

Sexual Mixing Models: A Comparison of Analogue Deterministic and Stochastic Models

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ABSTRACT

Models for sexual partner choice are discussed for the case of highly variable sexual activity in the population. It is demonstrated that the variances in the number of infected persons may be extremely large. For the random mixing model, higher order cumulants are also evaluated. On the basis of these results the applicability of deterministic models and models for expectations only are questioned. A general model is proposed for handling nonrandom, or correlated, mixing. The problem of inconsistency is overcome by considering the couples having sex as the natural unit in the model. In the case of s discrete homogeneous groups it is shown that only $\binom{s}{2}$ parameters defining the interaction between the groups can be chosen freely. Finally, the effect of correlation in partner choice is demonstrated by a bivariate lognormal model for partner choice.

INTRODUCTION

The HIV/AIDS epidemic has increased interest in mathematical models for sexually transmitted diseases (STD) with features quite different from those of other infections such as measles and rubella (German measles) [3]. A number of new models have been proposed over the past 5 or 6 years in order to understand and possibly control the spread of HIV infection. Realistic modeling requires knowledge about incubation time, migration and deaths, variable infectiousness, variable sexual activity, and pattern of partner choice. None of these problems is fully understood in relation to the spread of HIV, though estimates for the relevant parameters are constantly improving owing to an increased amount of data and the construction of realistic models.

In the present paper problems related to variable sexual activity and nonrandom partner choice are analyzed from a purely theoretical point of view without reference to particular diseases. However, the problems dealt with are of a general character and may be useful to research workers dealing with specific sexually transmitted diseases.

Proportionate mixing or random mixing has been used extensively by a number of authors [2, 6, 7, 9, 14]. Suppose that each member of the population has a different rate, denoted λ , of acquiring new sexual partners. For a particular person, λ is defined as the expected number of new partners per unit time. The value of λ varies from person to person, and in a large population its distribution can be approximated by a probability density. Random mixing may be thought of as if all members of the population who were going to have a new partner on a particular day met and chose a partner at random within this group. Anderson et al. [4] called this the heterogeneous-mixing model and showed that a sexually transmitted epidemic under these assumptions would take off exponentially at the rate $\mu(c^2 + 1)$, where μ and c are the expectation and coefficient of variation, respectively, of λ in the population.

We assume that any partnership results in transmission if one partner is infected and the other is susceptible. Alternatively, we may assume that transmission occurs with probability p . Then λ should be replaced by, say, $\lambda' = \lambda p$ in the theory that follows. The distribution of λ must then be replaced by the distribution of λ' . Since the theory to be presented is general with respect to the distribution of λ , there is no loss of generality involved in assuming $p = 1$. Notice also that the assumption that λ is gamma or lognormally distributed is not affected by choosing $p < 1$.

A number of alternatives to random heterogeneous mixing have been proposed in the literature. However, the step from random to nonrandom mixing is not at all trivial. The model has to meet certain requirements to be consistent, and though these conditions are simple and obvious, it is not straightforward to ensure that they are fulfilled [5]. In brief, the problem is the following: If a certain member of the population chooses new partners according to some model, how do we make sure that the choices are in agreement with the models used by those who are chosen? This problem has led many authors to make a number of simplifying assumptions about the mixing structure. The most common approach is to divide the population into homogeneous groups and assume that partners sometimes are chosen at random within the groups and sometimes between the groups [10, 12, 14]. Although this type of discrete model has certain advantages in being simple to formulate, one tends to lose the overview, owing to mathematical complications when it comes to the analysis of the model. Some authors have approached the problem by using continuous models [5, 11], assuming that the rate of partner change is continuously distributed in the population. Blythe and Castillo-Chavez [5] defined a mixing function $\rho(s, r)$, where

$$\int_r^{r+\Delta r} \rho(s, u) du$$

is supposed to be the fraction of partners that a person with activity (rate) s has among individuals with activities $(r, r + \Delta r)$. They gave the conditions that $\rho(r, s)$ must satisfy, with the remark that “these conditions are simple and obvious, but it is not easy to find functional forms that satisfy them simultaneously for all r, s , and time t .”

It is not a natural approach, either from a mathematical or a sociological point of view, to try to model this type of problem from the point of view of each particular individual in the population. The process of “choosing” sexual partners is extremely complicated, and the realized processes are probably not as exciting as people’s wishes or dreams in relation to partner choice. Therefore, the only natural units to build the model from are the couples having sex, not the individuals. As will be demonstrated, this also dramatically simplifies the mathematical problems and helps us to overcome the problem of inconsistency.

Throughout this paper we shall consider only one-sex populations. There are two main problems that will be dealt with: (1) To analyze in general the stochasticity in the number of infected individuals at a given point of time for the heterogeneous random mixing model and (2) to present a general theory for nonrandom mixing. In particular, we shall analyze the model for nonrandom mixing, or like-with-like preference, in the case that the λ ’s are lognormally distributed in the population and the nonrandomness is defined by a simple coefficient of correlation, ρ , possibly ranging from -1 to 1 . For $\rho = 0$ we are back to the random mixing model, $\rho > 0$ corresponds to like-with-like preference, and $\rho < 0$ corresponds to the opposite and is probably unrealistic for the spread of STD in human populations.

