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**"Simulation Studies on Stochastic Models with
Heterogeneously Mixing Contact Structures"**

**Carlos Castillo-Chavez
Biometrics Unit
Cornell University
Ithaca, NY 14853-7801
U.S.A.**

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**SIMULATION STUDIES ON STOCHASTIC
MODELS WITH HETEROGENEOUSLY
MIXING CONTACT STRUCTURES**

BY

**Carlos Castillo-Chavez, Samuel Fridman
and Shu-Fang Hsu Schmitz**

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Simulation studies on stochastic models with heterogeneously mixing contact structures

*Carlos Castillo-Chavez**, *Samuel Fridman[†]* and *Shu-Fang Hsu Schmitz[†]*

Abstract. This article concentrates on the study of the role of changing contact/social structures in heterogeneously mixing populations with applications to demography and epidemiology. A flexible framework of stochastic pair-formation models is revisited. We simulate demographic pair-formation models as continuous time Markov processes. The simulations focus on the effect of two distinct sets of partnership preferences. Suggestions and plans for future work are outlined.

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1. Introduction

Classical mathematical models in demography (Leslie 1945; Lotka 1922; MacKendrick 1926) concentrate on the dynamics of birth and death processes of female populations. They ignore the mating/marriage structures and their effect on social dynamics. The incorporation of mating structures or marriage functions was pioneered by both Kendall (1949) and Keyfitz (1949). Their work was extended by Fredrickson (1971), McFarland (1972), Parlett (1972), and Pollard (1973) two decades ago but with very limited impact. The HIV/AIDS epidemic attracted theoreticians' attention to the study of the effects of social dynamics on the spread of epidemics. Questions raised primarily by researchers interested in HIV/AIDS epidemiology have brought back interest in the modeling of marriage functions and their connection to social dynamics (Dietz 1988; Dietz and Haderler 1988; Haderler 1989a, b; Haderler and Nagoma 1990; Waldstätter 1989). Since then research in this area has grown at a fast pace.

Over the last few years, we (with several collaborators) have developed a mathematical approach for the systematic incorporation of very general contact structures in biological and/or sociological systems. This

* To whom correspondence should be sent. Biometrics Unit and Center for Applied Mathematics, 337 Warren Hall, Cornell University, Ithaca, NY 14853-7801

[†] Biometrics Unit, 337 Warren H ll, Cornell University, Ithaca, NY 14853-7801

approach is flexible and can be applied to the study of disease dynamics, frequency-dependent predation in heterogeneously mixing populations, the transmission dynamics of cultural traits, and general demographic processes (Castillo-Chavez *et al.* 1993b). In addition, we have made serious efforts to connect these models to data (Hsu Schmitz and Castillo-Chavez 1993).

In this paper we present a framework of stochastic pair-formation models that incorporate general contact/social structures. Simulations are conducted using two sets of partnership preferences to begin to address better their effects on variability of average behavior of the models. We organize this paper as follows: Section 2 introduces the approach to modeling contact/social structures; Section 3 outlines the implementation of this approach in an stochastic model; Section 4 presents the results of extensive simulations of a demographic two-sex stochastic model and compares the dynamics obtained from random mating with those obtained from non-random mating; Section 5 summarizes our results and outlines future work in this area.

2. The role of contact/social structures

The contact or social structure of a population plays a fundamental role in the transmission dynamics of diseases, cultural traits, genetic traits, etc. It has been modeled by assuming that the rate of transmission of the trait in consideration is directly proportional to those that have the trait and to those that do not (Anderson 1982; Anderson and May 1991; Bailey 1975; and references therein). The assumption that the rate of new "cases" (the incidence) is proportional to the product of "susceptibles" and "converts" (those infected), that is, the mass-action law, is useful but only in very limited circumstances. It is not very useful, for example, for the modeling of sexually transmitted diseases (STD's) if the interacting subpopulations vary in size over time. A thorough analysis of assumptions including those implicitly involved in the mass-action law in epidemiology has been carried out in a systematic fashion (Busenberg and Castillo-Chavez 1989, 1991).

The importance of the contact process on frequency dependent systems was recognized by Ross as early as 1911 in his work on malaria. The contact/social structure of the population must respond to demographic/epidemiological changes in the population. A flexible framework for the modeling of population interactions is being developed because several questions of theoretical and practical importance can not be properly studied under the existing framework. Some successful applications include those to food web dynamics (Velasco-Hernandez and Castillo-Chavez 1993), and those to cultural dynamics (Lubkin and Castillo-Chavez 1993).

Busenberg and Castillo-Chavez (1989, 1991) defined the contact/social structures through mixing/pair-formation matrices. In addition, they have provided a useful characterization of these matrices, which constitutes the basis of our further analysis. Consequently, we must introduce this framework. We begin with some needed notation and definitions:

$p_{ij}(t)$ = probability that a male in group i mixed with a female in group j at time t
given that he mixed with somebody;

$q_{ji}(t)$ = probability that a female in group j mixed with a male in group i at time t
given that she mixed with somebody;

$T_i^m(t)$ = number of males in group i at time t ;

$T_j^f(t)$ = number of females in group j at time t ;

b_i^m = average (assumed constant) number of female partners per group- i male per time unit,
= *per capita* pair-formation rate for group- i males;

b_j^f = average (assumed constant) number of male partners per group- j female per time unit,
= *per capita* pair-formation rate for group- j females.

Definition. $(p_{ij}(t), q_{ji}(t))$ is called a mixing/pair-formation matrix if and only if it satisfies the following properties at all times:

$$(A1) \quad 0 \leq p_{ij}(t) \leq 1, \quad 0 \leq q_{ji}(t) \leq 1.$$

$$(A2) \quad \sum_{j=1} p_{ij}(t) = 1 \text{ for all } i, \text{ and } \sum_{i=1} q_{ji}(t) = 1 \text{ for all } j.$$

$$(A3) \quad b_i^m T_i^m(t) p_{ij}(t) = b_j^f T_j^f(t) q_{ji}(t) \text{ for all } i, j.$$

$$(A4) \quad \text{If for some } i \text{ and/or some } j, \text{ we have } b_i^m b_j^f T_i^m(t) T_j^f(t) = 0 \text{ for some } t, \text{ then we define}$$

$$p_{ij}(t) \equiv q_{ji}(t) \equiv 0.$$

The only separable solution to (A1)–(A4) is the Ross solution given by $(\bar{p}_j(t), \bar{q}_i(t))$, where

$$\bar{p}_j(t) = \frac{b_j^f T_j^f(t)}{\sum_{i=1} b_i^m T_i^m(t)}, \quad \bar{q}_i(t) = \frac{b_i^m T_i^m(t)}{\sum_{k=1} b_k^f T_k^f(t)}.$$

Moreover, all solutions to (A1)–(A4) can be represented as multiplicative perturbations to the Ross solution.

