ON A GENETICS MODEL OF MORAN EVOLVING IN RANDOM ENVIRONMENTS

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SUMMARY. In a previous investigation [6], a model of a discretetime stochastic process (Z_n) evolving in a random environment controlled by an irreducible Markov chain (Y_n) was formulated wherein the bivariate process (Y_n, Z_n) is Markovian and the marginal process (Z_n) is a birth and death chain when conditioned on a fixed sequence of environmental states of (Y_n) . Conditions for the extinction and instability of (Z_n) were stated and proved. In a succeeding investigation [7] methods were obtained to calculate extinction probabilities when the probability of extinction is less than one and (Y_n) has finite state space. In this paper, these methods are applied to a genetics model of [4] to study gene fluctuations due to mutation influences subject to varying environmental conditions.

1. Introduction. Consider a bivariate stochastic process (Y_n, Z_n) , $n = 0, 1, 2, \cdots$ with state space $S_0 = \{1, \dots, m\} \times Z_0$ where Z_0 denotes the non-negative integers. In a previous investigation (Torrez [6]), we formulated a mathematical model to represent a discrete-time birth and death process evolving in a random environment in such a way that (i) the marginal process (Y_n) of (Y_n, Z_n) (called the environmental process or simply environment) is an irreducible Markov chain with state space $\{1, \dots, m\}$ and transition kernel K; (ii) given a realization of (Y_n) , the conditional distribution of (Z_n) is Markovian (but not time-homogeneous, in general). Indeed, when a sequence of environmental states (y_n) is given, the marginal process (Z_n) of (Y_n, Z_n) behaves like a birth and death process with transition probabilities

$$Pr[Z_{n+1} = z' | (Y_n, Z_n) = (y_n, z_n)] = \begin{cases} p_{z_n}^{(y_n)} & \text{if } z' = z_n + 1, \\ q_{z_n}^{(y_n)} & \text{if } z' = z_n - 1 \\ r_{z_n}^{(y_n)} & \text{if } z' = z_n \\ 0 & \text{otherwise} \end{cases}$$

where

$$0 \leq p_{z_n}^{(y_n)}, q_{z_n}^{(y_n)}, r_{z_n}^{(y_n)} \leq 1,$$

Received by the editors on December 1, 1977.

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and

$$p_{z_n}^{(y_n)} + q_{z_n}^{(y_n)} + r_{z_n}^{(y_n)} = 1$$

for all *n*. It should be noted that, since the sequence of environments is itself a stochastic process, in general the marginal process (Z_n) is not Markovian. When no particular sequence of environmental states is specified, we will refer to (Z_n) as a birth and death process in a random environment (BDRE). We denote the one step transition kernel of the (Y_n) -conditioned (Z_n) birth and death process by $P_u(z, z')$, i.e.,

$$P_y(z, z') = Pr[Z_{n+1} = z' | (Y_n, Z_n) = (y, z)].$$

We will set $P_y(0, 0) = 1$ for all $y = 1, \dots, m$ thus making 0 an absorbing state for (\mathbb{Z}_n) .

With the formulation (i) and (ii) above, (Y_n, Z_n) is a temporally non-homogeneous Markov process with transition kernel P given by

(1.2)
$$P[(y, z), (y', z')] = K(y, y')P_y(z, z').$$

Indeed (Y_n, Z_n) may be viewed as a "pieced-together" stochastic process each piece of which is a birth and death process conditioned or chosen by a fixed environmental state. Thus the evolving system (Z_n) changes its mode of evolution or mode of fluctuation due to changes in the environment controlled by a random process (Y_n) . (See [1] for a formulation of this type of stochastic model in a more abstract setting.) In a subsequent work [7] we describe a method for the calculation of extinction probabilities in the framework of the BDRE model. To illustrate these methods, we consider a stochastic model (Z_n) which represents genetic fluctuations due to mutation pressures influenced by varying environmental conditions. Birth and death models of these phenomena in constant environment have received considerable attention in the mathematical-biological literature [8, 4, 3].

