

Pair Formation in Sexually-Transmitted
Diseases

BU-1034-M

June, 1989

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PAIR FORMATION IN SEXUALLY-TRANSMITTED DISEASES

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Abstract

Most epidemiological models of sexually-transmitted diseases (STD's) consider populations of single individuals. These models assume that every encounter by a susceptible possibly involves a different partner and such individuals get infected, with a constant probability per encounter, by infected partners. In order to match the model with data it is assumed that the probability of infection per "encounter" sums over all sexual contacts during a partnership. Although in reality the majority of individuals live in steady partnerships, it is usually assumed that these models are good approximations.

Models that use a different approach show other results. This paper presents a brief overview of recent models that take into account pair formation and explicitly follow pairs in the equations. The effect of prostitution on the Dietz/Hadeler model is investigated. Some results are compared with those from the usual "single" models without pairs. Simulations show that the disease can spread up to three times more slowly in pair formation models than in the approximated models without pairs.

1. Pair Formation and Mixing

Population structure determines the pattern of the spread of a disease. In the AIDS epidemic, for example, there appear to be several risk groups with nonproportional mixing among them. Mixing behavior recently has received a great deal of attention (see for example Jacquez et al. (1988), Sattenspiel and Simon (1988), Hyman and Stanley (1988,1989), Blythe and Castillo-Chavez (1989)). However, most of the studies of sexually-transmitted diseases (STD's) concentrate on homosexual populations and have not dealt with the heterogeneities introduced by two sexes and pair formation. Although the majority of individuals live in steady partnerships, these models do not follow pairs in the equations. They implicitly assume that the duration of partnerships is zero and that all sexual contacts happen instantaneously. This approximation may be justified in highly sexually active subgroups, but otherwise one has to take into account the fact that pairs of susceptibles are practically immune and that pairs with at least one infected partner do not spread the disease outside the pairs as long as they remain together and do not have other partners. This can strongly influence the initial phase of an epidemic because the majority of existing pairs consist of susceptible individuals.

It is therefore important in the modelling of sexually transmitted diseases, as in human demography, to have a mathematical description of the formation and dissolution of pairs. Mixing behavior of individuals produces one constraint on pair formation. Before the formation of a pair there must be an encounter between possible partners. A first approach to pair formation is thus the "encounter-mating" model, in which pair formation involves two steps: the encounter of a possible partner and the decision whether to "mate". The mixing pattern determines the encounter step. The decision to mate is often treated as instantaneous step but this may not be true. Individual preferences are often not easily recognizable at the first encounter (Gimelfarb (1988a,b)). The two terms "mixing" and "preference" are often confused. The terms refer to different phenomena: mixing describes which individuals are met, preference describes which individuals are likely to be chosen (for instance as partners). Whereas mixing between subgroups must be symmetric, i.e. subgroup i mixes as many times with subgroup j as subgroup j mixes with subgroup i , preferences need not be symmetric. In models to describe mixing patterns in AIDS, preferences often are not considered.

Until about 1947 all population models considered only one sex. They typically focused on the female population because births are more easily attributable to the mother. But the same models were also applied to the male sex. Kuczynski (1932) calculated the female and male net reproduction numbers for France 1920-3 (the average number of daughters (sons) that will be born to a female (male)) and he found the female rate to be 0.977 and the male rate to be 1.194. One-sex models would therefore predict either a decrease or an increase of the population, depending on the sex. Kuczynski at that time explained these differences in the rates as being due to wars.

As a first attempt to overcome the inconsistencies in one-sex population models, A. H. Pollard (1948) attributed artificially the number of male births to females and the number of female births to males. Kendall (1948) suggested some different deterministic approaches to this so-called "two-sex problem". First he considered the simplest one-sex model

$$x' = (\lambda - \mu) x, \quad (1)$$

where $x(t)$ is the number of females at time t , λ the birth rate and μ the death rate. Then he generalized this equation to two sexes:

$$\begin{aligned} x' &= -\mu x + 1/2 \Lambda(x,y), \\ y' &= -\mu y + 1/2 \Lambda(x,y), \end{aligned} \quad (2)$$

where the term $\Lambda(x,y)$ is symmetric in x and y and describes the births due to males and females. It is easy to see by subtracting one equation from the other, that an initial excess of one sex will disappear in time in this model. Later Kendall (1949) considered a model that explicitly followed single females x , single males y , and couples p :

$$\begin{aligned} x' &= -\mu x + (\lambda + \mu)p - \varphi(x,y), \\ y' &= -\mu y + (\lambda + \mu)p - \varphi(x,y), \\ p' &= -2\mu p + \varphi(x,y), \end{aligned} \quad (3)$$

where the birth and death rates λ and μ are the same for males and females. $\phi(x,y)$ describes the number of new pairs. Kendall assumed $\phi(x,y)$ to be $\rho \min(x,y)$, $\rho = \text{const.}$ Although this model is quite realistic, it has the disadvantage of assuming that male and female birth and death rates are equal, which is often a poor approximation.