STOCHASTICITY IN THE HETEROGENEOUS RANDOM MIXING MODEL

For notational purposes, let us assume that the rate of partner change, λ , has a probability density $f(\lambda)$ in the population. However, the results of this section are generally valid for any distribution of the λ ’s with finite moments. Our purpose is to investigate the stochasticity in the growth of the epidemic without considering the effect of saturation when the number infected becomes large. We therefore assume infinite population size. It ought to be emphasized that this is a theoretical abstraction. When more than, say, 5% of the population is infected, a new partnership involves two infected persons with probability exceeding 0.0025, whereas we assume that this probability is zero. However, I have chosen to show graphical presentations up to periods of 10 years to indicate the asymptotic behavior of the theoretical model. In practice, saturation effects suppressing the spread may occur before this time, depending on the population size.

Let $\Lambda(t)$ denote $\sum \lambda$, where the sum is taken over the individuals infected at time t . Then, the probability of a new infected in $(t, t + \Delta t)$ given $\Lambda(t)$

is $\Lambda(t)\Delta t + o(\Delta t^2)$. According to the random mixing model, a person infected in $(t, t + \Delta t)$ has a λ value generated from the distribution $\lambda f(\lambda)/\mu$, where $\mu = E\lambda = \int_0^\infty \lambda f(\lambda) d\lambda$. Omitting higher order terms that vanish as $\Delta t \rightarrow 0$, $\Lambda(t)$ must obey the equation

$$E(e^{u\Lambda(t+\Delta t)} | \Lambda(t)) = e^{u\Lambda(t)} \{ [1 - \Lambda(t) \Delta t] + \Lambda(t) \Delta t R(u) \}, \quad (1)$$

where $R(u) = \int_0^\infty e^{u\lambda} \lambda f(\lambda) d\lambda / \mu$.

Now, taking the expectation of (1) with respect to $\Lambda(t)$, we obtain

$$E(e^{u\Lambda(t+\Delta t)}) = E(e^{u\Lambda(t)}) + [R(u) - 1] \Delta t E(\Lambda(t) e^{u\Lambda(t)}), \quad (2)$$

or

$$M(u, t + \Delta t) = M(u, t) + [R(u) - 1] \Delta t \frac{\partial}{\partial u} M(u, t), \quad (3)$$

where $M(u, t) = E(e^{u\Lambda(t)})$.

In the limit as $\Delta t \rightarrow 0$ we get the differential equation

$$\frac{d}{dt} M(u, t) = [R(u) - 1] \frac{\partial}{\partial u} M(u, t). \quad (4)$$

Introducing the cumulant generating function $K(u, t) = \ln M(u, t)$, we find the same equation,

$$\frac{\partial}{\partial t} K(u, t) = [R(u) - 1] \frac{\partial}{\partial u} K(u, t), \quad (5)$$

with the boundary condition $K(u, 0) = \lambda_0 u$ provided that the process starts at time $t = 0$ with $\Lambda(0) = \lambda_0$.

Now, taking the derivative of (5) with respect to u and evaluating at $u = 0$, we get

$$\frac{\partial}{\partial t} k_1(t) = \nu_1 k_1(t), \quad (6)$$

where $k_i(t)$ is the i th cumulant of $\Lambda(t)$ and $\nu_i = E\lambda^{i+1}/E\lambda$. Hence, the first cumulant is

$$k_1(t) = \lambda_0 e^{\nu_1 t}. \quad (7)$$

Notice that $\nu_1 = E\lambda^2/E\lambda = E\lambda(c^2 + 1)$, which is the same rate as was found by Anderson et al. [4].

The general solution of (5) is

$$K(u, t) = \psi(t - A(u)), \quad (8)$$

where ψ is any function and

$$A(u) = \int_u^\infty \frac{1}{R(x) - 1} dx, \quad A'(u) = -[R(u) - 1]^{-1}.$$

Requiring that $K(u, 0) = \lambda_0 u$, we have $\lambda_0 u = \psi(-A(u))$, or $\psi(u) = \lambda_0(A)^{-1}(-u)$, giving

$$K(u, t) = \lambda_0(A)^{-1}[A(u) - t]. \quad (9)$$

As λ_0 will be a common factor for all cumulants, we may without loss of generality put $\lambda_0 = 1$. From (9) we find, taking derivatives with respect to u ,

$$A'(K(u, t))K'(u, t) = A'(u),$$

which can be written

$$K'(u, t) = S(K(u, t))/S(u), \quad (10)$$

where $S(u) = R(u) - 1 = -A'(u)^{-1}$.