2. Calculating extinction probabilities for the BDRE. For the study of biostochastic processes for which the BDRE model is appropriate, it is of paramount importance to find conditions which determine instability and almost certain extinction of the process (for the use of the word "instability" in this context, see Harris [2]). The results obtained in the aforementioned reference (Torrez [6]) give such conditions, and for ease of reference we state them below as Theorem A and Theorem B.

THEOREM A (Instability of the BDRE). Suppose that for each $\nu \in \{1, \dots, m\}$,

(2.1)
$$\max_{1 \leq i \leq m} \Pr[\tau_{\nu} > n \mid Y_0 = i] \to 0 \text{ as } n \to \infty$$

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where $\tau_{\nu} = \min\{\inf[n \ge 1 : Y_n = \nu], +\infty\}$. Then

 $\Pr[Z_n \to 0 \text{ or } + \infty | (Y_0, Z_0) = (y, z)] = 1$

where

$$(y, z) \in S = S_0 \setminus (\{1, \cdots, m\} \times 0).$$

REMARK. The requirement stated in the introduction that (Y_n) be irreducible makes (y_n) a positive recurrent Markov chain on finite state space so that (2.1) is satisfied, and moreover implies that K possesses an invariant distribution $\{\pi_i\}$.

Recall the notation $\{p_k^{(i)}, q_k^{(i)}, r_k^{(i)}\}, 1 \leq i \leq m, k \geq 0$, expressed in (1.1) for the transition probabilities of the BDRE. Define $u(y, z) = \Pr[(Y_n, Z_n) \in \{1, \dots, m\} \times \{0\}$ for some $n \mid (Y_0, Z_0) = (y, z)]$ for $(y, z) \in S$. Then the harmonic function u(y, z) is the probability of extinction of the BDRE when the initial state (y, z) is in S. We now state

THEOREM B (Extinction of the BDRE). Assume that the quantities

$$\overline{q}_k = \max_{1 \le i \le m} q_k^{(i)}, \ \underline{q}_k = \min_{1 \le i \le m} q_k^{(i)},$$

$$\overline{p}_k = \max_{1 \le i \le m} p_k^{(i)}, \ \underline{p}_k = \min_{1 \le i \le m} p_k^{(i)}$$

are positive and that $q_{z}^{(y)} + r_{z}^{(y)} \ge \underline{q}_{z+1}^{(y)}$ for all $(y, z) \in S$. Let $\lambda_{k} = \prod_{j=1}^{k} [\underline{q}_{j}/\overline{p}_{j}]$ and $\mu_{k} = \prod_{j=1}^{k} [\overline{q}_{j}/\underline{p}_{j}]$, $k = 1, 2, \cdots$ and $\lambda_{0} = \mu_{0} = 1$.

1. If $\sum_{k=0}^{\infty} \lambda_k = +\infty$, then u(y, z) = 1 for every $(y, z) \in S$, i.e., extinction of the BDRE is almost certain.

2. If $\sum_{k=0}^{\infty} \mu_k < +\infty$, then u(y, z) < 1 for every $(y, z) \in S$, i.e., extinction of the BDRE has probability less than one.

When the conditions of Theorem B.1 are not met (or at least in the cases when the series $\sum_{k=0}^{\infty} \mu_k$ converges) so that extinction may occur with probability < 1 it is also of great interest to be able to calculate extinction probabilities of the BDRE. We do so in the following way: the Dirichlet equation Pu = u, where P is the transition kernel for (Y_n, Z_n) defined in (1.2), holds with boundary conditions u(y, 0) = 1 and $u(y, \infty) = \lim_{N \to \infty} u(y, N) = 0$. To approximate the probability u(y, z), we first find the harmonic solution u_N of the Dirichlet equation $P_N u_N = u_N$ with boundary conditions