Since 1949 numerous authors have worked on the two sex problem. Keyfitz (1972), Parlett (1972) and J.H. Pollard (1973) designed and discussed models with different mating functions and understood that a realistic mating function is definitely nonlinear. McFarland (1972) and Fredrickson (1973) specified some conditions that had to be satisfied by a mating function:

(i) Definiteness:

In the absence of males and females there should be no pair formation,

$$\phi(0,y) = \phi(x,0) = 0. \quad (4)$$

(ii) Homogeneity:

If the sex ratio remains constant, the pair formation increases proportional to the total population size,

$$\phi(\alpha x, \alpha y) = \alpha \phi(x,y) \quad \text{for all } \alpha, x, y \geq 0. \quad (5)$$

(iii) Monotonicity:

The pair formation increases if the number of males or females increases

$$u \geq 0, v \geq 0 \quad \text{then} \quad \phi(x+u, y+v) \geq \phi(x,y) \quad \text{for all } x, y \geq 0. \quad (6)$$

A consequence of the second condition is that all mating functions can be written in the form

$$\phi(x,y) = x g(y/x) = y h(x/y) \quad (7)$$

where g and h are functions for $x, y > 0$ of one variable. Hence we can interpret the number of formed pairs per unit time as the number of females times a function of the number of males per female describing the availability of males (or the number of males times another function describing the availability of females). The most common examples in the literature are the minimum function

$$\phi(x,y) = \rho \min(x,y), \quad (8)$$

the geometric mean

$$\phi(x,y) = \rho \sqrt{xy}, \quad (9)$$

and the harmonic mean

$$\phi(x,y) = 2\rho xy/(x+y). \quad (10)$$

These demographic models based on Kendall's model assume that the birth rate is linear in the number of pairs. To study the behavior, J. H. Pollard (1973) looked for exponential solutions. Hader et al. (1988) confirmed this approach with the theory of homogeneous evolution equations. This theory has also the potential of being applicable to a wider class of population models and epidemiological models (e.g. Nold (1980), Busenberg and van den Driessche (1989), Busenberg et al. (1989)). Hader et al. (1988) used this technique to investigate the qualitative behavior of a general two-sex model of the Kendall type. They added a break-up rate for pairs with a general pair-formation law, and showed that if the mortalities of

males and females do not differ very much there is a globally attractive two-sex exponential solution with constant sex ratio (see also Yellin and Samuelson (1974)). Instead of birth rates depending linearly on the number of pairs, one can also consider a constant recruitment rate κ in demographic models:

$$\begin{aligned}x' &= \kappa - \mu x + (\sigma + \mu)p - \varphi(x, y), \\y' &= \kappa - \mu y + (\sigma + \mu)p - \varphi(x, y), \\p' &= -(\sigma + 2\mu)p + \varphi(x, y),\end{aligned}\tag{11}$$

where σ is a constant break-up rate, μ the death rate (independent of sex, for simplicity) and φ satisfies the conditions (i)-(iii). In this model exponential solutions do not play an essential role because the equations are not homogenous. There is always a globally stationary solution (x, y, p) , where p is determined by the equation

$$\varphi(\kappa/\mu - p, \kappa/\mu - p) = (\sigma + 2\mu)p\tag{12}$$

If one assumes that the numbers of both sexes are approximately equal, then the mating functions (8)-(10) are essentially indistinguishable. What then is the value of discrimination among the mating functions? One area where the distinction becomes important is that of age-structured models. Pair formation clearly depends strongly on the ages of the individuals and the numbers in different age classes can be very different.

Several papers about mating models (e.g. Goodman (1967), Fredrickson (1971), Keyfitz (1972), Hoppensteadt (1975), Staroverov (1977), Haderler (1989a,b), and several others) have treated age structure, which I do not consider further in this paper. Goodman (1953) considers stochastic rather than deterministic models; other papers investigated mating functions in models of population genetics (e.g. Wilson (1973), Wagener (1976) or Karlin (1979)). An application of preferred or assortative mating in one-sex models is presented in Levin and Segel (1982).

