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LAWS OF LARGE NUMBERS FOR DYNAMICAL SYSTEMS  
WITH RANDOMLY MATCHED INDIVIDUALS

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## Abstract

Biologists and economists have analyzed populations where each individual interacts with randomly selected individuals. The random matching generates a very complicated stochastic system. Consequently evolutionary biologists have approximated such a system by a deterministic system. The justification of such an approximation is that the population is assumed to be very large and thus some law of large numbers must hold. In this paper we give an example for which this assumption does not hold. We then show that if we assume that the population is infinite then the stochastic and the deterministic system are the same. Finally, we show that if the process lasts finitely many periods and if the population is large enough then the deterministic model offers a good approximation of the stochastic model. In doing so we make precise what we mean by population, matching process, and evolution of the population.

# LAWS OF LARGE NUMBERS FOR DYNAMICAL SYSTEMS WITH RANDOMLY MATCHED INDIVIDUALS

Richard T. Boylan \*

## 1 Introduction

There is a large literature (see below) that studies dynamical system with individuals randomly matched in pairs, although the particular way with which people are matched is left unspecified. In this paper we describe ways of matching individuals and the properties of such matching schemes.

Fudenberg and Levine (1990) examine a model where there are  $n$  populations; each population consists of  $m$  different types where each type consists of a belief over what strategy the other individuals adopt. The proportion of population  $i$  that is of type  $j$  is denoted by  $p_{ij}$ . Every period each player from a population  $i$  is randomly and independently matched with one individual from every other population  $i'$  ( $i' \neq i$ ). Fudenberg and Levine assume that the probability with which a player meets a player from population  $i'$  and of type  $j$  is  $p_{i'j}$ . The randomly matched individuals play a game selecting strategies according to their beliefs and updating their beliefs according to the observed strategy choices of the other players. Fudenberg and Levine go on to characterize the steady states of the dynamics.

This type of model is very similar to the models that have been studied extensively in population genetics and evolutionary biology. <sup>1</sup> This similarity has led to a large literature on the application of evolutionary biology to game theory. <sup>2</sup> In this paper we assume that there is a large population. Each individual is matched anonymously to

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<sup>1</sup>Appendix C contains a brief discussion of these models.

<sup>2</sup>See Boylan (1990) and references therein.

exactly one other individual. There are  $m$  types of individuals. We keep the terminology vague so that the model can be applied to economics (where types are beliefs), evolutionary biology (where types are strategies), and to population genetics (where types are genotypes or alleles). The set of types is denoted by  $S$ , where

$$S = \{s_1, \dots, s_m\}.$$

The initial proportion of the population of type  $s_r$  is denoted by  $p_r$ ; we assume throughout that, for all  $s_r$  in  $S$ ,  $p_r$  is positive. The initial distribution of types in the population is denoted by  $p$  where  $p = (p_1, \dots, p_m)$ . Underlying the models we have mentioned is the conjecture that if the population is very large (possibly infinite) there exists a matching scheme such that for all types  $s_r$  and  $s_v$  the proportion of individuals of type  $s_r$  that are matched with individuals of type  $s_v$  is  $p_r p_v$  (almost surely).

In this paper we further assume that the matching scheme is implemented infinitely often and each individual's type is allowed to change in between periods. Again, underlying the models we mentioned is the conjecture that in every period the set of individuals adopting the same strategy is matched with the population average. This paper proves that there is a matching rule for which both conjectures are correct when individuals are represented by the set of natural numbers. Thus this paper answers the following questions that are usually left unanswered in the literature: How is the population characterized? What is the structure of the matching process? How are types assigned to individuals? What do we mean by each subpopulation facing the distribution of types equal to the population distribution? How do we characterize the evolution of the population from the random matching scheme?

Section 2 gives an example of how the dynamics for very large populations differs from the dynamics for infinite populations. Section 3 describes the problem of finding a matching technology for infinite populations such that all matches are equally likely. Section 4 proves the first conjecture. Sections 5 and 6 prove the second conjecture. Section 7 examines a matching scheme for finite populations. Appendix A briefly discusses the literature on the law of large numbers for a continuum of agents. Appendix C gives a brief overview of the biological literature related to matching schemes.

## 2 Matches over very large populations

A natural argument for supporting the conjecture in the introduction is the following: if the population is of size  $n$  then the probability that the matching rule does not behave as its expectation is  $q(n)$ . By the law of large numbers  $q(n)$  can be made arbitrarily small by taking  $n$  large. In other words for large populations the conjecture is approximately correct. As we will see in Section 7 this argument can be formalized if the matching scheme occurs finitely many times. In many cases, however, the matching scheme analyzed occurs infinitely many times, and it is thus possible that the small perturbations that occur in each period alter the process significantly in the limit. We construct an

example where this problem actually occurs. The example is taken from evolutionary biology because: (i) such models are very important in evolutionary biology, (ii) several economists have applied evolutionary models to game theory, and (iii) the mathematics in this example are very tractable.

Suppose that there is a population consisting of  $3M$  individuals (where  $M$  is an even number). Individuals have a very simple life: they are born at time  $t$  they interact with one randomly selected individual, give birth to new individuals and die at time  $t+1$ . The matching scheme is left unspecified but we assume that all matches occur with positive probability.<sup>3</sup> Individuals belong to three different types: 1,2,3. If an individual of type  $r$  interacts with an individual of type  $v$  then this individual has  $a_{rv}$  offsprings. All offsprings are of the same type as the parent. Suppose that the matrix  $A = (a_{vw})$  is as follows:

$$A = \begin{pmatrix} 1 & 2 & 0 \\ 0 & 1 & 2 \\ 2 & 0 & 1 \end{pmatrix}.$$

First notice that the population size stays constant: if individuals of type  $s_v$  and  $s_w$  meet they will have together  $2 = a_{vw} + a_{wv}$  offsprings and thus keep the population constant. Notice that, because of the 0 entry in the matrix  $A$ , at any period  $t$  there is a positive probability that one of the types disappears, which we denote by  $q_e^t$ . For any population distribution among types  $(M_1, M_2, M_3)$  (where  $M_1 + M_2 + M_3 = 3M$ ) there exists a set of matches for which one of the types totally disappears. Since all matches are possible these matches will have positive probability. Denote the probability that one type disappears when the population distribution is  $(M_1, M_2, M_3)$  by  $q_{M_1, M_2, M_3}$ . Let

$$q_e = \min_{\{(M_1, M_2, M_3) | M_1 + M_2 + M_3 = 3M\}} q_{M_1, M_2, M_3}.$$

Then, for all  $t$ ,  $q_e^t \geq q_e > 0$ .

Notice that if a type disappears it never comes back. Consequently, if the matching scheme is repeated infinitely often, the probability that a type will disappear is greater than

$$1 - \lim_{t \rightarrow \infty} (1 - q_e)^t = 1.$$

Let  $B_t$  be the set of events for which the trajectory attains one of the boundaries of the simplex by time  $t$ . From the previous remarks  $\{B_t\}$  is an increasing sequence and  $\lim_{t \rightarrow \infty} P(B_t) = 1$ ; therefore one of the types disappears in finite time. It is easy to see that if type  $s_v$  disappears then the population will converge to a population composed uniquely of individuals of type  $s_{v+1 \pmod{3}}$  (almost surely). Therefore the population will converge to one of the vertices of the simplex in finite time (almost surely). Since this result is true irrespective of the population size  $3M$ , it will also be true as  $M$  tends to infinity.

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<sup>3</sup>One way of describing the random matching scheme is to think of individuals as being drawn successively (without replacement) from an urn. The first and second individuals drawn are matched together, the third and fourth individuals drawn are matched together, and so on.

Let  $p_v$  be the proportion of the population of type  $s_v$ . In evolutionary biology the evolution for the population is analyzed according to the replicator model. The replicator model assumes that a proportion  $2p_v p_w$  of the matches are between individuals of type  $s_v$  and  $s_w$ . Then the proportion of the population of type  $i$  at time  $t + 1$  is related to the population at time  $t$  in the following way:

$$p_r^{t+1} = R_r(p^t) \equiv p_r^t \frac{\sum_v p_v^t a_{rv}}{\sum_v \sum_w p_v^t a_{vw} p_w^t}. \quad (1)$$

First suppose that the initial population is composed of a third of each type. Then the population will remain at the barycenter contrary to the behavior of the population when we examined the random matching rule.

