-related mortality and, therefore, increases the life expectancy of infected individuals.

Stochastic models of HIV have been proposed and studied by researchers. For example, Peterson et al [4] applied Monte-Carlo simulation technique in a population of intravenous drug users.

Greenhalgh and Hay [5] studied a mathematical model of the spread of HIV/AIDS among injecting drug users. Dalal *et al* [6] examined a stochastic model of AIDS and condom use. Dalal, *et al* [7] also studied a stochastic model for internal HIV dynamics. Ding *et al* [8] carried out risk analysis for AIDS control based on a stochastic

model with treatment rate. Tuckwell and Le Corfec [9] studied a stochastic model for early HIV-1 population dynamics. Waema and Olowofeso [10] studied a mathematical model for HIV transmission using generating function approach.

In this paper, deterministic and stochastic models to simulate the effects of antiretroviral therapy and counseling on HIV/AIDS transmission dynamics in a heterosexual population are presented. The deterministic model was proposed by Kimbir *et al* [11]. We now formulate the stochastic counterpart of the model by Kimbir *et al* [11].

The plan of this paper is as follows. Introductory part is presented in section 1. The deterministic model is presented in section 2. The stochastic counterpart of the deterministic model is developed in section 3. Numerical simulations are carried out in section 4. Discussion and conclusive remarks are passed in sections 5 and 6 respectively.

2. Formulation of the Deterministic Model

Kimbir and his collaborators proposed their model based on the following assumptions. The population is partitioned into three compartments: the number of susceptible individuals $S(t)$, the number of infected individuals $I(t)$ and the number of people receiving ART $R(t)$. It is assumed that recruitment into the S-compartment occurs at the rate bN. Death occurs in all the compartments at the rate μ. In addition, there is AIDS-related death which occurs at the rate α_0 in I-compartment. Infected individuals are treated at the rate δ. Members of the R-compartment die due to AIDS at the rate α. With the availability of free diagnosis, we assume that people are now aware of their HIV status and consequently the infected individuals should now go for antiretroviral therapy and counseling. People that have developed full-blown AIDS symptoms cannot transmit. Based on the above assumptions, Kimbir *et al* [11] formulated the following model.

$$\begin{aligned}\frac{dS}{dt} &= bN - B(t)S - \mu S,\\ \frac{dI}{dt} &= B(t)S - (\mu + \alpha_0 + \delta)I, \qquad (1)\\ \frac{dR}{dt} &= \delta I - (\mu + \alpha)R,\end{aligned}$$

where $N(t) = S(t) + I(t) + R(t)$.

The incidence rate is given by $B(t) = \frac{c\beta I + c'\beta' R}{N}$, where β is the probability of transmission by an individual in I-compartment, c is the number of sex partners for each member of the I-class, β' and c' are the probability of transmission and the number of sex partners respectively by an individual in R-compartment.

3. Stochastic Model of HIV/AIDS transmission dynamics

In order to obtain the Corresponding stochastic differential equation (SDE) model for system (1), we need to identify the forgoing deterministic model as a birth, death and migration process. This SDE formulation assumes there is demographic variability in births, deaths and migrations.

Let X_1, X_2, X_3 denote random variables for the numbers of susceptible, infected individuals and infected individuals on antiretroviral drug. Let the incremental changes in susceptible, infected and infected individuals on ART during the small time period Δt be denoted by Δx_1, Δx_2 and Δx_3 respectively. Then we define the vector Δx as

$\Delta x(t) = (\Delta x_1(t), \Delta x_2(t), \Delta x_3(t))^T$,

Where $\Delta x_i(t) = x_i(t + \Delta t) - x_i(t)$ for $i = 1, 2$ and 3.

The mean and the covariance matrix of Δx have the forms $E(\Delta x) = \mu \Delta t$ and $V(\Delta x) = C\Delta t$, respectively, where C is a positive definite matrix. From the work done by Allen *et al* [12], an explicit form for the matrix $B = \sqrt{C}$ exists for a given positive definite matrix C of order 2. Furthermore, the method of obtaining such a square root matrix is explained in Allen [12]. Then, the SDE model of the deterministic model of interest can be obtained in the form of $dx = \mu dt + Bdw$, where μ and $B = \sqrt{C}$ are defined as above. The variable $W = W(t)$ is a three dimensional wiener process. The notation

$dW = (dW_1, dW_2, dW_3)^T$ denotes the differential of the three dimensional Wiener process, because the wiener process is continuous but not differentiable. The incremental change in the wiener process satisfies.

