The Effect of Behavioural Change on the Prediction of R_0 in the Transmission of AIDS

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Diekmann *et al.* (1991) developed a model for calculating R_0 for a multi-state disease including pair formation and dissolution. This model is analogous to a model of Blythe and Anderson (1988) and Jacquez *et al.* (1988) which did not include pair formation. The model in Diekmann *et al.* (1991) is a generalization of the model of Diekmann *et al.* (1990). In the sequel to Diekmann *et al.* (1991), Dietz *et al.* (1993) investigated the effects of variable HIV-infectivity. This paper will summarize the model and results of Dietz *et al.* (1993) and will present further results obtained with the same model.

We assume four stages of HIV-infection, three pre-AIDS, and the final stage, AIDS. The parameters incorporated in the model are:

θ_i transition rate from infection state i to infection state $i+$ 1. $\theta_1 = 4.0$ per year; $\theta_2 = \theta_3 = 0.2$ per year;

$p_i(k)$ probability of infection by an infective of sex k in infection state i.

μ_0 death rate of susceptibles (both sexes).

μ_i death rate of infected individuals in infection state i. $\mu_i = 0.02$ per year $(i \neq 4)$; $\mu_4 = 0.5$ per year.

$\rho_i(k)$ partner acquisition rate of an individual of sex k in infection state i.

σ break-up rate
We pick σ as a function of ρ to guarantee that the total expected number of contacts is 500 for the infectious period.

s_{ij} probability that an infected individual in state i remains sexually active after separating from a partner in infection state j.
The effect of s will be demonstrated in the sequel.

β sexual contact rate.
$\beta = 100$ per year in the numerical calculations.

q probability per contact of use of condoms.
We take $q = 0$ for the calculations.

The pairings considered are (note [·] indicates male and (·) female, the

numbers refer to the stage of HIV infection and + or − means seropositive or seronegative):

For the male index case:

$$
\begin{array}{llll}
[+1] & [+2] & [+3] & [+4] \\
[+1](-) & [+2](-) & [+3](-) & [+4](-) \\
[+1](+1) & [+2](+1) & [+3](+1) & [+4](+1) \\
[+1](+2) & [+2](+2) & [+3](+2) & [+4](+2) \\
[+1](+3) & [+2](+3) & [+3](+3) & [+4](+3) \\
[+1](+4) & [+2](+4) & [+3](+4) & [+4](+4)
\end{array}
$$

The analogous cases with the square and round brackets exchanged for the female index case is also included in the model, but not presented here.

In Dietz *et al.* (1993) the matrix of transition probabilities between the pairing states taking the parameters above into account was presented as a matrix G, so that $-G^{-1}$ gives the waiting times in each of the pairing states. Then the multi-type branching process represented by the matrix M of secondary cases of males produced by females, respectively, secondary cases of females produced by males, is given by

$$
\begin{pmatrix} 0 & M_2 \\ M_1 & 0 \end{pmatrix}
$$

where M_1 describes the secondary male cases generated by a female, and M_2 describes the secondary female cases generated by a male.

By the theory of multi-type branching processes (result of Diekmann *et al.* (1991)), R_0 is given by the Perron-Frobenius (PF) eigenvalue of M, and the components of the corresponding eigenvector, v, give the probabilities, respectively, of starting in the following states (collectively exhaustive list of starting possibilities):

$$
\begin{array}{lll}
1 :[+1](+1) & 2 :[+1](+2) & 3 :[+1](+3) \\
4 :(+1)[+1] & 5 :(+1)[+2] & 6 :(+1)[+3]
\end{array}
$$

Next, we want to calculate the number of partners and the number of contacts after infection. For the number of partners, we dot the vector v with the vector whose components are:

1: to 3: the sum of the time spent in infection-pair state [+1], [+2], [+3] after starting in the infection-pair state [+1](+i), where i is the component 1 to 3, respectively.

4: to 6: the sum of the time spent in infection-pair state (+1), (+2), (+3) after starting in the infection-pair state (+1)[+i], where i is the component 4 to 6, respectively.
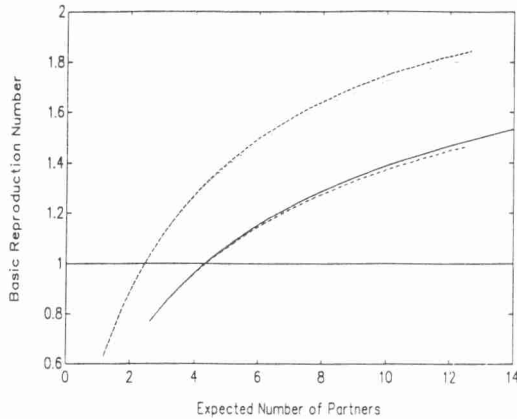
Figure 1

This dot product is then multiplied by ρ, the rate of acquisition of new partners.

To calculate the number of contacts within established partnerships, we multiply β, the contact rate within partnerships by the dot product of v with the vector of sums of times spent in partnerships. The total number of contacts is the sum of the two calculations from this and the previous paragraph.

The first graphics (see Figure 1) using this model compare the expected number of partners (after infection) versus R_0 for variable infectivity $p_i(k)$. Keeping the average infectivity constant, the four cases considered are:

I: sex dependent, time dependent: $p_1(1) = 0.05$, $p_2(1) = 0.001$, $p_3(1) = 0.01$, $p_4(k) = 0$, $p_1(2) = 0.025$, $p_2(2) = 0.0005$, $p_3(2) = 0.005$.

II: sex independent, time dependent: $p_1 = 0.0354$, $p_2 = 0.0007$, $p_3 = 0.0071$.

III: sex dependent, time independent: $p_{men} = 0.00654$, $p_{women} = 0.00327$.

IV: sex independent, time independent: all $p_i = 0.00462$.

Figure 1 shows the relationship: $R_0(\text{I}) \leq R_0(\text{II}) \leq R_0(\text{III}) \leq R_0(\text{IV})$.

Other (not previously reported) results:

- R_1, the basic reproduction ratio for men is the PF eigenvalue of M_1.

- R_2, the basic reproduction ratio for women is the PF eigenvalue of M_2.

- $R_0 = \sqrt{R_1 \cdot R_2}$.

- The variable s has a considerable effect on the the predictions of R_0 as a function of the expected number of partners (see Figure 2).
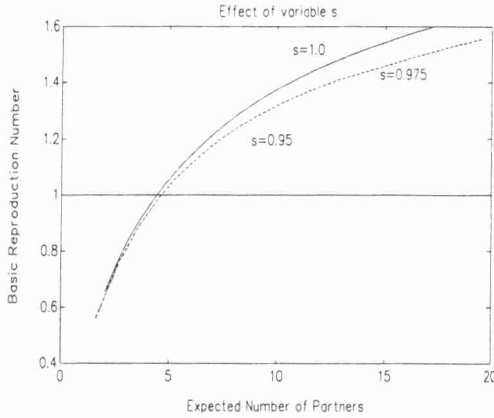
Figure 2

- In other calculations not presented here, distinguishing q_0, the probability of condom use at the first contact, from q, the probability of condom use on subsequent contacts was shown to have a negligible effect.

References

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