Explicitly,

$$p_{ij}(t) = \bar{p}_j(t) \left[\frac{R_j^f(t) R_i^m(t)}{\sum_{k=1} \bar{p}_k(t) R_k^f(t)} + \phi_{ij}^m \right], \quad q_{ji}(t) = \bar{q}_i(t) \left[\frac{R_i^m(t) R_j^f(t)}{\sum_{l=1} \bar{q}_l(t) R_l^m(t)} + \phi_{ji}^f \right],$$

where ϕ_{ij}^m denotes the degree of preference that males in group i have for females in group j , ϕ_{ji}^f denotes the degree of preference that females in group j have for males in group i . In addition, the following relationships must be satisfied:

$$0 \leq R_i^m(t) \equiv 1 - \sum_{k=1} \bar{p}_k(t) \phi_{ik}^m \leq 1,$$

$$0 \leq R_j^f(t) \equiv 1 - \sum_{l=1} \bar{q}_l(t) \phi_{jl}^f \leq 1,$$

and

$$\phi_{ij}^m = \phi_{ji}^f + R_i^m(t) R_j^f(t) \left[\frac{1}{\sum_{l=1} \bar{q}_l(t) R_l^m(t)} - \frac{1}{\sum_{k=1} \bar{p}_k(t) R_k^f(t)} \right].$$

We observe that if $\phi_{ij}^m = a$ (constant) and $\phi_{ji}^f = d$ (constant) for all i and j , then the general solution reduces to the Ross solution which corresponds to random heterosexual mixing.

Based on the above definitions and characterization, in the next section we introduce a stochastic analog to the deterministic epidemic model presented by Blythe *et al.* (1991). The applications of the mixing/pair-formation approach of Busenberg and Castillo-Chavez to stochastic models for sexually transmitted diseases that follow pairs are also discussed.

3. Stochastic pair-formation models

In this section, we formulate a stochastic pair-formation epidemiological model by using the approach that is common to interacting particle systems (for details, see Luo and Castillo-Chavez 1993; Luo *et al.* 1991). Extensions to model more complex scenarios should be quite evident from the following description.

We define

$$X = \{0, 1, \dots, L\} \times \{0, 1\} \times \{0, 1, \dots, N\} \times \{0, 1\} \setminus \{0\} \times \{0, 1\} \times \{0\} \times \{0, 1\},$$

and consider the explicit stochastic process

$$\xi_t : X \rightarrow \{0, 1, 2, \dots\}, \quad t \geq 0.$$

Let $x = (i, u; j, v) \in X$, where i and j denote the groups of males and females, u and v denote the epidemiological statuses of males and females, respectively. If we consider a STD that does not have a long latent period, does not provide permanent immunity, and does not cause significant mortality (e.g., gonorrhea, see Hethcote and Yorke 1984), then the possible values of u and v are either 0 (*susceptible*) or 1 (*infected*). For

$i > 0$ and $j > 0$, x gives the type of pair, that is, the male is from group i with epidemiological status u and the female is from group j with epidemiological status v . If $i = 0$ but $j > 0$, then x represents a single female in group j with epidemiological status v (the value of u is not relevant) and therefore we can define $x \equiv (0; j, v) \equiv (0, 0; j, v) \equiv (0, 1; j, v)$. Similarly, if $j = 0$ but $i > 0$, then x represents a single male in group i with epidemiological status u and again we can define $x \equiv (i, u; 0) \equiv (i, u; 0, 0) \equiv (i, u; 0, 1)$. Note that the case of $i = 0$ and $j = 0$ is not included in the domain X . Consequently, the stochastic process $\xi_t(x)$ gives the number of pairs of type x at time t if $i > 0$ and $j > 0$; it gives the number of single males of type x at time t if $i > 0$ and $j = 0$; and it gives the number of single females of type x at time t if $i = 0$ and $j > 0$.

To complete the characterization of $\xi_t(x)$, we define $S \equiv \{0, 1, 2, \dots\}^X$ and let $c : S \times S \rightarrow (0, \infty)$ be a real-valued function that models the flip rate. We view $\{\xi_t : t \geq 0\}$ as an S -valued Markov process with flip rate $c(\cdot, \cdot)$, i.e., if $\xi_t = \xi$ for some $t \geq 0$, then $c(\xi, \eta)$ denotes the instantaneous rate at which ξ_t may change to state η . Explicitly,

$$\text{Prob}(\xi_{t+h} = \eta | \xi_t = \xi) = c(\xi, \eta)h + o(h), \quad \forall t \geq 0.$$

The more specific definition of flip rates is as follows: for $\xi \in S$, $A \subset X$, $B \subset X$, and $A \cap B = \emptyset$, we define $\xi_B^A(x) \in S$ as

$$\xi_B^A(x) = \begin{cases} \xi(x) + 1 & \text{if } x \in A; \\ \xi(x) - 1 & \text{if } x \in B; \\ \xi(x) & \text{otherwise.} \end{cases}$$

Thus, the system $\{\xi_t\}$ consists of a series of changing elements in the set S , which is the set of all functions on X . The dynamics of the system is described by the rates $\{c(\xi, \eta) : \xi \neq \eta, \xi, \eta \in S\}$ at which the system changes.

We assume the existence of an underlying mixing/pair-formation matrix $(p_{ij}(\xi_t), q_{ji}(\xi_t))$ as described in Section 2. Since ξ_t is a function of t , the mixing matrix is also a function of t . We further assume that paired individuals do not look for other partners before they separate. As the time t changes, singles may form pairs, pairs may dissolve, the disease may be transmitted within pairs from an infective to a susceptible, the infectives may be cured, etc.

We use the indices m and f to identify the parameters associated with males and females regardless of their epidemiological status, and use M and F to characterize those parameters only associated with infected males and females, respectively. Then the flip rate $c(\cdot, \cdot)$ is calculated as follows:

a) Pair formation

For $i > 0, j > 0$,

$$\begin{aligned} c(\xi, \xi_{(i,u;0),(0;j,v)}^{(i,u;j,v)}) &= b_j^f \xi(0;j,v) q_{ji}(\xi) \frac{\xi(i,u;0)}{\xi(i,u;0) + \xi(i,1-u;0)} \\ &= b_i^m \xi(i,u;0) p_{ij}(\xi) \frac{\xi(0;j,v)}{\xi(0;j,v) + \xi(0;j,1-v)}; \end{aligned}$$

b) Pair dissolution (σ denotes the constant pair dissolution rate)

For $i > 0, j > 0$,

$$c(\xi, \xi_{(i,u;j,v)}^{(i,u;0),(0;j,v)}) = \sigma_{ij} \xi(i,u;j,v);$$

c) Transmission (δ denotes the constant transmission rate)

For $i > 0, j > 0$,

$$c(\xi, \xi_{(i,0;j,1)}^{(i,1;j,1)}) = \delta_F \xi(i,0;j,1), \quad c(\xi, \xi_{(i,1;j,0)}^{(i,1;j,1)}) = \delta_M \xi(i,1;j,0);$$

d) Recovery (γ denotes the constant recovery rate)