Next suppose that the initial population is not distributed equally among each type. The interior of the simplex is invariant under the map  $R$ . Thus if a trajectory starts in the interior of the simplex it cannot reach the boundary in finite time. Also the vertices of the simplex are repellors for the dynamics on the interior of the simplex. Let  $W: \Delta^3 \rightarrow \mathbf{R}$  be such that  $W(p) = \frac{1}{p_1 p_2 p_3}$ . Weising (1989) shows that  $W$  has a unique minimum at the barycenter and that along any trajectory  $W$  is strictly increasing. Thus the trajectory approaches the boundary of the simplex asymptotically. By looking at the law of motion we can see that the trajectory oscillates from a neighborhood of  $(1, 0, 0)$ , to a neighborhood of  $(0, 1, 0)$ , to a neighborhood of  $(0, 0, 1)$  and so on and that the time the trajectory takes to go from one neighborhood to another is increasing. Thus for any period  $T$  there is a period  $t > T$  such that  $p^t$  is far removed from any of the vertices and the  $\omega$ -limit (the set of accumulation points) of the trajectory is the whole boundary.

### 3 Matches over countably infinite number of agents

This section introduces the notation that will be used in this paper and discusses the problems of finding a random matching scheme for an infinite population. We assume that the population is countably infinite and is denoted by

$$\mathbf{N} = \{1, 2, \dots, n, \dots\}.$$

For convenience we represent the type space by the standard basis for  $\mathbf{R}^m$ ; i.e.,  $s_r$  is the  $m$  dimensional vector with a one on the  $r^{\text{th}}$  component and zeros on the other components. Let

$$\alpha: \mathbf{N} \rightarrow S \text{ be such that } \lim_{T \rightarrow \infty} \frac{1}{T} \sum_{i=1}^T \alpha(i) = p.$$

If  $\alpha(i) = s_v$  then individual  $i$  is of type  $s_v$ . The  $v^{\text{th}}$  component of the vector  $p$ ,  $p_v$ , represents the proportion of the population of type  $s_v$ .

Let  $\Sigma$  be the set of all possible pairwise matchings; i.e.,

$$\Sigma = \{\sigma: \mathbf{N} \rightarrow \mathbf{N} \mid \sigma \text{ is bijective and for all } i, \sigma^2(i) = i \text{ and } \sigma(i) \neq i\}.$$

A few remarks on the conditions that characterize  $\Sigma$ . The first condition says that each individual is matched exactly once. The second condition says that: ‘if John is matched with Paul then Paul is matched with John.’ The third condition states that an individual cannot be matched to himself.

We first show that there does not exist a probability space  $(\Sigma, \mathcal{F}, P)$  such that for all distinct players  $i, j, k \in \mathbf{N}$ , the event that player  $i$  is matched with player  $j$  and the event that player  $i$  is matched with player  $k$  are equally likely. Suppose that  $(\Sigma, \mathcal{F}, P)$  is such a probability space. Denote the probability that player  $i$  is matched with player  $j$  by

$$p(\sigma(i) = j) \equiv P(\{\sigma \in \Sigma \mid \sigma(i) = j\}).$$

In order for  $p$  to be well defined we need to assume that for all individuals  $i, j \in \mathbf{N}$ ,

$$\{\sigma \in \Sigma \mid \sigma(i) = j\} \in \mathcal{F}. \quad (2)$$

Suppose that  $p(\sigma(i) = j) \equiv q > 0$ . Notice that since each individual is matched once, the sets  $\{\sigma \in \Sigma \mid \sigma(i) = j\}$  and  $\{\sigma \in \Sigma \mid \sigma(i) = k\}$  are disjoint. Thus

$$p(\sigma(i) \in \mathbf{N}) = p\left(\bigcup_{j \in \mathbf{N}} \sigma(i) = j\right) = \sum_{j \in \mathbf{N}} p(\sigma(i) = j) = \infty.$$

This clearly contradicts the definition of a probability. Alternatively, if  $q = 0$  then  $p(\sigma(i) \in \mathbf{N}) = 0$  which is not consistent with the fact that individual  $i$  is matched once.

Clearly the assumption in equation 2 and the assumption that all matches are equally likely lead to this contradiction. In order to weaken the set of measurable sets we need to find another way to express the idea that all matches are equally likely. Alternatively, we could relax the assumption that all matches are equally likely. <sup>4</sup>

## 4 Construction of a probability measure over matches

In this section we will construct a probability space over the set of matches by considering the events: ‘the set of matches such that individual  $i$  is matched with an individual of type  $s_v$ ’ ( $\forall i \in \mathbf{N}, \forall s_v \in S$ ). We construct the probability space in an indirect way. First we define a probability over the space  $S^{\mathbf{N}}$ , which we call ‘the set of realizations of matches.’ The probability space  $(S^{\mathbf{N}}, \mathcal{B}, \mu)$  is defined by the property that the probability with which  $x_i$  (where  $x \in S^{\mathbf{N}}, i \in \mathbf{N}$ ) equals  $s_v$  is the proportion of individuals in the population of type  $s_v$ ,  $p_v$  (for all  $s_v \in S$ ). Then we show that this probability space generates a probability space over matches,  $(\Sigma, \mathcal{F}_\alpha^2, P_\alpha^2)$ . Thus calling elements in  $S^{\mathbf{N}}$  realizations of matches is justified since they can be derived from a probability over matches. This probability space is the  $(P_\alpha^2)$  unique probability space for which each individual expects to be matched with the population average. For this probability space

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<sup>4</sup>Another approach is to assume that there is a continuum of agents. A brief discussion of this approach is contained in Appendix A.

the set of events ‘individual  $i$  is matched with individual  $j$  is not measurable.’ If we let these events be measurable, as in the probability space  $(\Sigma, \mathcal{F}_\alpha^1, P_\alpha^1)$ , then these event will not be equally likely, although all individuals have the same probability of being matched with an individual that adopts strategy  $s_v$  (for all  $s_v \in S$ ).

We call  $S^{\mathbf{N}}$  the set of realizations of the matching process. Let  $x \in S^{\mathbf{N}}$ . If  $x(i) = s_r$  then individual  $i$  is matched with an individual of type  $s_r$ . The description of the relationship between  $\Sigma$  and  $S^{\mathbf{N}}$  and the derivation of the probability space over  $\Sigma$  are the objects of this section.

We consider each element in  $S^{\mathbf{N}}$  as the realization of an infinite sequence of *i.i.d.* random variables where the probability that  $x(i)$  equals  $s_v$  is  $p_v$ . If  $m = 6$  and  $p_v = 1/6$  (for  $v = 1, \dots, 6$ ) we can think of  $x$  as the outcome from rolling a dice infinitely many times. Let  $(S^{\mathbf{N}}, \mathcal{B}, \mu)$  be the probability space we just described where  $\mathcal{B}$  is the  $\sigma$ -algebra constructed by the finite dimensional rectangles, and  $\mu$  is the extension of the probability over the finite dimensional rectangles.<sup>5</sup> For all types  $s_r$ , let  $I_r \subset \mathbf{N}$  be the subset of the population of type  $s_r$ ; i.e.,

$$I_r(\alpha) = \{i \in \mathbf{N} \mid \alpha(i) = s_r\}.$$

Notice that each set  $I_r(\alpha)$  is infinite. Let  $X_{rv}(\alpha) \subset S^{\mathbf{N}}$  be the set of realizations of the matching process such that the proportion of individuals that are of type  $r$  and are matched with individuals of type  $v$  is  $p_r p_v$ ; i.e.,

$$X_{rv}(\alpha) = \{x \in S^{\mathbf{N}} \mid \lim_{T \rightarrow \infty} \frac{1}{T} \sum_{i=1}^T \alpha_r(i) x_v(i) = p_r p_v\}.$$

Then by the strong law of large numbers,  $\mu(X_{rv}(\alpha)) = 1$ .<sup>6</sup> Let  $X_\alpha$  be the set of realizations of the matching process such that for all  $s_r, s_v \in S$ , the proportion of individuals that are of type  $r$  and are matched with individuals of type  $v$  is  $p_r p_v$ ; i.e.,  $X_\alpha = \bigcap_r \bigcap_v X_{rv}(\alpha)$ . Notice that since  $X_{rv}$  is the finite intersection of sets of measure one,  $\mu(X_\alpha) = 1$ .

