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## Behavior Change and Non-Homogeneous Mixing

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## Abstract

Incorporating changes in behavior patterns has always been a thorny issue in the modeling of non-homogeneous mixing. The generalized "two-sex problem" in a multi-group population requires the solution of multiple matching constraints any time contact rates, selection patterns, or group sizes change. Previous papers have outlined a method for incorporating the effects of changes in group size, assuming contact and selection preferences remain constant (Morris, 1991). This paper will present methods for incorporating empirical or theoretical changes in group-specific contact rates and selection patterns. The approach combines iterative proportional scaling and log-linear models to estimate the changing behavioral parameters. These parameters can then be used to drive epidemic simulations. Such methods are particularly useful when full network data have been collected for only one period, but contact rate data have been collected over many periods. The approach can thus help to reduce the expense and political sensitivity of data collection. An application to age-structured mixing among gay men in New York City is presented.

Mixing patterns in multi-group populations are now recognized to have an important role in the population dynamics of disease (Hethcote and Yorke (1984); Sattenspiel (1987b); Anderson, et al. (1990)). Initially in response to the resurgence of gonorrhea and later with the rapid growth of the AIDS epidemic, selective mixing has become a major focus for epidemiological modelers. Various methods for summarizing the structure of selective mixing have been proposed (Gupta and Anderson (1989); Blythe, et al. (1991); Koopman, et al. (1991); Morris (1991)). Simulation studies show that these effects can be both strong and variable (Hyman and Stanley (1988); Haraldsdottir, et al. (1992); Morris (1993d)), and that they can bias the estimates of other epidemiological parameters if they are not

taken into account (Koopman, et al. (1991)). Analytic expressions for the effect of mixing on the reproductive rate (or number) of a disease and the definition of core groups are beginning to be developed (Diekmann, et al. (1990); Jacquez, et al. (1993)).

One of the major issues in modeling the mixing patterns of a multi-group population concerns the solution of multiple matching constraints in non-equilibrium populations. Constraints are imposed by the symmetry inherent in contact processes, i.e., if I meet you, then you have to meet me. This is a generalized version of the "two-sex problem" familiar to demographers. In its classical form this problem arises in life table modeling when births are projected on the basis of two-sex populations. The birth process implies a matching process between the age-structured populations of males and females, and these constraints become complicated when vital dynamics are considered (Pollard (1948); Schoen (1982)). In the context of disease transmission, the "two-sex" problem arises in modeling mixing patterns when the subgroup sizes, contact rates, or selection patterns change over time. The multiple matching constraints that must be satisfied in each case require explicit modeling.

The three sources of change -- size, activity and selection -- often arise in different contexts but they also interact. Subgroup sizes typically change in response to vital dynamics, e.g., differential birth and death rates, and differential disease-induced mortality. The former is responsible for the so-called "marriage squeeze" generated by the baby-boom, disrupting the typical pattern of age-matching in marriage (grooms slightly older than brides) as early baby-boom women faced a relative scarcity of older men, and late baby-boom men faced a similar scarcity of younger women (cite). Differential disease-induced mortality can raise similar issues. In the case of AIDS, for example, deaths due to disease may change the population age structure (Anderson, et al. (1988)), or the size of risk groups such as gay men or IVDUs. Each requires some change in the contact patterns of their partners. Changes in contact rates may also arise independently as the result of social and psychological dynamics. The most recent example is the dramatic reduction in unsafe sex reported by gay men since the identification of HIV ((1985); Martin (1987); Becker and Joseph (1988); Winkelstein, et al. (1988)). But similar effects arise in other diseases when clinical infection or quarantine removes an infectious person from general circulation. As with the change in subgroup size, the result is that a group becomes more or less available to its usual partners. The underlying dynamics, however, are different, and this must be recognized in the model. Finally, selection patterns may change independently, apart from (or in addition to) changes in either subgroup size or activity level. This, too, is a social-psychological dynamic. There is anecdotal evidence, for example, that men are choosing substantially younger women as sex partners in some countries in Africa in an attempt to avoid contact with the assumed higher HIV-prevalence among their female peers (Wawer et al., 1992).

