



Some generalized age-dependent branching processes  
by Kenny Sherman Crump

A thesis submitted to the Graduate Faculty in partial fulfillment of the requirements for the degree of  
DOCTOR OF PHILOSOPHY in Mathematics  
Montana State University  
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Abstract:

Several models for branching processes are investigated which extend the age-dependent model of Bellman and Harris (1952). These models are developed primarily to provide reasonable alternatives to the assumptions that individuals live and reproduce independently and that the death of a parent and the birth of offspring must occur simultaneously.

A process in which correlations occur among siblings is obtained by assuming the life-spans (as well as the numbers of offspring) of a group of siblings are exchangeable random variables. Other necessary probabilistic relations are governed by independence. The generating function of  $z^{(k)}(t)$ , the number of individuals alive at time  $t$  descending from  $k$  siblings born at time  $t = 0$ , satisfies a system of integral equations, which, upon differentiation, becomes a simple renewal equation for  $E[z^{(1)}(t)z^{(1)}(t+\tau)]$  which in certain cases leads to the result that  $Z^{(k)}(t)/e^{\alpha(2t + \tau)}$  converges in mean square to a r.v.  $W^{(k)}$  as  $t \rightarrow \infty$  and, in turn,  $W^{(k)}$  converges in mean square to a nondegenerate r.v.  $W$  as  $k \rightarrow \infty$ . In the binary case, the distribution of  $W^{(2)}$  is continuous and, provided  $1 - G_1(t) = O(e^{-\epsilon t})$ ,  $\epsilon > 0$ , it is also absolutely continuous.

Dependence between generations is introduced by assuming that if  $o_1, \dots, o_j, \dots$  is a sequence of individuals with  $o_j$  the parent of  $o_{j+1}$  then the life-spans of these individuals form a Markov chain. An integral equation satisfied by the generating function of the process is used to study the probability of extinction and the first moments. A simpler model with dependence between generations is also described and it is indicated how standard techniques may be employed to study this model.

A rather general birth-and-death process is considered in which an individual may give birth at various times during its life. The number of offspring  $N(t)$  born to an individual with life-span  $l$  during the age-interval  $[0, t]$  is defined by  $N(t) = K(t)$  if  $t \leq l$ , and  $N(t) = K(l)$  if  $t > l$ , where  $K(t)$  is an arbitrary counting process. Individuals are assumed to live and reproduce independently. If  $E[K(t)] < \infty$  for all  $t$  and  $E[K(0)] < 1$ , then  $Z(t)$ , the size of the population at time  $t$ , is finite a.s. The probability of extinction of  $Z(t)$  is the smallest nonnegative root of the equation  $s = E[\exp\{N(l)(\log s)\}]$ . A renewal-type integral equation is derived for  $M(t) = E[Z(t)]$ , and this equation is used to investigate the monotonicity and asymptotic properties of  $M(t)$ . Again,  $Z(t)/e^{\alpha t}$  converges in mean square (a.s. in some instances) to a r.v.  $W$  as  $t \rightarrow \infty$ . For the special case where  $K(t)$  is a compound Poisson process, the generating function of  $Z(t)$  satisfies a useful integral equation which is utilized in investigating the distribution of  $W$ . and in showing that Markov branching processes form a special case of this process.

In a process where the life-span of an individual depends on the size of his family, the first two moments satisfy systems of non-linear renewal-type integral equations. Asymptotic expressions for these moments are obtained using complex variable techniques.

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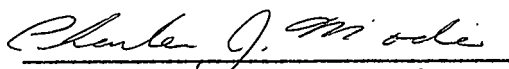
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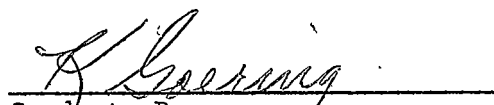
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ABSTRACT

Several models for branching processes are investigated which extend the age-dependent model of Bellman and Harris (1952). These models are developed primarily to provide reasonable alternatives to the assumptions that individuals live and reproduce independently and that the death of a parent and the birth of offspring must occur simultaneously.

A process in which correlations occur among siblings is obtained by assuming the life-spans (as well as the numbers of offspring) of a group of siblings are exchangeable random variables. Other necessary probabilistic relations are governed by independence. The generating function of  $Z^{(k)}(t)$ , the number of individuals alive at time  $t$  descending from  $k$  siblings born at time  $t = 0$ , satisfies a system of integral equations, which, upon differentiation, becomes a simple renewal equation for  $E[Z^{(1)}(t)Z^{(1)}(t+\tau)]$  which in certain cases leads to the result that  $Z^{(k)}(t)/e^{\alpha(2t+\tau)}$  converges in mean square to a r.v.  $W^{(k)}$  as  $t \rightarrow \infty$  and, in turn,  $W^{(k)}$  converges in mean square to a nondegenerate r.v.  $W$  as  $k \rightarrow \infty$ . In the binary case, the distribution of  $W^{(2)}$  is continuous and, provided  $1 - G_1(t) = O(e^{-\epsilon t})$ ,  $\epsilon > 0$ , it is also absolutely continuous.