For $i > 0, j > 0$, the recovery flip rates for one paired individual are

$$c(\xi, \xi_{(i,0;j,1)}^{(i,0;j,0)}) = \gamma_F \xi(i,0;j,1), \quad c(\xi, \xi_{(i,1;j,0)}^{(i,0;j,0)}) = \gamma_M \xi(i,1;j,0),$$

$$c(\xi, \xi_{(i,1;j,1)}^{(i,1;j,0)}) = \gamma_F \xi(i,1;j,1), \quad c(\xi, \xi_{(i,1;j,1)}^{(i,0;j,1)}) = \gamma_M \xi(i,1;j,1);$$

and the flip rate for both individuals in pairs is

$$c(\xi, \xi_{(i,1;j,1)}^{(i,0;j,0)}) = \gamma_{FM} \xi(i,1;j,1);$$

while for single infected individuals ($j = 0$ or $i = 0$) we have

$$c(\xi, \xi_{(i,1;0)}^{(i,0;0)}) = \gamma_M \xi(i,1;0), \quad c(\xi, \xi_{(0;j,1)}^{(0;j,0)}) = \gamma_F \xi(0;j,1);$$

e) Removal (μ denotes the constant removal rate from sexual activity)

For $i > 0, j > 0$,

$$c(\xi, \xi_{(i,u;j,v)}^{(i,u;0)}) = \mu_f \xi(i,u;j,v), \quad c(\xi, \xi_{(i,u;j,v)}^{(0;j,v)}) = \mu_m \xi(i,u;j,v);$$

while for single individuals ($j = 0$ or $i = 0$) we have

$$c(\xi, \xi_{(i,u;0)}^{(i,u;0)}) = \mu_m \xi(i,u;0), \quad c(\xi, \xi_{(0;j,v)}^{(0;j,v)}) = \mu_f \xi(0;j,v);$$

f) Recruitment (Λ denotes the constant recruitment rate for susceptible singles)

For $i > 0, j = 0$,

$$c(\xi, \xi_{(i,0;0)}^{(i,0;0)}) = \Lambda_i^m,$$

and for $i = 0, j > 0$,

$$c(\xi, \xi^{(0;j,0)}) = \Lambda_j^f;$$

g) Other

For any other $\eta \neq \xi$, we assume $c(\xi, \eta) = 0$.

h) $c(\xi, \xi) = - \sum_{\eta \neq \xi} c(\xi, \eta).$

This concludes the characterization of our stochastic epidemiological model with pairs. In the next section we outline the simulation procedure of a general stochastic process which includes the stochastic process described in this section. In addition, for illustrative purposes, we provide the results of several simulations of a particular case—the case when there is no infection.

4. Simulation of the stochastic process $\{\xi_t : t \geq 0\}$

We first describe the general approach to simulating jump Markov processes. From the construction of the flip rates we know that

$$c(\xi) = \sum_{\eta \neq \xi} c(\xi, \eta) < \infty.$$

If we let the sequence $0 = \rho_0 < \rho_1 < \dots$ denote the jump times of the process, then $\tau_n = \rho_n - \rho_{n-1}$ has an exponential distribution with rate $c(\xi_{\rho_{n-1}})$. Thus, the process can be simulated as follows:

- 1) First, set the initial state ξ_0 and assume that a sequence of n jump times $0 = \rho_0 < \rho_1 < \dots < \rho_n$ and their corresponding states ξ_{ρ_i} , $1 \leq i \leq n$, have been determined.
- 2) Get τ_{n+1} from $\exp\{\xi_{\rho_n}\}$ and let $\rho_{n+1} \equiv \rho_n + \tau_{n+1}$.
- 3) Set $\xi_{\rho_{n+1}} = \eta$ with probability $c(\xi_{\rho_n}, \eta)/c(\xi_{\rho_n})$
- 4) Define $\xi_t = \xi_{\rho_n}$ for $\rho_n \leq t < \rho_{n+1}$.

We proceed to simulate the stochastic model described in Section 3 in a very special situation. We assume that the infection rates δ_M and δ_F are equal to zero or, equivalently, that there are no infected individuals in the population. Hence, the recovery rates γ_M and γ_F have no meaning to us and are also excluded from the purely demographic model: individuals form and dissolve pairs. In addition, there is constant recruitment into single groups and constant removal from all groups.

Table 1. Initial group sizes and parameters for single males and females used in stochastic simulations

Single Group	Group Size	Recruitment Rate	Pair Formation Rate	Removal Rate
m_1	10000	1000	3.50	0.1
m_2	9000	900	3.00	0.1
m_3	8000	800	2.50	0.1
m_4	27000	2700	3.50	0.1
f_1	20000	2000	2.50	0.1
f_2	10000	1000	2.45	0.1
f_3	5000	500	2.30	0.1
f_4	35000	3500	2.59	0.1

Simulations were carried out using four groups of single males (m_1, m_2, m_3, m_4) and four groups of single females (f_1, f_2, f_3, f_4), which result in 16 possible pairing types ($m_1f_1, m_1f_2, \dots, m_2f_1, m_2f_2, \dots, m_4f_4$). The initial sizes, rates of recruitment, pair formation and removal of single male and female groups are presented in Table 1. The preference matrices are assumed to be $\{\phi_{ij}^m\} = \{\phi_{ji}^f\} = \text{diag}\{d, d, d, d\}$, where $d = 0$ or 1. The initial number of pairs was constrained to zero for all possible pairing types. Removal rates for paired individuals—just as those for singles—were held constant at 0.1. For this investigation, the pair dissolution rate, σ , is fixed at 5. A set of runs with 500 realizations each was allowed to simulate the process up to time $t = 6$.¹

We first describe the results for singles. For $d = 0$, the mean population sizes of 500 realizations stabilize at $t \approx 0.6$ (Figure 1, left panel). For $d = 1$, the mean population sizes also stabilize at about the same time, but the stable mean population sizes are smaller than that for $d = 0$, especially for m_4 and f_4 (Figure 1, right panel). The standard deviations increase with time for all groups in a similar way for both values of d , except that there is more fluctuation for m_4 and f_4 when $d = 0$ (Figure 2). Thus, the coefficients of variation also increase with time and those for $d = 0$ are smaller than those for $d = 1$.

The mean number of pairs of 500 realizations also stabilize at $t \approx 0.6$ (Figure 3). Compared with those for $d = 0$, the stable mean numbers of pairs of diagonal types, i.e., m_1f_1, m_2f_2, m_3f_3 , and m_4f_4 , are larger, and those of other types are smaller for $d = 1$. This result confirms that non-zero d in the hypothesized diagonal preference matrix provides a like-with-like mixing pattern, but its impact depends on ξ_i . The

1 All simulations were conducted on Quadra 950 and Quadra 700 Macintosh computers. We used a custom-developed Pascal program optimized for the specific design analyzed here (with four single male groups, four single female groups, and 16 pairing types). Typical simulations took about 4 hours to complete.

standard deviations behave in a similar way except that the difference between $d = 0$ and $d = 1$ for those non-diagonal types are very small (Figure 4). Unlike singles, the standard deviations for pairs don't change so much with time after $t \approx 0.6$ except for the type $m4f4$. Hence, the coefficients of variation fluctuate within a narrow range after $t \approx 0.6$. When $d = 1$, the diagonal types have smaller coefficients of variation, especially for $m1f1$, $m2f2$, and $m3f3$; but the non-diagonal types have slightly larger coefficients of variation. Figure 5 shows the patterns of mean number of pairs, standard deviations and coefficients of variation at time $t = 6$ for $d = 0$ and $d = 1$. It is evident that the value of d plays an important role in the contact structure.

