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Epidemiological Model of HIV/AIDS with Demographic Consequences

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Abstract

We take a simple mathematical model, with the aim of making clear some of the essential relations between epidemiological parameters and the overall course of HIV infection with various populations. Such models help to clarify what kinds of epidemiological data are needed to make predictions. We assume constant infectiousness, a constant rate of movement from HIV infection to AIDS disease and the same average rate of acquiring new heterosexual partners for all individuals. We begin with an analytic treatment of the demographic effects of HIV/AIDS, using a basic model in which male-to-female and female-to-male transmission rates are assumed equal. Some refinements to this basic model are discussed.

Keywords: Epidemiology, HIV/AIDS, susceptible, heterosexual transmission, homosexual transmission.

1. Introduction

Mathematical models to study the overall dynamics of transmission of HIV infections among particular risk groups. The models are essentially those of conventional mathematical epidemiology but modified to take account of important special features that make the transmission dynamics of HIV significantly different from that of, say, measles. Mathematical models of the transmission dynamics of HIV can facilitate the indirect assessment of certain epidemiological parameters, clarify what data is required to predict future trends, make predictions under various specified assumptions about the course of infection in individuals and patterns of sexual activity within defined populations (or changes therein) and, more generally, provide a template to guide the

interpretation of observed trends. These models explore the epidemiology of HIV/AIDS, but do not systematically explore the demographic implications. This basic model is defined, and its dynamical properties are discussed. It so happens that this basic model can be solved analytically; the general analytic solution is given and discussed. Some refinements to this basic model are also given.

2. A Basic Model with Demography and Epidemiology

2.1 Definition of the Model

Let us consider first the homosexual transmission of HIV within a population of males. Let the total population N(t) at time t be subdivided into X(t) susceptibles and Y(t) infecteds (assumed to also infectious) It is assumed that all infecteds move at a constant rate υ (that is, after an average incubation time 1/ υ) to develop full-blown AIDS, at which point they are regarded for the purpose of this model as effectively being removed from the population. Deaths from all other causes occur at a constant rate μ.

This simple system is described by the pair of first-order differential equations:

$$\frac{dX}{dt} = B - (\lambda + \mu)X, \tag{1}$$

$$\frac{dY}{dt} = \lambda X - (\upsilon + \mu)Y. \tag{2}$$

The dynamics of the total population, N=X+Y, thus obeys

$$\frac{dN}{dt} = B - \mu N - \upsilon Y. \tag{3}$$

Here B(t) is the net rate at which new recruits appear in this population, and λ(t) is the usual “force of infection”, representing the probability per unit time that a given susceptible will become infected. For a sexually transmitted disease such as HIV, we may write

$$\lambda = \beta c Y / N. \tag{4}$$

where β is the probability of acquiring infection from any one infected partner, Y/N is the probability that a randomly chosen partner will be infected, and c is the average rate at which partners are acquired.

The effective average over the distribution by degrees of sexual activity, c, is given explicitly as $c = \sum i^2 N / \sum_i N_i = m + \sigma^2/m$, where m is the mean and σ^2 the variance of the distribution of the number of new sexual partners per unit of time. Thus, c is not simply the mean but the mean plus the ratio of variance to mean, which reflects the disproportionate role played by highly active individuals, who are both more likely to acquire infection and more likely to transmit it. The total population size N may be

roughly partitioned into subgroups of sizeN_i, each of whom on the average acquire i new sexual partners per unit time (when$N = \sum_i N_i$).

The one additional assumption-which puts the demography into the closed system of equations—concerns the input of susceptible, B, which is given by the net birth rate:

$$B = \nu\,[N - (1-\varepsilon)Y\,] \tag{5}$$

where ν is the per capita birth rate (females per female, or equivalently offspring per capita for a 50:50 sex ratio) in the absence of infection. Let us assume that a fraction ε of all offspring born to infected mothers survive, while a fraction 1 –ε die effectively at birth; thus the net birth rate is diminished below νN by deaths at the rate ν (1–ε) Y, resulting from vertical transmission.