Dependence between generations is introduced by assuming that if  $o_1, \dots, o_j, \dots$  is a sequence of individuals with  $o_j$  the parent of  $o_{j+1}$  then the life-spans of these individuals form a Markov chain. An integral equation satisfied by the generating function of the process is used to study the probability of extinction and the first moments. A simpler model with dependence between generations is also described and it is indicated how standard techniques may be employed to study this model.

A rather general birth-and-death process is considered in which an individual may give birth at various times during its life. The number of offspring  $N(t)$  born to an individual with life-span  $\ell$  during the age-interval  $[0, t]$  is defined by  $N(t) = K(t)$  if  $t \leq \ell$ , and  $N(t) = K(\ell)$  if  $t > \ell$ , where  $K(t)$  is an arbitrary counting process. Individuals are assumed to live and reproduce independently. If  $E[K(t)] < \infty$  for all  $t$  and  $E[K(0)] < 1$ , then  $Z(t)$ , the size of the population at time  $t$ , is finite a.s. The probability of extinction of  $Z(t)$  is the smallest non-negative root of the equation  $s = E[\exp\{N(\ell)(\log s)\}]$ . A renewal-type integral equation is derived for  $M(t) = E[Z(t)]$ , and this equation is used to investigate the monotonicity and asymptotic properties of  $M(t)$ . Again,  $Z(t)/e^{\alpha t}$  converges in mean square (a.s. in some instances) to a r.v.  $W$  as  $t \rightarrow \infty$ . For the special case where  $K(t)$  is a compound Poisson process, the generating function of  $Z(t)$  satisfies a useful integral equation which is utilized in investigating the distribution of  $W$  and in showing that Markov branching processes form a special case of this process.

In a process where the life-span of an individual depends on the size of his family, the first two moments satisfy systems of non-linear renewal-type integral equations. Asymptotic expressions for these moments are obtained using complex variable techniques.

## Chapter I

### INTRODUCTION

#### 1.1 Statement of Problem

Generally speaking, a branching process is a mathematical model for the development of a population whose members reproduce and die, subject to laws of chance. For convenience, in this thesis we shall usually refer to the members of a population as "individuals", although the mathematical model being discussed may be applicable to bacteria, plants, atomic particles, or many other things. The reader interested in applications, as well as the basic theory of branching processes, may refer to the monograph by T. E. Harris (1963). Kendall (1966) gives an interesting account of the history of branching processes.

Most of the models for branching processes studied previously have incorporated the assumption that members of the population must not interfere with one another. In other words, they must live and reproduce independently. This assumption seems reasonable for some applications; e.g., when the population is composed of atomic particles, and there is on the average, a sizable distance between adjacent particles. However, for the study of complex biological populations, it would be advantageous to be able to introduce certain types of dependence among individuals, particularly among related individuals. Such an assumption might, for example, enable one to incorporate the effects of heredity into the framework of branching processes.

Another often undesirable feature of the more well-known models is



that the death of the parent<sup>1</sup> must occur simultaneously with the birth of offspring.<sup>2</sup> Although this feature has a natural application in populations of bacteria that reproduce by splitting, a model which allows reproduction to occur throughout the life of the parent would certainly be of interest.

The purpose of this thesis, then, is to formulate mathematical models for branching processes which incorporate some of the suggestions in the foregoing paragraphs, and then to investigate the properties of these models. Chapter II concerns a model in which the life-spans of siblings are correlated, as well as the numbers of offspring produced by siblings, but otherwise individuals live and reproduce independently. Next, two models are discussed in which an individual's life-span is influenced by the life-spans of his ancestors. In Chapter IV a fairly general process is studied wherein it is possible for an individual to give birth at various times during his life. Finally, in Chapter V a brief description of two processes is given. The first process deals with a special type of dependence between generations and the second process allows for the possibility of an individual becoming dormant and remaining in the population indefinitely but never having offspring.

Before proceeding to these models, however, it seems appropriate

- 
- 1 All of the processes discussed in this thesis consider only one sex, so an individual will have only one parent in the population.
  - 2 In age-independent processes such as Markov branching processes (Harris (1963)) it actually makes no difference whether we assume an individual dies at time  $t$  and is replaced by  $n \geq 1$  offspring or that he continues to live and has  $n - 1$  offspring at time  $t$ .

that we pause here to describe two of the most well-known branching processes and to state some results for these models which we will find convenient to refer to later. We shall also present some results from renewal theory which will be useful in the sequel.