The initial distribution in proportions of group sizes for single males is (19%, 17%, 15%, 50%) corresponding to the four groups, and for single females is (29%, 14%, 7%, 50%). When $d = 0$, the final distributions of single males and females are equal to the initial distributions. In addition, for paired individuals, the final distribution of female partners within each male group is the same as the initial distribution of single females; and the final distribution of male partners for each female group is the same as the initial distribution of single males (Figure 6, top panel). This is because $d = 0$ represents random mixing. Hence, if individuals choose their partners at random, then the final distribution in proportions of who-paired-with-whom is not only random but identical to the initial distribution (the Ross solution). When $d = 1$, we see a different picture (Figure 6, bottom panel) as expected: the diagonal proportions increase and other proportions decrease.

According to properties (A2) and (A3) in Section 2, at all times, $\sum_{j=1}^4 p_{ij}(t) = 1$, $\sum_{i=1}^4 q_{ji}(t) = 1$, and $b_i^m T_i^m(t) p_{ij}(t) = b_j^f T_j^f(t) q_{ji}(t)$ for $i, j = 1, 2, 3, 4$, where $T_i^m(t)$ and $T_j^f(t)$ are the number of single males in group i and single females in group j at time t , respectively. Hence, summing over i and j on both sides of the last equation yields

$$\sum_{i=1}^4 b_i^m T_i^m(t) = \sum_{i=1}^4 \sum_{j=1}^4 b_i^m T_i^m(t) p_{ij}(t) = \sum_{i=1}^4 \sum_{j=1}^4 b_j^f T_j^f(t) q_{ji}(t) = \sum_{j=1}^4 b_j^f T_j^f(t).$$

However, for both values of d , the simulation results show that $\sum_{j=1}^4 p_{ij}(t)$ and $\sum_{i=1}^4 q_{ji}(t)$ are not exactly equal to 1 (but not too far off), and that $\sum_{i=1}^4 b_i^m T_i^m(t)$ and $\sum_{j=1}^4 b_j^f T_j^f(t)$ are not equal when $t > 0$. For $d = 0$, the ratio of $\sum_{j=1}^4 b_j^f T_j^f(t)$ to $\sum_{i=1}^4 b_i^m T_i^m(t)$ sharply increases with time before $t \approx 0.6$, then fluctuates between 1.18 and 1.20, and finally stabilizes at about 1.19; for $d = 1$, the ratio also increases with time before $t \approx 0.6$, then fluctuates between 1.20 and 1.24, and finally stabilizes at about 1.22 (Figure 7). One possible reason for this inequality is that the jump Markov process used for our simulation counts events by integers. Thus, there is never a fraction of any event occurring during the time period between two consecutive events, which is not true for processes in which there is continuous change. Thus, it appears that the biases introduced by the jump Markov process during the initial stages of the simulation are preserved for all future times.

5. Conclusions

In this article we have revisited a general stochastic framework for the modeling of contact structures in biology and epidemiology. An application to demographic models that follow the dynamics of pairs is provided. This framework is so flexible that further applications to other areas of biology, sociology, and demography are possible (Castillo-Chavez *et al.* 1993b).

This research represents our initial efforts in understanding the role of social structures in demography and disease dynamics where stochasticity and partnership preferences play a major role. In the past, most deterministic models assumed a fixed social/behavioral structure, while most stochastic models used the mass-action law. The study of the transmission dynamics of HIV highlighted the limitations of some of these approaches. We have observed a large number of theoretical advances over the last few years (Castillo-Chavez 1989; Jewell *et al.* 1991; Anderson and May 1991; and Hethcote and Van Ark 1992). However, we have just begun to understand the effects of changing preference parameters in contact structures in population dynamics.

The simulation results confirm that non-zero diagonal elements in the preference matrix are associated with like-with-like mixing patterns. If random mixing is assumed, then the final mixing proportions are the same as the initial proportions of singles in different groups, i.e., the Ross solution. Simulation results obtained from using different initial conditions and parameters are provided by Castillo-Chavez *et al.* (1993a) for $d = 0$. The effect of other types of preference matrices (non-diagonal) will be explored in further studies. To reveal the relationship between stochastic and deterministic pair-formation processes, the simulation of an analogous deterministic model is being conducted. In addition, we are also trying to understand the underlying relationship between the male and female preference matrices, $\{\phi_{ij}^m\}$ and $\{\phi_{ji}^f\}$, in a two-sex mixing population.

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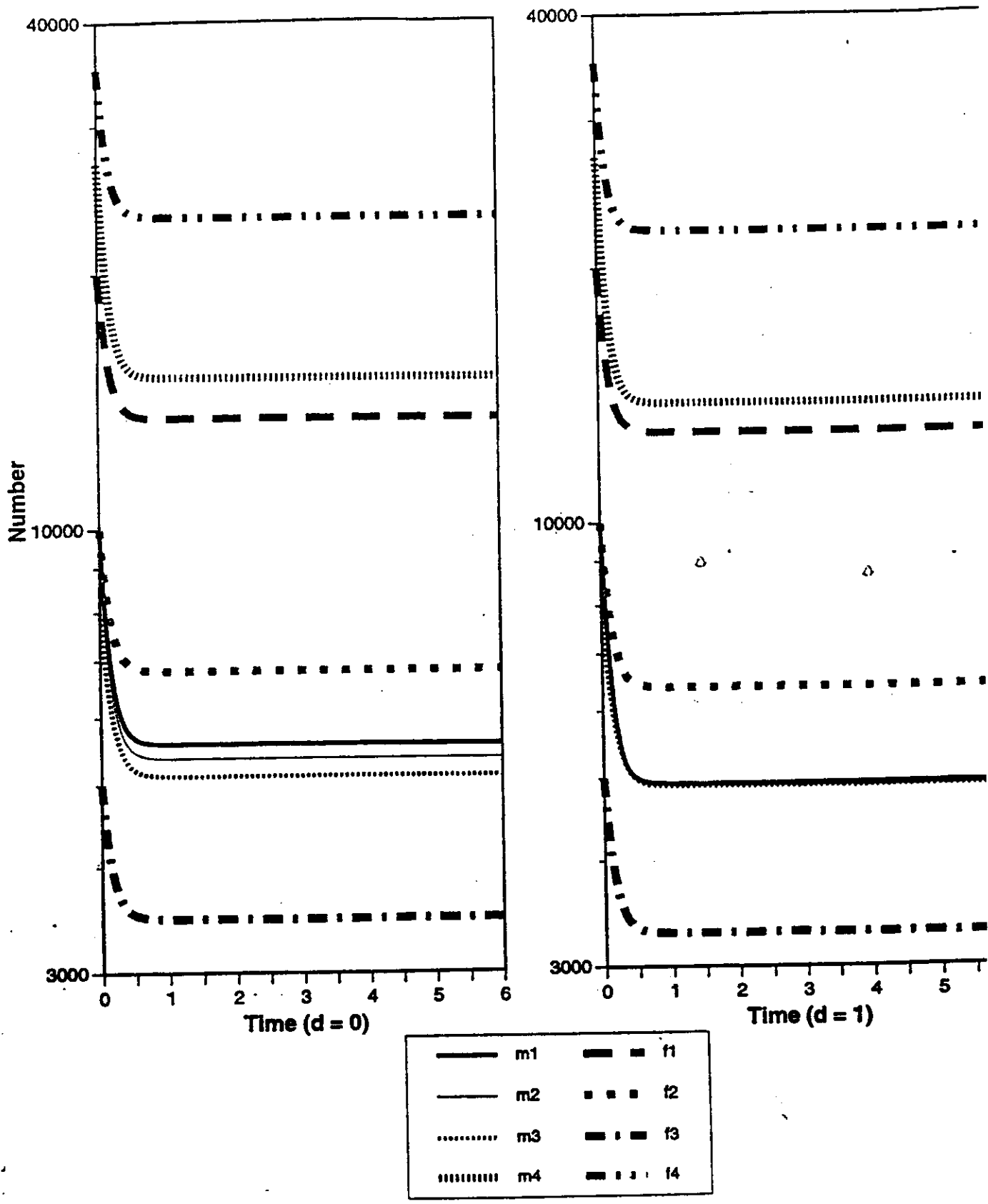