From the Taylor expansions

$$S(u) = \nu_1 u + \frac{1}{2} \nu_2 u^2 + \frac{1}{6} \nu_3 u^3 + \dots$$

and

$$K(u, t) = k_1(t)u + \frac{1}{2} k_2(t)u^2 + \frac{1}{6} k_3(t)u^3 + \dots$$

we can now evaluate higher order cumulants expressed by $k_i = k_i(t)$ by comparing coefficients. This is easy to perform with the symbol manipulation program MACSYMA [15], giving up to the fourth order

$$k_2 = \frac{\nu_2}{\nu_1} k_1(k_1 - 1), \quad (11)$$

$$k_3 = \left[k_1^3(\nu_1 \nu_3 + 3\nu_2^2) - 6k_1^2 \nu_2^2 + k_1(3\nu_2^2 - \nu_1 \nu_3) \right] / (2\nu_1^2) \quad (12)$$

and

$$k_4 = \left[k_1^4 (\nu_1^2 \nu_4 + 8\nu_1 \nu_2 \nu_3 + 9\nu_2^3) + k_1^3 (-9\nu_1 \nu_2 \nu_3 - 27\nu_2^3) \right. \\ \left. + k_1^2 (27\nu_2^3 - 6\nu_1 \nu_2 \nu_3) + k_1 (-\nu_1^2 \nu_4 + 7\nu_1 \nu_2 \nu_3 - 9\nu_2^3) \right] / (3\nu_1^3) \quad (13)$$

We can now easily compute variance, skewness, and kurtosis for $\Lambda(t)$ as functions of t . In the limit we find approximations valid for large values of t :

$$\lim_{t \rightarrow \infty} (\text{skewness}) = \left(\frac{\nu_1^2 \nu_3^2 + 6\nu_1 \nu_2^2 \nu_3 + 9\nu_2^4}{4\nu_1 \nu_2^3} \right)^{1/2} \lambda_0^{-1/2} \quad (14)$$

$$\lim_{t \rightarrow \infty} (\text{kurtosis}) = \frac{\nu_1^2 \nu_4 + 8\nu_1 \nu_2 \nu_3 + 9\nu_2^3}{3\nu_1 \nu_2^2} \lambda_0^{-1}. \quad (15)$$

Notice that in the general case of starting at λ_0 , all cumulants must be multiplied by λ_0 .

The coefficient of variation for $\lambda(t)$ is

$$C_\Lambda = (\nu_2 / \nu_1)^{1/2} (1 - e^{-\nu_1 t})^{1/2} / \lambda_0,$$

tending to $(\nu_2 / \nu_1)^{1/2} / \lambda_0$ as $t \rightarrow \infty$.

The variable $\Lambda(t)$ is not the number of individuals infected but is closely related to that number, say $N(t)$. In fact, defining

$$E\left(\frac{dN(t)}{dt}\right) = \lim_{\Delta t \rightarrow 0} E\left(\frac{N(t + \Delta t) - N(t)}{\Delta t}\right),$$

we have the relation

$$E\left(\frac{dN(t)}{dt} \middle| \Lambda(t)\right) = \Lambda(t). \quad (16)$$

Hence, $\Lambda(t)$ is the instantaneous growth rate of the epidemic. Taking the expectation of (16) with respect to $\Lambda(t)$, we get

$$E\left(\frac{dN(t)}{dt}\right) = E(\Lambda(t)) = \lambda_0 e^{\nu_1 t},$$

giving exactly by integration

$$E(N(t)) = 1 + \frac{\lambda_0}{\nu_1} (e^{\nu_1 t} - 1), \tag{17}$$

which is approximately the same as the expression given by Anderson et al. [4] because $\nu_1 = \mu(c^2 + 1)$. It is harder to find exact expressions for higher order cumulants. However, we have

$$\frac{\Lambda(t)}{N(t)} \xrightarrow{P} \nu_1$$

as $t \rightarrow \infty$. Hence, since the cumulants of

$$\Lambda(t)e^{-\nu_1 t}/\nu_1$$

tend to a limit as $t \rightarrow \infty$, we have for large values of t

$$\text{var } N(t) \approx \frac{\nu_2}{\nu_1^3} k_1(t) [k_1(t) - 1], \tag{18}$$

while the coefficients of variation, skewness, and kurtosis are approximately the same as for $\Lambda(t)$.

An alternative derivation of (5) and (10) is given in Appendix A.

NONRANDOM MIXING

GENERAL FRAMEWORK

For the random mixing model we may consider each instance of sexual intercourse as the realization of an associated bivariate random variable, where the components are the transmission rates for the two persons involved. The two rates are in this case independent. In general, however, the rates for the persons involved will be dependent.

Let the rate of sexual contacts in which the couple have personal rates in the intervals $(x, x + \Delta x)$ and $(y, y + \Delta y)$ be $mg(x, y) \Delta x \Delta y +$ higher order terms. In a one-sex population there is no particular distinction between the first and second variables. Choosing at random which to consider as the first, we obtain the symmetry requirement $g(x, y) = g(y, x)$. If m is the total rate of new formation of couples in the population, $\int \int g(x, y) dx dy = 1$, so that $g(x, y)$ actually is a distribution. As in the previous section, we let the number of persons with rates in the interval $(x, x + \Delta x)$ be $nf(x) \Delta x + o(\Delta x^2)$, where n is the population size, giving

