

DE GRUYTER

Paul A. Ballonoff

**MATHEMATICAL
FOUNDATIONS
OF SOCIAL
ANTHROPOLOGY**

Mathematical Foundations of Social Anthropology

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ERRATA

page 49

line 9 R^{j+1} for any positive integer n should read
 R^{j+k} for any positive integer k

page 81

line 3	$\pm 1/10$	<u>should read</u>	$\pm 1/100$
line 4	$\pm 10\%$ of L	<u>should read</u>	$\pm 5\%$ of L
line 8	10 times fewer	<u>should read</u>	100 times fewer

page 57

second half, following the words "Thus, if", and page 58, first half, including matrices M_1 and M_2 , should go to page 59, between matrices S, R^1 , L^1 , and paragraph starting with "Notice that either . . . "

page 129

reference to Ballonoff, P. A., 1974a: title should read
Mathematical Models of Social and Cognitive Structures.
Urbana: University of Illinois Press.

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PREFACE

Objective

Over the last several decades, at an increasing pace, social anthropology has witnessed mathematical formulations of its two most prominent branches: kinship and marriage. While not all anthropologists have welcomed intervention of "formal" methods, it is now clear that in any case they are here to stay. In the same period, we have also seen the development of formal, if not mathematical, treatment of myth, folktales, riddles, and other materials which form the core of cultural semantics.

Of these two major developments, the present author has largely been a contributor to the first, not the second; but he has also found that there are numerous problems, principally of interpretation, left unanswered and indeed unasked by the "pure" theory of marriage and kinship. On the other hand, there are quite a number of questions answered by the pure theory without reference to semiotic concepts.

In the present work we therefore set out after this objective: to outline the pure theory of marriage and kinship (which we shall call "marriage theory" for simplicity), to establish the independent existence of this field in the jungle of demographic and mathematical models, and to show its surprising potential for responding to some very critical questions. In a companion work, we will provide sufficient development of cultural semantic theory so that one may see both that many of the claims and methods of the less mathematical "structuralists" are indeed well justified, and to show that the fundamental structures which motivate marriage theory (namely, marriage rules) do indeed have a proper foundation in cultural theory. (In a sense, we hereby carry out the program of C. Levi-Strauss in Chapter 15 of Structural Anthropology.)

Philosophy

There is an important overlying philosophy of this work, reflected in the above division into two major topics, but also to be noted in marriage theory itself on several occasions. This philosophy may be stated as follows: the accessible results are limited by the available techniques. While this may seem trite, it appears to be a hard lesson. For example, we discuss early in the work that the major techniques of demography have limits of applicability well known to demographers. We are then able to gain results in marriage theory in the precise area of greatest weakness of demography. Similarly, we are able to at least fill one (small but) important gap in genetic theory. Likewise, when we abandon marriage theory to

finally enter cultural theory, we shall also abandon nearly all the mathematics of the work, save only for the necessities imposed by the rules of mathematical syntax. With a few byways on the path, we shall then arrive at a formal conceptualization of the ideas used intuitively in this work.

The present book is a text on theory, not history, and as such it contains only as much bibliography as necessary to develop the theory. This position is also justified by the fact that I have elsewhere published materials of historical nature (Ballonoff, 1974b, 1974c). On the other hand, to motivate or interpret the theoretical developments, it is often necessary to present short sections of an essentially philosophical nature. I hope the reader may find these helpful.

Readers Background

A comment on the presumed background of the reader is necessary. While there is certainly a necessity for presentation of results in forms readable to the untrained, to those trained, there is also an obvious need to present the result in the first place. Whatever may stand the first test then deserves the second, and since this is the first time (to the author's knowledge) that all aspects of the present problem have been treated in a single place from the same perspective, we admit from the outset its experimental nature. We shall worry about "popularization", if at all, only when it is clear that there is something to popularize.