## 1.2 The Galton-Watson Process

It was about 100 years ago that Watson and Galton (1874) formulated a model to study the problem of the extinction of family surnames. Because of the disappearance of the surnames of many families that had once occupied conspicuous positions, it had been conjectured that distinguished families are more likely to die out than ordinary ones. In order to explore this hypothesis, Galton recognized that it would be desirable to first know the probability that an ordinary family becomes extinct.

In the mathematical model developed by Galton and Watson for this purpose (called a Galton-Watson process), a man has probabilities  $p_0, p_1, p_2, \dots$  of having  $0, 1, 2, \dots$  sons and in turn each of these offspring has sons of his own with the same probabilities, and so on. The number of sons sired by any man is assumed independent of the number of male progeny of any other man.

An important role in the investigation of this process is played by the generating function

$$h(s) = \sum_{n=0}^{\infty} p_n s^n, \quad |s| \leq 1.$$

For instance, the smallest non-negative root of the functional equation

$h(s) = s$  turns out to be the probability that the male line originating from a single man will eventually terminate. If  $h'(1) \leq 1$  this root is one (assuming  $p_1 < 1$ ), but if  $h'(1) > 1$  this root is strictly less than one. (Due to an oversight, Watson concluded erroneously that this root was always equal to one.) Although the model of Galton and Watson was overlooked for many years, numerous papers on this model have appeared in the past two decades.

### 1.3 The Bellman-Harris Process

Bellman and Harris (1952) studied an extension of the Galton-Watson process in which the life-spans of individuals are also taken into consideration. A single individual born at time  $t = 0$  lives for a random length of time with distribution function  $G(t)$ . At the end of its life it is replaced by  $n$  offspring,  $n = 0, 1, 2, \dots$ , with probability  $p_n$ . These progeny, in turn, behave in the same way as the progenitor and so the process continues for as long as individuals are present. The life-span and the number of children of each member of the population have the same probability distributions as the corresponding ones for the original individual. The other necessary probabilistic relations are governed by independence, so that this process is completely determined by the distribution  $G(t)$  and the generating function  $h(s) = \sum p_n s^n$ . It is usually assumed that these functions satisfy the conditions  $G(0) = 0$ ,  $G(\infty) = 1$  and  $m \equiv h'(1) < \infty$ . All distribution functions that appear in this thesis are taken to be continuous from the right.

To avoid confusion, we shall call the random function  $Z(t)$

giving the size of the population at time  $t$  a Bellman-Harris process, although the term "age-dependent branching process" seems to be more in vogue in the literature. However, the latter expression also appropriately describes several other models discussed in this thesis.

The generating function  $F(s,t)$  of the random function  $Z(t)$  is defined by

$$F(s,t) = E[s^{Z(t)}] = \sum_{k=0}^{\infty} P[Z(t) = k] s^k, \quad t \geq 0, \quad |s| \leq 1. \quad (1.3.1)$$

Harris (1963) proves that  $F(s,t)$  satisfies the integral equation<sup>1</sup>

$$F(s,t) = s[1 - G(t)] + \int_0^t h[F(s,t-u)] dG(u). \quad (1.3.2)$$

Upon differentiating (1.3.2) with respect to  $s$  and putting  $s = 1$ , it follows that  $M(t) \equiv E[Z(t)]$  satisfies the renewal equation

$$M(t) = 1 - G(t) + m \int_0^t M(t-u) dG(u). \quad (1.3.3)$$

The following lemma summarizes some other well-known facts about  $M(t)$ .

---

1 In this thesis the symbol  $\int_a^b$  will mean  $\int_{[a,b]}$ . To denote  $\int_{[a,b)}$ ,  $\int_{(a,b]}$ , and  $\int_{(a,b)}$ , we will use  $\int_a^{b-}$ ,  $\int_{a+}^b$ , and  $\int_{a+}^{b-}$ , respectively.

Lemma 1.3.1: (i) Equation (1.3.3) has a unique solution that is bounded on every finite interval.

(ii) This solution may be written in the form

$$M(t) = 1 + (m-1) \sum_{k=1}^{\infty} m^{k-1} G_k(t), \quad (1.3.4)$$

where  $G_k$  is the  $k^{\text{th}}$  convolution of  $G$  with itself.