$\Delta Wi(t) = Wi(t + \Delta t) - Wi(t) \sim N(0, \Delta t)$.

Therefore, in order to formulate the SDEs, the mean matrix $E(\Delta x)$ and the covariance matrix $V(\Delta x)$ need to be computed, so that the vector μ and the matrix B can be obtained.

The various transitions and probabilities for the system (1) are as follows.

Table 1: The compartmental changes in small time period Δt

Transition	Probability
$(\Delta X)_1 = [1, 0, 0]^T$	$p_1 = bN\Delta t$
$(\Delta X)_2 = [-1, 1, 0]^T$	$p_2 = B(t)X_1\Delta t$
$(\Delta X)_3 = [-1, 0, 0]^T$	$p_3 = \mu X_1\Delta t$
$(\Delta X)_4 = [0, -1, 0]^T$	$p_4 = (\mu + \alpha_0)X_2\Delta t$
$(\Delta X)_5 = [0, -1, 1]^T$	$p_5 = \delta X_2\Delta t$
$(\Delta X)_6 = [0, 0, -1]^T$	$p_6 = (\mu + \alpha)X_3\Delta t$
$(\Delta X)_7 = [0, 0, 0]^T$	$1 - (p_1 + p_2 + p_3 + p_4 + p_5 + p_6)$

The system (1) will be changed into the stochastic differential equations in the form;

$\Delta X(t) = F(t, X(t)dt + B(t, X(t))dw(t)$ (2)

Where, $E(\Delta X) = \sum_{i=1}^{6} p_i (\Delta X)_i$

$$= \begin{pmatrix} bN - B(t)X_1 - \mu X_1 \\ B(t)X_1 - (\mu + \alpha_0 + \delta)X_2 \\ \delta X_2 - (\mu + \alpha)X_3 \end{pmatrix} \Delta t,$$

The covariance matrix $C = E((\Delta X)(\Delta X))^T$

$$= \sum_{i=1}^{6} p_i (\Delta X)_i (\Delta X)_i^T$$

$$= \begin{pmatrix} bN + B(t)X_1 & -B(t)X_1 & 0 \\ -B(t)X_1 & (B(t) + \mu)X_1 + (\mu + \alpha_0 + \delta)X_2 & 0 \\ 0 & 0 & (\mu + \alpha)X_3 \end{pmatrix} \Delta t$$

And $B = \sqrt{C}$.

Table 2: Data for HIV/AIDS model

Parameter	Value	Source
b	0.0366	USAID (2009)
μ	0.0166	USAID (2009)
c	variable	
c'	variable	
β	0.011-0.95	Mukandavire *et al* [1]
β'	0.011-0.95	Mukandavire *et al* [1]
δ	variable	
α_0	0.077	assumed
α	0.05	assumed
S	50,000	assumed
I	2	assumed
R	0	assumed

4. Numerical Simulation

The control parameters of the model are transmission coefficient for members in R-class, β', the proportion of infected members on ART,δ and the numbers of sex partners c and c'. While we keep the values of other parameters in Table 1 fixed, we have allowed the values of β', δ, c and c' to vary and investigated their effects on the spread of HIV/AIDS. The dynamics of the HIV/AIDS models $(1\ and\ 2)$ for various values of these control parameters are as shown in Figures $(1) - (13)$ below.