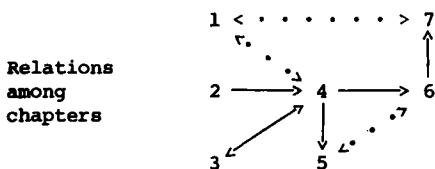
Marriage Theory as Biological Theory

While one section of this text will discuss certain contributions to genetics, in general, the reader with advanced knowledge of genetics or demography will find the present approach unusual. For example, in the "demographic" sections, we find particular family sizes represented as "equilibrium sizes" yet at the same time, we have no information on "age structure" of the population, so critical in the usual demographic mathematics. These same family size arguments likewise have nothing whatever to do with "selection" in the sense of the usual population genetics theory, since the very models which induce allocations of individuals by family, allow for the possibility that biological reproduction is random among mates. It is for these reasons that the present theory is not titled "Foundations of Population Biology" or the like. The present perspective is strictly social anthropological - if the results have implication for biology, it is only a fair return on the many insights that have crossed the boundary in the other direction.

HOW TO READ THIS WORK

Chapters are interrelated as shown in the chart below, using these symbols:

- strong dependence for concepts or development,
should be read in direction of the arrow.
- ↔ strong relation in content, may be read in either order.
- <..> related contents, order not important



Thus, one may find the "real meat" of the book by reading section 2.1, then chapters 4, 6, and 7. Chapters 5 and 6 are alternative approaches to the same or a similar problem, and in fact the results of 6 could all also be done in terms of the results of 5. Chapter 7 is more or less "philosophical" showing what might well be done with the scheme presented, while chapter 1 is "philosophical" in that it motivates the work by showing its existence (as a theorem!) and its distinction from other fields of study. Chapter 3, like chapter 5, shows one path that could be followed more extensively in future work.

Notice that this interrelationship of materials and short discussion suggests that in one sense this text is a treatment of the possible ways of working on "the marriage problem". Reading in the order of the chapter numbers will likely help perceive the survey from the more common to the least common methods, while reading "only for the meat" one might plunge directly into section 6.4. The Synopsis should help a reader decide his approach.

SYNOPSIS

Since this work is somewhat unusual both in content and purpose, in a field which is admittedly highly experimental, we present a short summary of the contents, purpose, and direction of each chapter.

CHAPTER 1: The essential problem of marriage theory is to characterize marriage rules and their relationships to population statistics. However, there is more than one way to do this and in chapter 1 we begin by presenting a short summary of a more standard approach to the problem than is used in the remainder of the text.

Section 1.1 summarizes a fixed class approach to subdivisions or classes in the population, and relies on relatively usual convex space methods. However, the approach does not allow a general enough conception of "marriage rule", and also ignores the large problem of the "network structure" of relationships between individuals in a population following a given rule.

Section 1.2 then discusses briefly the aims and achievements of classical demography, and points out that the areas of greatest weakness of demographic theory are precisely in interpretation and prediction of and from data such as that available in ethnographic observations.

CHAPTER 2: A considerable amount of the effort of theoretical anthropology has gone to the description of kinship systems. For the purposes of later chapters, we only need a small part of this apparatus, and we have described this part in section 2.1. A reader may therefore omit the rest of chapter 2.

However, one very large objective of this work is to argue that the proper mathematical conception of social anthropology will in fact also be a "global theory" for nearly all of the population statistics associated with human populations. Therefore, we have used up the remainder of chapter 2 to show how the apparently "trivial" results of section 2.1, when properly interpreted, can produce quite useful insights into a seemingly "established" field: population genetics. In fact, our interpretation of chapter 2 is in reality a subtle use of a continuous time sampled processes, in which we are essentially measuring differences between two points in time in the evolution of the genetic structure of a population. Where we differ from more usual models is in recognition, first, of the ability to treat the structural descriptive problem as no more than a log-transform of the statistical problem (and vice versa); and second, to place a great deal of trust in the conception of population structure as a continuous time process. In fact, although "structural" in purpose, the chapter places much more trust in this concept than

do even those works whose authors' careers depend upon statistical or stochastic models.

CHAPTER 3: There are two main problem areas noted in the above synopsis of chapter 1: description of the network of social ties in a population following a given rule, and prediction of the associated statistics. Chapter 3 is devoted primarily to a framework for the network problem stated in vector space terms, but it also describes how the empirical statistics of particular networks can be computed from the network descriptions. This chapter is therefore much more descriptive and far less analytic than other sections. In a sense, it is the most optimistic of the chapters, since it provides a framework for interpretation of results not yet available.