$$(2.2) u_{N}(y, 0) = 1$$

and

$$u_N(y, N) = 0.$$

Here P_N denotes the transition kernel for (Y_n, Z_n) restricted to the state space $S_N = \{1, \dots, m\} \times \{1, \dots, N\}$. With this formulation, u_N gives the probability that the process (Z_n) reaches state 0 before it reaches state N and by standard Markovian potential theory (see Syski [5]),

$$P_{N}[(y, z), (y', x')] \uparrow P[(y, z), (y', z')] \text{ and}$$
$$u_{N}(y, z) \uparrow u(y, z) \text{ as } N \to \infty$$

for (y, z), $(y', z') \in S_N$. We give two methods for calculating the function $u_N(y, z)$.

When the probabilities $\{p_z^{(y)}, q_z^{(y)}, r_z^{(y)}\}, (y, z) \in S$ are homogeneous, that is when they do not depend on the state z, an explicit solution for u_N is possible. The more general method, that is, when the transition probabilities depend on the state z, can be described as follows:

Since 0 is absorbing for (Z_n) , we have $r_0^{(y)} = r_N^{(y)} = 1$. (For the sake of convenience we will drop the subscript N from P_N and u_N and simply write P and u, respectively). We first represent the transition kernel P for (Y_n, Z_n) . From (1.1), we see that $P_y(z, z')$ is a square matrix (which we denote by $[P_u]$) of dimension N + 1:

	1	0	0	0	0	•••	•••	• • •	0	0
	$q_1^{(y)}$	0	$p_1^{(y)}$	0	0			• • •	0	0 0 0
	0	$q_2^{(y)}$	0	$p_2^{(y)}$	0	•••	• • •	• • •	0	0
$[P_{y}] =$.	•	•	•	•	•	•	•		
	.	•	•				•	•	•	0
	.	•	•		•	•	0	$q_{N-1}^{(y)}$	0	$p_{N-1}^{(y)}$
	Lo									1

From the definition of P,

$$P[(y, z), (y', z')] = K(y, y')P_y(z, z')$$

where $1 \leq y, y' \leq m, 0 \leq z, z' \leq N$. Thus P in block matrix form is

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$$[P] = \begin{bmatrix} K(1, 1)P_1 & \cdots & K(1, m)P_1 \\ \vdots & \vdots & \vdots \\ K(m, 1)P_m & \cdots & K(m, m)P_m \end{bmatrix}$$

This is an $m(N+1) \times m(N+1)$ matrix and the equations (2.2) have matrix formulation

$$(2.3) \begin{bmatrix} K(1, 1)P_{1} & \cdots & K(1, m)P_{1} \\ \vdots & \vdots & \vdots \\ \vdots & \ddots & \vdots \\ K(m, 1)P_{m} & \cdots & K(m, m)P_{m} \end{bmatrix} \begin{bmatrix} 1 \\ u(1, 1) \\ \vdots \\ u(1, N-1) \\ 0 \\ \vdots \\ u(1, N-1) \\ 0 \\ \vdots \\ u(m, 1) \\ \vdots \\ u(m, N-1) \\ 0 \end{bmatrix} = \begin{bmatrix} 1 \\ u(1, 1) \\ \vdots \\ u(1, N-1) \\ 0 \\ \vdots \\ u(1, N-1) \\ 0 \\ \vdots \\ u(m, 1) \\ \vdots \\ u(m, N-1) \\ 0 \end{bmatrix}$$

The result may be stated as follows:

THEOREM C. Let (Z_n) be a BDRE controlled by an environmental process (Y_n) . Let the transition probabilities of the BDRE be $\{p_z^{(u)}, q_z^{(u)}, r_z^{(u)}\}$ $(y, z) \in S$. Then the system (2.3) is equivalent to the vector difference equation