$$m \int [g(x, y) + g(y, x)] dy = nf(x)x.$$

Writing $h(x) = \int g(x, y) dy$, we have

$$2mh(x) = nxf(x),$$

which, after integration over x , gives

$$2m = nEX$$

and

$$h(x) = xf(x)/EX.$$

To obtain a consistent model we see that it is sufficient to require that the marginals of $g(x, y)$ are $xf(x)/EX$ in addition to the requirement that g is a symmetric two-dimensional distribution. The mixing function $\rho(r, s)$ of Blythe and Castillo-Chavez [5] is, in fact, just the conditional distribution defined by g ,

$$\rho(x, y) = \frac{g(x, y)}{\int g(x, y) dx} = \frac{g(x, y)}{h(y)}.$$

The same approach can be used in the discrete case. Consider a population of s groups with rates of partner change $\lambda_1, \lambda_2, \dots, \lambda_s$ and group sizes n_1, n_2, \dots, n_s . Then the total structure of the population is given by the two-dimensional symmetric discrete distribution $p(x, y)$, where x and y take the values $\lambda_1, \lambda_2, \dots, \lambda_s$. For any new contact the probability that the rates involved are x and y is then $p(x, y)$.

The marginal distributions must be $xq(x)/EX$, where $q(x) = n_i/n$ for $x = \lambda_i$, and $EX = \sum xq(x)$.

If the n_i and λ_i , and hence $q(x)$, are given, the marginals of $p(x, y)$ are given. Then, only $\binom{s}{2} = s(s-1)/2$ probabilities $p(x, y)$ can be chosen freely. When these are chosen, the remaining probabilities $p(x, y)$ can be calculated. We may say that $\binom{s}{2}$ is the number of degrees of freedom in the constructions of the dynamics between the groups. As an illustration let us choose $s = 3$. Then the number of probabilities that can be freely chosen is only $\binom{3}{2} = 3$. Put $\lambda_1 = 2$, $\lambda_2 = 3$, $\lambda_3 = 5$ (yr^{-1}), and $n_1 = n_2 = n_3$. Then the marginal distribution $xq(x)/EX$ is 0.2, 0.3, and 0.5 for $x = 2, 3$, and

5, respectively. Let us choose the diagonal probabilities $p(x, x)$ as indicated below:

0.1	?	?	0.2
?	0.2	?	0.3
?	?	0.4	0.5
0.2	0.3	0.5	1

Then we have chosen three probabilities, and there are no degrees of freedom left for choosing the probabilities indicating the between-groups relations. Actually, in this example the remaining probabilities are all 0.05. This lack of freedom in the choice of parameters is usually not realized by those working with discrete models. If one works with too large a number of parameters, the consequence is that a number of different parameter values correspond to equivalent models. The analysis then may seem to be a lot more complicated than it actually needs to be.

THE LOGNORMAL MODEL

In a human population, λ is typically distributed with large positive skewness. In fact, most people change partners very rarely, while only a small proportion of the population have large, and sometimes very large, values of λ . The lognormal distribution, with its very heavy right tail, typically meets these requirements for appropriate parameter values. On the other hand, the main purpose of this section is not to focus on the shape of the marginals, but rather to focus on the correlations representing deviations from random mixing. From this point of view, the lognormal seems to be a natural choice because it enables us to apply well-known results for the bivariate normal distribution.

Let us therefore assume that the rate of partner change is lognormally distributed in the population with parameters (μ, σ^2) . By this we mean that $\ln(\text{rate})$ is $N(\mu, \sigma^2)$. The first moment distribution corresponding to the marginals of $g(x, y)$, and denoted $h(x)$ in the previous section, is also the lognormal, but the parameters are $(\mu + \sigma^2, \sigma^2)$ (see, e.g., [1]). If the rates for a couple are (λ_1, λ_2) , we obtain an interesting class of consistent models by assuming that $(\ln \lambda_1, \ln \lambda_2)$ has a bivariate normal distribution with parameters $(\mu + \sigma^2, \mu + \sigma^2, \sigma^2, \sigma^2, \rho)$, where ρ is the correlation between $\ln \lambda_1$ and $\ln \lambda_2$. The distribution defining the structure, $g(x, y)$, is then the corresponding bivariate lognormal. If $\rho = 0$ we are back to the random mixing model. If $\rho > 0$, we have the situation where persons with high risk

are more likely to meet others with high risk than under random mixing. For $\rho < 0$, the opposite and probably less realistic situation occurs.

Introducing the standardized normal variates $U_i = (\ln \lambda_i - \mu - \sigma^2) / \sigma$, we obtain the appropriate bivariate lognormal if persons with the value U_1 choose partners with $U_2 = \rho U_1 + U \sqrt{1 - \rho^2}$, where U is $N(0, 1)$ and is independent of U_1 . Notice that we obtain the same model if the person with value U_2 chooses a partner with value $U_1 = \rho U_2 + U \sqrt{1 - \rho^2}$. Therefore we do not need to be concerned about the problem of who's choosing who and the possible inconsistency involved in modeling choices. By the above procedure, (U_1, U_2) are bivariate standard normal variates with correlation ρ . Transforming back to (λ_1, λ_2) , we have

$$\lambda_2 = \lambda_1^\rho e^{(\mu + \sigma^2)(1 - \rho)} e^{U\sigma \sqrt{1 - \rho^2}},$$

giving

$$E(\lambda_2^s | \lambda_1) = \lambda_1^{\rho s} \gamma(s, \rho),$$

where

$$\gamma(s, \rho) = \exp\left[(\mu + \sigma^2)s(1 - \rho) + (1/2)s^2\sigma^2(1 - \rho^2)\right].$$