In the AIDS epidemic, all of these factors are likely to be

changing in ways that will have important consequences for the eventual prevalence of the disease, and for the development of effective vaccination strategies. The challenge for epidemiology is that the data necessary to identify and model these changes will almost never be available. Longitudinal network data on patterns of sexual partnering would be needed, while at this point even cross-sectional network data are rare. Network data are difficult, time consuming and expensive to collect. When the topic involves sexual behavior, network methods are also intrusive to the respondent and politically sensitive, so that both funding and permission to collect the data may be hard to obtain (cf. (Laumann, et al. (1992))). These obstacles are sufficiently large that appropriate data may never be available in most settings. Methods for estimating the effects of these changes on mixing patterns, and for merging information from multiple sources, may thus be the only realistic option.

The discussion that follows generalizes the modeling framework presented in Morris (1991). Data on sexual partnerships are summarized in a "contact" or "mixing" matrix, where the rows and columns represent the subjects' and partners' attributes, and the cell counts represent pairs of individuals. The object of the mixing model is to predict these counts. If we let  $x_{ij}(t)$  denote the observed cell counts at time  $t$ , and  $m_{ij}(t)$  denote the predicted counts, then the model specifies that

$$m_{ij}(t) = K_{ij}(t) a_{ij}(t) \quad (1)$$

where

$$K_{ij}(t) = f(N_i(t)N_j(t), N(t))$$

is a term that depends only on the number in each subgroup,  $N(\cdot)(t)$ , and  $a_{ij}(t)$  represents the contact and selection preferences of groups  $i$  and  $j$ . By separating the effects of population size and preferences, this model enables each to vary independently. The resulting contact rates (as distinct from preferences) will change in response to either or both of the underlying factors. The general loglinear model for  $m_{ij}(t)$  can be written as

$$\log(m_{ij}(t)) = \log(K_{ij}(t)) + u(t) + u_1(i)(t) + u_2(j)(t) + \text{isu}(s=1, S, u_s(ij)(t)) \quad (2)$$

The  $K_{ij}(t)$  term is fit as an offset in the model (Numerical Algorithms Group (1985); Aitkin, et al. (1989)). The remaining  $u$ -terms are the loglinear decomposition of the preference term  $a_{ij}$ :  $u_1(i)$  is the marginal effect for row  $i$  and  $u_s(ij)$  is the effect of selection factor  $s$  on the  $ij$ 'th cell. The marginal effects represent the group-specific contact rate preferences (relative to the reference category  $u$ ). The selection effects represent the attribute-related preferences. These terms can be interpreted either as odds-ratios, or as simple multiplicative increments (decrements) to the probability of

a pair. The general approach taken below is to use data, where possible, to estimate the time-dependent parameters, and to treat the remaining parameters as constant.

For modeling disease transmission, the loglinear parameters can be substituted into the infection rate term,  $b_{SI}$ , of a compartmental model (actually  $b_{ijSiIj}$  in the multi-group model) to represent the heterogeneous mixing process. Letting  $c_i$  denote the contacts per unit time for group  $i$ ,  $p_{ij}$  denote the probability that this contact is with a member of group  $j$  and  $t_{ij}$  denote the per-partnership force of infection from  $i$  to  $j$ , then

$$\begin{aligned} b_{ij}(t) &= f(c_i p_{ij}(t) t_{ij}, N_j) \\ &= f(m_{ij}(t) t_{ij}, N_j N_i) \\ &= f(a_{ij}(t) t_{ij}, N) \end{aligned} \quad (3)$$

#### Modeling changes in sub-population sizes

Methods for dealing with changes in the population profile have been the focus of earlier papers (Blower and McLean (1991); Morris (1991)). Such methods may be used in several contexts. One is to update a mixing matrix when changes in subgroup size are known e.g., the change in the population age structure resulting from the baby boom. Data on changes in the population profile are likely to be available, as documenting such changes requires only survey or census estimates of subgroup frequency. Another context in which these methods may be used is to merge data from different sources, e.g., when full network data have been collected from a non-representative sample and the true population profile is known from another sources. Finally, these methods may be used during simulation, to update selection patterns at each step with the current population profile when there is differential disease-induced mortality among the subgroups.

Using the loglinear modeling framework described above, such changes only affect the offset term  $K_{ij}(t)$  in equation (2). In the absence of corresponding data on change in contact or selection preferences, these may be hypothesized to remain constant. The number of contacts between members of group  $i$  and members of group  $j$  then varies over time according to the model

$$\begin{aligned} \log(m_{ij}(t)) &= \log(K_{ij}(t)) + a_{ij} \\ a_{ij} &= u + u_1(i) + u_2(j) + i_{su}(s=1, S, u_s(ij)) \end{aligned} \quad (4)$$

As  $K_{ij}(t)$  changes, the marginal contact rates will, in general, not be preserved. The model simply specifies that the preferred contact rates for each group do not change. An application of this model will be examined below in conjunction with changing activity preferences.