Figure 1. Number of Singles, by Sex and Class. Simulations with $\sigma = 5.0$, $t \leq 6.0$, 500 Realizations, and $d = 0.0$ (Left) or $d = 1.0$ (Right).

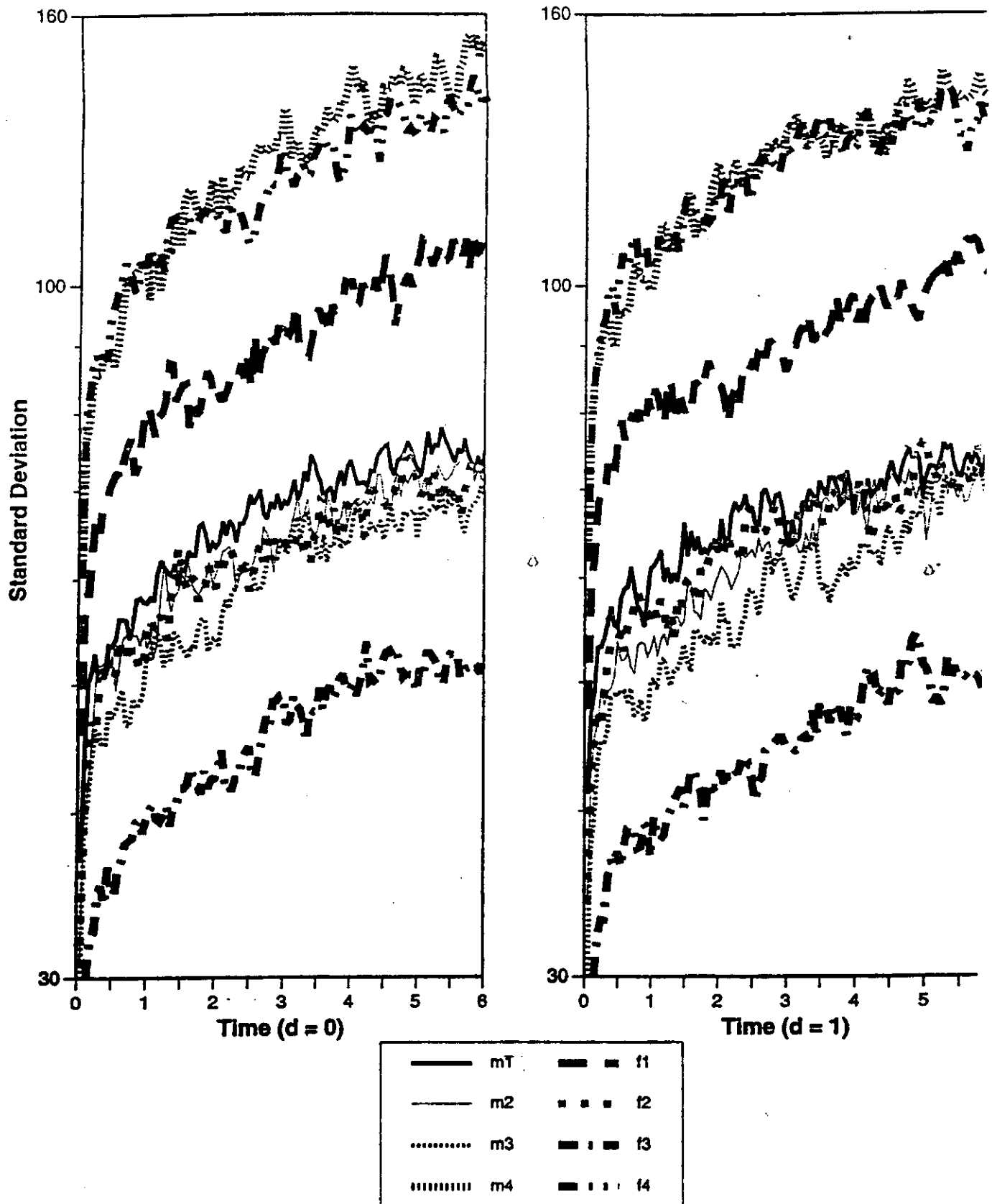


Figure 2. Standard Deviations for Singles, by Sex and Class. Simulations with $\sigma = 5.0$, $t \leq 6.0$, 500 Realizations, and $d = 0.0$ (Left) or $d = 1.0$ (Right).