It is convenient now to introduce the variable

$$X_s(t) = \sum_{i=0}^{N(t)} \lambda_{(i)}^s,$$

where $\lambda_{(i)}$ is the λ parameter for infected number i , and $N(t)$ is the number of infected persons at time t . Now, let $\lambda(t)$ denote the vector of λ values for those infected at time t .

$$\begin{aligned} E(X_s(t + \Delta t) | \lambda(t)) &= X_s(t) + \sum_{i=0}^{N(t)} \lambda_{(i)} \Delta t \lambda_{(i)}^{\rho s} \gamma(s, \rho) + o(\Delta t) \\ &= X_s(t) + X_{1+\rho s}(t) \Delta t \gamma(s, \rho) + o(\Delta t), \end{aligned}$$

giving

$$E\left(\frac{d}{dt} X_s(t) | \lambda(t)\right) = X_{1+\rho s}(t) \gamma(s, \rho).$$

Integrating over the distribution of $\lambda(t)$, we find the unconditional expectations

$$E\left(\frac{d}{dt} X_s(t)\right) = E(X_{1+\rho s}(t))\gamma(s, \rho).$$

Introducing the function

$$g(t, v) = E(X_{1/(1-\rho)+v}(t)),$$

we get the basic equation

$$\frac{d}{dt} g(t, v) = \alpha(v, \rho)g(t, \rho v), \tag{19}$$

where $\alpha(v, \rho) = \gamma(1/(1-\rho) + v, \rho)$, with initial condition $g(0, v) = \lambda_0^{1/(1-\rho)+v}$.

Notice that the expected number of infected persons at time t is

$$E(N(t)) = g(t, -1/(1-\rho)). \tag{20}$$

The special case of random mixing corresponds to $v = 0, \rho = 0$, giving

$$\frac{d}{dt} g(t, 0) = \alpha(0, 0)g(t, 0).$$

Inserting $\alpha(0, 0) = e^{\mu+(3/2)\sigma^2} = E\lambda^2/E\lambda$ and solving the differential equation, we again confirm the result of Anderson et al. [4] given by Equation (7).

Write Λ_t for the λ value of a person infected at time t . Then

$$E(X_s(t + \Delta t)) = E(X_s(t)) + E(\Lambda_t^s) \sum_{i=0}^{N(t)} \lambda_{(i)} \Delta t,$$

giving unconditionally

$$E(\Lambda_t^s) = \frac{d}{dt} \frac{E(X_s(t))}{E(X_1(t))}.$$

Introducing $g(\cdot, \cdot)$ and putting $s = 1$, we get

$$E(\Lambda_t) = \frac{g'(t, \rho/(1-\rho))}{g(t, \rho/(1-\rho))} = \frac{d}{dt} \ln g(t, \rho/(1-\rho)).$$

A numerical procedure for calculation of the function $g(t, v)$ is given in Appendix B.

RESULTS AND DISCUSSION

The process dealt with in the first section is a generalization of the classical Yule's process (see, e.g., [13]), which corresponds to the case of no variability in the transmission rates λ in the population. Mathematically we arrive at Yule's process by putting $R(u) = e^{\lambda_0 u}$. Inserting this in (A4) and solving the differential equation, we obtain the cumulant generating function for Yule's process,

$$K(u, t) = -\ln(e^{\lambda_0 t - u} + 1 - e^{\lambda_0 t}).$$

The corresponding growth rate for the epidemic is λ_0 .

Anderson et al. [4] demonstrated that large variability in sexual behavior, which is probably realistic in human populations, has the effect of increasing the growth rate at the early stage of the epidemic, as indicated by the exact result (17). The growth rate is actually $\mu(c^2 + 1)$, where μ is the growth rate for a homogeneous population (corresponding to λ_0 in Yule's process) and c is the coefficient of variation for the growth rate λ in the population.

This paper demonstrates that heterogeneity also has a substantial effect on the variance of the number of infected individuals at a given point of time. For large values of t the coefficient of variation for $\Lambda(t)$ is approximately $(\nu_2/\nu_1)^{1/2}/\lambda_0$. Thus, the variation in the process does not vanish as $t \rightarrow \infty$, but the standard deviation is actually proportional to the expected number of infected individuals. Writing γ for the coefficient of variation for the first moment distribution $xf(x)/\mu$, we have

$$\lim C_{\Lambda(t)}^2 = \nu_1(\gamma^2 + 1)/\lambda_0^2,$$

showing that heterogeneity in general also has a substantial effect on the coefficient of variation. These results agree well with findings of Falck [8], who simulated the beginning of an HIV epidemic in a population of 1200 individuals. Falck found very large variability when the process was repeated. Though his model is more realistic than the one treated in this paper, incorporating realistic incubation time and death rates, the findings of very large variances is a common fact. These variances are great enough to question the applicability of deterministic models for this type of process in general. One should also be aware of the stochasticity in the process when comparing the realizations of epidemics for different populations, for example, in different countries. Differences must be enormous to be indicative of significant differences in sexual habits.