(iii) If  $G$  is not a lattice distribution<sup>1</sup> and there exists an  $\alpha$  such that

$$m \int_0^{\infty} e^{-\alpha u} dG(u) = 1 \quad (1.3.5)$$

and

$$\int_0^{\infty} u e^{-\alpha u} dG(u) < \infty, \quad (1.3.6)$$

then

$$M(t)e^{-\alpha t} \rightarrow \frac{\int_0^{\infty} e^{-\alpha u} [1 - G(u)] du}{m \int_0^{\infty} t e^{-\alpha u} dG(u)} \quad \text{as } t \rightarrow \infty. \quad (1.3.7)$$

These results concerning the renewal equation (1.3.3) are all given

---

<sup>1</sup> We say that  $G$  is a lattice distribution if its only points of increase are integer multiples of some fixed number.

explicitly in Harris (1963) (with the exception of 1.3.4, which is easily deducible from Harris' Lemma 1, page 161). However, we shall prove parts (ii) and (iii) at the end of the next section to illustrate the results from renewal theory presented there.

#### 1.4 Some results from renewal theory

Since the moments of several of the processes to be studied satisfy renewal-type equations, rather extensive use will be made of the results in this section. The treatment of renewal theory given here is patterned after Feller (1966).

Throughout this section we shall suppose that  $F(t)$  and  $H(t)$  are finite, nondecreasing, continuous from the right and equal to zero when  $t \leq 0$ . Of considerable interest in renewal theory is the function

$$U(t) = \sum_{k=0}^{\infty} F_k(t), \quad (1.4.1)$$

where  $F_1 = F$ ,  $F_k$  is the  $k^{\text{th}}$  convolution of  $F$  with itself,  $k = 2, 3, \dots$ , and

$$F_0(t) = \begin{cases} 1 & \text{for } t \geq 0. \\ 0 & \text{for } t < 0. \end{cases}$$

Lemma 1.4.1: The function  $U(t)$  is finite for all  $t$ .

Proof This fact is well known but perhaps the following proof (similar to Mode (1968a)) is of interest. Let  $t$  be fixed. If  $F(t) < 1$ , then

$$U(t) = \sum_{k=0}^{\infty} F_k(t) \leq \sum_{k=0}^{\infty} F^k(t) = \frac{1}{1-F(t)} < \infty.$$

If  $F(t) \geq 1$ , then

$$\int_0^t e^{-ax} dF(x) < 1,$$

for some  $a > 0$ . If we let

$$\bar{F}(u) = \int_0^u e^{-ax} dF(x) \quad 0 \leq u \leq t,$$

it can be shown using Laplace transforms or other techniques that the  $k^{\text{th}}$  convolution of  $\bar{F}(u)$  with itself is given by

$$\bar{F}_k(u) = \int_0^u e^{-ax} dF_k(x) \quad 0 \leq u \leq t.$$

It follows from the case  $F(t) < 1$  that

$$\sum_{k=0}^{\infty} \bar{F}_k(t) < \infty.$$

But

$$\sum_{k=0}^{\infty} F_k(t) \leq e^{at} \sum_{k=0}^{\infty} \bar{F}_k(t)$$

and the lemma is therefore proved. The proof of the next result is similar to that of Lemma 2.5.1 and will be omitted.

Lemma 1.4.2: If  $f(t)$  is bounded and  $f(t) \rightarrow A$  as  $t \rightarrow \infty$  and  $F(\infty) < \infty$ , then

$$\int_0^t f(t-u)dF(u) \rightarrow AF(\infty) \quad \text{as } t \rightarrow \infty. \quad (1.4.2)$$

Parts (i) and (ii) of the following lemma are often called Blackwell's theorem and the key renewal theorem, respectively.

Lemma 1.4.3: Suppose  $F$  is not a lattice distribution and  $F(\infty) = 1$ .

Then

(i)

$$U(t) - U(t-h) \rightarrow \frac{h}{\int_0^{\infty} ydF(y)} \quad \text{as } t \rightarrow \infty \quad (1.4.3)$$

for every fixed  $h > 0$ ,

(ii) if  $f(t)$  is the difference of two bounded nondecreasing functions which are both integrable on  $[0, \infty]$  and  $f(t) = 0$  for  $t < 0$ , then

$$\int_0^t f(t-y)dU(y) \rightarrow \frac{\int_0^{\infty} f(y)dy}{\int_0^{\infty} ydF(y)} \quad \text{as } t \rightarrow \infty. \quad (1.4.4)$$

The proof of this lemma may be found in Feller (1966).



Corollary: If  $H(\infty) < \infty$ ,  $F(\infty) = 1$ , and  $V(t)$  satisfies the equation

$$V(t) = H(t) + \int_0^t V(t-y)dF(y),$$

then

$$\frac{V(t)}{t} \rightarrow \frac{H(\infty)}{\int_0^{\infty} ydF(y)} \quad \text{as } t \rightarrow \infty. \quad (1.4.5)$$

Proof: The proof follows from Lemmas 1.4.2 and 1.4.3 (i) by applying the technique set forth in XI.3 of Feller (1966).

