

SOME GENERAL RESULTS ON RANDOM WALKS, WITH GENETIC APPLICATIONS

P. A. P. MORAN

(received 11 June 1962)

1. Introduction

Consider a random Markovian process in which the state of the system is defined by a random variable which can take the finite set of values $i = 0, 1, \dots, N$, and which is such that transitions can only occur from any state i to the two nearest states $i \pm 1$. This restriction brings about an essential simplification of the theory for the basic reason that in order for the system to move from state i to state j ($i < j$ say) it must first move to $i+1$, then $i+2$ and so on until it reaches j . From this it follows that the first passage distribution from i to j is the convolution of the first passage distributions from i to $i+1$, $i+1$ to $i+2$, \dots , $j-1$ to j each of which is comparatively easy to find.

In this paper we exemplify the resulting simplification in two ways. In the first we consider a continuous time process and obtain explicit representations of the Laplace transforms, with respect to time, of the first passage distributions and the transition probability densities. In the second we consider a process with one absorption state and obtain an explicit expression for the mean time of absorption. Under certain symmetry assumptions this can be generalised to the case of two absorption states and is then used to obtain the mean time required for a genetic population to become homozygous when the heterozygote is selectively advantageous over equally fit homozygotes.

2. The continuous-time random walk

Suppose that time is continuous and that the probabilities of moving from a state i to $i-1$ and $i+1$ in the time interval $(t, t+dt)$ are equal to $\mu_i dt + o(dt)$ and $\lambda_i dt + o(dt)$ respectively. We take $\lambda_i > 0$, $\mu_i > 0$ except that $\mu_0 = \lambda_N = 0$. Then starting from any initial state k the probabilities, $p_{ik}(t)$, of being in the state i at time t satisfy the differential equations:

$$\begin{aligned}
 p'_{0k}(t) &= -\lambda_0 p_{0k}(t) + \mu_1 p_{1k}(t), \\
 (1) \quad p'_{ik}(t) &= \lambda_{i-1} p_{i-1,k}(t) - (\lambda_i + \mu_i) p_{ik}(t) + \mu_{i+1} p_{i+1,k}(t) \quad (i = 1, \dots, N-1), \\
 p'_{Nk}(t) &= \lambda_{N-1} p_{N-1,k}(t) - \mu_N p_{N,k}(t).
 \end{aligned}$$

The resulting process is usually described as a finite Birth and Death Process with birth coefficients λ_i and death coefficients μ_i . In general the solutions of these equations is of the form

$$(2) \quad p_{ik}(t) = \sum_{s=0}^N a_{is} e^{\theta_s t}$$

where the a_{is} are constants chosen to fit the initial conditions, and the θ_s are the roots of the matrix

$$(3) \quad \begin{bmatrix} -(\lambda_0 + \theta) & \mu_1 & & & & \\ \lambda_0 & -(\lambda_1 + \mu_1 + \theta) & \mu_2 & & & \\ & \lambda_1 & -(\lambda_2 + \mu_2 + \theta) & & & \\ & & & \dots & & \\ & & & & \dots & \\ & & & & & \mu_N \\ & & & & & -(\mu_N + \theta) \end{bmatrix}$$

whose determinant we write as $M(\theta)$. The roots of (3) are known to be all real and distinct but it can be quickly verified that even for very simple definition of λ_i and μ_i as functions of i , the θ_s are usually very complicated and difficult to evaluate.

Karlin and McGregor ([6], [7]) have represented the transition probabilities of Birth and Death process as the Laplace-Stieltjes transforms of products of polynomials, the integrals being taken with respect to discrete distribution functions whose points of increase are the roots of $M(\theta)$. The use of this representation involves finding these roots and it is convenient to put off doing this as long as possible. Here we give a different representation by showing how the Laplace transforms, with respect to time, of the $p_{ik}(t)$ can be represented as the ratios of polynomials satisfying recurrence relations which are necessarily very similar to those of Karlin and McGregor.

