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Continuous Approximation of Dynamical Systems with Randomly Matched Individuals

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Biologists and economists have analyzed populations in which each individual interacts with randomly selected individuals. Because random matching generates a very complicated stochastic process, biologists and economists frequently approximate the population dynamics by a deterministic process. This paper examines the limit of random matching schemes as the population grows, matches occur very frequently, and the proportion of the population paired in a matching becomes very small. In the limit, the population evolves according to a differential equation. The proof of convergence depends either on the existence of a global attractor or on finiteness of the time horizon. *Journal of Economic Literature* Classification Numbers: C73, C78, D83.

1. INTRODUCTION

Many important models consider large populations with randomly matched individuals.[1] In such models, the matching process is usually not defined, but the stochastic process it generates is assumed to be

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[1] Reference [4] analyzes a game played repeatedly by randomly matched players. Individuals belong to a finite number of types, where a type is defined to be a belief over the strategy the other individuals adopt. References [5, 9] study a market where traders are randomly and pairwise matched. In some job search models (see, for instance, [11]) workers and employees are randomly matched. In biology, genes are randomly matched to determine a phenotype (see, for instance, [3]) and animals are randomly matched against competitors for scarce resources (see, for instance, [8]).

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approximated by a particular deterministic process.[2] The purpose of this paper is to give conditions under which a deterministic process is a good approximation to a random matching process.

In the model, each individual is of a type. Individuals update their types after they are matched to other individuals. Specifically, an individual's new type depends on the type of the matched individual. The random matching process considered in this paper is defined by a population size, the frequency with which individuals are matched, and the proportion of the population paired in each matching.

The approximation results can be stated by considering a sequence of random matching processes. In such a sequence, the population size goes to infinity, the time interval between matches goes to zero, and the proportion of the population paired at each point in time goes to zero. Corresponding to the sequence of random matching processes there is a sequence of trajectories which describe the evolution of each matching process over time. Corollary 1 states that the trajectories converge to the solution of a differential equation. Proposition 1 gives numerical bounds for deviations of the random matching process and allows us to prove Corollary 1 and Proposition 2 (and hence Corollary 2). Corollary 2 gives conditions under which the limiting behavior of the deterministic process approximates the limiting behavior of the random matching process; namely, the differential equation which approximates the random matching process must have a globally stable point. The paper ends with an example where the deterministic process has one locally asymptotically stable stationary point (a sink) and three unstable stationary points. Each unstable stationary point is an absorbing state for the random matching process. Furthermore, for any initial population, the random matching process converges to one of the unstable points in finite time.

Ideally, for all time periods, the deterministic process would be close to the random population process with high probability. However, the approximation deteriorates as the time horizon increases unless the deterministic approximation has a globally stable point. This requirement is a strong one and typically is not satisfied. Consequently, we should be cautious when characterizing random matching processes using results derived from a deterministic process.

This note is closely related to [2], but the results are different because the matching schemes are different. In both cases, individuals behave the

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[2] One exception is [10] who considers an uncountable number of buyers (of measure k) and sellers (of measure 1). The random matching process is such that the probability with which a subset of buyers is matched to a subset of sellers which has measure m is equal to m. Reference [10] proves by a law of large numbers that the proportion of sellers that is not matched to any buyer is e^{-k}. However, such a model cannot be applied to the models listed above where individuals are matched to at most one individual.

same in a given matching. However, the number of matchings in [2] is one per individual, while the number of matchings per individual in this note is random and converges to a Poisson process as the population grows. The limiting deterministic process is different in the two cases, showing that aggregate dynamics are sensitive to the fine structure of the matching process.

This paper considers large, but finite, populations. Reference [2] shows that there is no random matching processes that satisfies a list of apparently innocuous and intuitive requirements when the population is taken to be the natural numbers. Reference [9] points out the same result when the population is indexed by an interval,[3] The urn results used in this paper are a slight modification of the results in [2]. The method of proving the continuous approximation is taken from [13].

2. APPROXIMATION

The population $P(N)$ consists of individuals $\{1, ..., N\}$. Individuals are of m different types, where a generic type is labeled by s_r.

Individuals are randomly pairwise matched at time $t = \alpha(N)$, $2\alpha(N)$, ... At each period, the fraction of the population that is matched is $\alpha(N)$. For instance if $\alpha(N) = 1$, then the entire population is matched at time 1, 2, 3, ... If $\alpha(N) = \frac{1}{2}$, then half of the population is matched at time $\frac{1}{2}$, 1, $\frac{3}{2}$, ... The proportion of the population which is matched and the frequency with which the population is matched are chosen in such a way that, for a time period of length 1, the number of pairs matched is $N/2$.