As an application of the results of this section and also to illustrate techniques that will be used later, we now give the

Proof of Lemma 1.3.1:

It can be easily verified that  $M(t)$  defined by (1.3.4) satisfies equation (1.3.3). If we define  $F(t) = mG(t)$ , then

$$M(t) = 1 + \frac{(m-1)}{m} \sum_{k=1}^{\infty} F_k(t)$$

and it follows from Lemma 1.4.1 that this last expression is finite, which proves (ii). If we define

$$\bar{G}(t) = m \int_0^t e^{-\alpha u} dG(u),$$

$$\bar{f}(t) = (1 - G(t))e^{-\alpha t},$$

$$\bar{M}(t) = M(t)e^{-\alpha t},$$

and

$$\bar{U}(t) = \sum_{k=0}^{\infty} \bar{F}_k(t),$$

then (1.3.3) becomes

$$\bar{M}(t) = \bar{f}(t) + \int_0^t \bar{M}(t-u) d\bar{G}(u). \quad (1.4.6)$$

The solution of (1.4.6) is given by

$$\bar{M}(t) = \int_0^t \bar{f}(t-y) d\bar{U}(y),$$

and (iii) of Lemma 1.3.1 now follows from (ii) of Lemma 1.4.3.

The interested reader may consult Feller (1941) for the proof of uniqueness.

## Chapter II

### CORRELATION AMONG SIBLINGS

#### 2.1 Introduction

In this chapter we shall study an age-dependent branching process in which the independence assumptions of the Bellman-Harris process described in Section 1.3 are relaxed so that interactions may occur among siblings. Individuals that are not siblings continue to live and reproduce independently; in particular, there is no interaction between individuals in different generations.

The process begins with  $k$  siblings born at time  $t = 0$ . The life-spans, as well as the numbers of offspring, of these siblings are correlated. At the end of its life an individual is replaced by its offspring who are correlated in the same way as the siblings in the first generation. As is generally true, the relaxation of independence assumptions makes matters more complicated. In order to have some homogeneity on which to base the analysis of the process, we shall assume that the life-spans  $l_1, \dots, l_n$  of any group of  $n$  siblings have the same joint distribution function  $G_n(x_1, \dots, x_n)$ , and this function is invariant under permutations of the  $x$ 's. In the literature, this property of  $G_n(x_1, \dots, x_n)$  is expressed by saying that the random variables  $l_1, \dots, l_n$  are "exchangeable" or "interchangeable". Likewise, we shall assume that the numbers of offspring of siblings are exchangeable random variables. Intuitively, these assumptions say that one would expect all groups of  $n$  siblings to behave in the same way which seems to be a natural first step in relaxing assumptions of independence.

Harris (1963) discusses briefly, for the case of binary reproduction, how a Bellman-Harris process can be modified to include dependence between sister cells. The model he discusses is a special case of the process described above.

Data of Powell (1955) suggests that in bacterial populations the life-spans of sister cells are correlated while the life-spans of mother and daughter are not. If this is true, the study of bacterial populations could be an important application of the results obtained in this chapter.

## 2.2 The probability space

Although we shall be primarily concerned with analytic properties of the process, we shall base the development of these properties upon an underlying probability space. The construction of this space follows that of Harris (1963), Chapter 6, and much of the notation used here is borrowed from that source.

Let us denote the collection of all finite sequences  $i_1, \dots, i_k$ , where  $i_1, \dots, i_k$  and  $k$  are positive integers, by  $\mathcal{J}$ . For each  $I \in \mathcal{J}$ , let  $\langle I \rangle$  represent a distinct individual whose line of descent is given by  $I$ . For example,  $\langle 213 \rangle$  is the third child of  $\langle 21 \rangle$ , who, in turn, is the first child of  $\langle 2 \rangle$ . Since we are assuming that all children of an individual appear simultaneously, the ordering "first child", "second child", etc., has no real significance. The collection  $\langle 1 \rangle, \langle 2 \rangle, \dots$  is called the first generation and we shall not be concerned with ancestors of these individuals. We say naturally that two individuals of the form  $\langle i_1 \dots i_{k,n} \rangle$  and  $\langle i_1 \dots i_{k,m} \rangle$  are siblings. By fiat, all members of

the first generation are siblings. Similarly, if  $I_1 = i_1, \dots, i_k$  and  $I_2 = i_1, \dots, i_j$  with  $j \geq k$ , we say that  $\langle I_2 \rangle$  is a descendent of  $\langle I_1 \rangle$ . We note that according to this definition, every individual is a descendent of himself.