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<sup>5</sup>Formally, a finite dimensional rectangle is a set of the form

$$B = \{x \in X \mid x_i \in B_i \text{ for all } i \text{ in } J\}$$

where  $J$  is a finite subset of  $\mathbf{N}$  and for all  $i$  in  $J$ ,  $B_i$  is a subset of  $S$ . Let

$$\mu_J(B) = \prod_{i \in J} \left( \sum_{s \in B_i} p_s \right).$$

Let  $\mathcal{B}$  be the  $\sigma$ -algebra generated by the finite dimensional rectangles. By Neveu (1965) Proposition V.1.2 there exists a probability measure over  $(S^{\mathbf{N}}, \mathcal{B})$  such that for all  $J$ -dimensional rectangles,  $B$ ,  $\mu(B) = \mu_J(B)$ .

<sup>6</sup>Let  $X_i = \alpha_r(i) x_v(i)$ . Then,  $\{X_i\}$  is a sequence of independent random variables with finite variance,  $\sigma_i$ . Furthermore,  $\sum_{i=1}^{\infty} \frac{\sigma_i^2}{i^2} < \infty$ , and thus by the Kolmogorov’s law of large numbers (see for instance Rao (1984) Theorem 6, page 60),  $\lim_{T \rightarrow \infty} \frac{1}{T} \sum_{i=1}^T X_i = p_r p_v$  (almost surely).

For all  $x \in X_\alpha$  and for all types  $s_r, s_v$ , let  $A_{rv}^x$  be the set of players of type  $s_r$  that are matched with an individual of type  $s_v$ ; i.e.,

$$A_{rv}^x \equiv \{i \in \mathbf{N} \mid \alpha(i) = s_r, x(i) = s_v\}.$$

Notice that each of the sets  $A_{rv}^x$  has countably many elements and thus can be enumerated as follows:

$$A_{rv}^x = \{a_{rv}^x(1), a_{rv}^x(2), \dots\}.$$

For any two different types  $s_r$  and  $s_v$  let

$$\begin{aligned} \sigma_\alpha^x(a_{rr}^x(i)) &= \begin{cases} a_{rr}^x(i+1) & \text{if } i \text{ is odd,} \\ a_{rr}^x(i-1) & \text{if } i \text{ is even;} \end{cases} \\ \sigma_\alpha^x(a_{rv}^x(i)) &= a_{vr}^x(i). \end{aligned}$$

Clearly  $\sigma_\alpha^x \in \Sigma$ .

Let  $\sigma_\alpha: X_\alpha \rightarrow \Sigma$  be such that  $\sigma_\alpha(x) = \sigma_\alpha^x$ . The function  $\sigma_\alpha$  is injective since  $\alpha \circ \sigma_\alpha^x = x$ .

Next we will construct two different probability spaces for matches. In the first probability space the events “individual  $i$  is matched with individual  $j$ ” and “individual  $i$  is matched with individual  $k$ ” are not equally likely. The second probability space is the coarsest measure for which each subpopulation  $I_r(\alpha)$  is matched with the population average. Notice that for this probability measure the event “individual  $i$  is matched with individual  $j$ ” are not measurable. <sup>7</sup>

Since  $\sigma_\alpha$  is injective, by identifying  $x$  and  $\sigma_\alpha^x$  we can construct a probability over  $\Sigma_\alpha = \sigma_\alpha(X_\alpha)$ . Formally, let  $\mathcal{F}_\alpha$  be the  $\sigma$ -algebra generated by  $\sigma_\alpha(\mathcal{B} \cap X_\alpha)$  and let  $P_\alpha = \mu \circ \sigma_\alpha^{-1}$ . Then,  $(\Sigma_\alpha, \mathcal{F}_\alpha, P_\alpha)$  is a probability measure.

We can extend this probability over all  $\Sigma$  by letting  $\mathcal{F}_\alpha^1$  be the  $\sigma$ -algebra generated by  $\mathcal{F}_\alpha$  and  $\Sigma \setminus \Sigma_\alpha$  and letting  $P_\alpha^1(A) = P_\alpha(A \cap \Sigma_\alpha)$ .

**Theorem 1**  $(\Sigma, \mathcal{F}_\alpha^1, P_\alpha^1)$  is a probability measure for which the event  $\{\sigma \in \Sigma \mid \sigma(i) = j\}$  is measurable.

*Proof:* Let  $B_i^n$  be the event “ $i$  is the  $n^{\text{th}}$  player selecting strategy  $\alpha(i)$  and matched with an individual adopting strategy  $\alpha(j)$ .” Let  $N_i = \{k \leq i \mid \alpha(k) = \alpha(i)\}$ . Then

$$\begin{aligned} B_i^n &= \bigcup_{\{N' \subset N_i \mid |N'|=n\}} \{x \in S^{\mathbf{N}} \mid x(i) = \alpha(j), \forall k' \in N', x(k') = \alpha(j), \\ &\quad \text{and } \forall k'' \in N_i \setminus N', x(k'') \neq \alpha(j)\}. \end{aligned}$$

<sup>7</sup>In Section 3 we showed that for a probability space over  $\Sigma$  either the events “individual  $i$  is matched with individual  $j$ ” are not measurable or they are not equally likely.

Thus  $B_i^n$  is the finite union of rectangles and is thus measurable. Similarly, let  $B_j^n$  be the event “ $j$  is the  $n^{\text{th}}$  player selecting strategy  $\alpha(j)$  and matched with an individual adopting strategy  $\alpha(i)$ .” Clearly,  $B_j^n$  is measurable. Let  $B^n = B_i^n \cap B_j^n$  and let  $B = \bigcup_{n \leq \min\{i,j\}} B^n$ . Clearly,  $B_n$  is measurable and  $x \in B$  if and only if  $\sigma_\alpha(x)(i) = j$ . Therefore,

$$\sigma_\alpha(B) = \{\sigma \in \Sigma \mid \sigma(i) = j\} \in \mathcal{F}_\alpha^1,$$

and thus the event that individual  $i$  is matched with individual  $j$  is measurable. ■

Let  $\phi_\alpha: \Sigma \rightarrow S^{\mathbb{N}}$  be defined by  $\phi_\alpha(\sigma) = \alpha \circ \sigma$  and let  $Y_\alpha = \phi_\alpha(\Sigma)$ . Let  $(S^{\mathbb{N}}, \mathcal{B}', \mu')$  be the completion of the measure space  $(S^{\mathbb{N}}, \mathcal{B}, \mu)$ .

**Lemma 1**  $X_\alpha \subset Y_\alpha$ . Consequently,  $\mu'(Y_\alpha) = 1$ .

*Proof:* Let  $x \in X(\alpha)$ . Then  $\sigma_\alpha(x) \in \Sigma$  and  $\phi_\alpha(\sigma_\alpha(x)) = x$ . Therefore,  $x \in Y(\alpha)$ . Consequently,  $\mu'(Y_\alpha) = 1$  since  $X_\alpha \subset Y_\alpha$  and  $\mu'(X_\alpha) = 1$ . ■

The probability measure  $\mu'$  is restricted over  $Y_\alpha$  by setting:

$$\mathcal{B}_Y = \mathcal{B}' \cap Y_\alpha, \mu_Y(A) = \mu'(A \cap Y_\alpha).$$

Let  $\mathcal{F}_\alpha^2$  be the  $\sigma$ -algebra on  $\Sigma$  generated by  $\phi^{-1}(\mathcal{B}_Y)$  and let  $P_\alpha^2 = \mu_Y \circ \phi_\alpha$ .

**Theorem 2**  $(\Sigma, \mathcal{F}_\alpha^2, P_\alpha^2)$  is a probability measure.

*Proof:* Follows from the previous lemma, the fact that  $\mu(X_\alpha) = 1$ , and Proposition 2.12 (page 21) in Breiman (1968). ■

For either probability measure we have thus proven the following theorem.

**Theorem 3** Let  $I_r(\alpha)$  be the subset of the population of type  $s_r$ . Suppose that the proportion of the population of type  $s_v$  is  $p_v$ . Suppose that people are matched at random according to the matching rule  $(\Sigma, \mathcal{F}_\alpha, P_\alpha)$ . Then the proportion of the population  $I_r(\alpha)$  that is matched with an individual of type  $s_v$  is  $p_v$  (almost surely).

## 5 Extension of the probability of the realizations of matches

In the previous section we defined a probability over the set of realizations of the matching process. In order to do that we had to assume that the assignment of types,  $\alpha$ , was such that the Cesaro average converges; i.e.,  $\alpha \in A$  where

$$A = \{ \alpha \in S^{\mathbf{N}} \mid \lim_{T \rightarrow \infty} \frac{1}{T} \sum_{i=1}^T \alpha(i) \text{ exists and is strictly positive} \}.$$

In this section we dispense with this assumption; i.e., we define a probability over the realization of matches for all  $\alpha \in S^{\mathbf{N}}$ . This is done by means of a measurable extension of the averaging which we denote by  $g$ .