Write

$$(4) \quad P_{ik}(\theta) = \int_0^\infty e^{-\theta t} p_{ik}(t) dt,$$

which exists for all $\theta > 0$. We then have

$$(5) \quad \int_0^\infty e^{-\theta t} p'_{ik}(t) dt = \theta P_{ik}(\theta) - \delta_{ik},$$

where δ_{ik} is Kronecker's δ . The set of equations (1) becomes

$$(6) \quad \begin{aligned} -\delta_{0k} &= -(\lambda_0 + \theta) P_{0k}(\theta) + \mu_1 P_{1k}(\theta), \\ -\delta_{1k} &= \lambda_0 P_{0k}(\theta) - (\lambda_1 + \mu_1 + \theta) P_{1k}(\theta) + \mu_2 P_{2k}(\theta), \\ &\dots \\ -\delta_{Nk} &= \lambda_{N-1} P_{N-1,k}(\theta) - (\mu_N + \theta) P_{Nk}(\theta). \end{aligned}$$

The matrix of coefficients on the right hand side of (6) is given by (3) and thus whenever $M(\theta) \neq 0$ we can solve (6) in the form

$$(7) \quad P_{ik}(\theta) = M_{ik}(\theta)M(\theta)^{-1},$$

where $M_{ik}(\theta)$ is a matrix obtained by replacing the $(i+1)$ th column in (3) by a column consisting of zeros except for -1 in the $(k+1)$ th row.

We can now find $M_{ik}(\theta)$ in a simpler form. Write $L_i(\theta)$ for the determinant of the matrix of the first $i+1$ rows and columns of (3), and $N_i(\theta)$ for the determinant of the last $N-i+1$ rows and columns. Then $L_N(\theta) = N_0(\theta) = M(\theta)$, and $L_0(\theta) = -(\lambda_0 + \theta)$, $N_N(\theta) = -(\mu_N + \theta)$. It is convenient to make the convention that $L_{-1}(\theta) = N_{N+1}(\theta) = 1$.

When $i = k$ examination of $M_{ik}(\theta)$ shows that expansion by the $(i+1)$ th column gives

$$(8) \quad M_{ik}(\theta) = -L_{i-1}(\theta)N_{i+1}(\theta).$$

By inspection of the determinant we also see that if $i > k$,

$$(9) \quad M_{ik}(\theta) = (-1)^{i-k+1} \lambda_k \lambda_{k+1} \cdots \lambda_{i-1} L_{k-1}(\theta) N_{i+1}(\theta),$$

and if $i < k$,

$$(10) \quad M_{ik}(\theta) = (-1)^{k-i+1} \mu_{i+1} \mu_{i+2} \cdots \mu_k L_{i-1}(\theta) N_{k+1}(\theta).$$

Hence the problem of finding the Laplace transforms of the transition probabilities is reduced to that of evaluating the determinants $L_i(\theta)$ and $N_i(\theta)$ for all i .

Inspection of (3) shows that

$$(11) \quad L_i(\theta) = -(\lambda_i + \mu_i + \theta)L_{i-1}(\theta) - \lambda_{i-1}\mu_i L_{i-2}(\theta)$$

for $i = 1, \dots, N$, using the above convention about $L_{-1}(\theta)$, and similarly

$$(12) \quad N_i(\theta) = -(\lambda_i + \mu_i + \theta)N_{i+1}(\theta) - \lambda_i \mu_{i+1} N_{i+2}(\theta).$$

It is useful to relate these results to first passage time distributions. Write $q_{ik}(t)dt$ for the probability that a first passage to state i occurs in the interval $(t, t+dt)$ when the system was in state k at time $t = 0$, and define the Laplace transform by

$$(13) \quad Q_{ik}(\theta) = \int_0^\infty e^{-\theta t} q_{ik}(t) dt.$$

Similarly let $s_k(t)dt$ be the probability that the system remains in the state k from $t = 0$ until $t > 0$ and then leaves k in the interval $(t, t+dt)$. Clearly

$$s_i(t)dt = (\lambda_i + \mu_i) e^{-(\lambda_i + \mu_i)t} dt,$$

and the Laplace transform is

$$(14) \quad S_i(0) = \nu_i(\nu_i + \theta)^{-1},$$

where $\nu_i = \lambda_i + \mu_i$.