#### Modeling changes in contact rates

It is not uncommon for simple behavioral data, such as contact rates, to be collected over time. Network data, however, are often collected only at one time point, if at all. When there have been significant changes in contact rates over time, simulating disease transmission will require that the mixing matrix be adjusted. Changes in contact rates present a slightly different modeling problem than changes in group size. With both the subgroup sizes and contact rates known, the margins of the matrix are fixed at each time point. In contrast to the case described above, adjustments to the matrix must now preserve the known marginal totals.

In the absence of data on whether selection patterns are changing in response to the marginal changes, a natural hypothesis is that they remain constant. Changes in contact rates thus index the reference category and marginal effects in equation (2) by time, but leave the selection effects constant:

$$\begin{aligned} \log(m_{ij}(t)) &= \log(K_{ij}(t)) + a_{ij}(t) & (5) \\ a_{ij}(t) &= u(t) + u_1(i)(t) + u_2(j)(t) + \text{isu}(s=1, S, \\ &\quad \text{us}(ij)) \end{aligned}$$

If contact rates are increasing or decreasing at a constant rate, time can be modeled as a continuous variate, adding a single interaction parameter to the prediction equation for each of the marginal effects. If the trends are not as regular, time may be treated as a discrete variable to represent the observed pattern. In the log-linear context, constant selection preferences are equivalent to assuming that the internal odds-ratios of the matrix do not change.

The effects of changing contact rates are captured in the marginal parameters  $u_1(i)(t)$  and  $u_2(j)(t)$  above. If these parameters could be expressed as simple functions of the observed marginal totals, as they can be in standard linear models, the adjustment of the  $a_{ij}$  would be a straightforward matter of updating the parameters by substituting the new margins for the old ones. In generalized linear models, however, the marginal parameters are instead multiplicative functions of the fitted  $m_{ij}$ , so this approach is not possible.

It is relatively simple to derive the maximum likelihood estimates (MLEs) for the  $m_{ij}(t)$ , however, and use these to construct the parameter estimates. For a table with known marginal totals and interaction structure (here the observed odds-ratios), the MLEs can be computed using iterative proportional scaling (IPS). This method is also known as the Deming-Stephan algorithm, standardization or "raking" the cross-tabulated data.

The IPS algorithm updates the cell counts by sequentially multiplying the rows and columns by the ratio of the desired contact rates and the current rates for each group. Letting  $m_{ij}(k)$  represent the  $k$ 'th iteration, and  $c \cdot (*)$  represent the final desired contact rate,

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mij(1)  =      mij(0) f(ci(*),ci(0))
mij(2)  =      mij(1) f(cj(*),cj(1))
mij(3)  =      mij(2) f(ci(*),ci(2))

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The first iteration conforms the row margins to the desired contact rate. This will generally change the contact rates for the column margins, so the second iteration conforms the column margins to the desired rate, changing the marginal contact rates for the rows, and the iteration process continues.

It has been shown that this algorithm always converges (Haberman (1974)), and that the resulting estimates are the MLEs of the fitted values under the hypothesis of no change in the interaction structure (Birch (1965)). That IPS preserves the interaction structure within the matrix is clear, as the odds-ratios which represent this structure in the loglinear model are unaffected when rows or columns of a matrix are multiplied by an arbitrary constant. The parameters from equation (5) can be recovered by fitting the model to the IPS-adjusted matrix.

#### Example

In this section we will apply both of the methods above to adjust a matrix of age-matching in sexual partnerships among gay men. The adjustment will compensate for both the decline in the age-group specific prevalence of unsafe sex (a change in group size) and for the reduction in the number of partners among those who continue to report engaging in unsafe sex (a change in contact rates).

The analysis is based on data from the Longitudinal AIDS Impact Project (LAIP), a panel study of gay men in New York City. The study began in 1985 and seven waves of interviews have now been completed. Using structured face-to-face interviews this project has collected a wide range of information on the social and sexual network characteristics of respondents, as well as their serostatus. The original sample of 746 men was selected using a combination of stratified probability sampling, targeted sampling, and snowball sampling. The sample was augmented for the last two waves by a cohort of younger men (18-23 years old) in order to compensate for the age-bias introduced by the panel design. For further information on the sample and data from this project see (Martin and Dean (1990)).