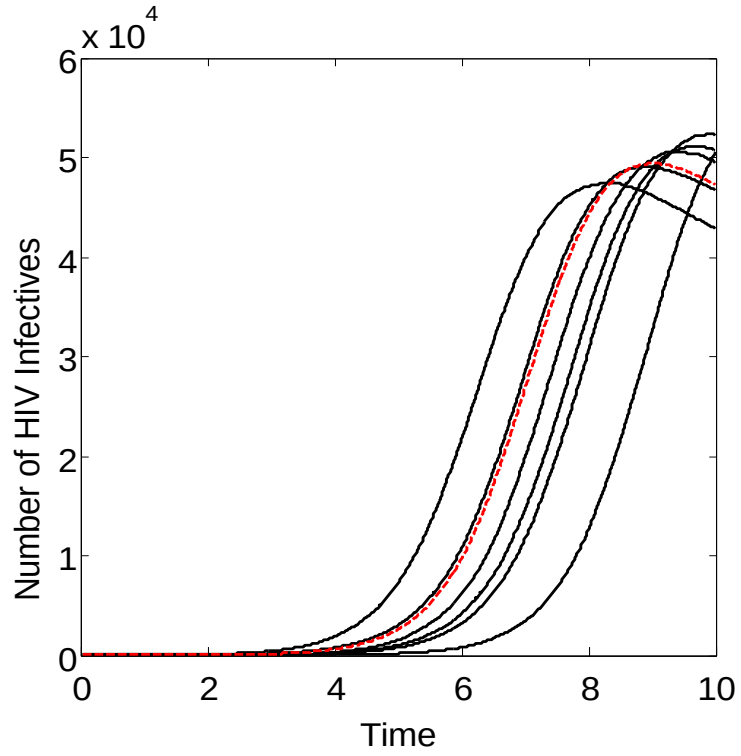

Figure 1: Sample paths of the stochastic model (black) and the trajectory of the deterministic model(red) $c=3, c'=3, \beta=0.5, \beta'=0.5, \delta=0.2$

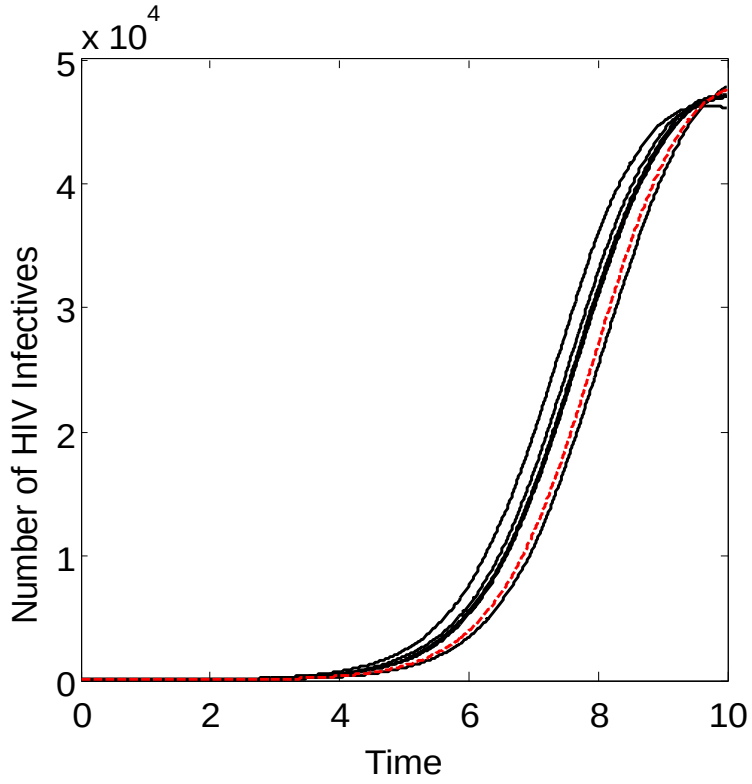

Figure 2: Sample paths of the stochastic model (black) and the trajectory of the deterministic model(red) $c=3, c'=3, \beta=0.5, \beta'=0.011, \delta=0.2$