A rather simple framework that makes the problem of nonrandom, or correlated, mixing rather tractable is proposed by considering the couples

having sex as the natural unit in the model. As a corollary to the general result we found the number of degrees of freedom in parameter choices for discrete models. If there are s homogeneous groups in the population, only $\binom{s}{2}$ parameters defining the interactions between the groups can be chosen freely. If one constructs models of this type using a larger number of parameters, those exceeding $\binom{s}{2}$ in number are actually redundant. For each set of parameters there will always exist an equivalent model with $\binom{s}{2}$ parameters only.

For the case of correlated mixing I have only been able to calculate the expected values of the number of infected individuals for the particular case that the distribution of rates of partner change in the population is lognormal. Figures 1 and 2 show the expectations $E\Lambda(t)$ and $EN(t)$, respectively, for $\rho = 0.0, 0.1, \dots, 0.8$, $\mu = 0.05 \text{ (yr}^{-1}\text{)}$, and $c = 2$. Calculations are performed for starting values $\lambda_0 = 0.1, 1, \text{ and } 10 \text{ (yr}^{-1}\text{)}$. The result does not come as a surprise. The effect of a positive correlation is very great, we may say dramatic, remembering that logarithmic scales are used. Note also that the value of λ_0 is very important when ρ is large. If the first person infected is a member of a high-risk group (large λ_0), the epidemic takes off very rapidly. On the other hand, if λ_0 is small, a positive ρ may have a suppressing effect on the epidemic in the beginning. This is because a positive correlation increases the chance that only low-risk persons will be infected initially. However, the virus will eventually reach the high-risk groups and cause something like an explosion in the number of infected individuals. Simulation studies are required in order to understand more deeply the consequences of correlated mixing. Data containing information on the bivariate distribution of (λ_1, λ_2) for couples are also needed but are probably difficult to obtain in practice.

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APPENDIX A. THE FORWARDS AND BACKWARDS EQUATION FOR THE PROCESS

If, rather than starting with one infected individual at $t = 0$ with rate λ_0 , we started with two with rates $\lambda_0^{(1)}$ and $\lambda_0^{(2)}$, $\lambda_0^{(1)} + \lambda_0^{(2)} = \lambda_0$, we would obviously get the same process $\Lambda(t)$. That is, the processes are additive in the λ_0 's. As a consequence, defining

$$M(u, t) = Ee^{u\Lambda(t)},$$

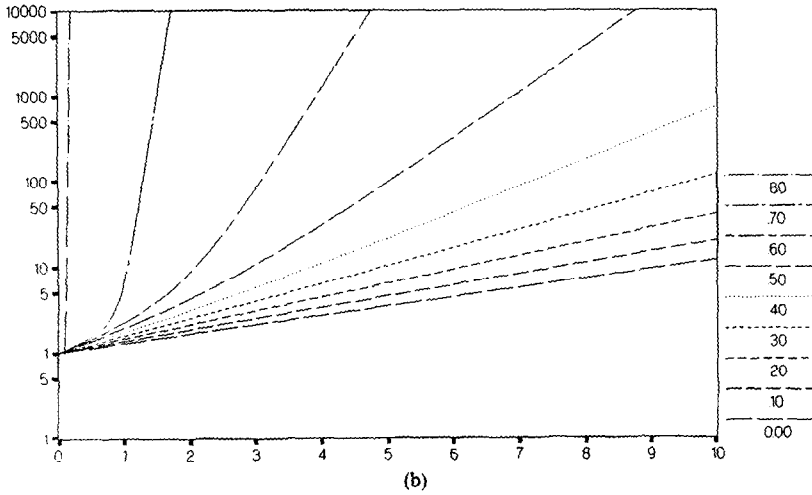
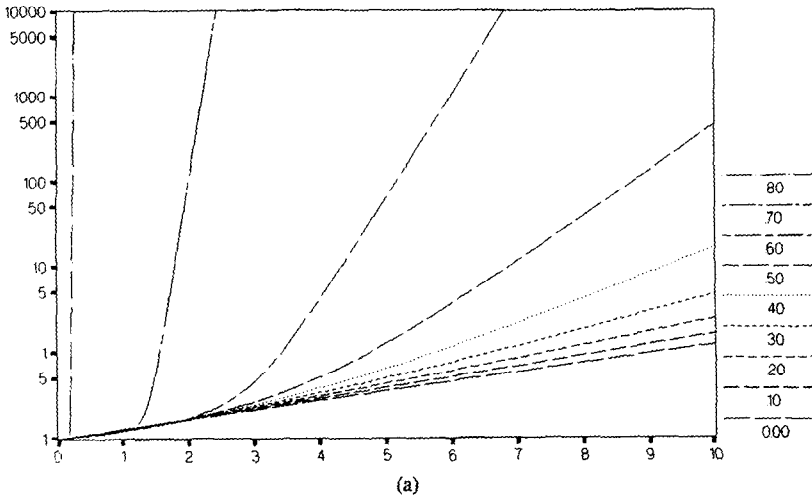
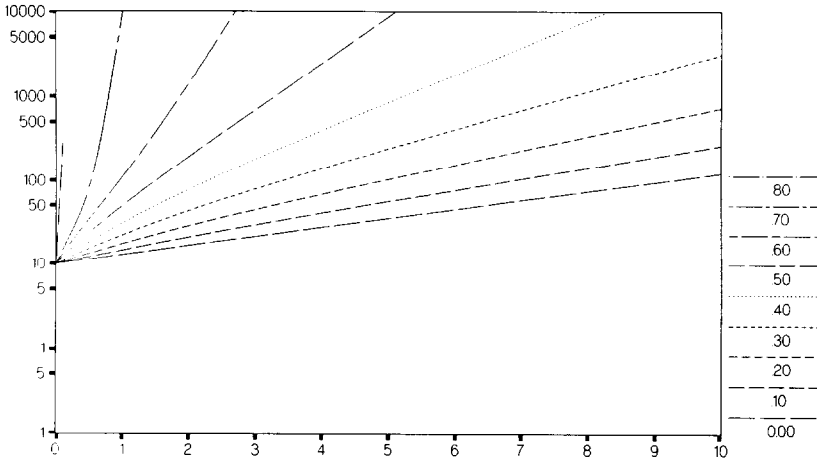