Equations (1)–(5) give a complete description of the dynamical behaviour of this model system, under the interplay of intrinsic demographic factors (births and disease–free deaths, characterized by the parameters ν and μ) and epidemiological factors (horizontal and vertical transmission and resulting deaths, characterised by the parameters βc, υ and ε). Equations (1)-(5) can be written as a pair of equations for N(t) and Y(t)

$$\frac{dN}{dt} = N\left((\nu-\mu) - [\upsilon + (1-\varepsilon)\nu]\frac{Y}{N}\right) \tag{6}$$

$$\frac{dY}{dt} = Y\left((\beta c - \mu - \upsilon) - \beta c\frac{Y}{N}\right) \tag{7}$$

Let us define r to be the disease-free growth rate of the population, Λ the initial exponential growth rate of the infection (from very low values) within the population and θ represents the additional mortality rates associated with infection [both from the direct effects of horizontally transmitted infection, υ, and from the effects of vertical transmission which can depress effective birth rates, ν (1- ε)]:

$$r \equiv \nu - \mu, \tag{8}$$

$$\Lambda \equiv \beta c - (\mu + \upsilon)\,, \tag{9}$$

$$\theta \equiv \upsilon + \nu\,(1-\varepsilon)\,. \tag{10}$$

Equations (6) and (7) now take the tidier form

$$\frac{dN}{dt} = N\left[r - \theta\frac{Y}{N}\right], \tag{6a}$$

$$\frac{dY}{dt} = Y\left[\Lambda - \beta c\,\frac{Y}{N}\right]. \tag{7a}$$

2.2 Reproductive Rate

Whether an infection can establish itself and spread within a population is determined by the key parameter R_o, the basic reproductive rate of infection. R_o is the average number of secondary infections produced by one infected individual in the early stages of an epidemic (when essentially all contacts are susceptible); clearly the infection can maintain itself within the population only if R_o exceeds unity. For a sexually transmitted disease(STD), R_o depends on c, which is essentially the average rate at which new sexual partners are acquired, on β, the average probability that infection is transmitted from an infected individual to a susceptible partner (per partner contact) and on the average duration of infectiousness.

The basic reproductive rate for HIV infection, R_o, is related to the parameters β, c and $\frac{1}{(\mu+\upsilon)}$, and hence to Λ by the formula $R_o = \beta c \frac{1}{(\mu+\upsilon)}$ and if $R_o < 1$ there will be no epidemic.

2.3 Asymptotic Properties

The asymptotic behaviour of the pair of Equations (6) and (7) can be determined by observing that–so long as Λ > r–both N(t) and Y(t) will eventually settle to behave as $e^{\rho t}$. In the limit t → ∞, equations (6) and (7) then give two equations for the two unknown quantities ρ *and* Λ, where κ is the (asymptotically constant) ratio $\frac{Y}{N}$;

$$\rho = r - \theta\kappa, \tag{11}$$

$$\rho = \kappa - \beta c. \tag{12}$$

The asymptotic fraction infected, $\Lambda = \frac{Y}{N}$, can be written, after some algebraic manipulation, as

$$= \frac{\Lambda - r}{(\Lambda - r) + \varepsilon\nu} \tag{13}$$

Asymptotically, the exponential rate at which both the total population, N(t), and the number infected, Y(t), grow can be written as

$$\rho = -(\mu + \upsilon) + \frac{\varepsilon\nu\,(\Lambda + \mu + \upsilon)}{(\Lambda - r + \varepsilon\nu)} \tag{14}$$

this expression for ρ is positive if $\varepsilon\nu$ exceeds the $(\mu + \upsilon)\frac{\Lambda - r}{\Lambda}$ and otherwise is negative (corresponding to the population declining exponentially).

2.4 Exact Solution of the Basic Model

For an exact solution of the pair of Equations (6) and (7), let us first define

$$\emptyset\,(t) = \frac{Y\,(t)}{N\,(t)}.$$

It follows that $\frac{d\emptyset}{dt} = \frac{Y}{N}\left(\frac{dY/dt}{Y} - \frac{dN/dt}{N}\right)$ (15)

We thus have for $\emptyset\,(t)$the simple logistic equation

$$\frac{d\emptyset}{dt} = \emptyset\,[a - b\emptyset]. \tag{16}$$

Here the parameter combinations a and b have been defined for notational simplicity as

$$a = \Lambda - r, \tag{17}$$

$$b = a + \varepsilon\nu. \tag{18}$$

The boundary condition in Equation (16) is that $\emptyset\,(0) = \Delta$, wher Δ is defined as the fraction of the population who are infected at some initial time t=0: $\Delta \equiv$ Y(0) / N(0). Equation (16) has the routine solution

$$\emptyset\,(t) = \frac{\Delta e^{at}}{1+\left(\frac{b}{a}\right)\Delta(e^{at}-1)} \tag{19}$$