2. Two-Sex Models in Sexually Transmitted Diseases

Dietz (1987, 1988) and Dietz and Haderler (1988) presented a two-sex model for diseases spread through sexual contacts among heterosexuals. They assumed that a pair begins with the first sexual contact and that an individual can be member of only one pair at a time. The population is divided into eight disjunct classes:

x_0 single females, noninfected;

- x_1 single females, infected;
- y_0 single males, noninfected;
- y_1 single males, infected;
- p_{00} pairs, both partners noninfected;
- p_{01} pairs, only male infected;
- p_{10} pairs, only female infected;
- p_{11} pairs, both partners infected.

Individuals are recruited only into the noninfected single classes with a constant rate κ . Single females and males are removed with constant death rates μ_0 (uninfected) or μ_1 (infected), and by forming a pair. Pairs end by breaking up or by death of one partner. The break-up rate is a constant σ . Furthermore it is assumed that the probability of infection in one sexual contact is a constant h and that the average number of sexual contacts within a pair is β . Then the model equations read:

$$\begin{aligned}
 dx_0/dt &= \kappa - \mu_0 x_0 + (\mu_0 + \sigma)p_{00} + (\mu_1 + \sigma)p_{01} - \varphi_{00} - \varphi_{01}; \\
 dy_0/dt &= \kappa - \mu_0 y_0 + (\mu_0 + \sigma)p_{00} + (\mu_1 + \sigma)p_{10} - \varphi_{00} - \varphi_{10}; \\
 dx_1/dt &= -\mu_1 x_1 + (\mu_0 + \sigma)p_{10} + (\mu_1 + \sigma)p_{11} - \varphi_{10} - \varphi_{11}; \\
 dy_1/dt &= -\mu_1 y_1 + (\mu_0 + \sigma)p_{01} + (\mu_1 + \sigma)p_{11} - \varphi_{01} - \varphi_{11}; \\
 dp_{00}/dt &= -(2\mu_0 + \sigma)p_{00} + \varphi_{00}; \\
 dp_{01}/dt &= -(\mu_0 + \mu_1 + \sigma + h\beta)p_{01} + (1-h)\varphi_{01}; \\
 dp_{10}/dt &= -(\mu_1 + \mu_0 + \sigma + h\beta)p_{10} + (1-h)\varphi_{10}; \\
 dp_{11}/dt &= -(2\mu_1 + \sigma)p_{11} + h\beta p_{01} + h\beta p_{10} + h\varphi_{01} + h\varphi_{10} + \varphi_{11}.
 \end{aligned} \tag{13}$$

This model contains the demographic model (11) if there is no infection in the population and I will call it the Dietz/Hadeler or PSI-model (Pair formation - SI - model). The pair formation φ is defined by

$$\varphi_{ij}(x_0, x_1, y_0, y_1) = \rho_{ij} y_j x_i / (x_0 + x_1) \tag{14}$$

which is derived from a model where males of type j meet females of type i with fraction $x_j/(x_0 + x_1)$ and mate with a constant rate ρ_{ij} without competition (male dominance). Although this function satisfies the conditions (i), (ii), (iii) it has the effect that for very small numbers of females there are a larger number of pairs formed than the total number of females. To avoid this problem the authors assume in their paper that the number of females is greater than or equal to the number of males.

Alternatively, assume that females of type i will encounter males of types 0 and 1 in the proportions $\alpha_{i0} : \alpha_{i1}$ and that males of type j will encounter females of types 0 and 1 in the

proportions $\beta_{0j} : \beta_{1j}$, $\alpha_{i0} + \alpha_{i1} = 1$ and $\beta_{0j} + \beta_{1j} = 1$. Assume that α_{ij} and β_{ij} are density dependent, i.e.

$$\alpha_{ij} = \alpha_{ij}(y_0, y_1), \quad \beta_{ij} = \beta_{ij}(x_0, x_1). \quad (15)$$

Furthermore, again let be ρ_{ij} be the probability that a female of type i forms a pair with a male of type j , given a meeting. Then

$$\varphi_{ij}(x_0, x_1, y_0, y_1) = \frac{2\rho_{ij} \alpha_{ij} x_i \beta_{ij} y_j}{(\alpha_{ij} x_i + \beta_{ij} y_j)}. \quad (16)$$