FIG. 1. The expected potential for infection, $EA(t) = EdN(t)/dt$, as a function of time t . The distribution of transmission rates λ in the population is lognormal with mean $\mu = 0.05$ and coefficient of variation $c = 2$. The correlation ρ varies from 0 to 0.8 in steps of 0.1 as indicated. One person infected at $t = 0$ with (a) $\Lambda(0) = \lambda_0 = 0.1 \text{ yr}^{-1}$; (b) $\lambda_0 = 1 \text{ yr}^{-1}$; (c) $\lambda_0 = 10 \text{ yr}^{-1}$.



(c)

FIG. 1. (continued)

we have

$$M(u, t) = M_0(u, t)^{\Lambda(0)},$$

where $M_0(u, t)$ is the generating function for a process starting at $t = 0$ with $\lambda_0 = 1$. Now, considering two points of time, $r + s > r > 0$, we have

$$\begin{aligned} M_0(u, r + s) &= EE(e^{u\Lambda(r+s)} | \Lambda(r)) \\ &= EM_0(u, s)^{\Lambda(r)} = Ee^{K_0(u,s)\Lambda(r)} \\ &= M_0(K_0(u, s), r), \end{aligned}$$

where $K_0(u, t) = \ln M_0(u, t)$.

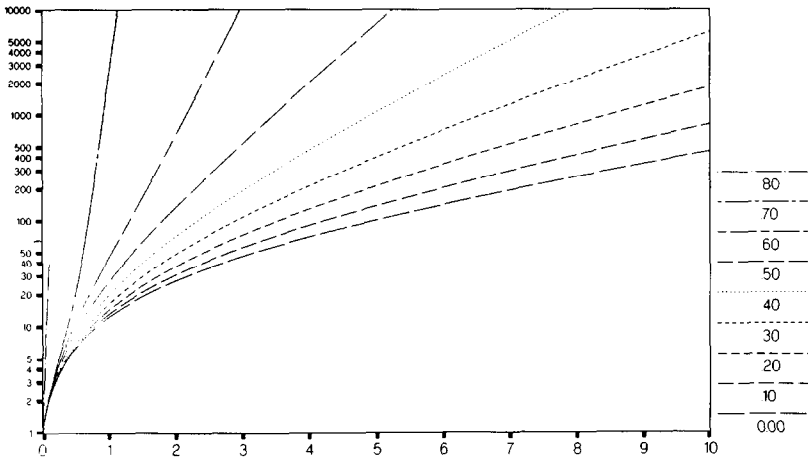
Hence, for the cumulant generating function we obtain

$$K_0(u, r + s) = K_0(K_0(u, s), r). \tag{A1}$$

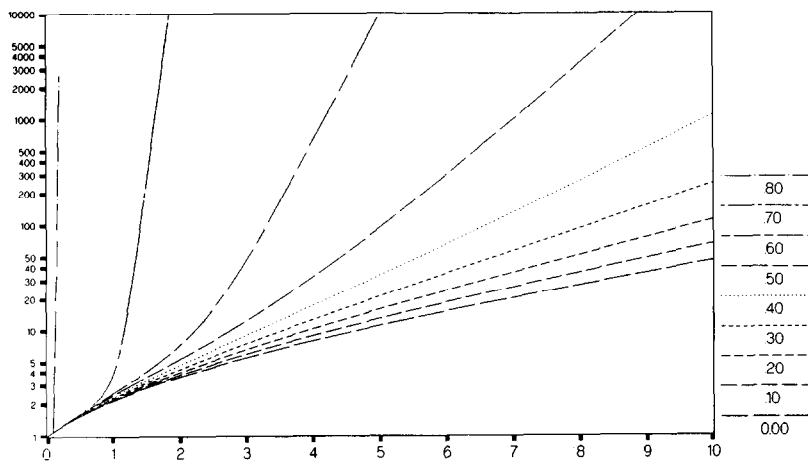
Considering the limits of (A1) as $s \rightarrow 0$ and $r \rightarrow 0$, we obtain the forwards and backwards equations, respectively, for $\lambda_0 = 1$, and the same equation for general initial conditions,

$$\frac{d}{dt} K(u, t) = [R(u) - 1] \frac{d}{du} K(u, t), \tag{A2}$$

$$\frac{d}{dt} K(u, t) = R(K(u, t)) - 1, \tag{A3}$$



(a)