(2.4)
$$U_{k} = P_{k}^{*}U_{k+1} + R_{k}^{*}U_{k} + Q_{k}^{*}U_{k-\nu}$$
$$k = 1, \dots, N-1$$

with boundary conditions $U_0 = \hat{1}$, $U_N = \hat{0}$, where $\hat{1}$ and $\hat{0}$ are the $m \times 1$ identity and zero vectors respectively, and

$$P_{i}^{*} = \begin{bmatrix} K(1, 1)p_{i}^{(1)} & \cdots & K(1, m)p_{i}^{(1)} \\ \vdots & & \vdots \\ K(m, 1)p_{i}^{(m)} & \cdots & K(m, m)p_{i}^{(m)} \end{bmatrix}$$

$$Q_{i}^{*} = \begin{bmatrix} K(1, 1)q_{i}^{(1)} & \cdots & K(1, m)q_{i}^{(1)} \\ \vdots & & \vdots \\ K(m, 1)q_{i}^{(m)} & \cdots & K(m, m)q_{i}^{(m)} \end{bmatrix}$$

$$R_{i}^{*} = \begin{bmatrix} K(1, 1)(1 - p_{i}^{(1)} - q_{i}^{(1)}) & \cdots & K(1, m)(1 - p_{i}^{(1)} - q_{i}^{(1)}) \\ \vdots & & \vdots \\ K(m, 1)(1 - p_{i}^{(m)} - q_{i}^{(m)}) & \cdots & K(m, m)(1 - p_{i}^{(m)} - q_{i}^{(m)}) \end{bmatrix}$$

$$U_k = (u(1, k), \cdots, u(m, k))',$$

and

$$-\vec{q}_1 = (-q_1^{(1)}, \cdots, -q_1^{(m)})',$$

(Here "'" denotes transpose).

Since there are no known methods to solve the vector difference equation (2.4) explicitly, we must solve the system numerically. It can be shown [7] that the equation (2.4) is equivalent to the system

	$\begin{bmatrix} R_1^* - I \end{bmatrix}$	<i>P</i> ₁ *	0	0	0	• • •	0 7	۲ آ	U ₁ -		$-\vec{q}$
	Q_2^*	$R_2^* - I$	P_2^*	0	0	• • •	0		U_2		0
	0	Q_3^*	$R_{3}^{*} - I$	P ₃ *	0	• • •	0		U_3		0
(2.5)										=	
	0						0				
	· ·								•		•
		•	•	Q_{N-2}^*	$_{2}R_{N-2}^{*}$ -	– I	P_{N-2}^*	U			0
	0	•	•	•	Q_{N-1}^*		$R_{N-1}^* - I$	U			0

where I is the $m \times m$ identity matrix.

Call the block matrix on the left-hand side of (2.5) A. Then A is a socalled band matrix, i.e., a matrix with non-0 entries only along the main diagonals and sub- and super-diagonals. There are powerful computing algorithms for solving systems involving such matrices so that we may calculate U_k for N very large. We illustrate this method with the example in the next section.

GENETICS MODEL

3. A genetics model of Moran evolving in a random environment. In this section, we illustrate the result of the previous section by considering a gentics model, first proposed by Moran [4], to study the effects of mutation influences on gene frequencies.

Consider a haploid population of fixed size N consisting of allele types a and A. The state of the process (Z_n) , $n = 0, 1, 2, \dots$, represents the number of a alleles in the n^{th} generation. An allele is to be replaced at the (n + 1)st generation by another chosen randomly from the population. Let γ_1 and γ_2 denote, respectively, the probability that an *a*-type mutates to an *A*-type, and that an *A*-type mutates to an *a*type. This simple model of gene frequency fluctuations can be formulated as a discrete-time birth and death chain with a finite number of states with transition probabilities (see Karlin and McGregor [3])

$$p_k = \lambda_k / (\lambda_k + \mu_k), q_k = 1 - p_k, 1 \leq k \leq N - 1$$

where

$$\lambda_k = \Pr[\text{allele } a \text{ population increases } | Z_n = k]$$
$$= (1 - k/N)[(k/N)(1 - \gamma_1) + (1 - k/N)\gamma_2]$$