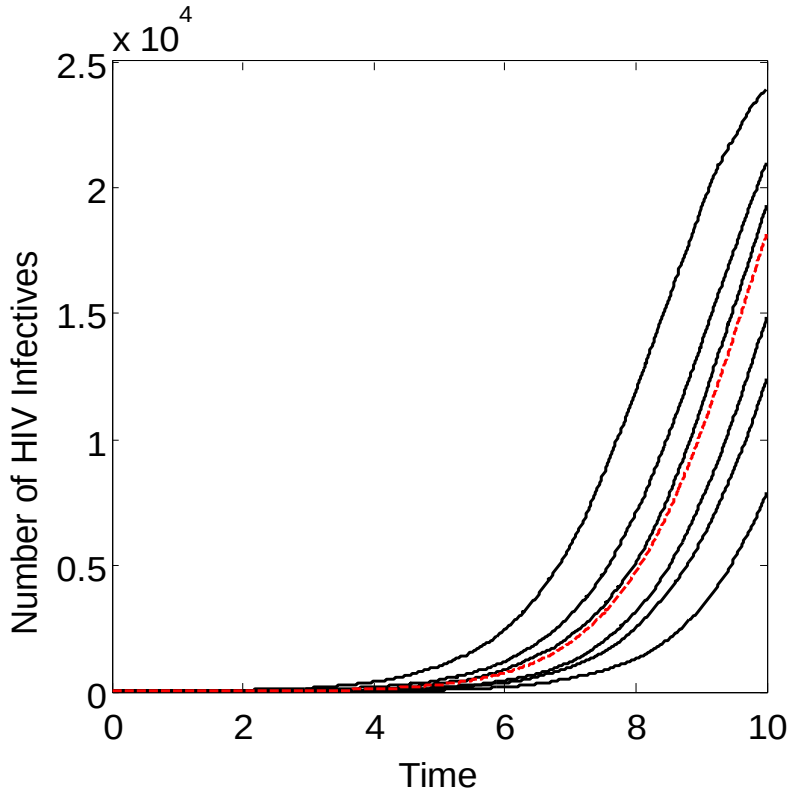

Figure 3: Sample paths of the stochastic model (black) and the trajectory of the deterministic model (red)
$c=3$, $c'=3$,$\beta=0.5$,$\beta'=0.011$,$\delta=0.5$

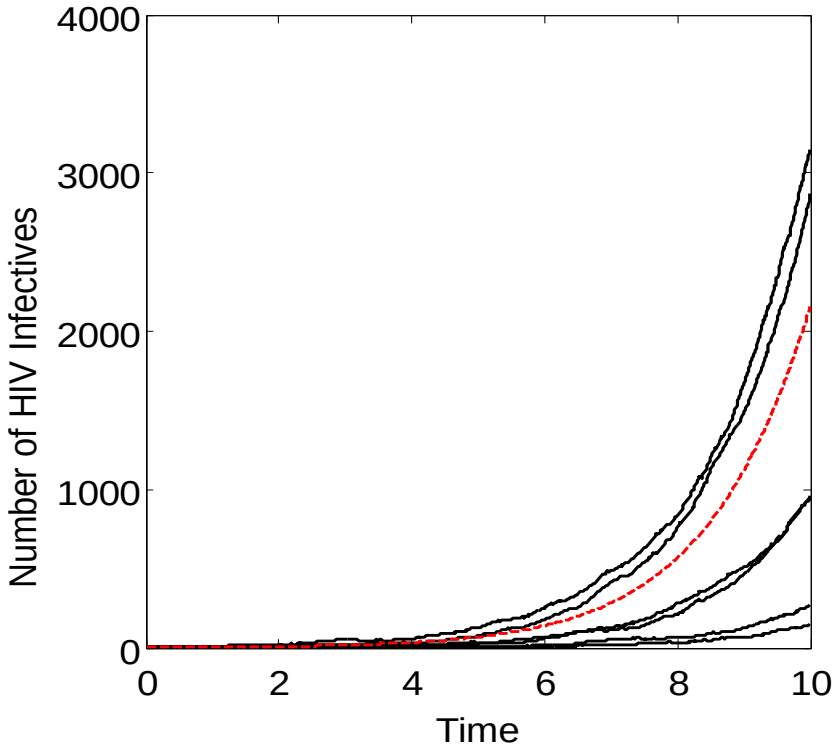

Figure 4: Sample paths of the stochastic model (black) and the trajectory of the deterministic model (red)
$c=3$, $c'=3$,$\beta=0.5$,$\beta'=0.011$,$\delta=0.8$