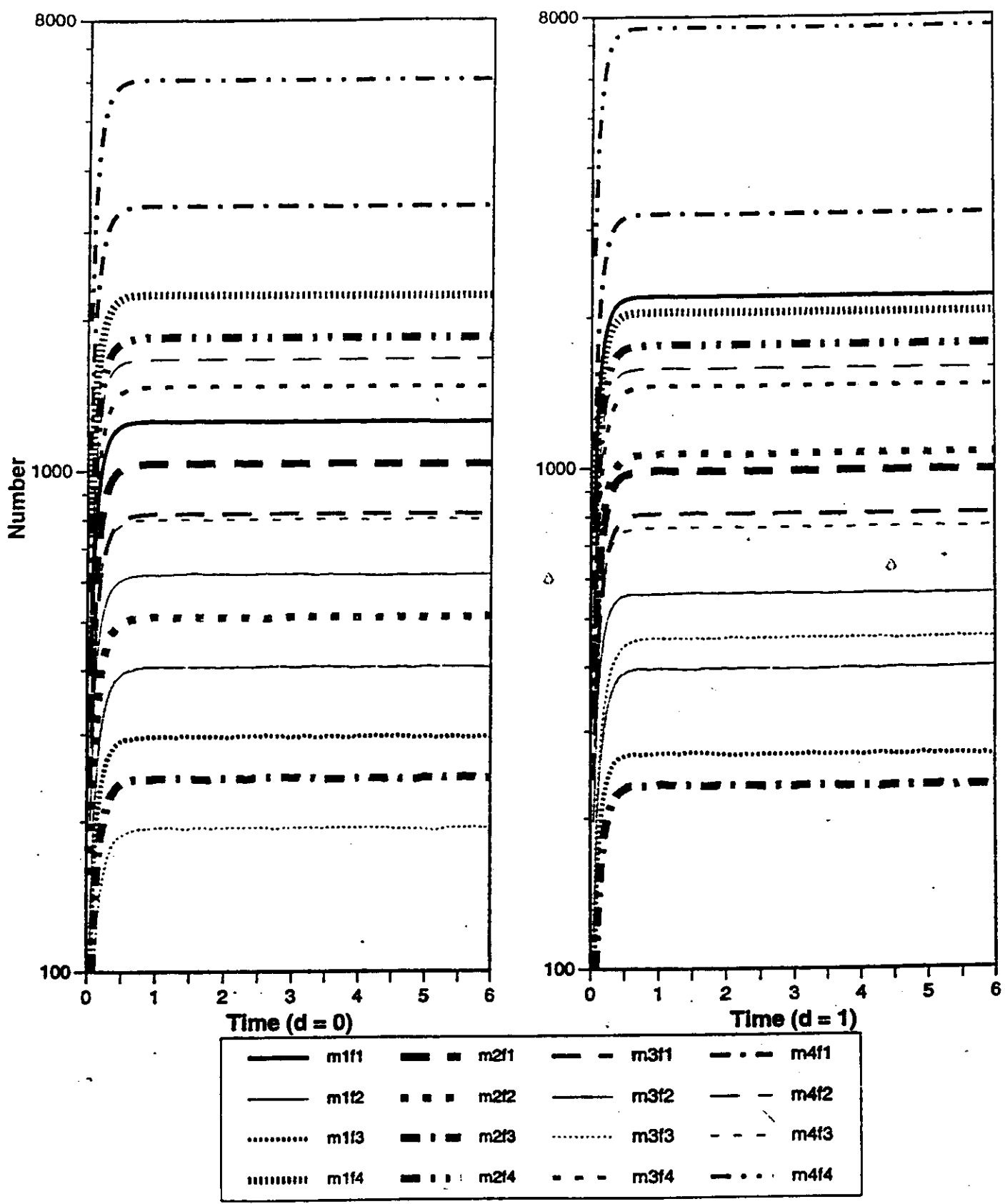


Figure 3. Number of Pairs, by Pair Type. Simulations with $\sigma = 5.0$, $t \leq 6.0$, 500 Realizations, and $d = 0.0$ (Left) or $d = 1.0$ (Right).

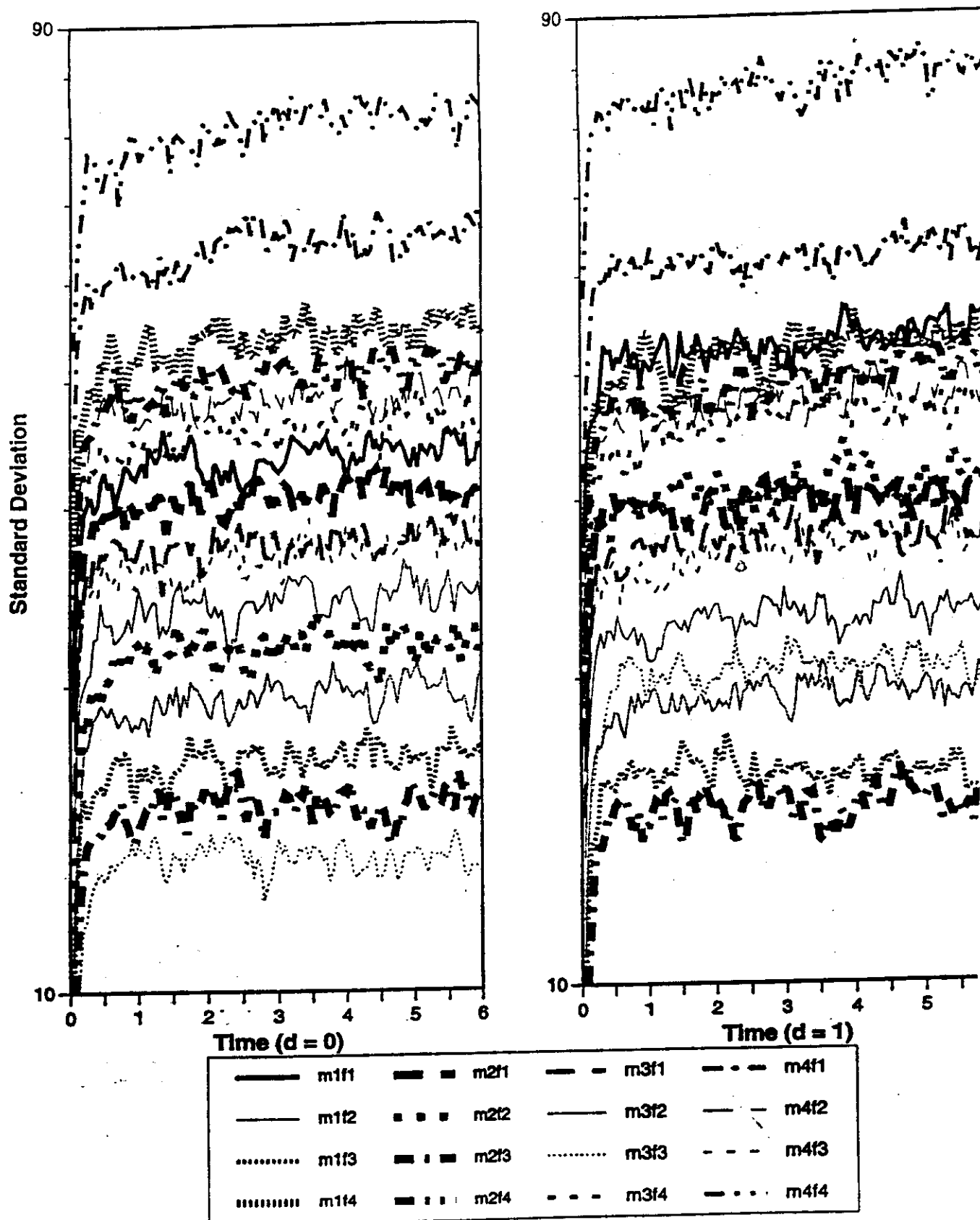


Figure 4. Standard Deviation for Pairs, by Pair-Type. Simulations with $\sigma = 5.0$, $t \leq 6.0$, 500 Realizations, and $d = 0.0$ (Left) or $d = 1.0$ (Right).