In order to prove the existence of a measurable extension we need both a topological and a measurable structure for  $S^{\mathbf{N}}$ . The space  $S^{\mathbf{N}}$  is endowed with the product topology; this makes  $S^{\mathbf{N}}$  a complete, separable, metric space<sup>8</sup> and  $(S^{\mathbf{N}}, \mathcal{B})$  a measurable space where  $\mathcal{B}$  is the Borel  $\sigma$ -algebra.

Let  $G: S^{\mathbf{N}} \rightarrow \mathbf{R}^m$  be such that for all  $\alpha \in S^{\mathbf{N}}$ ,  $G(\alpha)$  is the lim sup of  $\alpha$ ; i.e.,

$$G(\alpha) = \{ a \in \mathbf{R}^m \mid \exists \{T_n\}_n \text{ such that } \lim_{n \rightarrow \infty} \frac{1}{T_n} \sum_{i=1}^{T_n} \alpha(i) = a \}.$$

Notice that since  $\{ \frac{1}{T} \sum_{i=1}^T \alpha(i) \}_{T \in \mathbf{N}}$  is an infinite sequence belonging to the  $m$ -dimensional simplex it has a convergent subsequence and thus  $G(\alpha)$  is nonempty.

**Lemma 2** *The correspondence  $G$  is closed-valued and measurable.*

*Proof:* Fix  $\alpha \in S^{\mathbf{N}}$ , let  $\{a^m\}_m$  be such that  $a^m \in G(\alpha)$  and  $a^m \rightarrow a$ . For all  $n \in \mathbf{N}$ , let  $\{T_n^m\}_n$  be such that

$$\lim_{n \rightarrow \infty} \frac{1}{T_n^m} \sum_{i=1}^{T_n^m} \alpha(i) = a^m.$$

For each  $m \in \mathcal{N}$ , let  $n(m)$  be such that

$$\left\| \frac{1}{T_{n(m)}^m} \sum_{i=1}^{T_{n(m)}^m} \alpha(i) - a^m \right\| < 1/m \quad \text{and} \quad n(m) > n(m-1).$$

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<sup>8</sup>One possible metric is  $d$ , where for all  $\alpha, \beta \in S^{\mathbf{N}}$ ,

$$d(\alpha, \beta) = \sum_{i \in \mathbf{N}} \frac{|\alpha(i) - \beta(i)|}{2^i(1 + |\alpha(i) - \beta(i)|)}.$$

Then it is each to check that  $\lim_{m \rightarrow \infty} \frac{1}{T_{n(m)}^m} \sum_{i=1}^{T_{n(m)}^m} \alpha(i)$ . Therefore,  $a \in G(\alpha)$  and  $G(\alpha)$  is closed.

Let  $F \subset \mathbf{R}^m$  be closed. Then,

$$\begin{aligned} G^{-1}(F) &= \{\alpha \in S^{\mathbf{N}} \mid G(\alpha) \cap F \neq \emptyset\} \\ &= \{\alpha \in S^{\mathbf{N}} \mid \exists \{T_n\}_n \text{ such that } \lim_{n \rightarrow \infty} \frac{1}{T_n} \sum_{i=1}^{T_n} \alpha(i) \in F\} \\ &= \bigcap_{n \in \mathbf{N}} \bigcap_{\tau \in \mathbf{N}} \bigcup_{T > \tau} F_{T,n} \end{aligned}$$

where

$$\begin{aligned} F_{T,n} &= \{\alpha \in S^{\mathbf{N}} \mid \frac{1}{T} \sum_{i=1}^T \alpha(i) \in B(F, \frac{1}{n})\} \text{ and} \\ B(F, \frac{1}{n}) &= \{a \in \mathbf{R}^m \mid \exists b \in F \text{ such that } \|a - b\| < \frac{1}{n}\}. \end{aligned}$$

Since for all  $T$  and  $n$ ,  $F_{T,n} \in \mathcal{B}$ ,  $G^{-1}(F) \in \mathcal{B}$  and  $G$  is measurable. ■

**Lemma 3** *The correspondence  $G$  has a measurable selection  $g$ .*

*Proof:* The Kuratowski–Ryll–Nordziewski Theorem (see for instance Theorem 14.2.1 in Klein and Thompson (1984)) states that any closed-valued measurable correspondence into a separable metric space has a measurable selection. Thus the result follows from Lemma 2. ■

Notice that for all  $\alpha \in A$ ,  $g(\alpha) = \lim_{T \rightarrow \infty} \frac{1}{T} \sum_{i=1}^T \alpha(i)$  and thus  $g$  is the extension we are looking for.

Let  $B$  be a finite measurable rectangle in  $S^{\mathbf{N}}$ ; i.e.,

$$B = \{x \in S^{\mathbf{N}} \mid x(i) \in B_i \text{ for all } i \text{ in } J\},$$

where  $J \subset \mathbf{N}$  is a finite set and for all  $i$  in  $J$ ,  $B_i \subset S$ . Then let  $\mu(\alpha, B)$  be the probability that if the population selects strategies according to  $\alpha$ , then for all  $i \in J$ , individual  $i$  is matched with an individual of type  $B_i$ ; i.e.,

$$\mu(\alpha, B) = \prod_{i \in J} \left( \sum_{s \in B_i} g_s(\alpha) \right).$$

The function  $\mu(\alpha, \cdot)$  can clearly be extended so that  $(S^{\mathbf{N}}, \mathcal{B}, \mu(\alpha, \cdot))$  is a probability measure.

**Lemma 4** *The function  $\mu$  is a stochastic kernel.*

*Proof:* In order to check the measurability of  $\mu(\cdot, B)$  it is sufficient to consider the case where  $B$  is a finite dimensional rectangle (Neveu (1965), page 75). For this case,  $\mu(\cdot, B)$  is clearly a continuous function of  $g(\alpha)$ . Therefore,  $\mu(\cdot, B)$  is a measurable function. ■

## 6 Repeated matching scheme

In this section we define the notation to describe a population which is matched infinitely many times and in which after each period individuals' type may change. We extend the results of Section 4 for this context.

Let  $\tau: S \times S \rightarrow S$  be such that if at time  $t$  an individual of type  $s_v$  is matched with an individual of type  $s_w$  then at time  $t + 1$  the individual is of type  $\tau(s_v, s_w)$ .<sup>9</sup><sup>10</sup> In order to guarantee that no type disappears immediately we assume that for all types  $s_r$  there exist types  $s_v$  and  $s_w$  (where  $r, v, w$  can be equal) such that  $t(s_v, s_w) = s_r \in S$ . Let  $t: S^{\mathbf{N}} \times S^{\mathbf{N}} \rightarrow A$  be such that for all  $i \in \mathbf{N}$ ,  $x, \alpha \in S^{\mathbf{N}}$ ,

$$t(x, \alpha)(i) \equiv \tau(\alpha(i), x(i)).^{11}$$

If at time  $t$  individual  $i$  is of type  $\alpha(i)$  and is matched with an individual of type  $x(i)$  then, at time  $t + 1$ , individual  $i$ 's type is  $t(\alpha, x)(i)$ . For all  $x \in S^{\mathbf{N}}$  and for all  $\alpha \in S^{\mathbf{N}}$ , the functions  $t: S^{\mathbf{N}} \times \{x\} \rightarrow S^{\mathbf{N}}$  and  $t: \{\alpha\} \times S^{\mathbf{N}} \rightarrow S^{\mathbf{N}}$  are continuous<sup>12</sup> (and thus measurable) and hence and jointly measurable.<sup>13</sup>

Let  $Z = S^{\mathbf{N}} \times S^{\mathbf{N}}$  and let  $\mathcal{C} = \mathcal{B} \otimes \mathcal{B}$ . Let  $Q: Z \times \mathcal{C} \rightarrow [0, 1]$  be such that for all  $(\alpha, x) \in Z$  and all  $(B, B') \in \mathcal{C}$ ,

$$Q((\alpha, x), (B, B')) = \chi_B(t(\alpha, x)) \mu(t(\alpha, x), B').^{14}$$

---

<sup>9</sup>This law of motion includes the learning models and the evolutionary models with constant populations.

<sup>10</sup>A more general model would allow for a stochastic law of motion; i.e.,

$$\tau: S \times S \times [0, 1] \rightarrow S$$

where  $\tau$  is measurable and  $(S, \mathcal{P}(S))$  and  $([0, 1], \mathcal{B}([0, 1]))$  are measurable spaces (where  $\mathcal{P}(S)$  is the power set and  $\mathcal{B}(S)$  is the Borel  $\sigma$ -algebra). The map becomes stochastic after we define a probability measure over  $([0, 1], \mathcal{B}([0, 1]))$ .