On the other hand, the material in this chapter is not yet the final framework chosen for treatment of the problem. Therefore, since a very short summary of one use of the operators defined in chapter 3 is provided in section 4.3, a reader who finds chapter 3 obtuse or difficult, or who is not interested in the network problem, may omit it and read section 4.3 instead. Such a reader should realize that section 4.3 is more concerned with the "minimal" case, while chapter 3 is concerned with any network.

CHAPTER 4: Numerous authors have noted that various kinship and marriage rules have a smallest representation. (The introduction to chapter 3 gives a few references to these.) The problem of chapter 4 is to rigorously define a conception of "marriage rule", and to find the minimal structures associated with these rules.

It is important to note that the definition of marriage rule in this chapter is not the same as the definition of chapter 1. In chapter 1, the definition depended on (essentially) class labels; in chapter 4, the definition is in terms of "kinship ties". Actually, we are free to interpret the vocabulary of chapter 4 (since it is mathematical definition, not empirical description) in many different ways, and a very important problem arises: under what (mathematical) conditions is the framework of chapter 4 equivalent to that of chapter 1?

An intuitive answer comes from recognition that those famous "Australian systems" appear to be describable by either technique, and that furthermore, the marriage matrix of any minimal system (see chapter 3 or section 4.3) is also a permutation matrix, hence a trivial example of a marriage rule in the sense of chapter 1. However, the marriage matrix of an arbitrary population is not equivalent to the marriage rule of chapter 1, largely due to the non-uniqueness or complete absence of labels by class of persons in a system described only by kinship, since

this last description is a relation between individuals. Therefore the general problem of comparing the mathematics of chapter 1 and 4 will be a problem in formal kinship: under what conditions does a kinship labeling of a population form a partition of the population which is preserved over time by the marriage system?

CHAPTER 5: The idea of preservation implies that under certain conditions, a system may not preserve itself. Chapter 4 presents one way to preserve: if a population is empirically as small as its structural minimum and follows its rules precisely so that it always forms the minimal graph, then it will also survive — with a particularly probability. Chapter 5 is devoted to computing that probability for minimal and other systems from the point of view of reliability engineering. My fondest hope is that someone will read this chapter and realize that its problem is correct but its treatment totally incorrect. Then we may hopefully have some real progress.

CHAPTER 6: We must recognize that the marriage rule and hence the structural number of a particular population following that rule may have little apparent relation to the empirical network of relations or empirical population size of the system. (Unless the empirical size is close the the minimal size!) For example, most states of the United States have a marriage law whose structural number is 4, but have population sizes in the millions. This is somewhat larger than the minimal size of eight persons per generation for a rule of number 4.

Therefore, chapter 6 is devoted to two questions: what are the average population statistics associated with a rule independently of the size of the population using the rule; and which rules does one expect to find under what conditions?

In reading the technical sections of this chapter, the reader should clearly keep in mind that the combinatorial argument given here is a "dummy variable" technique: we obtain results independent of the population size. However we also obtain strict descriptions of minimal sizes. (A useful mathematical problem would be to obtain formulae in the framework of chapter 3 which also described the expected network statistics.) We then extend the results to a much greater variety of demographic statistics and show how to interpret the U.S. Census of 1970.

CHAPTER 7: As might be expected from a final chapter, this chapter talks more of what may be possible than what has been done. It also tries to place the present work as an example of a more general class of problems in science: the relationship of structural to statistical theories.

CHAPTER 1: THE GENERAL FRAMEWORK

1.0 Introduction

The most comprehensive prior attempt at a single framework for problems of marriage theory is that of J. H. B. Kemperman (1967). In a series of four simultaneously published papers, Kemperman outlined the general problem in the context of convex spaces and carried out certain applications of interest to population genetics. However, these papers also give clear evidence that the author was aware of other applications.

In the present chapter, we present the principal definitions and results of Kemperman's first paper, which was the most general. Our definitions and theorems will closely follow those of Kemperman, but the explanations given here may differ widely or narrowly from those of the original paper. Therefore, to give specific credit, we shall note with "K. ---" (where --- shows the page number of the original text) material which is direct quotation or close paraphrase (principally definitions or theorems). The reader should assume all other text is the opinion of the present author. However, we strongly recommend a reading of the original materials, in this and all other sections.