The random matching scheme works as follows. In each period, individuals are put in a large urn and then drawn in pairs, without replacement. The number of pairs drawn is $\alpha(N)N/2$ (by assumption an integer); individuals drawn together are matched to one another.[4]

If an individual of type s_r is matched with an individual of type $s_{r'}$, the individual of type s_r becomes a type $\tau(s_r, s_{r'})$ while the individual of type $s_{r'}$ becomes a type $\tau(s_{r'}, s_r)$.

Let $p_r^N(k)$ be the proportion of individuals of type s_r after k periods of matchings, when the population size is N. The random matching and the updating rule generate the Markov chain $\{p^N(k)\}$. Let $p_r^N\langle t\rangle$ be the proportion of individuals of type s_r at time t. For $x \in \mathbf{R}$, let $[x]$ be the integer part of x. Then $p^N\langle t\rangle = p^N([t/\alpha(N)])$. Figure 1 illustrates the

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[3] After discussing this result they state "We believe that the conceptual imperfections of this approach are, in principle, properly dealt with by limit theorems." This is exactly the approach taken in this paper.

[4] Let $n^N(t, i)$ be the number of times that individual i has been matched after time t. If $\lim_{N \to \infty} \alpha(N) = 0$, then $n^N(t, i)$ converges to a Poisson process with mean t.

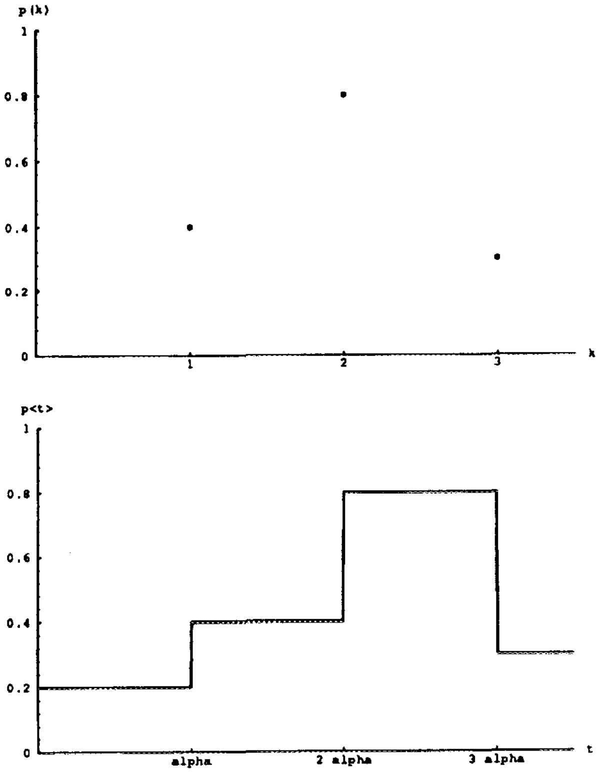

FIG. 1. A realization of $p(k)$ and corresponding $p\langle t\rangle$: $p(k)$ is the proportion of the population of type s_1 after k matchings, $p\langle t\rangle$ is the proportion of the population of type s_1 at time t (after $[t/\alpha]$ periods of matchings). As α converges to 0, $p\langle t\rangle$ converges to the solution of a particular differential equation.

relationship between $p^N(k)$ and $p^N\langle t\rangle$ in a model where there are only two types.

Let $\tau^{-1}(s_r)$ be the set of matches that lead the first individual to be a type s_r; i.e., $\tau^{-1}(s_r) \equiv \{(v, w) : \tau(s_v, s_w) = s_r\}$. Let p_r be the proportion of the population which is of type s_r and let $p = (p_1, ..., p_m)$. Let $F_r(p)$ be the expected change in the proportion of the population which is of type s_r after the next matching time; specifically, $F_r(p) = \sum_{\tau^{-1}(s_r)} p_v p_w - p_r$. Let $p(t)$ be the solution of the differential equation $\dot{p}(t) = F(p(t))$, $p(0) = p^0$, where $p^0 \in \Delta^m$.[5] Such a solution exists and is unique since F is polynomial.

The initial population, $p^N(0)$, is assumed to be deterministic, and for all r, $|p_r^N(0) - p_r^0| < 1/N$.[6]

[5] $\Delta^m = \{p \in \mathbf{R}^m_+ : \sum_r p_r = 1\}$.