Because of the linear arrangement of the states and the fact that nearest neighbour transitions only are permitted we can find the $M_{ik}(\theta)$ in terms of the $Q_{ik}(\theta)$. Consider first $M_{ii}(\theta)$.

$p_{ii}(t)$ is the probability that the system is in state i at time t if it was also in state i at $t = 0$. This could have happened in three different ways.

In the first there might have been no change in the interval $(0, t)$. This has probability $e^{-\nu_i t}$. In the second the system stays in i until a time $u (< t)$, passes to $i-1$ in $(u, u+du)$, passes back to i for the first time after u in $(v, v+dv)$, where $u < v < t$, and then whatever happens after v , is in i at time t . The probability of this sequence is

$$\mu_i e^{-\nu_i u} q_{i,i-1}(v-u) p_{ii}(t-v) du dv.$$

The third possibility is similar but the system moves to $i+1$ in $(u, u+du)$ and back to i for the first time in $(v, v+dv)$. Adding these possibilities we have

$$p_{ii}(t) = e^{-\nu_i t} + \int_0^t \int_0^v e^{-\nu_i u} \mu_i q_{i,i-1}(v-u) p_{ii}(t-v) du dv + \int_0^t \int_0^v e^{-\nu_i u} \lambda_i q_{i,i+1}(v-u) p_{ii}(t-v) du dv.$$

Taking Laplace transforms we have

$$P_{ii}(\theta) = (\nu_i + \theta)^{-1} + \mu_i (\nu_i + \theta)^{-1} Q_{i,i-1}(\theta) P_{ii}(\theta) + \lambda_i (\nu_i + \theta)^{-1} Q_{i,i+1}(\theta) P_{ii}(\theta),$$

and hence

$$(15) \quad P_{ii}(\theta) = \{ \nu_i + \theta - \mu_i Q_{i,i-1}(\theta) - \lambda_i Q_{i,i+1}(\theta) \}^{-1}.$$

If $k < i$, it is also clear that

$$(16) \quad Q_{ik}(\theta) = Q_{k+1,k}(\theta) Q_{k+2,k+1}(\theta) \cdots Q_{i,i-1}(\theta),$$

and

$$(17) \quad P_{ik}(\theta) = Q_{ik}(\theta) P_{ii}(\theta).$$

Next we must find the Q 's. Consider $Q_{i+1,i}(\theta)$. A first passage from i at $t = 0$ to $i+1$ at t can occur in two ways. In the first there is no change between $t = 0$ and $t-dt$, but during $(t-dt, t)$ there is a jump from i to $i+1$. This has probability

$$\lambda_i e^{-\nu_i t} dt.$$

In the second there is no change between 0 and u ($0 < u < t$), a jump to $i-1$ in $(u, u+du)$, a first passage from $i-1$ to i in $(v, v+dv)$

($0 < u < v < t$), and a first passage from i to $i+1$ in $(t-dt, t)$. Integrating over the values of u and v , this has probability

$$\int_0^t \int_0^v e^{-v\mu} \mu_i q_{i,i-1}(v-u) q_{i+1,i}(t-v) du dv dt.$$

Taking Laplace transforms we obtain

$$Q_{i+1,i}(\theta) = \lambda_i(v_i + \theta)^{-1} + \mu_i(v_i + \theta)^{-1} Q_{i,i-1}(\theta) Q_{i+1,i}(\theta),$$

and hence

$$(18) \quad Q_{i+1,i}(\theta) = \lambda_i \{v_i + \theta - \mu_i Q_{i,i-1}(\theta)\}^{-1},$$

which provides us with a recurrence relation for the $Q_{i+1,i}(\theta)$ from which they can be found successively starting from

$$(19) \quad Q_{1,0}(\theta) = \lambda_0(\lambda_0 + \theta)^{-1}.$$

Similarly we have

$$(20) \quad Q_{i-1,i}(\theta) = \mu_i \{v_i + \theta - \lambda_i Q_{i,i+1}(\theta)\}^{-1},$$

and]