We shall be interested in only two facts about each individual; the length of its life and the number of children it has. For each  $I \in \mathcal{I}$  let  $l_I$  and  $v_I$  denote the life-span and the number of offspring of  $\langle I \rangle$ , respectively. The life-span  $l_I$  may be any non-negative real number and  $v_I$  may be any non-negative integer.

Definition 2.1.1: By a family history we mean a sequence

$$\omega = (l_1, v_1; l_{11}, v_{11}; l_2, v_2; \dots) \quad (2.2.1)$$

where the subscripts range over all elements of  $\mathcal{I}$  in some arbitrary but fixed order. The collection of all such family histories shall be denoted by  $\Omega$ .

It should be pointed out that many  $\omega \in \Omega$  correspond to the same realization of the growth of an actual population. This is because each  $\omega$  gives information about individuals who are never born. For example  $v_1 = 3$  means that  $\langle 1 \rangle$  has three children, but  $l_{14}$  represents the life-span of the fourth child of  $\langle 1 \rangle$ . It might seem more natural to define  $\Omega$  so that each  $\omega \in \Omega$  would contain only the following information: the life-spans of the  $k$  individuals in the first generation and the number of offspring of each, the life-spans of these offspring and the number of offspring they have, and so on. Everett and Ulam (1948) and

Otter (1949) have constructed spaces of this type, although they consider only generation sizes.

In view of these remarks, Definition 2.2.1 may seem rather artificial, but it certainly does no harm to have "finer" events in a probability space than those one is actually concerned with. Moreover, this definition makes  $\Omega$  a countably infinite product of spaces that are either the non-negative real line or the non-negative integers, which is a great help in defining the  $\sigma$ -algebra  $\mathcal{G}$  and probability measure  $P$ , and also in deriving integral equations as we shall see.

The problem discussed here is not unlike that of computing probabilities in a certain dice game. Although one is only interested in events such as "the sum of the numbers is seven", it is more convenient to define the basic space as a product space (the set of all ordered pairs of integers from one to six) whose elements correspond to "finer" events. The main difference in this simple example and our situation is that our "finer" events are not actually observable.

As mentioned before, the set  $\Omega$  may be represented as an infinite product space

$$\Omega = B_1 \times B_2 \times B_3 \times \dots \quad (2.2.2)$$

where each  $B_i$  is either the non-negative real line or the set of non-negative integers. In the former case, let the  $\sigma$ -algebra  $\mathcal{G}_i$  on  $B_i$  be the Borel sets, and in the latter case, let the  $\sigma$ -algebra  $\mathcal{G}_i$  on  $B_i$  be the power set of  $B_i$ . Then define the  $\sigma$ -algebra  $\mathcal{G}$  on  $\Omega$  as the

minimal  $\sigma$ -algebra over the class of all cylinders of the form

$$\prod_{k=1}^N A_k \times \prod_{k=N+1}^{\infty} B_k$$

where  $N$  is any positive integer and  $A_k \in \mathcal{G}_k$ ,  $k = 1, 2, \dots, N$ .

We must now define a probability measure  $P$  on the measurable space  $(\Omega, \mathcal{G})$ . For each  $k = 1, 2, \dots$ , let  $G_k(x_1, \dots, x_k)$  be a distribution satisfying

(i) if  $x_j < 0$  for some  $j$ ,  $1 \leq j \leq k$ , then

$$G_k(x_1, \dots, x_k) = 0 \tag{2.2.3}$$

(ii) the function  $G_k(x_1, \dots, x_k)$  is symmetric in its arguments; i.e.,

$$G_k(x_{i(1)}, \dots, x_{i(k)}) = G_k(x_1, \dots, x_k) \tag{2.2.4}$$

where  $i(\cdot)$  is any permutation of  $1, \dots, k$ , and

(iii) the family of distributions is consistent<sup>1</sup> in the sense that

$$G_{k-1}(x_1, \dots, x_{k-1}) = G_k(x_1, \dots, x_{k-1}, \infty), \tag{2.2.5}$$

We shall frequently denote  $G_k(x_1, \dots, x_k)$  simply by  $G(x_1, \dots, x_k)$ .

<sup>1</sup> Condition (iii) is weaker than the usual definition of consistency, but (ii) and (iii) taken together imply consistency as it is usually defined.