[6] We cannot necessarily pick $p_r^N(0) = p_r^0$ because $p_r^N \in \{k/N\}_{k \leq N}$.

Ideally, we would like a result such as $\forall \varepsilon, \delta > 0$, $\exists T^*$, N^* such that $\operatorname{Prob}(\|p(t) - p^N\langle t\rangle\| \geqslant \delta) \leqslant \varepsilon$ for all $t \geqslant T^*$ and $N \geqslant N^*$. This result is false as shown by the example at the end of the paper. Hence, we prove a weaker result, Proposition 1, which is proven in Appendix A.

PROPOSITION 1. *For all* $\delta > 0$ *and* $t \geqslant 0$, *if* $\delta e^{-C_1 t} > C_2 \alpha(N) + 1/N$, *then*

$$\operatorname{Prob}(\|p(t) - p^N\langle t\rangle\| \geqslant \delta) \leqslant \frac{2tm^2(1+m)}{N(\delta e^{-C_1 t} - C_2 \alpha(N) - 1/N)^2},$$

where C_1 *is such that* $\max_r |F_r(p) - F_r(q)| \leqslant C_1 \|p - q\|$ *and* $C_2 = \max_{r,p} |F_r(p)|$.

Note that the probability with which the stochastic process, $\{p^N\langle t\rangle\}$, is within δ of the deterministic process is an increasing function of the population size, N, and a decreasing function of time, t. Furthermore, the size of δ is an increasing function of t and, if $\alpha(N)$ is nonincreasing, a decreasing function of N.

From now on, $\lim_{N \to \infty} \alpha(N) = 0$.

COROLLARY 1. *For all* $t \geqslant 0$ *and* $\delta > 0$, $\lim_{N \to \infty} \operatorname{Prob}(\|p(t) - p^N\langle t\rangle\| \geqslant \delta) = 0$.

Corollary 1 is not strong enough to motivate learning models where an individual updates his type according to the pairings in that period.[7] However, it can be generalized. Let ρ_{rv} denote the proportion of (s_r, s_v) pairs in a matching. The updating rule, $H\colon \mathbf{R}^{m^2} \to \mathbf{R}^m$ is a function of $\rho = (\rho_{vw})$ such that for some $K > 0$, $\max_{r,\rho} \|DH_r(\rho)\| \leqslant K$. Let $F(p) = H(pp^T)$. Then Corollary 1 still holds, as was shown in [1].

Corollary 1 states that the deterministic process approximates the random matching process over bounded time intervals. At the end of the paper, there is an example where the limiting behavior of the two processes is very different. Corollary 2 states that if the deterministic process is globally asymptotically stable, then the limiting behavior of the deterministic process provides a good approximation of the limiting behavior of the random matching process.

Let A^N be the Cesaro average for the random matching process; i.e., for all $B \subset \Delta^m$,

$$A^N(B) = \lim_{K \to \infty} \frac{1}{K} \sum_{k=1}^{K} \operatorname{Prob}(p^N(k) \in B \mid p(0) = p).^8$$

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[7] See, for instance, [6].

[8] This limit always exists as a probability measure because $\{p^N(k)\}$ is a finite Markov chain, as follows simply from [14, p. 541].

The probability measure A^N is invariant; i.e., for all k and B, $A^N(B) = \int \text{Prob}(p^N(k) \in B \mid p(0) = p)\, dA^N(p)$. Since A^N is a probability measure over a compact set, there is a weakly convergent subsequence, $\{A^{N_j}\}$, where $\lim_{j \to \infty} A^{N_j} = A$. Let $G_t(p) = p(t)$, where $p(t)$ is such that $\dot{p}(t) = F(p(t))$, $p(0) = p$.

PROPOSITION 2. *A is an invariant probability measure of G_t; i.e., $A = AG_t^{-1}$.*

Proof. Let $P^N(B \mid p)$ denotes the probability that $p^N\langle t \rangle \in B$ given that $p^N\langle 0 \rangle = p$. By Proposition 1, $P^N(\cdot \mid p)$ converges weakly to $\delta_{G_t(p)}$ uniformly with respect to p. Hence by weak convergence arguments, $\lim_{j \to \infty} \int P^{N_j}\, dA^{N_j} = \int \delta_{G_t(p)}\, dA = AG_t^{-1}$. Therefore, $AG_t^{-1} = \lim_{j \to \infty} \int P^{N_j}\, dA^{N_j} = \lim_{j \to \infty} A^{N_j} = A$. ▮