This function is a generalization of the harmonic mean (10) and of the preferential mating in Levin and Segel (1982). If we assume random mixing,

$$\alpha_{ij} = y_j / (y_0 + y_1), \quad \beta_{ij} = x_i / (x_0 + x_1), \quad (17)$$

the mating function (16) simplifies to (see also Hadelar and Ngoma (1989))

$$\varphi_{ij}(x_0, x_1, y_0, y_1) = \frac{2\rho_{ij} x_i y_j}{(x_0 + x_1 + y_0 + y_1)}. \quad (18)$$

If, furthermore, $x_i = y_i$ for $i=0,1$ (18) is exactly the same function as (14). Dietz and Hadelar (1988) showed that there is always a trivial noninfected stationary solution $(\bar{x}_0, \bar{x}_1, 0, 0, \bar{p}_{00}, 0, 0, 0)$. They derived a threshold condition for existence of another stationary solution which is determined by the sign of D , where

$$D = h\rho_{01} [2\mu_1(\mu_1 + \sigma) + \sigma(\mu_0 + \sigma + \beta)] - \mu_1(2\mu_1 + \sigma)(\rho_{01} + \sigma + \mu_0 + \mu_1 + h\beta). \quad (19)$$

Stability analysis is carried out for the special case with symmetric assumptions and no disease-induced mortality.

Dietz (1988) compares these results to those of a simplified model which does not explicitly follow pairs. He matches the probability of infection appropriately by adjusting the parameters of the simplified model. Even so, with realistic parameters, the PSI-model reaches its equilibrium about three times more slowly than the approximate model. Also the equilibrium prevalence of the disease is significantly lower in the original model.

The Dietz/Hadelar model presents an initial step towards the development of more general models of disease transmission. A realistic approach to AIDS must take into account more

complex social and sexual behavior. For instance the use of an average number of sexual contacts within a pair is doubtful. Furthermore, individuals can also get infected through sexual partners other than their "social" partner, such as prostitutes or steady liasons. One should also build both homosexual pairing and needle sharing by IV drug users into the model. Another idea is to extend the model to variable infectivity over time (see Castillo-Chavez (1989)).

Hadeler and Ngoma (1988) considered a model similar to the PSI-model where they considered vertical transmission. In some diseases the time scales of the recruitment rate and of the demographic process are roughly equal. In this case it may be appropriate to define the recruitment to be linear in the numbers of pairs. Mathematically the model contains Kendall's model (3) if there is no infection. In this case exponential solutions play an important role and the authors use the stability analysis in Hadeler et. al. (1988).

3. Pair Formation Models with Female Prostitutes

Models omitting pair formation and the PSI-model may be seen as two extreme approximations to describe STD's. The former may best describe individuals with many different partners and the latter may best describe individuals who do not have more than one steady partnership at a time. Dietz (1988) showed in simulations that in the PSI-model the virus spread much more slowly, even if in models without pairs the rate of encounters and the infection rate per encounter are matched appropriately. If individuals have more than one steady partner at a time, i.e. if they have liasons or visit prostitutes, it is expected that the disease will spread faster than in the PSI-model. But how much does this aspect influence the disease? Do pair formation models with more heterogeneities, such as short-term liasons, still show that the disease is spread more slowly and that the prevalence of infectives is lower than in models without pairs? In order to investigate these questions let us introduce two additional classes of female prostitutes, F_0 and F_1 . Again, 0 means noninfected, 1 infected. For simplicity assume that the interaction of prostitutes and males consists of a single sexual contact with duration zero. Prostitutes become infected through males and transmit the virus into the male population but have no interaction with females (see Fig.2). Let ψ_{sdt} and ψ_{cdt} be the number of sexual contacts per unit time with prostitutes by single men and paired men respectively. One can assume that ψ_s and ψ_c are linear in the male variable,

$$\psi_s(F_i, y_j) := \theta y_j F_i / (F_0 + F_1), \quad (20)$$

$$\psi_c(F_i, p_{kj}) := \xi p_{kj} F_i / (F_0 + F_1). \quad (21)$$

Let κ_F be the constant recruitment rate of noninfected prostitutes and v_0, v_1 the rates at which noninfected and infected prostitutes retire from their business. Let the "social" pair formation be described by the harmonic mean function (16). Since my interest is to look at the possible effects of prostitutes in the dynamics of a STD, we start by random mixing (17,18). The new model reads:

$$\begin{aligned}
dx_0/dt &= \kappa - \mu_0 x_0 + (\mu_0 + \sigma)p_{00} + (\mu_1 + \sigma)p_{01} - \varphi_{00} - \varphi_{01}; \\
dy_0/dt &= \kappa - \mu_0 y_0 + (\mu_0 + \sigma)p_{00} + (\mu_1 + \sigma)p_{10} - \varphi_{00} - \varphi_{10} - h\psi_s(F_1, y_0); \\
dx_1/dt &= -\mu_1 x_1 + (\mu_0 + \sigma)p_{10} + (\mu_1 + \sigma)p_{11} - \varphi_{10} - \varphi_{11}; \\
dy_1/dt &= -\mu_1 y_1 + (\mu_0 + \sigma)p_{01} + (\mu_1 + \sigma)p_{11} - \varphi_{01} - \varphi_{11} + h\psi_s(F_1, y_0); \\
dp_{00}/dt &= -(2\mu_0 + \sigma)p_{00} + \varphi_{00} - h\psi_c(F_1, p_{00}); \\
dp_{01}/dt &= -(\mu_0 + \mu_1 + \sigma + h\beta)p_{01} + (1-h)\varphi_{01} + h\psi_c(F_1, p_{00}); \\
dp_{10}/dt &= -(\mu_1 + \mu_0 + \sigma + h\beta)p_{10} + (1-h)\varphi_{10} - h\psi_c(F_1, p_{10}); \\
dp_{11}/dt &= -(2\mu_1 + \sigma)p_{11} + h\beta p_{01} + h\beta p_{10} + h\varphi_{01} + h\varphi_{10} + \varphi_{11} \\
&\quad + h\psi_c(F_1, p_{10}); \\
dF_0/dt &= \kappa_F - v_0 F_0 - h\psi_s(F_0, y_1) - h\psi_c(F_0, p_{01}) - h\psi_c(F_0, p_{11}); \\
dF_1/dt &= -v_1 F_1 + h\psi_s(F_0, y_1) + h\psi_c(F_0, p_{01}) + h\psi_c(F_0, p_{11}).
\end{aligned} \tag{22}$$

I will call this model the PSI+P model.

Again there is always a noninfected state $(\bar{x}_0, \bar{x}_0, 0, 0, \bar{p}_{00}, 0, 0, 0, \bar{F}_0, 0)$. Assume that the rate of pair formation does not depend on the infection

$$\rho_{00} = \rho_{01} = \rho_{10} = \rho_{11} = \rho, \tag{23}$$

and furthermore that the pair formation rate with prostitutes is the same for single and coupled men,

$$\theta = \xi. \tag{24}$$

The Jacobian of the system in the noninfected state shows the stability behavior in this infection-free state. After some cumbersome calculations one gets the threshold condition

$$\begin{aligned}
D_1 &= v_0 \kappa h^2 [(d_1 \rho^2 + d_2 \rho + d_3)(2\mu_0 + \sigma) + (f_1 \rho^2 + f_2 \rho + d_3)\rho] \theta^2 \\
&\quad + (l_1 \rho^2 + l_2 \rho + l_3) \kappa_F \mu_0 (\rho + 2\mu_0 + \sigma_{11})
\end{aligned} \tag{25}$$

for the noninfected state to be locally asymptotically stable. Here

$$d_1 = -[\mu_1 a(1-h)^2 + b^2] < 0,$$

$$d_2 = -2\mu_1 c_1 [(1-h)a + b] < 0,$$

$$d_3 = -\mu_1 c_1^2 (2\mu_1 + \sigma) < 0,$$

$$f_1 = d_1 + h^2 a c_2 < 0,$$

$$f_2 = -[c_1 \{a(2\mu_1(1-h) + h^2\beta) + 2\mu_1 b\} + h^2\beta^2(1-h)a] < 0,$$