Similarly, suppose that for each  $k$  and each set of non-negative integers  $j_1, \dots, j_k$ ,  $P_{j_1, \dots, j_k}$  is a non-negative number satisfying

$$(i) \quad \sum_{j_1=0}^{\infty} \dots \sum_{j_k=0}^{\infty} P_{j_1 \dots j_k} = 1, \quad (2.2.6)$$

$$(ii) \quad P_{j_{i(1)} \dots j_{i(k)}} = P_{j_1 \dots j_k} \quad (2.2.7)$$

where  $i(\ )$  is any permutation of  $1, \dots, k$ , and

$$(iii) \quad \sum_{j_k=0}^{\infty} P_{j_1 \dots j_k} = P_{j_1 \dots j_{k-1}} \quad (2.2.8)$$

Now let  $S_1, \dots, S_k, \dots$  be the partition of  $\mathcal{J}$  into equivalence classes determined by the equivalence relation " $I_1$  is equivalent to  $I_2$  if and only if  $\langle I_1 \rangle$  and  $\langle I_2 \rangle$  are siblings". Then  $\Omega$  may be written as

$$\Omega = L_{S_1} \times V_{S_1} \times L_{S_2} \times V_{S_2} \times \dots$$

where

$$L_{S_j} = \prod_{I \in S_j} L_I$$

and



$$V_{S_j} = \prod_{I \in S_j} V_I$$

each  $L_I$  being the non-negative real line, and each  $V_I$  being the set of non-negative integers.

The functions  $G_k(x_1, \dots, x_k)$   $k = 1, 2, \dots$  form a family of consistent distribution functions which determines a probability on each  $L_{S_j}$  by Kolmogorov's fundamental theorem (Kolmogorov (1933)). Likewise, the  $p_{i_1} \dots p_{i_k}$  determine a probability on each  $V_{S_j}$  by the same theorem. These probabilities then determine a probability  $P$  on  $(\Omega, \mathcal{G})$  according to the product probability theorem (Loeve (1963), p. 91). The following facts are immediate consequences of the definition of  $P$ .

(i) For any  $k$  siblings,  $G_k(x_1, \dots, x_k)$  is the joint distribution function for their life-spans, and  $p_{i_1} \dots p_{i_k}$  is the joint probability function for the numbers of offspring they have. It follows that for each  $I \in \mathcal{I}$ , the collections  $\{l_{I_1}, \dots, l_{I_k}, \dots\}$  and  $\{v_{I_1}, \dots, v_{I_k}, \dots\}$  are sequences of exchangeable random variables.

(ii) The life-spans  $l_I$  are independent of the numbers of offspring  $v_I$ .

(iii) If none of the individuals  $\langle I_1' \rangle, \dots, \langle I_k' \rangle, \dots$  are siblings of the individuals  $\langle I_1'' \rangle, \dots, \langle I_k'' \rangle, \dots$  then the collection of life-spans  $\{l_{I_1'}, \dots, l_{I_k'}, \dots\}$  is independent of the collection  $\{l_{I_1''}, \dots, l_{I_k''}, \dots\}$ , and a corresponding statement is true for the numbers of offspring.

### 2.3 The branching stochastic process

We shall be primarily interested in the random function  $Z^{(k)}(t)$  giving the number of individuals alive at time  $t$  in a process that begins

with  $k$  siblings born at time  $t = 0$ .

Definition 2.3.1: For each  $t \geq 0$ ,  $\omega \in \Omega$ , and  $I = i_1, \dots, i_k \in \mathcal{J}$ , let

$$X_I(t, \omega) = \begin{cases} 1 & \text{if } i_2 \leq v_{i_1, \dots, i_k} \leq v_{i_1, \dots, i_{k-1}}, \\ & l_{i_1} + \dots + l_{i_1, \dots, i_{k-1}} \leq t, \\ & \text{and } l_{i_1} + \dots + l_{i_1, \dots, i_k} > t \\ 0 & \text{otherwise} \end{cases} \quad (2.3.1)$$

and

$$Z_j(t, \omega) = \sum X_I(t, \omega) \quad (2.3.2)$$

where the sum is taken over all descendants of  $\langle j \rangle$ , and

$$Z^{(k)}(t, \omega) = \sum_{j=1}^k Z_j(t, \omega) \quad (2.3.3)$$

We shall often, for convenience, suppress the  $\omega$  in these functions. Expression (2.3.1) simply says that  $X_I(t) = 1$  if  $\langle I \rangle$  is ever born and is alive at time  $t$ , and  $X_I(t) = 0$ , otherwise. Therefore,  $Z_j(t)$  is the number of descendants of  $\langle j \rangle$  alive at time  $t$  and  $Z^{(k)}(t)$  is the number of individuals alive at time  $t$  who descend from  $\langle 1 \rangle, \dots, \langle k \rangle$ .

Theorem 2.3.1: The functions  $X_I(t, \omega)$ ,  $Z_j(t, \omega)$ , and  $Z^{(k)}(t, \omega)$  are all measurable in  $t$  for each fixed  $\omega$  and measurable in  $\omega$  for each fixed

t.