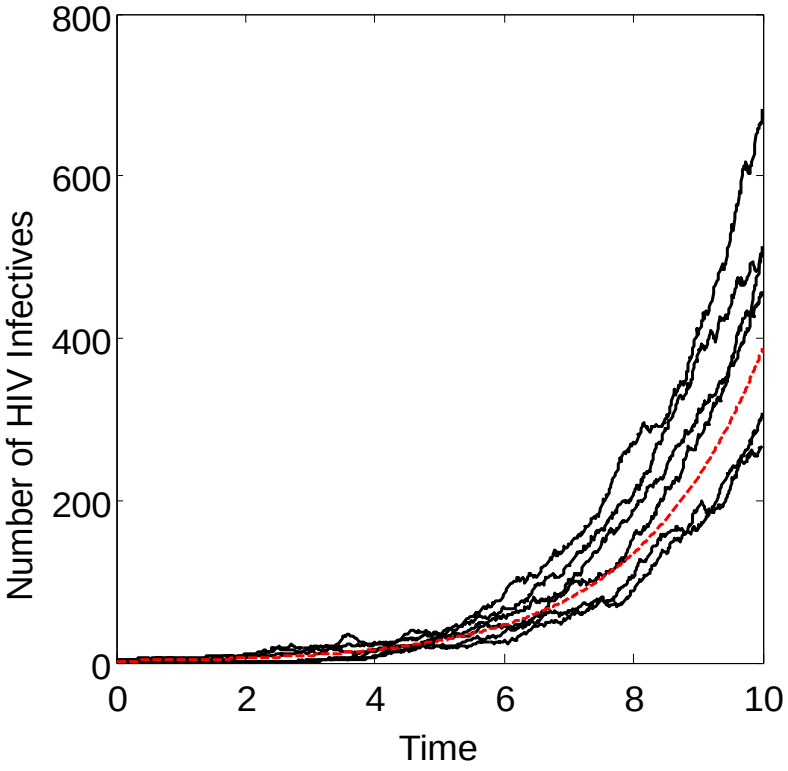

Figure 5: Sample paths of the stochastic model (black) and the trajectory of the deterministic model (red)
$c=3$, $c'=3$,$\beta=0.5$,$\beta'=0.011$,$\delta=1$

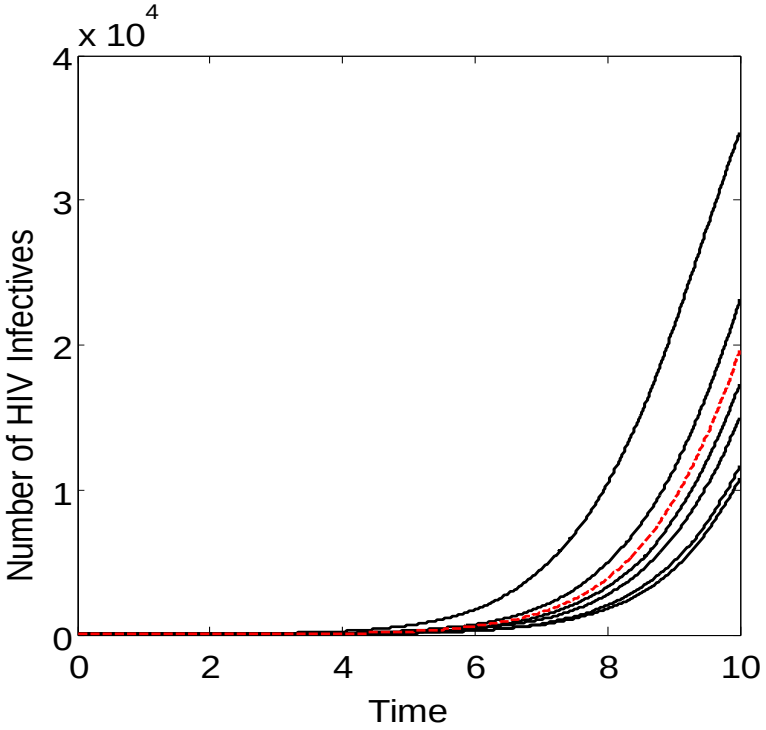

Figure 6: Sample paths of the stochastic model (black) and the trajectory of the deterministic model (red)
$c=2$, $c'=2$,$\beta=0.5$,$\beta'=0.5$, $\delta=0.2$

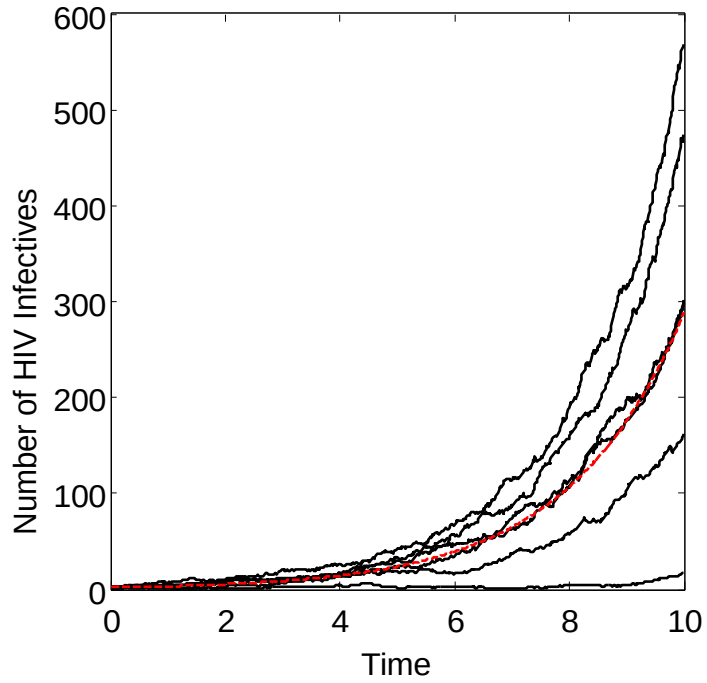

Figure 7: Sample paths of the stochastic model (black) and the trajectory of the deterministic model (red) $c=2$, $c'=2$,$\beta=0.5$,$\beta'=0.011$, $\delta=0.5$