<sup>11</sup>If  $\tau$  is stochastic then  $t: S^{\mathbf{N}} \times S^{\mathbf{N}} \times [0, 1]^{\mathbf{N}} \rightarrow A$  is such that for all  $i \in \mathbf{N}$ ,  $x, \alpha \in S^{\mathbf{N}}$ ,  $\xi \in [0, 1]^{\mathbf{N}}$ ,

$$t(x, \alpha, \xi)(i) \equiv \tau(\alpha(i), x(i), \xi_i).$$

<sup>12</sup>Suppose  $\alpha^n \rightarrow \alpha$  and let  $m > 0$ . Then there exists an  $N$  such that for all  $n \geq N$  and for all  $i \leq m$ ,  $\alpha^n(i) = \alpha(i)$ . Thus for all  $n \geq N$  and for all  $i \leq m$ ,  $t(\alpha^n, x)(i) = t(\alpha, x)(i)$ . Therefore,  $t(\alpha^n, x) \rightarrow t(\alpha, x)$  and  $t(\cdot, x)$  is continuous. The same proof shows that  $t(\alpha, \cdot)$  is continuous.

<sup>13</sup>The proof that the continuity of each section implies joint measurability is in Appendix B.

<sup>14</sup>For the case where  $\tau$  is stochastic let  $\lambda$  be the Lebesgue measure over  $[0, 1]^{\mathbf{N}}$ . For all  $\alpha, x \in S^{\mathbf{N}}$ , let  $\rho_{\alpha, x}$  be the probability measure on  $(S^{\mathbf{N}}, \mathcal{B})$  defined by

$$\rho_{\alpha, x}(B) = \lambda(\{\xi \in [0, 1]^{\mathbf{N}} | t(\alpha, x, \xi) \in B\}).$$

Then,

$$Q((\alpha, x), (B, B')) = \int_B \mu(t, B') d\rho_{\alpha, x}(t).$$

$Q((\alpha, x), (\alpha', x'))$  is the probability that if at time  $t$  the population has types assigned by  $\alpha$  and is matched according to  $x$ , then at time  $t+1$  the population has types assigned by  $\alpha'$  and is matched according to  $x'$ .

**Lemma 5** *The function  $Q$  is a transition probability, i.e., for each  $C \in \mathcal{C}$ ,  $Q(\cdot, C)$  is measurable and for each  $z \in Z$ ,  $Q(z, \cdot)$  is a probability measure.*

*Proof:* Fix  $z \in Z$ . Then  $Q(z, \cdot)$  is the product of two probability measures and is thus a probability. Fix  $C = (B, B') \in \mathcal{C}$ . Notice that  $Q(\cdot, C)$  is the product of two measurable functions of  $t$  and that  $t$  is a measurable function of  $z$ . Therefore,  $Q(\cdot, C)$  is a measurable function. ■

Let  $\bar{Z} = \times_{n \in \mathbb{N}} Z$  and  $\bar{\mathcal{C}} = \otimes_{n \in \mathbb{N}} \mathcal{C}$ .

**Theorem 4** *There is a unique probability  $\bar{Q}_{z_0}$  over  $(\bar{Z}, \bar{\mathcal{C}})$  such that for every finite dimensional rectangle,  $C_1 \times \cdots \times C_J \times \times_{n=J+1}^{\infty} S^{\mathbb{N}}$ ,*

$$\bar{Q}_{z_0}[C_1 \times \cdots \times C_J \times \times_{n=J+1}^{\infty} S^{\mathbb{N}}] = \int_{C_1} Q(z_0, z_1; dz_1) \cdots \int_{C_J} Q(z_{J-1}, z_J; dz_J).$$

*Proof:* This follows from the Ionescu Tulcea theorem (see for instance Neveu (1965), Proposition V.1.1). ■

For each  $\alpha$  let  $X_\alpha$  be the set of realizations of the matching rule such that each subpopulation is matched with the population average. By the results in Section 4, for all  $\alpha \in A$ ,  $\mu(\alpha, X_\alpha) = 1$ .

**Lemma 6** *The correspondence  $X: A \rightarrow S^{\mathbb{N}}$  is measurable and closed valued.*

*Proof:* The proof is exactly the same as the proof of Lemma 2. ■

**Lemma 7** *The graph of  $X$  is measurable.*

*Proof:* Klein and Thompson (1984) prove (Proposition 13.2.2 and Proposition 13.2.4) that the graph of a closed measurable function is measurable. Thus this result follows directly from Lemma 6. ■

**Theorem 5** *Suppose that the initial population types are described by  $\alpha_0 \in A$  and is matched according to  $x_0 \in X_{\alpha_0}$ . Then at every period each subpopulation is matched with the population average (almost surely).*

*Proof:* Let  $C = \text{graph } X$  and let  $z \in C$ . Clearly,  $\chi_{t(z)}(t(z)) = 1$  and by the results in Section 4,  $\mu(t(z), X_{t(z)}) = 1$ . Then since  $t(z) \in A$  we get that  $(t(z), X_{t(z)}) \in \text{graph } X$  and thus,

$$Q(z, C) \geq Q(z, (t(z), X_{t(z)})) = \chi_{t(z)}(t(z)) \mu(t(z), X_{t(z)}) = 1.^{15}$$

Since for all  $z \in C$ ,  $Q(z, C) = 1$ , then for all  $J \in \mathbb{N}$ ,

$$\bar{Q}_{z_0}[C \times \cdots \times C \times_{n=J+1}^{\infty} Z] = \int_C Q(z_0, z_1; dz_1) \cdots \int_C Q(z_{J-1}, z_J; dz_J) = 1.$$

■

Since in each period each subpopulation is matched with the population average, given an initial population,  $\alpha$ , we can compute the distribution of types at any given period  $t$ ,  $g^t(\alpha)$ . Specifically, by letting

$$g^1(\alpha) = \sum_v \sum_w g_v(\alpha) g_w(\alpha) t(s_v, s_w),$$

and we define recursively  $g^t(\alpha)$  by

$$g^t(\alpha) = g^{t-1}(g^1(\alpha)).$$

---

Next we want to show that the probability  $\bar{Q}_{z_0}$  is generated by some probability measure over the set of matches.

Let  $\phi: \Sigma^{\mathbb{N}} \times A^{\mathbb{N}} \rightarrow \bar{Z}$  be such that

$$\phi(\{\sigma_i\}, \{\alpha_i\}) = \{(\alpha_i \circ \sigma_i, \alpha_i)\}.$$

Let  $Y = \phi(\Sigma^{\mathbb{N}} \times A^{\mathbb{N}})$  and let  $(\bar{Z}, \bar{\mathcal{C}}', Q')$  be the completion of the measure  $(\bar{Z}, \bar{\mathcal{C}}', \bar{Q}_{z_0})$ . Using the same arguments as in Lemma 1 we can show that  $\text{graph } X \subset Y$  and thus  $Q'(Y) = 1$ . The probability  $Q'$  is restricted over  $Y$  by setting

$$\mathcal{C}_Y = \mathcal{C} \cap Y \quad \text{and} \quad Q_Y(C) = Q'(C \cap Y).$$

Let  $\mathcal{F}$  be the  $\sigma$ -algebra generated by  $\phi^{-1}(\mathcal{C}_Y)$  and let  $P = Q_Y \circ \phi$ . Using the same argument as in Section 4 we get the following result.

**Theorem 6**  $(\Sigma^{\mathbb{N}} \times A^{\mathbb{N}}, \mathcal{F}, P)$  is a probability measure.

---

<sup>15</sup>In order to prove that  $Q(z, C) = 1$  we had to show that  $C$  was measurable. An alternative way to proving the same results is to show that the set  $C$  is *thick* (i.e.,  $A \in \mathcal{C}, A \cap C = \emptyset \Rightarrow P(A) = 0$ ) and thus  $\bar{Q}(x, C) = 1$  where  $\bar{Q}$  is the extension of  $Q$  over the trace  $\sigma$ -algebra  $\mathcal{C}(\mathcal{C})$  such that  $\bar{Q}(A \cap C) = Q(A)$  (see Rao (1981), page 15, Theorem 5).