$$l_1 = v_1 b [(1-h)\mu_1(2\mu_1 + \sigma) - h\sigma c_2],$$

$$l_2 = 2v_1\mu_1^2 c_1 [(1-h)a + b] > 0,$$

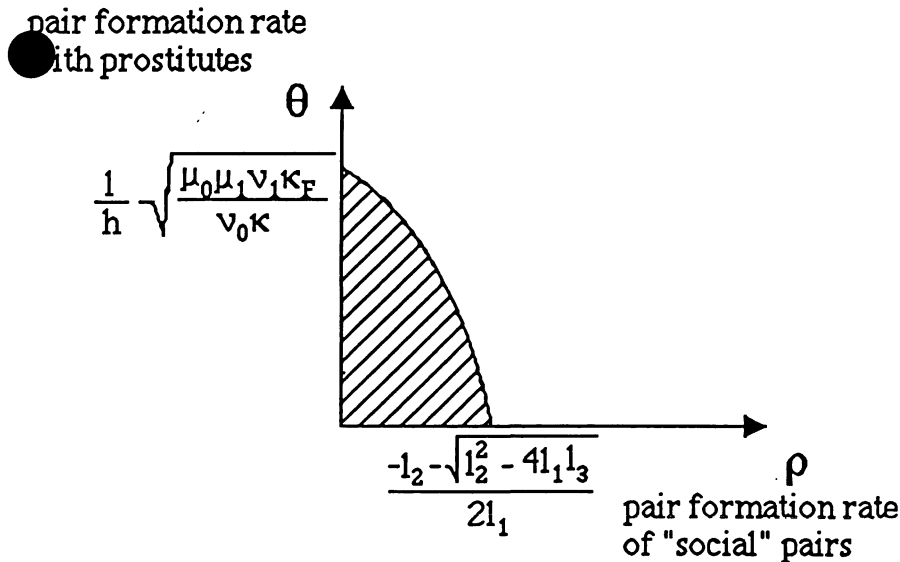
$$l_3 = v_1(2\mu_1 + \sigma)\mu_1^2 c_1^2 > 0,$$

and $a = \mu_1 + \sigma$, $b = h(\mu_0 + \sigma + \beta) + \mu_1$, $c_1 = \mu_0 + \mu_1 + \sigma + h\beta$,
 $c_2 = \mu_0 + \mu_1 + \sigma + \beta$.

If there is no pair formation with prostitutes ($\theta = \xi = 0$), then the threshold condition is identical to that in the Dietz/Hadeler model. Fix $h, \mu_0, \mu_1, \sigma, \beta, v_0, v_1, \kappa, \kappa_F$ and vary ρ, θ . Then we have the two cases:

Case 1 ($l_1 < 0$)

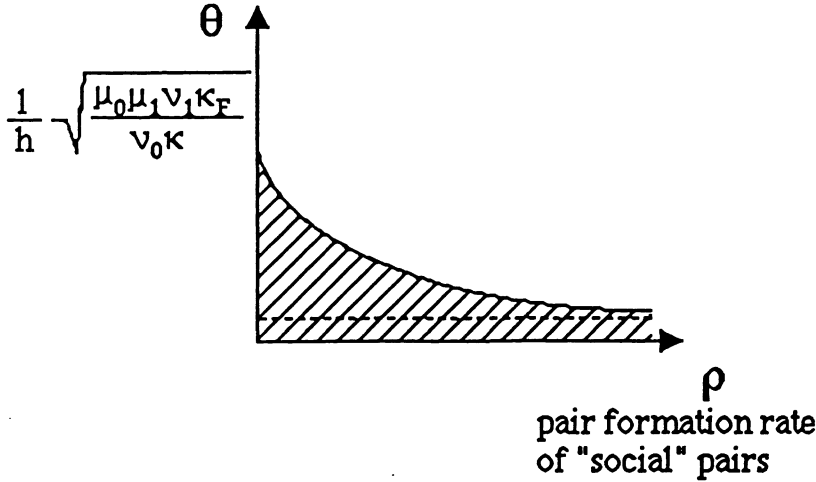
If the average number β of sexual contacts within a pair or the infection probability h is "high", then $l_1 < 0$, and we get the following domain of stability:



Case 2 ($l_1 > 0$)

If β or h is "low" then $l_1 > 0$. In that case the "social" pair formation does not play an important role in the spread of the disease. For every ρ there is an interval $[0, \theta_0]$ where the disease-free equilibrium is still stable.

pair formation rate
with prostitutes



In order to understand the effect of considering a class of female prostitutes in pair formation models let us approximate another model. If the break-up rate σ tends to infinity in the PSI+P model we arrive at the following model which neglects pairs:

$$\begin{aligned}
 dx_0/dt &= \kappa - \mu_0 x_0 - 2kqx_0y_1/(x_0+x_1+y_0+y_1); \\
 dy_0/dt &= \kappa - \mu_0 y_0 - 2kqx_1y_0/(x_0+x_1+y_0+y_1) - h\theta y_0F_1/(F_0+F_1); \\
 dx_1/dt &= -\mu_1 x_1 + 2kqx_0y_1/(x_0+x_1+y_0+y_1); \\
 dy_1/dt &= -\mu_1 y_1 + 2kqx_1y_0/(x_0+x_1+y_0+y_1) + h\theta y_0F_1/(F_0+F_1); \\
 dF_0/dt &= \kappa_F - v_0 F_0 - h\theta y_1 F_0/(F_0+F_1); \\
 dF_1/dt &= -v_1 F_1 + h\theta y_1 F_0/(F_0+F_1).
 \end{aligned} \tag{26}$$