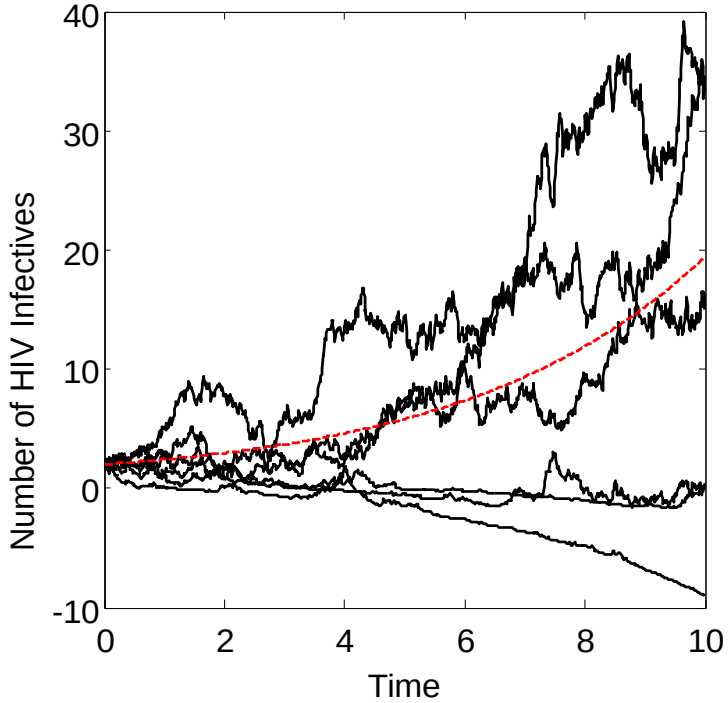

Figure 8: Sample paths of the stochastic model (black) and the trajectory of the deterministic model (red) $c=2$, $c'=2$,$\beta=0.5$,$\beta'=0.011$, $\delta=0.8$

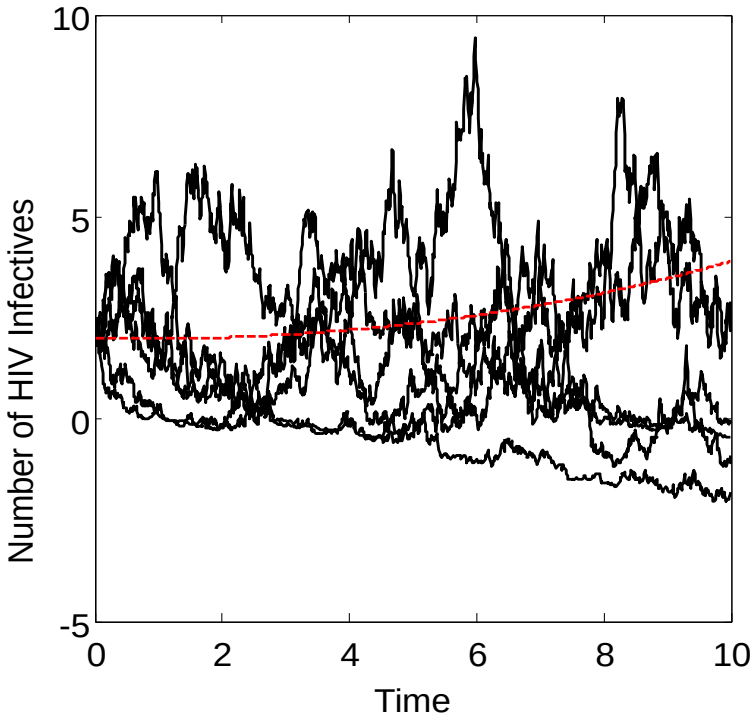

Figure 9: Sample paths of the stochastic model (black) and the trajectory of the deterministic model (red) $c=2$, $c'=2$,$\beta=0.5$,$\beta'=0.011$, $\delta=1$