COROLLARY 2. *Suppose the deterministic process has a globally asymptotically stationary point; i.e., for all initial conditions, $\lim_{t \to \infty} p(t) = \tilde{p}$. Then, $\lim_{N \to \infty} A^N = \delta_{\tilde{p}}$. Consequently, for each neighborhood of $\tilde{p}$, U, if N is large enough, then $p^N(k)$ is outside of U (at most) a finite number of times.*

Proof. Since $\tilde{p}$ is a globally asymptotically stationary point, $\delta_{\tilde{p}}$ is the unique invariant measure, and all convergent subsequences $\{A^{N_j}\}$ converge to $\delta_{\tilde{p}}$. Therefore, $\{A^N\}$ converges to $\delta_{\tilde{p}}$. ▮

Corollary 2 cannot be extended to the case where the deterministic process is only localy asymptotically stable. For instance, suppose there are six different types. Types are updated as follows: $\tau(s_1, s_1) = \tau(s_1, s_2) = s_1$, $\tau(s_1, s_3) = s_6$, $\tau(s_2, s_1) = s_4$, $\tau(s_2, s_2) = \tau(s_2, s_3) = s_2$, $\tau(s_3, s_1) = \tau(s_3, s_3) = s_3$, $\tau(s_3, s_2) = s_5$, for $i \in \{1, 2, 3\}$, j, $k \in \{4, 5, 6\}$, where $j \neq k$, $\tau(s_j, s_i) = \tau(s_i, s_j) = \tau(s_j, s_j) = s_{j-3}$, and $\tau(s_j, s_k) = s_j$.

In the deterministic process $\tilde{p}_1 = \tilde{p}_2 = \tilde{p}_3 = (3 + 3\sqrt{13})/54$, $\tilde{p}_4 = \tilde{p}_5 = \tilde{p}_6 = (1/3) - (3 + 3\sqrt{13})/54$ is a sink; i.e., $\tilde{p}$ is a stationary point and all the eigenvalues of DF have negative real parts. Thus (see [7, p. 181]) there is a neighborhood $U \subset \Delta^6$ of $\tilde{p}$ such that if $p(0) \in U$, then for some positive constants B and c and for all t, $|p(t) - \tilde{p}| \leqslant Be^{-tc} |p(0) - \tilde{p}|$. The other stationary points, $e_1 = (1, 0, 0, 0, 0, 0)$, $e_2 = (0, 1, 0, 0, 0, 0)$, $e_3 = (0, 0, 1, 0, 0, 0)$, are unstable (this follows from the fact that DF has a positive eigenvalue and the corollary in [7, p. 187]).

For any population $p^N(k)$ we can construct a finite number of matchings after which all individuals are of one type (which could be s_1, s_2, or s_3). Furthermore, for any population size we can find a lower bound for such a probability (see Appendix B). Therefore, in finite time, the population becomes of only one type. Consequently, if $\{A^{N_j}\}$ converges, then $\lim_{j \to \infty} A^{N_j} = \alpha\delta_{e_1} + \beta\delta_{e_2} + \gamma\delta_{e_3}$, for some nonnegative constants α, β, γ.

APPENDIX A

This section proves Proposition 1. The proof makes use of Lemma 1.

LEMMA 1. *For large N,*

$$E[p_r^N(k+1) - p_r^N(k) \mid p^N(k)] = \alpha(N)\, F_r(p^N(k))$$

$$\mathrm{Var}[p_r^N(k+1) - p_r^N(k) \mid p^N(k)] \leqslant 2m(m+1)\,\frac{\alpha(N)}{N}.$$

Proof (*Lemma*). Consider the subpopulation consisting of the $\alpha(N)N$ individuals drawn. Let $x_i = 1$ if the ith pair is of type (s_r, s_v) and zero otherwise. Let ρ_{rv}^N denote the proportion of (s_r, s_v) matches; i.e.,

$$\rho_{rv}^N = \frac{2}{\alpha(N)N} \sum_i x_i.$$

Note that the random variables $\{x_i\}_i$ are exchangeable. Thus,

$$E\left(\sum_i x_i\right) = \sum_i E(x_i) = \frac{\alpha(N)N}{2}\, E(x_1).$$

Let N be large enough so that the terms $p_r N - 1$, $p_r N - 2$, $p_r N - 3$ can be approximated by $p_r N$. Then

$$E(x_1) = \frac{p_r N}{N}\,\frac{p_v(N - \delta_{rv})}{N-1} \approx p_r p_v$$

and

$$E(\rho_{rv}^N) \approx \frac{2}{\alpha(N)N}\,\frac{\alpha(N)N}{2}\, p_r p_v = p_r p_v.$$

