

Modelling the Spread of HIV/AIDS Epidemic

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Abstract: In this paper, a deterministic mathematical model for the spread of HIV/AIDS in a variable size population through horizontal transmission is considered. The existence of a threshold parameter, the basic reproduction number, is established, and the stability of both the disease-free equilibrium and the endemic equilibrium is discussed in terms of R_0 .

Key words: spread of HIV/AIDS, horizontal transmission, threshold, stability

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1 Introduction

Many recent theoretical, experimental and field studies have challenged the old wisdom that parasites evolve to become harmless to their hosts. Longevity within the host often comes at the expense of other characteristics of evolutionary value to parasites, that is, the spread of replication, transmissibility and resistance to the host's immune response (see [1]). These patterns have also been observed in the context of HIV. The serious consequences of infection with the HIV virus, according to the prevailing view, which is the agent for AIDS, have stimulated many works on the epidemiological implications of this infection (see [2]).

In recent decades, there have been several investigations on infectious diseases using deterministic mathematical models with or without demographic factors (see [3]). Similarly, we investigate in this work, the transmission of HIV, by considering a basic model with three compartments. Determinating the steady state solutions and analysing their stability represent the main part of our analysis, in which we also address the question of whether or not the disease can invade the host population and under what conditions it happens.

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2 Model Formulation

We consider a sample of population of size $N(t)$ at time t , with a constant inflow rate π of susceptibles. The size $N(t)$ is divided into three subclasses of susceptibles $S(t)$, chronic infectives $I(t)$ and patients who have developed AIDS $A(t)$ with a natural death rate d in each class. The constant progression rate to AIDS is denoted by γ , so that $\frac{1}{\gamma}$ years is the mean duration of stay in the compartment $I(t)$.

In this simple HIV model, we assume that the transmission of the disease for the heterosexual population occurs horizontally, that is, due to direct contact. We also assume a homogenous mixing of the population, so the average number of contacts with susceptibles, adequate for the transmission of the infection, of one infective per unit time is given by $c\beta_i \frac{S}{N}$, where $i = 1, 2$. The incidence rate, the number of new cases, that arise per unit time in this model, is given by $(c\beta_1 I + c\beta_2 A) \frac{S}{N}$, where the probabilities of transmitting infection from the infective partner to the susceptible partner are given by β_1 and β_2 respectively for infectives in compartments I and A . Individuals acquire new sexual partners at a rate c and the average number of adequate contacts of an infective per unit time is given by $c\beta_i$, $i = 1, 2$. The total sexually active population is given by

$$N(t) = S(t) + I(t) + A(t).$$

The transfer diagram is given by Fig. 2.1.

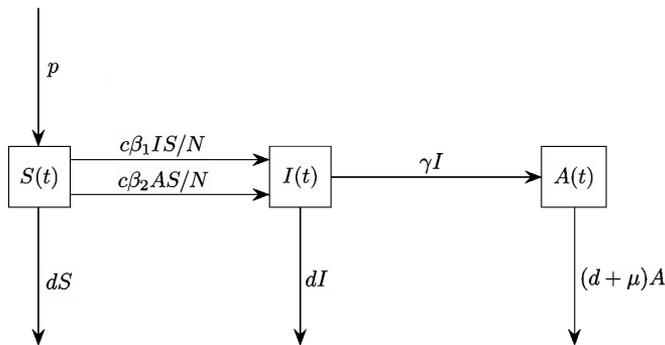


Fig. 2.1

The transfer diagram Fig. 2.1 leads to the formulation of the autonomous differential system

$$\frac{dS}{dt} = \pi - \frac{(c\beta_1 I + c\beta_2 A)}{N} S - dS, \tag{2.1}$$

$$\frac{dI}{dt} = \frac{(c\beta_1 I + c\beta_2 A)}{N} S - (d + \gamma)I, \tag{2.2}$$

$$\frac{dA}{dt} = \gamma I - (d + \mu)A. \tag{2.3}$$

Adding the equation (2.1) to (2.3) gives

$$\frac{dN}{dt} = \pi - dN - \mu A. \tag{2.4}$$