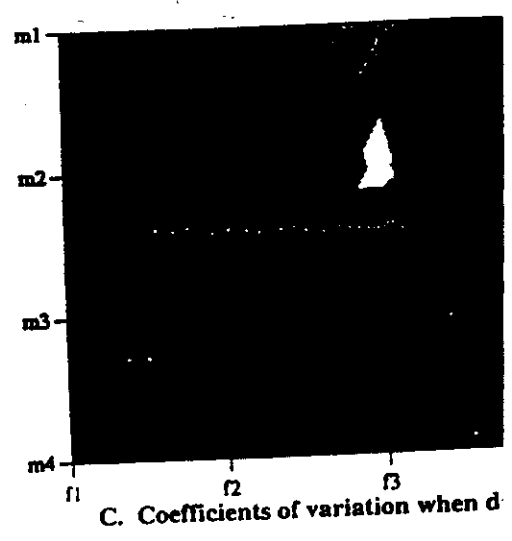
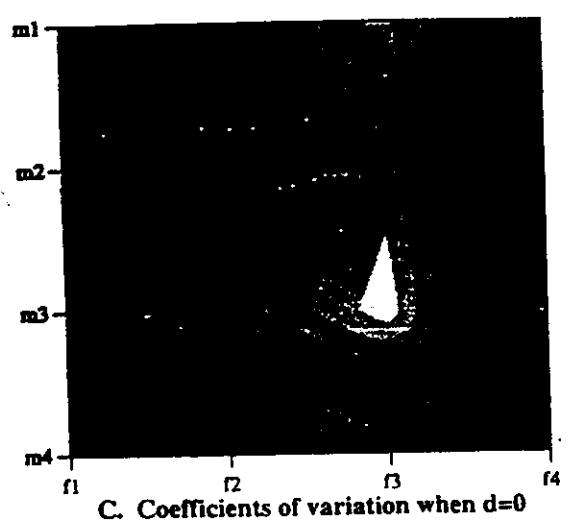
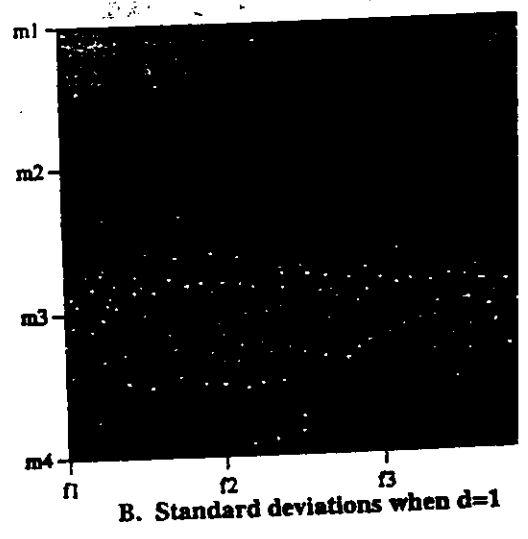
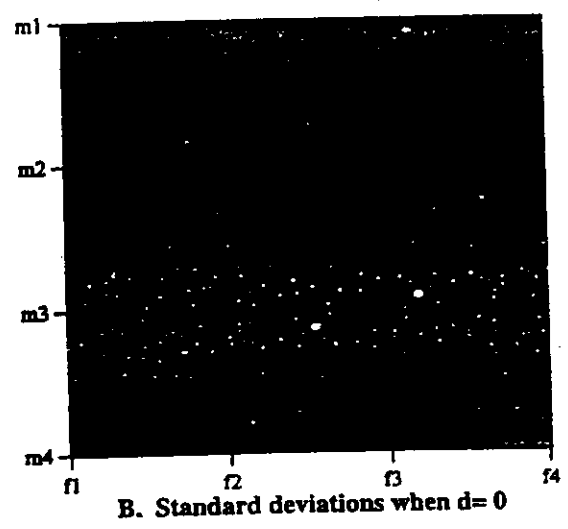
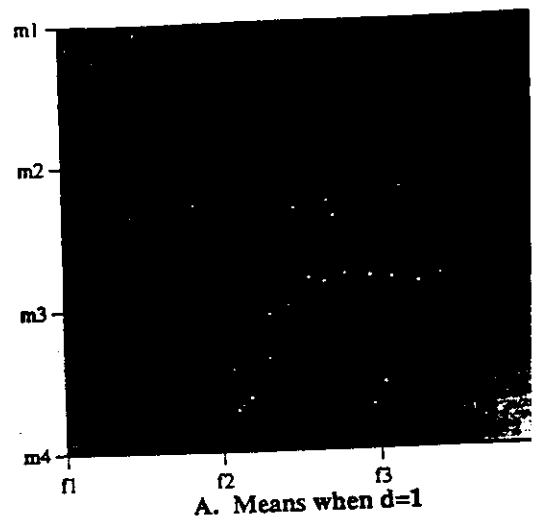
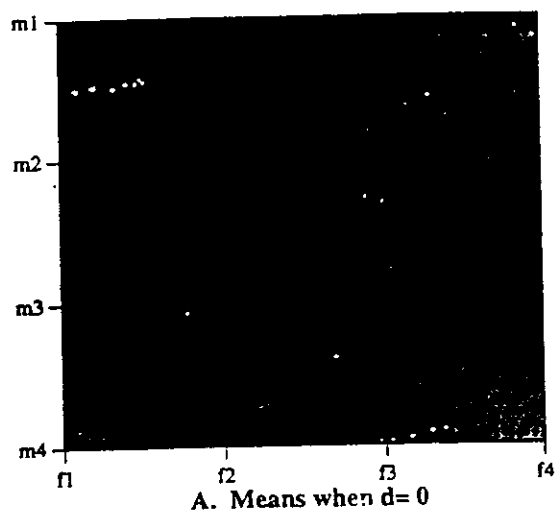


Figure 5. Contour Plots for All Pair Types $\epsilon : t = 6.0$. Simulations with $\sigma = 5.0$, 500 Realizations, and $d = 0.0$ (Left) or $d = 1.0$ (Right).