Note that $x_i^2 = x_i$. Then, by exchangeability of the random variables $\{x_i x_j\}_{j \neq i}$,

$$\begin{aligned}\mathrm{Var}\left(\sum_i x_i\right) &= E\left[\left(\sum_i x_i\right)^2\right] - \left[E\left(\sum_i x_i\right)\right]^2\\ &= \sum_{i \neq j} E(x_i x_j) + E\left(\sum_i x_i\right) - \left[E\left(\sum_i x_i\right)\right]^2\\ &= \frac{\alpha(N)N}{2}\left(\frac{\alpha(N)N}{2} - 1\right) E(x_1 x_2) + E\left(\sum_i x_i\right) - E\left[\left(\sum_i x_i\right)\right]^2.\end{aligned}$$

Since

$$E(x_1 x_2) = \frac{p_r N}{N} \frac{p_v N - \delta_{rv}}{N-1} \frac{p_r N - 1 - \delta_{rv}}{N-2} \frac{p_v N - 1 - 2\delta_{rv}}{N-3} \approx p_r^2 p_v^2,$$

then

$$\operatorname{Var}(\rho_{rv}^N) \approx \frac{4}{\alpha(N)^2 N^2} \left\{ \frac{\alpha(N) N}{2} \left(\frac{\alpha(N) N}{2} - 1 \right) p_r^2 p_v^2 \right.$$

$$\left. + p_r p_v \frac{\alpha(N) N}{2} - p_r^2 p_v^2 \frac{\alpha(N)^2 N^2}{4} \right\}$$

$$= \frac{2}{\alpha(N) N} p_r p_v (1 - p_r p_v).$$

If the individuals are matched according to $\{\rho_{rv}\}$, then

$$p_r^N(k+1) = \sum_{\tau^{-1}(s_r)} \alpha(N)\ \rho_{vw}^N(k) + p_r^N(k) - \alpha(N) \sum_{v} \rho_{rv}^N(k).$$

Consequently,

$$E[p_r^N(k+1) - p_r^N(k) \mid p^N(k)] = \alpha(N) \sum_{\tau^{-1}(s_r)} p_v^N(k)\ p_w^N(k) - \alpha(N)\ p_r^N(k)$$

$$= \alpha(N)\ F_r(p^N(k)).$$

Since $\operatorname{Cov}(X, Y) \leqslant \max\{\operatorname{Var}(X), \operatorname{Var}(Y)\}$,

$$\operatorname{Var}[p_r^N(k+1) - p_r^N(k) \mid p^N(k)] \leqslant \alpha(N)^2\ m(m+1) \max_{rv} \operatorname{Var}(\rho_{rv}^N)$$

$$\leqslant \alpha(N)^2\ m(m+1) \frac{2}{\alpha(N) N}. \quad \blacksquare$$

By definition, $p_r(t) = p_r^0 + \int_0^t F_r(p(u))\, du$. Note that

$$\int_0^{k\alpha(N)} F_r(p^N \left(\left[\frac{u}{\alpha(N)} \right] \right) \Big) du = \sum_{s=0}^{k-1} \int_{s\alpha(N)}^{(s+1)\alpha(N)} F_r \left(p^N \left(\left[\frac{u}{\alpha(N)} \right] \right) \right) du$$

$$= \sum_{s=0}^{k-1} \alpha(N)\ F_r(p^N(s)).$$

Let $\{m_r(k)\}$ be the martingale defined by

$$m_r(k) = p_r^N(k) - p_r^N(0) - \sum_{s=0}^{k-1} E[p_r^N(s+1) - p_r^N(s) \mid p^N(s)].$$

Thus,

$$\begin{aligned} p_r^N(k) &= m_r(k) + p_r^N(0) + \sum_{s=0}^{k-1} E[p_r^N(s+1) - p_r^N(s) \mid p^N(s)] \\ &= m_r(k) + p_r^N(0) + \alpha(N) \sum_{s=0}^{k-1} F_r(p^N(s)) \\ &= m_r(k) + p_r^N(0) + \int_0^{k\alpha(N)} F_r\left(p^N\left(\left[\frac{u}{\alpha(N)}\right]\right)\right) du. \end{aligned}$$