$$(21) \quad Q_{N-1,N}(\theta) = \mu_N \{\mu_N + \theta\}^{-1}.$$

We now show that

$$(22) \quad Q_{i+1,i}(\theta) = -\lambda_i L_{i-1}(\theta) L_i(\theta)^{-1},$$

and

$$(23) \quad Q_{i-1,i}(\theta) = -\mu_i N_{i+1}(\theta) N_i(\theta)^{-1}.$$

Equation (22) is clearly true for $i = 0$ from (19) and the known values of $L_{-1}(\theta)$ and $L_0(\theta)$. Supposing that (22) is satisfied for all values of i up to $i = s$, substituting in (18) and using the recurrence relation (11) we see that (22) is true for $i = s+1$, and therefore for $i = 0, 1, \dots, N$. (23) may be similarly verified.

Substituting in (16) and (17) we find for $k < i$,

$$(24) \quad P_{ik}(\theta) = \frac{(-i)^{i-k} \lambda_k \dots \lambda_{i-1} L_{k-1}(\theta) N_{i+1}(\theta)}{\{(v_i + \theta) L_{i-1}(\theta) N_{i+1}(\theta) - \mu_i \lambda_{i-1} L_{i-2}(\theta) N_{i+1}(\theta) - \lambda_i \mu_{i+1} L_{i-1}(\theta) N_{i+2}(\theta)\}},$$

which is otherwise obvious by expanding (7).

The advantage of this method of procedure is that in any particular case we can obtain $L_i(\theta)$ and $N_{N-i}(\theta)$ explicitly for small values of i and knowing the recurrence relation we can try to guess the resulting polynomials. A systematic investigation of all the simplest functions λ_i, μ_i would be desirable. Here we draw attention to a few known cases.

3. Special cases

If either all the λ_i , or all the μ_i , are zero, the roots of (3) are obvious and it is not in principle difficult to write down an explicit solution. In particular if all $\mu_i = 0$ and the λ_i are constant the equations are easy to solve. If $\mu_i = 0$ and $\lambda_i = \lambda i$ we have the well-known linear birth process. If $\mu_i = 0$ and λ_i is a quadratic function of i we have a quadratic birth process considered by John [5].

If λ_i and μ_i are both non-zero constants the recurrence relations can be solved explicitly and inversion of the Laplace transforms results in modified Bessel functions of the first kind (Heathcote and Moyal [3]).

Not many other explicit solutions are known. When N is infinite and $\lambda_i = \lambda i$, $\mu_i = \mu i$ we have the well known simple birth and death process first solved by Palm (see Kendall [9]). It is usually more realistic in practice to put an upper bound to the size of the population, thus making the methods of the present paper applicable, and for biological populations the natural approach is to construct an analogue of the deterministic logistic process in the manner described by Kendall. We suppose that the population is confined between two limits N_1, N_2 so that $0 \leq N_1 \leq i \leq N_2$, and that the birth and death rates per individual are linear functions of i ;

$$(25) \quad \lambda_i = \lambda i(N_2 - i),$$

$$(26) \quad \mu_i = \mu i(i - N_1).$$

This makes the death rate per individual increase linearly with i , and the birth rate per individual decrease linearly. In order to get simpler equations Prendiville [14] suggested that (25) and (26) be modified to

$$(27) \quad \lambda_i = \lambda(N_2 - i),$$

$$(28) \quad \mu_i = \mu(i - N_1),$$

thus making the birth and death rates per individual proportional to $N_2 i^{-1} - 1$ and $1 - N_1 i^{-1}$ respectively, which vary in the right direction. He did not, however, publish his analysis and the first published solution was given by Takashima [15].

The present theory makes the reason for the simplicity of the solution clearer. Shifting the origin of definition of i to N_1 we can write (27) and (28) in the form

$$(29) \quad \lambda_i = \lambda(N - i),$$

$$(30) \quad \mu_i = \mu i,$$

and the roots of the determinant $M(\theta)$ come out simply by using the factorisation of the determinant

$$(32) \quad T_i = t_i + t_{i+1} + \dots + t_{N-1}.$$

If the system is in state i it will remain there for a period s_i and then move either to $i-1$ or to $i+1$, where s_i clearly has a geometric distribution,

$$\text{prob}(s_i = n) = r_i^{n-1}(1-r_i), \quad n = 1, 2, \dots$$

Thus

$$(33) \quad E(s_i) = (1-r_i)^{-1}.$$

If the system moves to $i+1$, s_i will be the first passage time. If it moves to $i-1$ the expected remaining time to reach $i+1$ will be $t_{i-1} + t_i$.