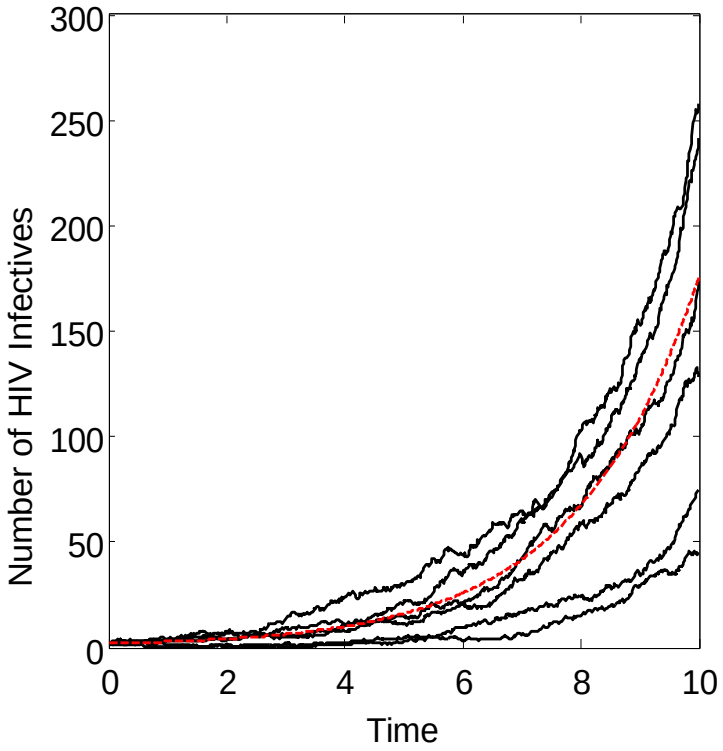

Figure 10: Sample paths of the stochastic model (black) and the trajectory of the deterministic model (red) $c=1$, $c'=1$,$\beta=0.5$,$\beta'=0.5$, $\delta=0.2$

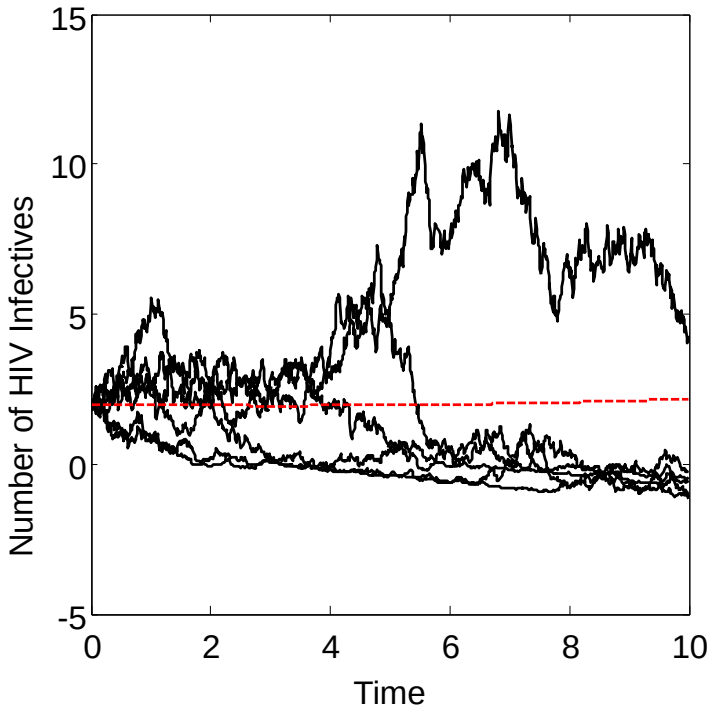

Figure 11: Sample paths of the stochastic model (black) and the trajectory of the deterministic model (red) c=1, c'=1,β=0.5,β'=0.011, δ=0.5