Here k is the number of partners per unit time and q is the probability of getting infected from one partner. This model assumes that all sexual contacts with one partner occur at the same time. k and q take the place of the parameters ρ , σ , β , h in the original model. For this model the threshold (compare with (25)) is

$$D_2 = v_1 \mu_0 \kappa_F (kq)^2 + \mu_1 h^2 \kappa v_0 \theta^2 - v_1 \mu_0 \mu_1^2 \kappa_F. \tag{27}$$

To get a sense of the difference between these models with and without pairs, let us assume some realistic values for the parameters. In the noninfected state the total number of (single and coupled) females and males must each be κ/μ_0 . Let κ be 200,000 per year and $\mu_0 = 0.02$ per year, so that the number of individuals at risk in the infection-free state is 20 million (Hethcote and Yorke (1984)). Let us further assume that κ_F is 16,667, $v_0 = 0.067$ and $v_1 = 0.125$ per year. Then

in the infection-free equilibrium we have about 250,000 prostitutes. Let ρ be 4.5 per year, θ be 1 and σ be 0.46 per year, $\mu_1 = 0.1$, $h = 0.002$ and $\beta = 100$ per year. To match the probability of infection and the pair formation rate in both models, we use the formulas

$$c = (\mu_0 + \sigma)^{-1} + \rho^{-1}$$

and

$q = 1 - (1-h)c$, where $c = 1 + \beta/(\mu_0 + \sigma)$
as in Dietz (1988). We then calculate $k = 0.43$ and $q = 0.342$ per year.

These parameters yield case 1 in the pair formation model (22). For both models PSI+P and (26) the infection free state is unstable. The models differ in the time to approach the equilibrium. Simulations show that if the noninfected state is unstable, there is always an endemic equilibrium. The model without pairs reaches its equilibrium more than twice as fast as the original model with pairs. The infection prevalence in the endemic equilibrium is significantly lower in the pair formation model (see Fig. 1).

	Maximum		Equilibrium	
	after	% infected	after	% infected
Model without pairs (26) $\theta = 0$	148.5 years	31.4 %	348.5 years	31.1 %
PSI+P model $\theta = 0$	513.5 years	14.8 %	689 years	14.8 %
Model without pairs (26) $\theta = 1$	148 years	32.1 %	349.5 years	31.5 %
PSI+P model $\theta = 1$	488 years	15.3 %	665.5 years	15.3 %

Fig. 1 : Comparison of simulations of the PSI+P model and model (23). The time to equilibrium is measured when the distance of the trajectory and the equilibrium is for the last time more than 1000 individuals.