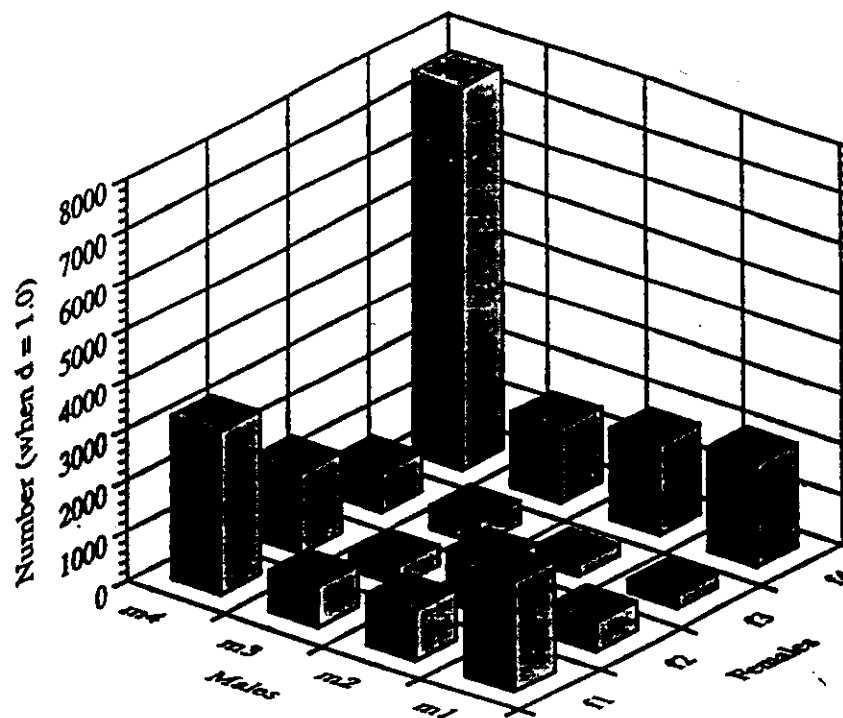
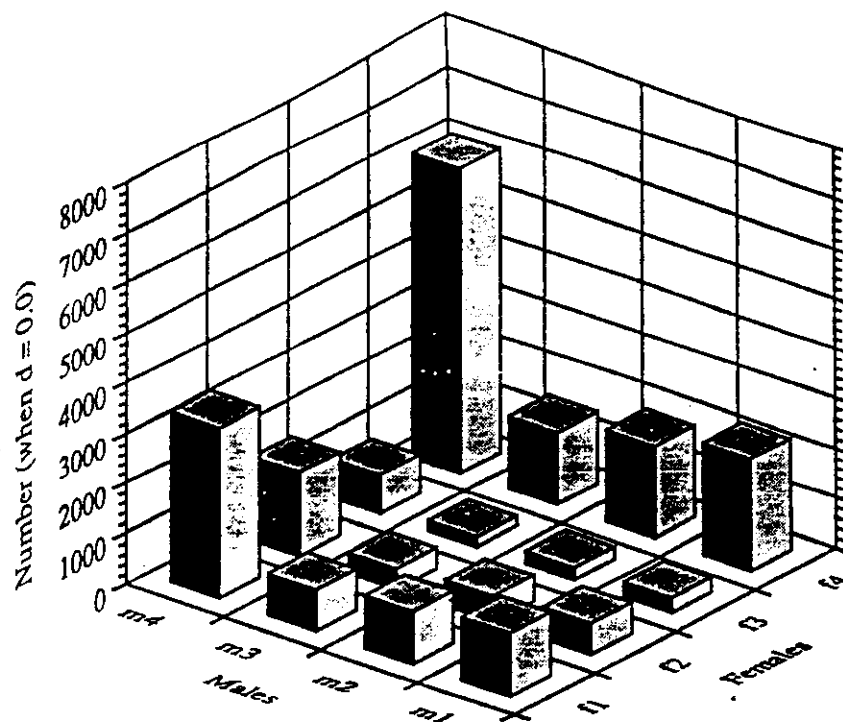


Figure 6. Stable Populations, at $t = 6.0$, by Pair Type. Simulations with $\sigma = 5.0$, 500 Realizations, and $d = 0.0$ (Top) or $d = 1.0$ (Bottom).

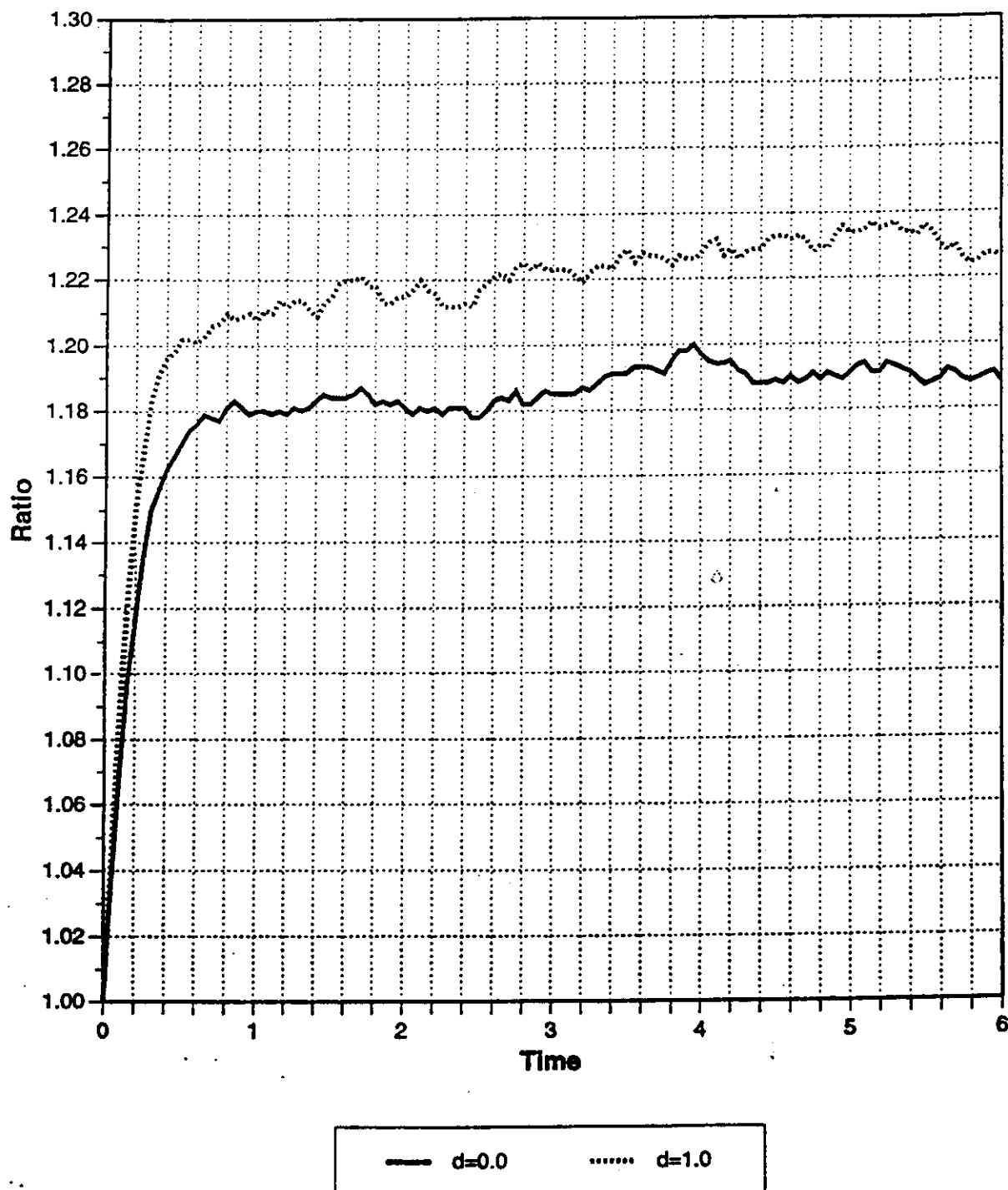


Figure 7. Ratio of $\Sigma b_j T_j^l / \Sigma b_j T_j^m$ Over Time for a Large Population. Simulations with $\sigma = 5.0$, $t \leq 6.0$, 500 Realizations, and $d = 0.0$ or $d = 1.0$.