1.1 Basic Ideas

We assume a population consisting of m types of males and f types of females. Using i to index male types and j to index female types, we can define a set of ordered pairs (i, j) in $M \times F$, the cross product of the M of the m male types and the set F of the f female types.

We may define a new set T as

$$T = \{(i, j): i \text{ and } j \text{ are a prohibited mating type}\}$$

We call T the set of prohibited pairs. If $(i, j) \in T$, we call (i, j) admissible. Note that in the simplest case $m = f$, and for each pair $(i, j) \in T$ there is a positive constant K which is the number of male and female offspring of each pair of individuals of pair-type (i, j) .

(K. 247) For each admissible type (i, j) and each $k = 1, \dots, m$ the expected number K_{ijk} of male offspring is equal to the expected number of female offspring of type k . Also, $f_{ijk} \leq 0$, and $\sum_n f_{ijk} = 1$. (Note that this condition could be done away with, and not affect other development.)

(K. 247) If we have p_1, \dots, p_m nonnegative numbers, with $\sum^n p_i = 1$. and consider a population of Np_i males of each type i in a total population of size N , and Np_j females of each type j , then we call the vector $p = (p_1, \dots, p_m)$ the type distribution of the population of males, and $q = (q_1, \dots, q_f)$ the type distribution of females.

Notice that in genetics, the type distribution would refer, for example to relative frequencies of genotypes, while in social anthropology it will refer, for example, to relative frequencies of clan members or lineage members. In fact, any partition of the members of a population will be suitable to define a type distribution of the population into the subsets of the given partition. However, one difficulty we may note (treated more extensively in White, 1963, Chapter 1; Boyd, 1971; and Lorrain, 1974) is that some methods of partitioning the population are constructed from the "viewpoint" of a particular member of the population, while other methods are independent of "viewpoint".

For example, whether or not an individual has a particular given family name is generally not dependent on who provides the list of names (e.g., civil records serve well in many cases), but who is a "first cousin" of whom will provide different partitions of the population relative to each particular individual. We note that this difference in perspective becomes unimportant (e.g., results in isomorphic partitions) in particular cases treated by White, and subsequently others (Courrege, 1974, and the above references), but we also note that the framework of the present chapter only applies strictly to populations with partitions independent of "perspective". (Atkins, 1974, has a method for always partitioning a population essentially according to patri- or matri-lineal descent, which is also compatible with the notion of type distribution.)

Kemperman next defines the idea of system of mating, with the disclaimer that he is not interested in "which particular system is most likely to be followed" by a particular group. However, as will be apparent in Chapter 6, that is precisely one question we seek to answer.

DEFINITION 1.1 (K. 248) Let S_n denote the collection of all type distributions $p = (p_1, \dots, p_n)$. By a system of mating we shall mean a rule which associates to each $p \in S_n$ a set of n^2 nonnegative numbers p_{ij} ($i, j = 1, \dots, n$) not all zero, satisfying

$$(1) \quad \sum_{i=1}^n p_{ij} \leq p_j \quad \text{and} \quad \sum_{j=1}^n p_{ij} \leq p_i$$

(for $i = 1, \dots, n$ and $j = 1, \dots, n$ respectively) and

$$(2) p_{ij} = 0 \text{ if } (i, j) \in T$$

This is equivalent to a system of n^2 nonnegative functions $G_{ij}(*)$ on S_n satisfying
 $\sum_{i,j} G_{ij} > 0, G_{ij}(p) \equiv 0 \text{ when } (i, j) \notin T.$

In such a population, the number of pairs of each type (i, j) is $C_{ij} = N p_{ij}$
if N is the number of each sex, and $P_{ij} = G_{ij}(p)$.

This notation allows one characterization of random mating, which not incidentally also corresponds to the method used by Darwin to compute expected isonomous marriages in a given population. In particular, for $(i, j) \notin T$, let $G_{ij}(p) = p_i p_j$. One might call this completely random mating if $|T| = 0$, but conditionally random mating otherwise.