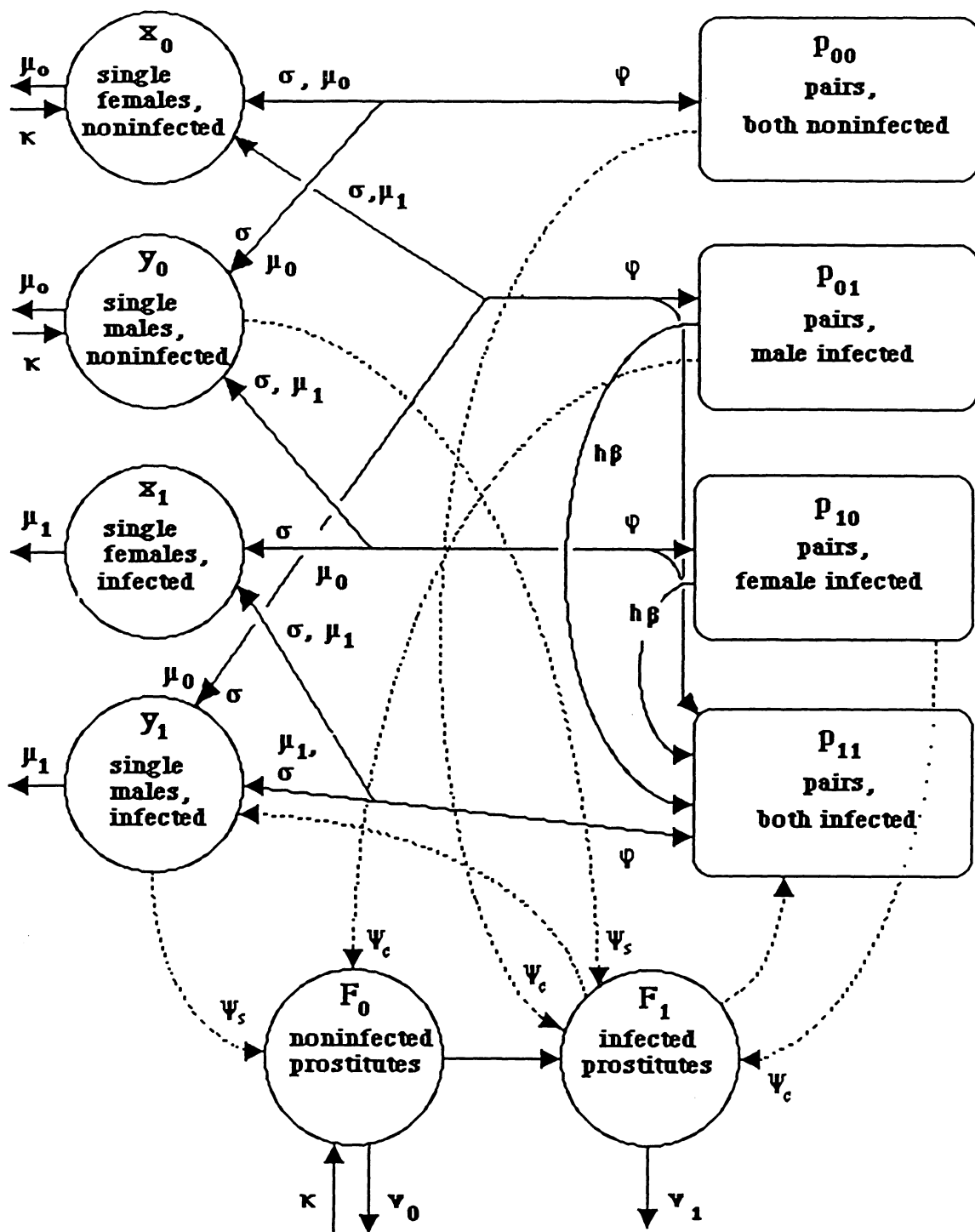


Fig.2: Possible interactions in a two-sex model of heterosexuals with prostitution.

Discussion

A brief overview of pair formation and two-sex models in epidemics has been presented. The model of Dietz and Haderl has been extended by considering an additional class of female prostitutes to look at the effects of female prostitution on the dynamics of pair formation models. It was assumed that prostitutes interact only with the male population. Social structure other than sex still has been ignored.

Simulations indicate that only high values of θ , the rate at which males visit prostitutes, alter the course of the disease significantly. This result depends strongly on the transmission probability per sexual contact. As in the Dietz/Hadeler model, a comparison to a model not explicitly considering pairs shows that the prevalence of the disease in the pair formation model is much lower than in the model without pairs, even if prostitution is considered. Whereas in the model without pairs the equilibrium prevalence for certain realistic parameters is about 30%, the pair formation model with female prostitutes shows a prevalence of about 15%. Simulations indicate also that the equilibrium is reached twice as fast in the model without pairs. (see Fig.1).

In reality prostitutes are not a social class "outside of society"; their mixing behavior is much more complex. In models with prostitution there are a lot of uncertainties. Estimates of the number of prostitutes in the United States lie inbetween 80,000 and 800,000 (Castillo-Chavez, personal communication). It is also difficult to get an idea of the magnitude of θ .

Unfortunately pair formation models are very cumbersome to analyze and the number of parameters that have to be estimated is very large. Although simulations cannot replace analytical treatment, one may get some useful insights into the behavior of these models.

Acknowledgements. I would like to thank Carlos Castillo-Chavez and Simon A. Levin whose ideas and suggestions made this work possible. This work was partially supported by the German Exchange Program (DAAD) 315/402/690/9 and by Hatch Project NYC 151-409, USDA, to Carlos Castillo-Chavez. I wish also to thank Fred Adler and Dan Grünbaum for reading and correcting the text and Karl P. Hadeler for valuable comments on the paper, as well as the Center for Applied Mathematics, Cornell University, for supporting my work.

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