Notice that if a>0 $(\Lambda > r)$, the ratio $\emptyset\,(t)$ will tend to the asymptotic value a/b obtained above, Equation (13) ; if a<0, the fraction infected tends to zero, even though R_0 for the infection may exceed unity. Substituting the explicit expression (19) for $\emptyset = Y/N$ into Equation (6) for N(t) and integrating, we get

$$\mathrm{N(t)=N(0)}\; e^{rt}\left(1 + \frac{b}{a}\Delta(e^{at} - 1)\right)^{-\theta/b} \tag{20}$$

Remember that r is the disease-free population growth rate, Equation (8), and the parameter combinations θ, a, b are defined by Equations (10), (17), (18) respectively. This exact solution confirms the qualitative results obtained above: if a<0, the population grows at its disease-free rate, r; if a>0, the population eventually behaves as $e^{\rho t}$, where the expression ρ=r–θa/b can be seen to be equivalent to Equation (14).

In the case where $\rho < 0$, so that asymptotically the population declines, these exact results enable us to say exactly how long it will take before the population ceases its previous pattern of growth, and begins to decline. This turnover point occurs when dN/dt=0, which can be seen to occur at a time t_c given by

$$t_c = \frac{1}{\Lambda - r}\; ln\left\{\frac{r\left[1 - \Delta\left(\frac{b}{a}\right)\right]}{\Delta\left[\theta - r\left(\frac{b}{a}\right)\right]}\right\} \tag{24}$$

Thus if the fraction infected at t=0 is Δ, then the time elapsed before population growth begins to become negative is given roughly by

$$t_c \sim \frac{ln\left(\frac{1}{\Delta}\right)}{\Lambda - r}\,. \tag{25}$$

3. Some Refinements to the Basic Model

3.1 Heterosexual Transmission

In developed countries, the extent to which HIV infection can be transmitted by heterosexual contacts is uncertain. HIV infections in females come from contact with bisexual males, transfusion recipients, haemophiliacs and intravenous drug users. If such female are not themselves a significant source of infection back into the homosexual/bisexual community (through contacts with uninfected bisexuals), we would expect the incidence of HIV infections among the female partners of bisexuals initially to rise roughly in proportion to the incidence among homosexual males.

We would expect the ratio of HIV infection among female partners of bisexuals to that among bisexual males to be $\sim \beta_1 c_1/\beta c$, where β and c are as previously defined, β_1 is the transmission probability for male-to-female contact, and c_1 is the mean number of new female partners acquired by a bisexual male, per unit time. We expect this ratio to be significantly less than unity, because β_1 is less than β, and c_1 is significantly less than c.

3.2 Basic Model with Heterosexual Transmission

We discussed a basic model HIV transmission in a single-sex population. Now we extend to the heterosexual transmission of HIV, and its demographic consequences. We should recognize that, in general, transmission rates from males to females are not identical with those from females to males. Writing N_1 and N_2 for the total populations of males and females, respectively, and similarly writing $Y_1$and Y_2 for numbers of infected males and females, let us replace the pair of Equations (6) and (7) for the symmetrical case with the more general system of four equations:

$$\frac{dN_1}{dt} = \nu[N_2 - (1-\varepsilon)Y_2] - \mu N_1 - \upsilon Y_1, \quad (26)$$

$$\frac{dN_2}{dt} = \nu[N_2 - (1-\varepsilon)Y_2] - \mu N_2 - \upsilon Y_2, \quad (27)$$

$$\frac{dY_1}{dt} = \beta_2 c_2 \frac{Y_2}{N_2}(N_1 - Y_1) - (\mu + \upsilon)Y_1, \quad (28)$$

$$\frac{dY_2}{dt} = \beta_1 c_1 \frac{Y_1}{N_1}(N_2 - Y_2) - (\mu + \upsilon)Y_2. \quad (29)$$

Here the parameters ν, μ, υ and ε are exactly as defined before. Births depend only on the female population (possible effects on fertility of male: female sex ratios below unity are ignored), and it is assumed that sex ratios at birth are 50:50, with females producing male and female offspring at the equal rates ν.