In many applications we will not be interested in the actual matches but only in the evolution of the population. Let  $\nu: S^{\mathbf{N}} \times \mathcal{B} \rightarrow [0, 1]$  be such that for all  $\alpha \in S^{\mathbf{N}}$  and  $B \in \mathcal{B}$ ,

$$\nu(\alpha, B) = \mu(\alpha, t_{\alpha}^{-1}(B)).$$

For all  $\alpha, \alpha' \in S^{\mathbf{N}}$ ,  $\nu(\alpha, \alpha')$  is the probability that if at time  $t$  the population's types are described by  $\alpha$ , then at time  $t + 1$  the population's types are assigned by  $\alpha'$ .

**Lemma 8** *The function  $\nu$  is a transition probability; i.e., for each  $B \in \mathcal{B}$ ,  $\nu(\cdot, B)$  is measurable and for each  $\alpha \in S^{\mathbf{N}}$ ,  $\nu(\alpha, \cdot)$  is a probability.*

*Proof:* This follows from Theorem 6.2 of Futia (1982). ■

Let  $\bar{S} = \times_{n \in \mathbf{N}} S^{\mathbf{N}}$  and  $\bar{\mathcal{B}} = \otimes_{n \in \mathbf{N}} \mathcal{B}$ .

**Theorem 7** *There is a unique probability  $\bar{\nu}_{\alpha_0}$  on  $(\bar{S}, \bar{\mathcal{B}})$  such that for every finite dimensional rectangle,  $B_1 \times \cdots \times B_J \times \times_{n=J+1}^{\infty} S^{\mathbf{N}}$ ,*

$$\bar{\nu}_{\alpha_0}[B_1 \times \cdots \times B_J \times \times_{n=J+1}^{\infty} S^{\mathbf{N}}] = \int_{B_1} \nu(\alpha_0, \alpha_1; d\alpha_1) \cdots \int_{B_J} \nu(\alpha_{J-1}, \alpha_J; d\alpha_J).$$

*Proof:* This follows from the Ionescu Tulcea theorem (see for instance Neveu (1965), Proposition V.1.1). ■

**Proposition 1** *If  $\alpha_0 \in A$  then  $\nu_{\alpha_0}[A^{\mathbf{N}}] = 1$ .*

*Proof:* Follows since we showed in Section 4 that  $\nu(\alpha_0, A) = 1$ . ■

## 7 The law of motion for finite populations and finite number of periods

A justification of the analysis of the deterministic model for finite population is that we are just interested in following the law of motion for a finite number of periods,  $T$ . This section proves that for a large enough population the model is approximately correct.

Let  $p_v^t$  be the proportion of individuals of type  $s_v$  at time  $t$ . The initial proportion  $p^0$  is given while the other proportions are computed by assuming that each type is matched with the population average. For any type  $s_r$  let  $\{x_r^i\}$  be a sequence of random variables such that (for all  $i$  and  $v$ ) the probability that  $x_r^i = s_v$  is  $p_v$  and let  $\mu$  be the probability

defined over the whole sequence of  $\{x_r^i\}$  (as discussed in section 2.4). If the population size is  $N$  the population is denoted by  $P(N)$ , where  $P(N) = \{1, \dots, N\}$ . For any period  $t = 1, \dots, T$ , let  $\alpha^t: P(N) \rightarrow S$  denote the assignment of strategies in the population. The initial population  $\alpha^0$  is given while the populations in the other periods are obtained by the law of motion  $\tau$  (which is described in Section 2.6) and the matching rule. Individuals are matched as in section 2.3; i.e., the individuals of type  $s_r$  that draw a random variable with value  $s_v$  are matched with the individuals of type  $s_v$  that draw a random variable with value  $s_r$ . Since these groups are finite we will not always be able to match all individuals this way. Thus the remaining individuals are matched in some arbitrary way.

**Theorem 8** *For any  $T > 0$ ,  $\epsilon > 0$  and for any  $\delta > 0$  there exists a positive integer  $N'$  such that for all population sizes  $N > N'$  and all strategies  $s_v$  the following holds: with probability greater than  $1 - \delta$  the proportion of the population  $P(N)$  adopting strategy  $s_v$  at time  $T$ ,  $\frac{1}{N} \sum_{i=1}^N \alpha_v^T(i)$ , is within  $\epsilon$  of  $p_v^T$ .*

*Proof:* The idea behind the proof is the following. We find a uniform upper bound (uniform over time period and strategy) for the proportion of the population which adopts a particular strategy at a time period and which is not matched according to the population average (with probability  $1 - q$ ). The upper bound and  $q$  can be made arbitrarily small by taking the population to be large enough. Then for almost all possible histories we can find a subpopulation which behaves exactly according to the deterministic model. Again the proportion of the population in this subpopulation can be made arbitrarily close to one by taking the population to be large enough.

Fix  $T > 0$ ,  $\epsilon > 0$ , and  $\delta > 0$ . Let  $\xi > 0$  be such that  $(1 - \frac{\epsilon}{\xi})^{2^T} > 1 - \epsilon$ , let  $\underline{p} = \min_{v,t \leq T} p_v^t$ , and let  $N$  be greater than  $N'$  where

$$N' = \frac{T\xi^2}{4\delta\epsilon^2\underline{p}^3(1-\frac{\epsilon}{\xi})^T}.$$

Let  $e^v$  be the vector with 1 on the  $v^{\text{th}}$  component and zeros on the other components. Then  $\{x_r^i \cdot e^v\}_i$  is a sequence of Bernoulli random variables and thus if  $n$  is greater than  $n'$ , where

$$n' = \frac{T\xi^2}{4\delta\epsilon^2\underline{p}^2},$$

then

$$\mu\left(\left|\frac{1}{n} \sum_i x_r^i \cdot e^v - p_v\right| \geq \frac{\epsilon p}{\xi}\right) \leq \frac{\delta}{T}.^{16}$$

<sup>16</sup>Bernoulli's weak law of large numbers is proved (see Shiryaev (1984), page 47), by showing that if  $\{x_i\}$  is a sequence of Bernoulli random variables with  $E(x_i) = p$  then

$$P\left\{\left|\frac{1}{n} \sum_{i=1}^n x_i - p\right| \geq \epsilon\right\} \leq \frac{1}{4n\epsilon^2}.$$

Suppose that the number of individuals adopting any strategy  $s_r$  is greater than  $n$  and the distribution of strategies in the population is given by  $p$ . Then, with probability greater than  $1 - \frac{\delta}{T}$ ,

$$\max_{r,v} \frac{|p_r p_v - \frac{1}{|\{i \in P(N) | \alpha(i)=r\}|} \sum_{\{i \in P(N) | \alpha(i)=r\}} x_r^i \cdot e^v|}{p_r p_v} < \frac{\epsilon}{\xi}.$$

Consequently, with probability greater than  $1 - \delta/T$  the proportion of individuals matched according to the correct proportions is  $1 - \frac{\epsilon}{\xi}$ . But, with probability greater than  $1 - \frac{\delta}{T}$ , at each period there are at least  $N \underline{p} (1 - \frac{\epsilon}{\xi})^T > n'$  individuals adopting any strategy  $s_v$  and thus a proportion  $1 - \frac{\epsilon}{\xi}$  of the population is matched according to the population proportion. Hence, with probability greater than  $1 - \delta$  at every period  $t = 1, \dots, T - 1$ , there is a  $(1 - \frac{\epsilon}{\xi})$  proportion of the population which is matched according to the population proportions. Define recursively  $P_1 = \{ \text{individuals matched with the population average} \}$ ,  $P_t = \{ \text{individual matched with subpopulation } P_{t-1} \text{ average} \}$ . Hence with probability  $1 - \delta$ ,  $\frac{|P_T|}{N} \geq (1 - \frac{\epsilon}{\xi})^{2T}$ . Thus with probability  $1 - \delta$  the population will be within  $1 - (1 - \frac{\epsilon}{\xi})^{2T} < \epsilon$  of  $p^T$ . ■

## 8 Conclusion

Biologists and economists have analyzed populations where each individual interacts with randomly selected individuals. The random matching generates a very complicated stochastic system. Consequently biologists have approximated such a system by a deterministic system. The justification of such an approximation is that the population is assumed to be very large and thus some law of large numbers must hold. In the paper we give an example for which this assumption does not hold. This does not mean that this kind of approximation may never hold, but that the correctness of the approximation depends on properties of the law of motion. This paper shows that if we assume that the population is infinite then the stochastic and the deterministic system are the same.

Note that all the proofs hold if the set of type,  $S$ , is countably infinite. In this case admissible proportions,  $p$ , must be such that:  $p > 0$ ,  $\sum_{s \in S} p_s = 1$ , and  $\lim_{s \rightarrow \infty} p_s = 0$ . However, we are not aware of any study of such models.