Proof: The proof follows easily from Definition 2.3.1 and the fact that all of the coordinate functions  $l_I$  and  $v_I$  are measurable.

The representation of  $Z^{(k)}(t)$  to be given in the following lemma will be crucial when we derive an integral equation for the generating function of  $Z^{(k)}(t)$ . For each  $\omega = (l_1, v_1; l_{11}, v_{11}; l_2, v_2; \dots)$  define  $\omega_1 = (l_{11}, v_{11}; l_{111}, v_{111}; l_{12}, v_{12}; \dots)$ . Let  $\Omega_1$  be the set of all such  $\omega_1$  and let  $\Omega_0$  be the set of all sequences of the form  $(l_1, v_1; l_2, v_2; l_3, v_3; \dots)$ . Then the space  $\Omega$  may be represented in the form

$$\Omega = \Omega_0 \times \Omega_1 \times \Omega_2 \times \dots \quad (2.3.4)$$

Lemma 2.3.1: If  $l_1 \leq t, \dots, l_i \leq t, l_{i+1} > t, \dots, l_k > t$  and  $v_1 > 0, \dots, v_i > 0$  for some  $i, 1 \leq i \leq k$ , then

$$Z^{(k)}(t, \omega) = k - i + \sum_{j=1}^i Z^{(v_j)}(t - l_j, \omega_j). \quad (2.3.5)$$

Remark: The proof of this lemma is similar to that of Theorem 6.1, page 129 of Harris (1963) and will be omitted. The content of the lemma is illustrated by Figure 1 which represents the first stages of the evolution of a family that begins with three siblings in the first generation. For this particular family history, we have  $k = 3, i = 2, v_1 = 2, v_2 = 3, v_3 = 3, Z^{(v_1)}(t - l_1, \omega_1) = 2, Z^{(v_2)}(t - l_2, \omega_2) = 4$ , and  $Z^{(k)}(t, \omega) = 7$ . The reader may verify that these values are in agreement with (2.3.5).

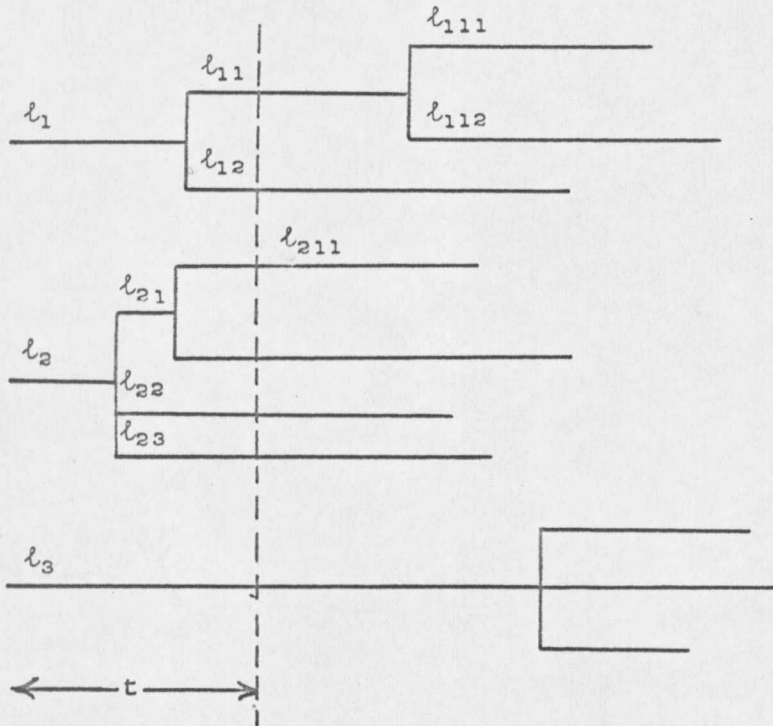


Figure 1

Early stages in the development of a family history

2.4 System of integral equations for the generating functions

Definition 2.4.1: For  $t \geq 0$ ,  $|s| \leq 1$ ,  $k = 1, 2, \dots$ , let

$$F(s, t, k) = \sum_{r=0}^{\infty} P[Z^{(k)}(t) = r] s^r = E \left[ s^{Z^{(k)}(t)} \right]. \quad (2.4.1)$$

Rather than derive an integral equation for  $F(s, t, k)$  for each fixed  $k$  similar to (1.3.2) we shall instead derive a system of integral equations in which each equation involves all of the functions  $F(s, t, k)$   $k = 1, 2, \dots$ .

It follows from Definition 2.4.1 that

















































































































































































































































































































