For the last two waves of the survey, respondents who reported any anal intercourse without the use of a condom have been asked to report the ages of the men with whom they had anal sex. Insertive and receptive sex were reported separately, and the ages of up to eight partners were recorded. The reported ages were fairly well distributed, with only a small tendency to round to multiples of five. The original age-matching matrix is given in Table 1 below.

Age of receptive partner:

Age of  
insertive partner:  
17-24

25-34  
 35-44  
 45-54total  
 pairs  
 Ncontact  
 rate17-24682116151.0425-3493818672750.9535-4432125756610.9145-54177519  
 181.08total pairs19735219162N15756118169contact  
 rate1.250.970.851.030.96

Table 1. Age-matching matrix for 1990-1991 LAIP data. These data represent an average of the patterns of selection observed in the last two years of the survey, corrected for sampling bias and the tendency for reports of insertive anal sex to be higher than receptive reports.

In the prior years of the survey, age-matching information was not collected. Respondents were asked, however, whether they engaged in unsafe anal sex, how frequently, how often they used condoms, and how many partners (new and repeat) they had in that year. Substantial changes in behavior occurred during this time. Two prior time points will be examined here: pre-AIDS and 1985, the first year of the survey. The data on pre-AIDS behavior patterns were collected as retrospective reports in 1985 with questions prefaced by "In the year before you heard about HIV/AIDS, did you...". Almost all of the respondents reported hearing about AIDS by 1981. The prevalence of unsafe anal intercourse and the number of new partners reported at each time point is presented in Table 2 below.

Behavior	Age Group	Pre-AIDS	Ins	Rec1985	Ins	Rec1991	Ins	Rec%	reporting
anal sex	15-24	1.98	3.66	3.25	9.72	4.41	6.73	5.55	5.64
new partners/yr	15-24	11.0	4.5	3.9	1.2	1.1	1.1	1.2	1.1
	25-34	11.2	10.5	4.3	3.9	1.1	1.3	1.5	1.3
	35-44	15.3	4.9	4.0	1.0	0.7	1.4	5.9	11.6
	45-54	3.8	4.8	1.2	0.9	1.1	1.1	1.1	1.1

Excludes persons in mutually monogamous relationships in 1991  
 2 5% trimmed mean (median), unsafe partners only

Table 2. Changes in risk behavior over time in the LAIP survey.

As in every major survey of sexual behavior of gay men in the US, the prevalence of reported unsafe sex in this sample has declined dramatically from the pre-AIDS period. The decline was not, however, the same for each age group: among the three oldest age-groups 15-20% report no unsafe sex in 1991, compared to nearly 40% among the youngest age group. Strong declines can also be observed in the number of new partners among those reporting unsafe sex. Here the 5% trimmed mean number of new partners was over 10 per year in the pre-AIDS era, and has dropped to just under 1 new partner per year in

1991. The reduction is roughly the same for each age group.

One of the primary questions one would like to examine using these data is whether the observed changes in behavior have been sufficient to bring the epidemic below the reproductive threshold. Given the observed heterogeneity in both contact rates and mixing patterns, it is also important to understand what effect these will have on the future of the epidemic.

Simulation is the only way to investigate this question. If all of the necessary parameters were confidently known (including the age-specific HIV prevalence and the distribution of infectivity during the latency period) it would be possible to simulate the path simply from 1991. These parameters are not well known, however, so it is important to assess the adequacy of the model by using it to simulate the initial years of the epidemic and compare the results against some known statistics, such as surveillance data on AIDS incidence among gay men. The means that 1990-91 mixing matrix in Table 1. will have to be adjusted for changes in the size of the exposed population and contact rates over this period.

These adjustments to the mixing matrix involve both of the methods described above. The original 1991 matrix must first be adjusted for the changes in group size using the  $K_{ij}(t)/K_{ij}(91)$  ratio. It must then be further adjusted using IPS to match the changing contact rates. The order of adjustment matters, as the group-size adjustment does not preserve the observed contact rates and must therefore be performed first.

The adjusted matrices for 1985 and the pre-AIDS period are presented in the four tables of Table 3. The first adjustment changes the size each group (the column labeled 'N'). The second adjustment conforms the marginal contact rates to those observed in each year using IPS. Convergence was obtained after five iterations. Discreteness in the number of persons generates small differences between the final contact rates and the rates observed in the original data.