and

 $\mu_k = \Pr[\text{allele a population decreases} \mid Z_n = k]$

$$= (k/N)[(k/N)\gamma_1 + (1 - k/N)(1 - \gamma_2)].$$

Of course $r_0 = r_N = 1$ thus making 0 and N absorbing states. Suppose the population is exposed to "good" and "bad" external conditions (e.g., beneficial and adverse chemical, climatic, or radioactive factors) which determine varying mutation rates. Further suppose that the selection of these varying mutation rates, which we denote by $\gamma_j^{(i)}$, $1 \leq i, j \leq 2$, is controlled by an irreducible Markov chain with transition matrix

$$K = \begin{bmatrix} .55 & .45 \\ .6 & .4 \end{bmatrix}$$

If we specify that N = 51 and

$$\gamma_1^{(1)} = .5$$
 $\gamma_2^{(1)} = .75$
 $\gamma_1^{(2)} = .15$ $\gamma_2^{(2)} = .8$

then we may calculate the BDRE transition probabilities $\{p_k^{(i)}\}, i = 1, 2, 1 \le k \le 50$ and obtain the results listed in Table 1. From K, it is clear that the environmental process chooses the "good" environment

more often (indeed, the stationary measure is $\pi = (.57, .43)$) and in this environment, mutation rates favor *a* alleles, so that extinction of these types becomes nearly impossible. A quick glance at Table 1 verifies this.

z	$p_{z}^{(1)}$	$p_{z}^{(2)}$	u(1, z)	u(2, z)
1	.993	.995	$.701 imes 10^{-2}$	$.512 imes10^{-2}$
2	.985	.989	$.905 imes10^{-4}$	$.653 imes10^{-4}$
3	.977	.984	$.182 imes10^{-5}$	$.128 imes10^{-5}$
4	.968	.979	$.507 imes10^{-7}$	$.349 imes10^{-7}$
5	.959	.973	$.183 imes10^{-8}$	$.123 imes10^{-8}$
6	.949	.968	$.829 imes10^{-10}$	$.550 imes10^{-10}$
7	.939	.962	$.518 imes10^{-11}$	$.361 imes10^{-11}$
8	.927	.956	$.1 \times 10^{-11}$	$.898 imes10^{-12}$
9	.915	.950	$.736 imes 10^{-12}$	$.728 imes10^{-12}$
10	.903	.944	$.716 imes10^{-12}$	$.715 imes10^{-12}$
11	.889	.938	$.714 imes10^{-12}$	$.714 \times 10^{-12}$
12	.875	.931	0	0
13	.860	.925	0	0
14	.845	.918	0	0
15	.828	.911	0	0
16	.811	.904	0	0
17	.793	.896	0	0
18	.775	.888	0	0
19	.755	.880	0	0
20	.735	.872	0	0
21	.715	.863	0	0
22	.693	.854	0	0
23	.671	.845	0	0
24	.648	.835	0	0
25	.625	.825	0	0
26	.600	.814	0	0
27	.576	.802	0	0
28	.551	.790	0	0
29	.525	.778	0	0
30	.500	.764	0	0
31	.473	.750	0	0
32	.447	.735	0	0
33	.420	.719	0	0
34	.393	.702	0	0
35	.367	.684	0	0
36	.340	.664	0	0

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37	.313	.643	0	0
38	.286	.620	0	Ő
39	.260	.595	0	Ő
			-	
40	.234	.567	0	0
41	.208	.537	0	0
42	.182	.503	0	0
43	.157	.466	0	0
44	.133	.424	0	0
45	.109	.377	0	0
46	.086	.232	0	0
47	.063	.261	0	0
48	.041	.188	0	0
49	.023	.102	0	0
50	0	0	0	0

TABLE 1

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