The male-to-female transmission probability is β_1, and males acquire new female partners at the epidemiologically effective average rate c_1. Thus $\beta_1 c_1$ represents the

overall male-to-female transmission rate. Similarly, $\beta_2\, c_2$ represents the overall female-to-male transmission rate. It should be emphasized that inconsistencies can arise in our formulation of equations (26) –(29), because they do not ensure that the number of female partners of males remains equal to number of male partners of females at all times (which must be true). By ignoring any effects of age structure and assuming the initial sex ratio is 50:50 we will have male and female contacts in balance before the advent of HIV/AIDS so long as $m_{1-}\ m_2$ (which, as just mentioned, does not necessarily imply $c_1 - c_2$). But AIDS will not usually remove equal numbers of males and females in Equations (26)–(29). In this event, the patterns in the distributions of acquiring new sexual partners must change over time, in such a way as to keep the total number of male and female contacts equal. If we write the corresponding, asymptotically constant ratios $Y_1 / N_1 \rightarrow \kappa_1\,, Y_2 / N_2 \rightarrow \kappa_2,$ and $N_1 / N_2 \rightarrow \xi,$ then we get four equations for the four quantities $\rho, \kappa_1, \kappa_2,$ and $\boldsymbol{\xi}$ that characterize the asymptotic behaviour of this system:

$$[\rho + \mu + \upsilon\kappa_1]\xi = \nu\,[1 - (1 - \varepsilon)\kappa_2], \tag{30}$$

$$[\nu(1 - \varepsilon) + \upsilon]\kappa_2 = \nu - \mu - \rho, \tag{31}$$

$$(\rho + \mu + \upsilon)\kappa_{1=}\, \beta_2 c_2 \kappa_2\, (1 - \kappa_1,), \tag{32}$$

$$(\rho + \mu + \upsilon)\kappa_{2=}\, \beta_1 c_1 \kappa_1\, (1 - \kappa_2,)\,. \tag{33}$$

The asymptotic analysis of the basic model, equations (11) and (12), gave us the pair of relations κ=$(r - \rho)/\theta$ and κ=(Λ - ρ) / βc, respectively. In this more general model, equation (30) immediately gives us a relation between κ_2 and ρ:

$$\kappa_2 = \frac{r - \rho}{\theta}. \tag{34}$$

Here r and θ are exactly as defined earlier in Equations (8) and (10), respectively. By eliminating κ_1 between the two equations (32) and (33), we get a second relation between κ_2 and ρ, as follows:

$$\kappa_2 = \frac{\beta_1 c_1 \beta_2 c_2 - (\rho + \mu + \upsilon)^2}{\beta_2 c_2\, (\beta_1 c_1 + \rho + \mu + \upsilon)} \tag{35}$$

The pair of equations (34) and (35) now give us a quadratic equation for ρ. The remaining member of the set of equations (30)–(33), namely Equation (30) give us an expression for the asymptotic sex ratio, $\xi = N_1 / N_{2,,}$ once ρ (and thence κ_2 and κ_1) have been determined.

To derive the relation between these more general results and those for the basic, symmetric, model, we define $\overline{\beta c}$ to be the geometric mean of the transmission rates $\beta_1\, c_1$ and $\beta_2\, c_2$:

$$\overline{\beta c} = (\beta_1 c_1 \beta_2 c_2)^{1/2} \tag{36}$$

Then Equation (35) can be expressed as $\kappa_2 = \left[\frac{\Lambda-\rho}{\overline{\beta c}}\right]\left[\frac{\overline{\beta c}+\rho+\mu+\upsilon}{\overline{\beta c}+\alpha(\rho+\mu+\upsilon)}\right]$ (37)

Here we have written $\Lambda = \overline{\beta c} - (\mu + \upsilon)$ in direct with the previous definition (9), and $\alpha = \beta_2 c_2 / \overline{\beta c}$. The transmission of HIV infection to females by bisexual males is a process whose initial dynamics is essentially determined by R_o for transmission among homosexual males, thereafter the question of its transmission and maintenance by purely heterosexual contact arises. The basic reproductive rate for such heterosexual transmission of HIV [20], R_o', is given by $R_o' = (\beta_1 \beta_2 c_1 c_2)^{1/2} / (\mu + \upsilon)$. If the second factor in square brackets in Equation (37) were put equal to unity, Equations (34) and (37) would give exactly the results for ρ obtained from equations (11) and (12) in the basic model, with βc interpreted as the geometric mean of male-to-female and female-to-male overall transmission rates. This approximation is exact if α =1, and is a good approximation so long as $\overline{\beta c}$ is significantly greater than μ +υ +ρ. In general, however, we need to solve a quadratic equation to evaluatc ρ, and to explore the properties of Equations (26)–(29) numerically. In short, the symmetric, basic model is likely to be a reliable guide to the more general case, provided $\overline{\beta c}$ significantly exceeds μ+υ + ρ.

4. Conclusion

Simple mathematical models of the transmission dynamics of human immunodeficiency virus help to clarify some of the essential relations between epidemiological factors, such as distributed incubation periods and heterogeneity in sexual activity, and the overall pattern of the AIDS epidemic. They also help to identify what kinds of epidemiological data are needed to make predictions of future trends.

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