Finally, the matching technologies defined in the paper depend on the particular distribution of strategies in the population. It remains an open question whether matching schemes exist that are independent of the distribution of strategies and for which individuals are matched with individuals that adopt strategies in the same proportion as the population as a whole.

## Appendix A: Populations with a continuum of agents

This section follows Feldman and Gilles (1985). Suppose that the population is represented by the unit interval,  $I = (0, 1]$ . Let  $\mathcal{I}$  denote the Lebesgue measurable sets of  $I$  and let  $\lambda$  be the Lebesgue measure on  $I$ . The fact that the population selects strategies according to  $x$  is represented by partitioning  $I$  as follows:

$$I = (0, x_1] \cup (x_1, x_1 + x_2] \cup \dots \cup (1 - x_m, 1].$$

Let  $\mathcal{B}$  be the Borel sets of  $I$ . Let  $(\Omega, \mathcal{F}, P)$  be a probability space determined by the randomized matching process. Let  $\{X(\cdot, i)\}_{i \in I}$  be a family of random variables, where for all  $i \in I$ ,  $X(\cdot, i): \Omega \rightarrow \{0, 1\}$  is such that

$$p(X(\cdot, i) = 1) \equiv P(\{\omega: X(\omega, i) = 1\}) = x_r.$$

The event  $X(\omega, i) = 1$  denotes that individual  $i$  is matched with an individual who selects strategy  $r$ ;  $X(\omega, i) = 0$  denotes that individual  $i$  is matched with an individual who does not select strategy  $r$ . Then in order for the conjecture given in the introduction to be correct to following needs to be true: for every  $B \in \mathcal{B}$

$$\int_B X(\omega, i) \lambda(di) = x_r \sigma(B). \quad (3)$$

For any sample  $\omega \in \Omega$ , define the set function  $v_\omega: \mathcal{B} \rightarrow \mathfrak{R}_+$  by

$$v_\omega(B) = \int_B X(\omega, i) \lambda(di).$$

Since  $v_\omega$  is absolutely continuous with respect to  $\lambda$ ,  $\lambda \gg v_\omega$ , by the Radon-Nikodym theorem there exists a unique measurable function  $f$  such that

$$v_\omega(B) = \int_B f(a) \lambda(da). \quad (4)$$

But if equation 3 holds then by setting  $f \equiv x_r$ , equation 4 is satisfied. Therefore since  $f$  is unique  $X(\omega, \cdot) = x_r (\lambda)$  a.e.. But since  $x_r \notin \{0, 1\}$  this is not an admissible value for  $X$ . Thus 3 cannot hold for all possible strategy partitions over the player set.

Green (1989) has shown that if the distribution of strategies in the population is described by a different partitioning then the conjecture may hold.

It still remains to be shown that there exists a probability space  $(\Omega, \mathcal{F}, P)$  and a sequence of random variables  $\{X(\cdot, i)\}$  which correspond to a random matching process such that the conjecture holds.

Finally, modeling a very large population as a countable set seems a better approximation than modeling it as a continuum.

## Appendix B: Joint measurability of a function with continuous sections

**Theorem 9** *Let  $(X, \mathcal{B})$  be a measure space where  $X$  is a separable complete metric and  $\mathcal{B}$  is the Borel  $\sigma$ -algebra. Let  $f: X \times X \rightarrow X$  be such that for all  $x \in X$ ,  $f: \{x\} \times X \rightarrow X$  and  $f: X \times \{x\} \rightarrow X$  are continuous. Then  $f$  is measurable.*

*Proof:* Since  $X$  is a separable metric space, the Borel  $\sigma$ -algebra  $\mathcal{B}$  has a denumerable subfamily,  $\mathcal{D}$  generating  $\mathcal{B}$  (see for instance Parthasarathy (1967) Theorem 1.8). Let

$$\mathcal{D} = \{D_1, \dots, D_n, \dots\}.$$

Let

$$\begin{aligned} \mathcal{F}^n &= \{F_1 \cap F_2 \cap \dots \cap F_n \mid \text{where } F_i = D_i \text{ or } F_i = X \setminus D_i\} \\ &\equiv \{F_1^n, \dots, F_{m(n)}^n\}. \end{aligned}$$

Notice that  $\mathcal{F}^n$  is a partition of  $X$  and that  $\mathcal{F}^n \subset \mathcal{B}$ . For all  $i$  and  $n$  choose  $y_i^n$  such that  $y_i^n \in F_i^n$ . Finally, let

$$f_n(x, y) = \sum_{i=1}^{m(n)} f(x, y_i^n) \chi_{X \times F_i^n}.$$

---

Notice that the continuity of  $f: X \times \{c\} \rightarrow X$  easily implies the continuity of the function  $g: X \times X \rightarrow X$  where  $g(x, y) = f(x, c)$ . Thus  $f_n(x, y)$  is a measurable function. Fix  $y \in X$  and for all  $n$  let  $i(n)$  be such that  $y \in F_{i(n)}^n$ . Notice that  $F_{i(n)}^n \subset F_{i(n-1)}^{n-1}$  and that  $F_{i(n)}^n \downarrow \{y\}$ . Then,

$$\lim_{n \rightarrow \infty} f_n(x, y) = \lim_{n \rightarrow \infty} f(x, y_{i(n)}^n) = f(x, \lim_{n \rightarrow \infty} y_{i(n)}^n) = f(x, y).$$

The function  $f$  is hence the pointwise limit of a sequence of measurable functions and is thus measurable. ■

## Appendix C: Brief review of Biology

In this appendix we describe the relationship between the issues raised in this paper and models considered in population genetics and evolutionary biology.

### Population Genetics

This section is based on Cavalli-Sforza and Bodmer (1971). In the models we consider, the phenotype (e.g., eye color) is determined by the action of two genes at one locus. Genes are assumed to be of two types (alleles):  $A_1$  and  $A_2$ . Individuals are of three types (genotypes):  $A_1A_1$ ,  $A_1A_2$ , and  $A_2A_2$ . When two individuals mate they each produce gametes (reproductive cells). Gametes receive one of the parent's genes. An offspring is produced by the union of a gamete from each parent. When two individuals of types  $aa'$  and  $bb'$  mate they produce offsprings of type  $ab$ ,  $ab'$ ,  $a'b$ , and  $a'b'$  with equal probability. Another assumption describes which individuals mate. **“Matings take place at random with respect to the genetic differences being considered and in a population of infinite size”** (Cavalli-Sforza and Bodmer (1971), page 45). All individuals mate at the same time and then are completely replaced by their offsprings. Thus the dynamics of the process depends on the random matching of individuals and the random selection of genotypes for the offsprings. Suppose the initial relative frequency of alleles  $A_1$  and  $A_2$  is  $p_1$  and  $p_2$  ( $p_1 + p_2 = 1$ ). Then the Hardy-Weinberg theorem states that in the next period the relative frequency of the genotypes  $A_1A_1$ ,  $A_1A_2$ ,  $A_2A_2$  is respectively  $p_1^2$ ,  $2p_1p_2$ , and  $p_2^2$ . This theorem is ‘proved’ (just as in the original papers by Hardy (1908) and Weinberg (1908)) by computing the expected proportion with which each of the matches occurs. No explicit modeling of the matching scheme and no derivation of a law of large numbers is given. Furthermore there seems to be some confusion in the literature about whether the population needs to be infinite or very large. Feller (1967) (page 135) writes: “In a large population the actually observed frequencies of the three genotypes in the filial generation will be close to the theoretical probabilities.” And in a footnote at the end of this sentence: “The statements is made precise by the law of large numbers and the central limit theorem, which permit us to estimate the effect of chance fluctuations.” Hofbauer and Sigmund (1988) (page 9) write: “A few more premises were used implicitly in the derivation. For instance we equated “frequency” with “probability.” This is admissible in the limiting case of very large populations.”