(b)

FIG. 2. The expected number of infected persons $EN(t)$ as a function of time. The parameters in the processes (a), (b), and (c) are the same as in Figure 1.

where $R(u)$ is the moment-generating function for the first moment distribution $xf(x)/EX$ defined in the main text. Equating (A2) and (A3), we obtain

$$\frac{d}{du} K(u, t) = \frac{S(K(u, t))}{S(u)}, \tag{A4}$$

where $S(u) = R(u) - 1$.

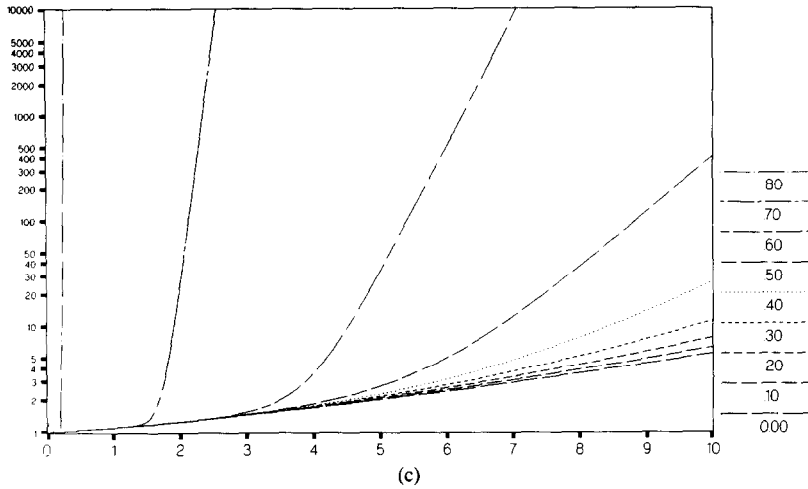


FIG. 2. (continued)

APPENDIX B. NUMERICAL EVALUATION OF $g(t, v)$

From the basic differential equation

$$\frac{d}{dt} g(t, v) = \alpha(v, \rho) g(t, \rho v),$$

we find

$$\frac{d^n}{dt^n} g(0, v) = \beta_n \lambda^{1/(1-\rho) + \rho^n v_0}$$

where $\beta_n = \prod_{i=0}^{n-1} \alpha(\rho^i v, \rho)$ and $\beta_0 = 1$.

The Taylor expansion for $g(t, v)$ is then

$$g(t, v) = \lambda_0^{1/(1-\rho)} \sum_{n=0}^{\infty} \beta_n \lambda_0^{\rho^n v} \frac{t^n}{n!}.$$

When ρ is not very close to 1, ρ^n approaches 0, and the terms of the expansion approach those of the expansion of the exponential function.

For $r > 1$, we define

$$\begin{aligned} h_r(t, v) &= \frac{\beta_r}{\alpha(0, \rho)^r} \lambda_0^{1/(1-\rho)} e^{\alpha(0, \rho)t} \\ &= \lambda_0^{1/(1-\rho)} \frac{\beta_r}{\lambda(0, \rho)^r} \sum_{n=0}^{\infty} \frac{\alpha(0, \rho)^n}{n!} t^n. \end{aligned}$$

We now write $g(t, v)$ as $[g(t, v) - h_r(t, v)] + h_r(t, v)$ and expand the difference in the brackets, giving

$$g(t, v) = \lambda_0^{1/(1-\rho)} \sum_{n=0}^{\infty} (\beta_n \lambda_0^{\rho n v} - \beta_r \alpha(0, \rho)^{n-r}) \frac{t^n}{n!} + h_r(t, v).$$

If we now approximate by summing only up to $n = r$, the error is

$$\begin{aligned} & \lambda_0^{1/(1-\rho)} \sum_{n=r+1}^{\infty} (\beta_n \lambda_0^{\rho n v} - \beta_r \alpha(0, \rho)^{n-r}) \frac{t^n}{n!} \\ &= \lambda_0^{1/(1-\rho)} \frac{\beta_r}{\alpha(0, v)} \sum_{n=r+1}^{\infty} \left(\prod_{i=r}^{n-1} \frac{\alpha(\rho^i v, \rho)}{\alpha(0, \rho)} \lambda_0^{\rho^i v} - 1 \right) \frac{(\alpha(0, \rho) t)^n}{n!}. \end{aligned}$$

In practice, if $\rho < 0.7$, the error term can be ignored if we put $r = 5$. On the other hand, the computation time is quite small even if we choose, for example, $r = 30$.

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