Thus

$$t_i = (1-r_i)^{-1} + q_i(t_{i-1} + t_i)(1-r_i)^{-1}$$

so that

$$(34) \quad p_i t_i = 1 + q_i t_{i-1}.$$

It is also possible to obtain a recurrence formula for the variance of the first passage time from t to $t+1$ but this is more complicated.

Since $t_0 = p_0^{-1}$ we can find t_1, t_2, \dots in succession, thus obtaining

$$t_1 = \frac{1}{p_1} + \frac{q_1}{p_0 p_1},$$

$$t_2 = \frac{1}{p_2} + \frac{q_2}{p_1 p_2} + \frac{q_1 q_2}{p_0 p_1 p_2},$$

and in general

$$(35) \quad t_i = \frac{1}{p_i} + \frac{q_i}{p_{i-1} p_i} + \dots + \frac{q_1 \dots q_i}{p_0 p_1 \dots p_i}$$

$$= \sum_{k=0}^{i-1} \frac{q_{i+1} q_i \dots q_{i-k+1}}{p_{i+1} p_i p_{i-1} \dots p_{i-k}}.$$

From (35) T_i can be found by summation. These results can be found in Harris [2] and Chung (see references in the latter's book [1]), and also Hodges and Rosenblatt [4]. Notice that similar methods can be used with continuous time models.

The above theory depends essentially on the assumption that there is only one absorbing state. However, we can still deal with the case where both $i = 0$ and $i = N$ are absorbing states if we have the symmetry condition $q_i = p_{N-i}$. To do this we identify the states i and $N-i$ which is now permissible. If N is even and equal to $2M$ we get a Markov chain with $M+1$ states E_0, E_1, \dots, E_M such that E_0 is not an absorbing state but E_M is.

5. An application to genetics

We now apply this result to discuss the behaviour of some genetic populations. The majority of such populations consist of diploid individuals but the mathematics is then so complicated that for the most part mathematical geneticists have been content to study models in which the individuals are haploid and the effects of selection are of such a kind as to provide a good imitation of the diploid case.

One model of such a population is as follows (Moran [10] [11]). Suppose the population consists of $N = 2M$ haploid individuals which are genetically either A or a . The number of A individuals is i and defines the state of the system where $i = 0, 1, \dots, N$. At successive unit intervals of time a haploid individual, chosen at random, dies and is replaced by a new individual which is A or a with probabilities equal to the relative proportion of these in the population before the death occurred. If the system was in the state i , it can only move to the states $i-1$, i , and $i+1$ at each step, and does so with probabilities,

$$(36) \quad \begin{aligned} p_{i-1,i} &= i(N-i)N^{-2}, \\ p_{i,i} &= \{i^2 + (N-i)^2\}N^{-2}, \\ p_{i+1,i} &= i(N-i)N^{-2}. \end{aligned}$$

The behaviour of this process has been very thoroughly studied and in particular Watterson [16] showed that if it starts from the state j , the expected number of steps to one of the absorbing states $0, N$, is given by

$$(37) \quad \begin{aligned} E(T_j) &= N(N-j)\{(N-1)^{-1} + \dots + (N-j)^{-1}\} \\ &\quad + Nj\{(N-1)^{-1} + \dots + (j-1)^{-1}\}. \end{aligned}$$

This can be obtained by the above methods as we shall see, and so also can Watterson's similar formula for $\text{Var}(T_j)$.

One of the main problems in the study of genetic models of this kind is to determine how fast real genetic populations become homozygous as the result of random assortment of genes. In the haploid models this corresponds to the states $j = 0, N$ and we often use the expression "rate of progress to homozygosity" for such models in spite of the fact that there are no zygotes, the individuals being haploid. Thus what we are really concerned with is the rate of absorption into the states $j = 0, N$ and in so far as the haploid model is an adequate description of the real diploid population, this provides an answer to the problem.