The model just described is generalized to the case where genotypes differ in fitness (the expected number of offsprings). Denote by  $w_{ii}$  the fitness of the genotype  $A_{ii}$ . If the initial relative frequency of alleles  $A_1$  and  $A_2$  is  $p_1$  and  $p_2$  then the next period frequency of the genotypes  $A_1A_1$ ,  $A_1A_2$ ,  $A_2A_2$  is respectively

$$\frac{w_{11}p_1^2}{d}, \frac{2w_{12}p_1p_2}{d}, \frac{w_{22}p_2^2}{d},$$

where  $d = w_{11}p_1^2 + 2w_{12}p_1p_2 + w_{22}p_2^2$ .<sup>17</sup> Then the frequency of alleles  $A_1$  in the next

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<sup>17</sup>Notice that in genetics it is always assumed that  $w_{ij} = w_{ji}$ .

period is

$$p'_1 = \frac{w_{11}p_1^2 + w_{12}p_1p_2}{d}, \quad p'_2 = \frac{w_{22}p_2^2 + w_{12}p_1p_2}{d}.$$

This model easily generalizes to the case where there are  $m$  alleles,  $A_1, \dots, A_m$ . The law of motion for the alleles is the same as equation 1 (where  $w_{ij} = a_{ij}$ ). This model has also been analyzed when the matches occur infinitely often; e.g., Fisher (1930) and more recently Losert and Akin (1983) analyze the properties of the limiting distributions of genotypes; i.e.,  $\lim_{t \rightarrow \infty} p^t$ .

The model just described is closely related to the model considered in this paper. The set of types in this model is the set of genotypes. For instance, in the case where there are only two alleles,

$$S = \{A_1A_1, A_1A_2, A_2A_2\}.$$

The law of motion  $\tau$  in this model is stochastic; for instance

$$\tau(A_1A_1, A_1A_2) = \frac{1}{2} \delta_{A_1A_1} + \frac{1}{2} \delta_{A_1A_2}.$$

Thus in order to prove the Hardy-Weinberg theorem in this context we need to generalize the model for stochastic laws of motions.

The Hardy-Weinberg theorem and the law of motion in equation 1 can be derived from a different set of assumptions on the reproductive scheme. Individuals form a large number of gametes. A small proportion of the gametes formed unite with gametes of the opposite sex. Thus, the distribution of genotypes in the next generation is found by a sample of the gametes (and hence of the alleles) in the population. Specifically if the proportion of alleles  $A_1$  and  $A_2$  is respectively  $p_1$  and  $p_2$  then the next generation is obtained by drawing  $2N$  gametes where we assume that the probability of drawing a gamete of type  $A_1$  is  $p_1$  and the probability of drawing a gamete of type  $A_2$  is  $p_2$ . Then the expected proportion of alleles of any type is given by equation 1 where  $p_i$  is the proportion of alleles of type  $A_i$  and  $a_{ij}$  is the number of offsprings of a genotype  $A_iA_j$ . Again no law of large numbers has been derived for this system. However, geneticists realize that the deterministic element of the model is due to the assumption of large population.

The stochastic element created by small population is considered in the models of 'random genetic drift.' Suppose that there are  $N$  individuals and that the population size stays constant from generation to generation. If the population proportion of allele  $A_1$  is  $p_1$  then the next period population is formed by drawing  $2N$  gametes from an urn that contains a proportion  $p_1$  of gametes of type  $A_1$ . This model is approximately correct if the number of gametes is large enough (and thus we can consider the sampling procedure as sampling with replacement). The binomial distribution gives the the gene frequency distribution after one period. Kimura (1964) derived the gene frequency distribution after  $n$  generations. At any generation the mean number of genes of type  $A_1$  is  $p_1$  although eventually one of the alleles is fixed in all populations. The proportion of populations in which  $A_1$  is eventually fixed is  $p_1$ . The probability of fixation at generation

$t$ ,  $P(t, p_1)$ , depends on the initial gene frequency,  $p_1$ , and the population size,  $N$ . Kimura (1964) showed that

$$P(t, p_1) \approx 1 - 6p_1(1 - p_1)e^{-\frac{t}{2}N}$$

and Ewens (1969) computed the mean fixation time to be

$$4N[p_1 \log p_1(1 - p_1) \log(1 - p_1)].$$

Thus this model underscores the difference between the expected gene frequency and the real gene frequency.

## Evolutionary Biology

This section follows Maynard Smith (1982) (10–23). There is an infinite population of individuals identical in all respects except for how they behave in a two-person contest. In this contest there are only two possible strategies: to act as a hawk (denoted by  $H$ ) and to act as a dove (denote by  $D$ ). Each individual is paired off at random with one other individual. Individuals reproduce their kind asexually. The number of offspring for an individual that adopts strategy  $i$  and is matched with an individual that adopts strategy  $j$  ( $i, j \in \{H, D\}$ ) is  $W_0 + E(i, j)$ .<sup>18</sup> If  $p$  is the frequency of individuals adopting strategy  $H$  then it is asserted that the number of offsprings of individuals that select strategy  $i$ ,  $E(i)$ , is

$$E(i) = W_0 + pE(i, H) + (1 - p)E(i, D)$$

and that the frequency  $p'$  of individuals selection  $H$  in the next period is

$$p' = p \frac{E(H)}{pE(h) + (1 - p)E(D)}.$$

This model can clearly be generalized to the case where there are  $m$  strategies,  $s_1, \dots, s_m$ . The law of motion for this system is the one described in equation 1 where  $a_{rv} \equiv W_0 + E(s_r, s_v)$ . Again there seems to be some confusion as to whether the population is assumed to be infinite or very large as in Hines (1987).

Suppose that the population stays constant; i.e.,  $a_{rv} + a_{vr} = 2$ . Then if we require the number of individuals of each type to be nonnegative integers then for all strategies  $s_r$  and  $s_v$ ,  $a_{vr} \in \{0, 1, 2\}$ . Thus the model described in Section 6 describes the replicator model where

$$\tau(s_v, s_w) = \begin{cases} s_v & \text{if } a_{vw} \neq 0 \\ s_w & \text{if } a_{vw} = 0. \end{cases}$$

The results in this paper show that if the population is countably infinite then equation 1 describes the behavior of the process (almost surely).

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<sup>18</sup>If the parent lives more than one period the number of offsprings includes the parent.

## References

- Boylan, R. 1990. Evolutionary equilibria resistant to mutation. Social Science Working Paper No. 729.
- Breiman, L. 1968. *Probability*. Reading, Mass.: Addison-Wesley.
- Cavalli-Sforza, L. L. and W. F. Bodmer. 1971. *The genetics of human populations*. San Francisco: W. H. Freeman and Company.
- Ewens, W. J. 1969. *Population genetics*. London: Methuen.
- Feldman, M. and C. Gilles. 1985. An expository note on individual risk without aggregate uncertainty. *Journal of Economic Theory* 35.
- Feller, W. 1967. *An introduction to probability theory and its applications*, third ed., volume I. New York: John Wiley & Sons, Inc.
- Fisher, R. A. 1930. *The genetical theory of natural selection*. Oxford: Clarendon Press.
- Fudenberg, D. and D. Levine. 1990. Steady state learning and self-confirming equilibrium. Mimeograph.
- Futia, C. A. 1982. Invariant distributions and the limiting behavior of Markovian economic models. *Econometrica* 50:377–408.
- Green, E. 1989. Individual-level randomness in a nonatomic population. Working Paper # 227.
- Hardy, G. H. 1908. Mendelian proportions in mixed population. *Science* 28:49–50. Reprinted in J. H. Peters, ed. *Classic Papers in Genetics*. Englewood Cliffs, N. J.: Prentice-Hall, 1959.
- Hines, W. G. S. 1987. Evolutionary stable strategies: a review of basic theory. *Theoretical Population Biology* 31:195–272.
- Hofbauer, J. and K. Sigmund. 1988. *The theory of evolution and dynamical systems*. Cambridge: Cambridge University Press.
- Kimura, M. 1964. *Diffusion models in population genetics*. London: Methuen.
- Klein, E. and A. Thompson. 1984. *Theory of correspondences*. New York: Wiley.
- Losert, V. and E. Akin. 1983. Dynamics of games and genes: discrete versus continuous time. *Journal of Mathematical Biology* 17:241–251.
- Maynard Smith, J. 1982. *Evolution and the theory of games*. Cambridge: Cambridge University Press.
- Neveu, J. 1965. *Mathematical foundations of the calculus of probability*. San Francisco: Holden-Day.

- Parthasarathy, K. R. 1967. *Probability measures on metric spaces*. New York: Academic Press.
- Rao, M. M. 1981. *Foundations of stochastic analysis*. New York: Academic Press.
- Rao, M. M. 1984. *Probability theory with applications*. New York: Academic Press.
- Shiryayev, A. N. 1984. *Probability*. New York: Springer-Verlag.
- Weinberg, W. 1908. On the demonstration of heredity in man. *Reprinted in* S. H. Boyer, ed. *Papers on Human Genetics*. Englewood Cliffs, N.J.: Prentice-Hall, 1963.
- Weising, F. 1989. Evolutionary stability and dynamics stability in generalized 'rock-scissors-paper' games. Working Paper No. 27.