The loglinear summary parameters for the final matrices are presented in Table 4. The declines in activity were not regular enough that time could be modeled as a continuous variable, so the time effect was modeled instead as a discrete factor. The selection preferences were summarized in a differential assortative bias factor and a diagonal quadrant block. The models were fit using the statistical package GLIM, the first level of each factor is taken as the reference category and takes the parameter value 1. For the row and column estimates, this is the 18-24 year olds, for the homophily terms it is the off-diagonal cells, and for the block term it is the off-diagonal 4-cell block for each quadrant of the submatrix.

Exponentiated Parameter for: Effects: t=81 t=85 t=91 Main:

Reference cat. u(t):

(t)

6.33\*



2.73\*  
0.85\* Rows             $u_1(i)(t)$ :insertive  
2(t)2.221.821.593(t)2.171.471.204(t)1.211.031.38 Columns     $u_2(j)(t)$ :  
receptive 2(t)1.651.881.413(t)1.581.350.914(t)1.151.511.06Selection  
 $us(ij)$ :Constant Exponentiated Parameter: assortative  
16.15\*20.51\*31.11\*42.13\* block diagonal quadrant2.08\*\*  $p < 0.05$

Table 4. Loglinear summary parameters for the original 1991, and adjusted 1985 and pre-AIDS matrices.

The model above fits the data almost too well, with a residual deviance of 2.45 on 22 degrees of freedom. A simple model of proportional mixing that preserved the time-specific margins would use only 5 less parameters (the selection effects at the bottom of the table). The only parameters to reach standard levels of statistical significance are the reference category, which indexes the general decline in contact preferences for each year, and the selection effects. The group-specific differences in contact preferences over time are uniformly insignificant. A more parsimonious model is thus suggested, dropping the preference differentials. This model, however, provides an unacceptable fit (residual deviance of 92.54 on 34 degrees of freedom). An acceptable model will thus need to index at least some of the group-specific differentials. Given the amount of pre-analysis data manipulation, and the small numbers of observations in 1991, significance levels are best treated as a rough guide here. The apparent "overfitting" of the model in Table 2 may not be a real problem.

Initial simulations using the parameter estimates from Table 2 (calibrated against AIDS surveillance data in New York City for the risk group "men who have sex with men") suggests that the current patterns of behavior are just on the boundary of reducing the epidemic spread below the reproductive threshold. If these data on behavior are accurate, and the patterns are maintained in the future, then the disease would eventually die out in the absence of other sources of infection (e.g., links with IDUs). If, on the other hand, respondents have under-reported the number of new partners they have, the result could be quite different. Assuming two new partners per year (instead of the one reported), the disease would instead become endemic, with seroprevalence levels of about 50% among the exposed population in the oldest group, and about 25% among the youngest (Morris (1993d)).

#### Modeling changes in selection preferences

When longitudinal network data are available, loglinear models can be used to examine whether the selection patterns have changed in ways not attributable to changes in group sizes or contact rates. The selection preference parameters in the model can now be indexed by time (equation 2), and various hypotheses may be tested. Again, if the trends over time are monotonically increasing or decreasing, e.g.,

a rise or fall in the strength of the assortative bias, the time index can be modeled as a continuous variate, with corresponding gains in parsimony.

The LAIP survey has two years of age-matching data, collected in 1990 and 1991. The mixing matrix in Table 1 above represented an average of these two years, but they can also be treated as distinct. The two matrices are presented in Table 5. The numbers are small, and a one-year difference in time may be expected to yield little difference in selection effects, but the data do provide an opportunity to test this hypothesis. Neither group sizes nor relative contact rates have changed much between the two years, so a simple model to examine here would be time-dependent uniform assortative bias, indexing only the reference category and a single parameter for assortative mixing by time:

$$\log(m_{ij}(t)) = \log(K_{ij}) + u(t) + u_1(i) + u_2(j) + u(ij)(t) \quad t=1,2$$

The hypothesis of interest is whether  $u(ij)(2)$  is significant, and it is not here. The residual deviance for the model of constant selection effects is 20.38 on 24 degrees of freedom. The reduction in deviance gained by adding the additional parameter for changing selection is a remarkably small 0.27.

## Conclusion

Loglinear methods provide a general class of models that are flexible enough to solve many of the important problems in heterogeneous mixing. The multiple matching constraints posed by a non-equilibrium population, whether the changes are due to variation in group sizes, contact rates or selection patterns, can be handled effectively with these methods. The summary parameters are interpretable and easily integrated into the compartmental modeling framework, and the procedures for hypothesis testing make the search for parsimonious models a relatively simple task.

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