The probability that $j \neq 0, N$ will be asymptotically equal to $C\lambda^t$, where C is a constant, λ is the largest non-unit root of the matrix of transition probabilities, and t is the number of birth-death events. Much research has been devoted to the calculation of C and λ for varying genetic

assumption but hardly any progress has been made when there is any kind of selection. In particular the most interesting case arises when, in populations of diploids, the heterozygote Aa has a selective advantage over the two homozygotes AA and aa . This leads to the simplest example of a "selectively balanced polymorphism", and it is of great practical interest to determine how large such selective forces must be to keep a natural population polymorphic for a given number of generations.

In such circumstances λ has not been found and would be extremely difficult to find theoretically. However, a different approach can be made by calculating not the probability that the process is heterozygous as a function of t , but simply the mean time necessary to become homozygous. We shall show that the mathematics is then not difficult provided the two homozygotes, AA and aa , have equal selective value.

In a haploid model, diploid selection has no meaning. However, a satisfactory model could be constructed by modifying the transition probabilities in the haploid model in such a way that the change in gene frequency from t to $t+1$ has the mean and variance it should have in a diploid model.

Consider first what happens in an infinitely large population with diploid individuals which are AA , Aa , or aa . Let the frequency of the A gene be p , and assume random mating so that the frequencies of the AA , Aa , and aa individuals are p^2 , $2pq$, and q^2 ($q = 1-p$). Suppose that AA and aa have the same selective value unity, and that the heterozygote Aa has the relative selective value $1+s$ where $s > 0$. It is then well known and easy to show that the expected change in gene frequency from one generation to the next is approximately

$$(38) \quad \Delta p = -spq(p-q)$$

the approximation being satisfactory when s is small compared with unity.

Since iN^{-1} is the relative gene frequency in the haploid model, and since one generation corresponds to N birth-death events, a suitable model is given by

$$\begin{aligned} p_{i+1,t} &= p_t = i(N-i)N^{-2}\{1 - \frac{1}{2}sN^{-1}(2i-N)\}, \\ p_{i,t} &= r_i = \{i^2 + (N-i)^2\}N^{-2}, \\ p_{i-1,t} &= q_t = i(N-i)N^{-2}\{1 + \frac{1}{2}sN^{-1}(2i-N)\}. \end{aligned}$$

We can now find the mean time of absorption. Suppose N is even and equal to $2M$. Since $p_i = q_{N-i}$ we can replace the system by a Markov chain with $M+1$ states E_k , $k = 0, 1, \dots, M$, for which

$$\begin{aligned} p_{k+1,k} &= p_k = (4M^2)^{-1}(M^2 - k^2)\{1 - \frac{1}{2}skM^{-1}\}, & (k > 0), \\ p_{k,k} &= r_k = (2M^2)^{-1}(M^2 + k^2), \\ p_{k-1,k} &= q_k = (4M^2)^{-1}(M^2 - k^2)\{1 + \frac{1}{2}skM^{-1}\}, & (k > 0). \end{aligned}$$

We substitute from these in (32) and (35) and obtain

$$(39) \quad E(T_i) = \sum_{j=i}^{M-1} \sum_{k=0}^j A_{jk},$$

where

$$(40) \quad A_{jk} = \frac{4M^2(N+sj) \cdots (N+s(j-k+1))}{\{M^2 - (j-k)^2\} \{1 - \frac{1}{2}s(j-k)M^{-1}\} (N-sj) \cdots (N-s(j-k+1))}$$

$$= \frac{4M^2\Gamma(Ns^{-1}+j+1)\Gamma(Ns^{-1}-j)}{\{M^2 - (j-k)^2\} \{1 - \frac{1}{2}s(j-k)M^{-1}\} \Gamma(Ns^{-1}+j-k+1)\Gamma(Ns^{-1}+k-j)}.$$

We assume that s is of the same order as M^{-1} and we put $s = \sigma M^{-1}$ where σ is to be kept fixed as M gets large. Consider the expression

$$\Gamma(x+a)\Gamma(x+b)^{-1}$$

where a and b are kept fixed and x increases indefinitely. Using Stirling's formula this is asymptotically equal to

$$x^{a-b} \exp \left\{ b-a + (x+a-\frac{1}{2}) \log(1+ax^{-1}) - (x+b-\frac{1}{2}) \log(1+bx^{-1}) \right\}.$$