Let C_1 be such that $\max_r |F_r(p) - F_r(q)| \leqslant C_1 \|p - q\|$, let $C_2 = \max_{r,p} F_r(p)$, and set $k = [t/\alpha(N)]$. Then

$$\begin{aligned} \left|p_r(t) - p_r^N\left(\left[\frac{t}{\alpha(N)}\right]\right)\right| &\leqslant |m_r(k)| + \int_0^t \left|F_r(p(u)) - F_r\left(p^N\left(\left[\frac{u}{\alpha(N)}\right]\right)\right)\right| du \\ &\quad + |p_r^N(0) - p_r^0| + \int_{k\alpha(N)}^t \left|F_r\left(p^N\left(\left[\frac{u}{\alpha(N)}\right]\right)\right)\right| du \\ &\leqslant |m_r(k)| + \frac{1}{N} \\ &\quad + C_1 \int_0^t \left\|p(u) - p^N\left(\left[\frac{u}{\alpha(N)}\right]\right)\right\| du + C_2\alpha(N). \end{aligned}$$

Let $M^2(k) = \max_r m_r^2(k)$. Then

$$\begin{aligned} \left\|p(t) - p^N\left(\left[\frac{t}{\alpha(N)}\right]\right)\right\| &\leqslant M(k) + \frac{1}{N} + C_2\alpha(N) \\ &\quad + C_1 \int_0^t \left\|p(u) - p^N\left(\left[\frac{u}{\alpha(N)}\right]\right)\right\| du. \end{aligned}$$

Gronwall's lemma (see [12, p. 499]) states that if ϕ is a locally bounded Borel function of $\mathbf{R}_+$ such that for all t, $\phi(t) \leqslant a + b\int_0^t \phi(s)\,ds$, then $\phi(t) \leqslant ae^{bt}$. Letting $\phi(t) = \|p(t) - p^N([t/\alpha(N)])\|$, we get that

$$\left\|p(t) - p^N\left(\left[\frac{t}{\alpha(N)}\right]\right)\right\| \leqslant \left[M(k) + \frac{1}{N} + C_2\alpha(N)\right] e^{C_1 t}.$$

By Lemma 1, $E(M^2(k)) \leqslant 2km^2(1+m)\,\alpha(N)/N$. Chebychev's inequality states that for all $\eta > 0$, $P(|\xi| \geqslant \eta) \leqslant E\xi^2/\eta^2$. Thus if $\delta e^{-C_1 t} > C_2\alpha(N) + 1/N$, then

$$\begin{aligned}\operatorname{Prob}\left(\left\|p(t) - p^N\left(\left[\frac{t}{\alpha(N)}\right]\right)\right\| \geqslant \delta\right) &\leqslant \operatorname{Prob}\left(M(k) \geqslant \delta e^{-C_1 t} - C_2\alpha(N) - \frac{1}{N}\right)\\ &\leqslant \frac{2km^2(1+m)\,\alpha(N)}{N(\delta e^{-C_1 t} - C_2\alpha(N) - 1/N)^2}\\ &\leqslant \frac{2tm^2(1+m)}{N(\delta e^{-C_1 t} - C_2\alpha(N) - 1/N)^2}.\end{aligned}$$

APPENDIX B

This section examines the example at the end of the paper and computes the lower bound for the probability with which the population converges, in a finite number of periods, to one of the unstable stationary points.

In order to make the probability as small as possible, suppose $\alpha(N)N = 2$. First we show how we get to a situation where for some $i \in \{1, 2, 3\}$, $p_i(k) + p_{i+3}(k) = 0$. Without loss of generality, pick $i = 2$.

First we eliminate type s_5 by matching each individual of type s_5 against another individual of type s_5 (if there is only one individual of type s_5 left, this individual is matched against an individual of type s_2). This takes less than $N/2$ periods. The probability of such a sequence of matchings is greater that N^{-N}. Then we eliminate s_2 by matching each individual of type s_2 with an individual of type s_1. Again, this step takes less than $N/2$ periods and the probability of such a sequence of matchings is greater than N^{-N}.

Next we show that if for some $i \in \{1, 2, 3\}$, $p_i(k) + p_{i+3}(k) = 0$, then we can get to a situation where for some $j \in \{1, 2, 3\}$, $p_j = 1$.

Suppose $p_2 + p_5 = 0$. First we eliminate type s_4 by matching each individual of type s_4 against another individual of type s_4 (and if this is not possible, then against an individual of type s_1). Then we match each invidual of type s_1 against an individual of type s_3. This takes at most N periods and occurs with probability greater than N^{-2N}.

Hence, the whole population is of only one type in less than $2N$ periods with probability greater than N^{-4N}.

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