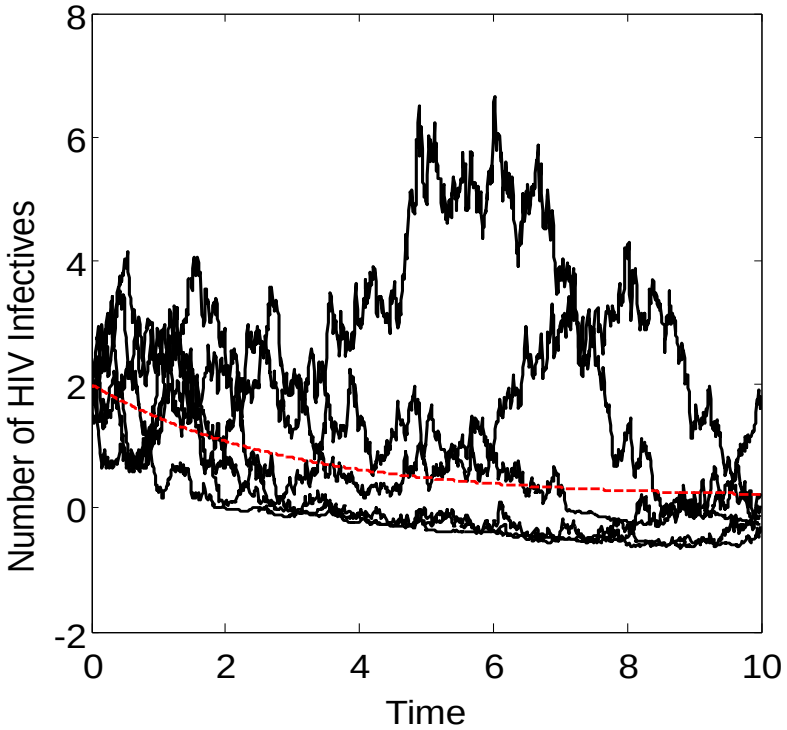

Figure 12: Sample paths of the stochastic model (black) and the trajectory of the deterministic model (red) c=1, c'=1,β=0.5,β'=0.011, δ=0.8

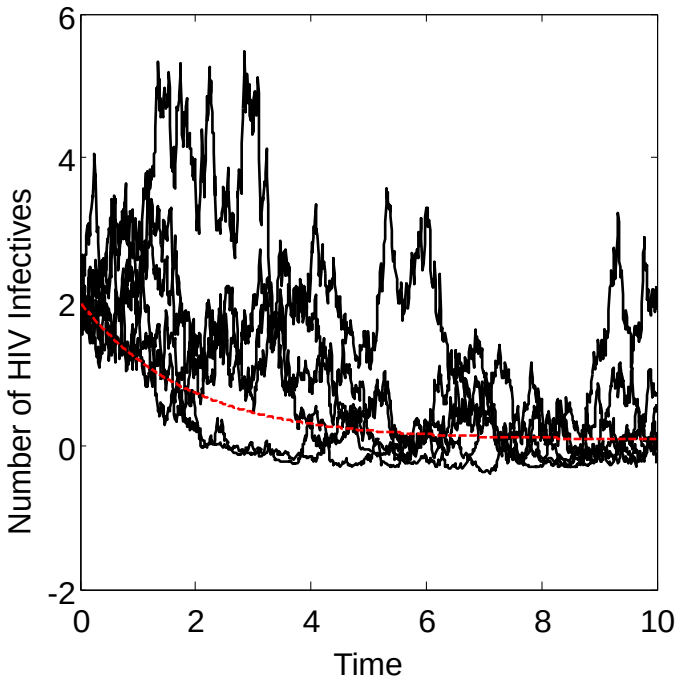

Figure 13: Sample paths of the stochastic model (black) and the trajectory of the deterministic model (red) $c=1$, $c'=1$,$\beta=0.5$,$\beta'=0.011$, $\delta=1$

5. Discussion of Results

In this paper, we constructed an equivalent stochastic differential equation model from a deterministic model and studied both to simulate the effects of antiretroviral therapy and counseling on the transmission dynamics of HIV/AIDS in a heterosexual population. The parameters of the model are in Table 1. The models are presented in sections 2 and 3. The numerical results are as shown in Figures $(1)-(13)$. The numerical results show that reducing the numbers of sex partners, c and c', reducing the transmission probabilities, β and β' and increasing the rate of treatment, δ can bring the spread of HIV/AIDS under control.

6. Conclusion

In this paper, deterministic and stochastic models of HIV/AIDS, considering the proportion of the infected persons on the ART, the transmission coefficient and the number of sex partners as control parameters, are presented. The stochastic counterpart of the deterministic model demonstrates the noise inherent in the transmission mechanism. The stochastic model shows that the disease can die in scenarios where the deterministic model predicts persistence of disease. However, effective treatment and counseling can control HIV/AIDS.

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