Expanding the logarithm and taking the largest term we get

$$x^{a-b} \exp \left\{ \frac{1}{2}(a^2-b^2)x^{-1} - \frac{1}{2}(a-b)x^{-1} \right\}.$$

Using this result in (40) we find that A_{jk} is asymptotically equal to

$$4M^2\{M^2 - (j-k)^2\}^{-1} \exp \frac{1}{2}\sigma M^{-2}k(2j-k+1).$$

We can therefore approximate to the double sum in (39) by the integral

$$4M^2 \int_x^1 \int_0^y \{1 - (y-z)^2\}^{-1} \exp \frac{1}{2}\sigma z(2y-z) dz dy,$$

where $x = iM^{-1}$, i being the initial state. Putting $u = y-z$ this becomes

$$(41) \quad 4M^2 \int_x^1 \int_0^y (1-u^2)^{-1} \exp \frac{1}{2}\sigma(y^2-u^2) du dy.$$

In the particular case $x = 0$ so that the process starts with the numbers of A , a genes equal, this is easily transformed into

$$(42) \quad E(T_i) = 4M^2 \int_0^1 (1-u^2)^{-1} \exp -\frac{1}{2}\sigma u^2 \int_u^1 \exp \frac{1}{2}\sigma y^2 dy du,$$

which can be fairly easily evaluated in particular cases by numerical integration. When $\sigma = 0$, (41) can be verified to be asymptotically to equal to (37) which can also be derived directly from (39).

References

- [1] Chung, K. L., *Markov Chains with stationary transition probabilities*. Grundlehren der Mathematischen Wissenschaften. Band 104. Springer (1960).
- [2] Harris, T. E., First passage and recurrence distributions. *Trans. Amer. Math. Soc.* **73**, (1952) 471–486.
- [3] Heathcote, C. R. and Moyal, J. E., The random walk (in continuous time) and its application to the theory of queues. *Biometrika* **46**, (1959) 400–411.
- [4] Hodges, J. L. and Rosenblatt, M., Recurrence time moments in random walks. *Pacific J. Math.* **3**, (1953) 127–136.
- [5] John, P. W. M., The quadratic birth process (Abstract). *Ann. Math. Statistics* **27**, (1956) 865.
- [6] Karlin, S. and McGregor, J. L., The differential equations of birth-and-death processes and the Stieltjes moment problem. *Trans. Amer. Math. Soc.* **85**, (1957) 489–546.
- [7] Karlin, S. and McGregor, J. L., The classification of birth-and-death processes. *Trans. Amer. Math. Soc.* **86**, (1957) 366–400.
- [8] Karlin, S. and McGregor, J. L., On a genetics model of Moran. *Proc. Cam. Phil. Soc.* **58**, (1962).
- [9] Kendall, D. G., Stochastic processes and population growth. *Jour. Roy. Statist. Soc. B.* **11**, (1949) 230–264.
- [10] Moran, P. A. P., Random processes in genetics. *Proc. Cam. Phil. Soc.* **54**, (1958) 60–71.
- [11] Moran, P. A. P., *The statistical processes of evolutionary theory*. Oxford University Press. 1962.
- [12] Muir, T., *History of the Theory of Determinants*. Vol. 3, (1911) p. 432.
- [13] Painvin, L., Sur un certain système d'équations linéaires. *Jour. de Math. (de Liouville)* (2) iii, (1858) 41–46.
- [14] Prendiville, B. J., Discussion of a paper by D. G. Kendall. *Jour. Roy. Stat. Soc. B.* **11**, (1949) 273.
- [15] Takashima, M., Note on evolutionary processes. *Bull. Math. Stat.* **7**, (1956) 18–24.
- [16] Watterson, G. A., Markov chains with absorbing states: a genetic example. *Ann. Math. Stat.* **32** (1961) 716–729.

Institute of Advanced Studies,
The Australian National University,
Canberra