Kemperman defines, but does not develop, the possibility that if w is a random variable, $p_{ij} = G_{ij}(p, w)$. Note that in population genetics, numerous special cases of $G_{ij}(p, w)$ have been studied, including subdivision of the population (Wahlund, 1975), and migration (see references in Crow and Kimura, 1974) but most such models essentially regard w as having an effect on the entire vector p and study the resulting effect on particular p_{ij} 's. We can also regard selection as normally studied in population genetics as a case where w acts as an operator (not always linear) on $G_{ij}(p)$. However, we could also interpret selection as introduction of a random variable or particular operator into the computation of f_{ijk} .

Under conditionally random mating, a portion $N p_{io}$ of the males and $N p_{oj}$ of the females remain unmated. For that matter, there may also be unmated individuals under completely random mating, depending on the sex ratio and our assumptions on mating sequence, etc. The unmated proportions of males and of females respectively are given by:

$$(3) P_{io} = p_i - \sum_{i=1}^f p_{ij}, \quad P_{oj} = p_j - \sum_{i=1}^m p_{ij}$$

for each i and each j .

(K. 249) The proportion of unmated individuals will be called the mating ratio denoted by c , a nonnegative number ≤ 1 , equal to

$$(4) 1 - c = \sum_{i=1}^m p_{io} = \sum_{j=1}^f p_{oj} = \sum_{i=1}^m \sum_{j=1}^f p_{ij}$$

Kemperman notes that the type of distribution $p^{(t)}$ of the t^{th} generation may converge to a limiting distribution. A very simple example of this is the Gada system of Ethiopia as modeled by Hoffman (1971), or any other system with Markovian

behavior. Such a limiting distribution is called the stable distribution, and will "usually satisfy"

$$(5) \quad \sum_{i=1}^m \sum_{j=1}^f G_{ij}(p) f_{ijk} = cp_k$$

(K. 250) where $k = 1, \dots, n$ and

$$(6) \quad c = \sum_{i=1}^m \sum_{j=1}^f G_{ij}(p), \quad 0 \leq c \leq 1.$$

Kemperman offers two conditions necessary for a vector p to be a stable type distribution. We list these below.

$$1. \quad \sum_{i=0}^m p_{ij} = \sum_{i=0}^m p_{ji} = p_j$$

$$2. \quad \sum_{i=1}^m \sum_{j=1}^f p_{ij} f_{ijk} = cp_k$$

with c given as in (6). For a given c , the set of all matrices $[p_{ij}]$ which satisfy these conditions will be denoted by Π_c . (Note that $p_{ij} = 0$ if $(i, j) \notin T$). Denote the corresponding set of vectors p_c by P_c .

Although we shall not here develop the convex space foundations of marriage theory, we note that Kemperman's developments so far, from the perspective of a fixed value of c , allow us to consider Π_c and P_c as compact, convex polyhedral subsets of their respective euclidian spaces. By study of the "extreme points" of such spaces, one gains a complete knowledge of the possible equilibria of particular systems. Kemperman applies these ideas in later sections of the paper, not reviewed here.

Notice that the most significant difference of Kemperman's approach from the usual approaches to population models of any type (social or biological) is precisely the preference to embed ideas in a geometric rather than strictly analytic framework. This difference is not trivial, since it appears that a geometric insight is essential to understanding social anthropology. This point will be more apparent in the chapter on the theory of structural numbers, but we submit that Kemperman's choice of foundations have more than an accidental relationship to his awareness of the possible breadth of application. However, (K.261) Kemperman is also aware of the "usual" Perron-Frobenius results upon which "normal" population models are built.

Condition 2 above has two totally different interpretations depending on whether we are considering social theoretic or genetic applications. If we interpret

genetically, then it essentially says "no selection". However, if we interpret as a rule on the social assignment of offspring to parents, then condition 2 allows all parental types not in T an equal chance at the "available" offspring, but says nothing whatever about selection in the genetic sense. In other words, there is nothing in Kemperman's model which prohibits our interpreting the numbers f_{ijk} as indicating the proportion of the offspring per generation given the labels "produced by i and j and put in class k" independently of which couple actually produced the offspring. Or, in still other words, adoption which gives the family name of foster parents to adopted offspring is permitted. Likewise, "cheating" is also possible, providing no one ever "knows".

We now present a most fundamental theorem, which encourages us to proceed.

THEOREM: Suppose there are no non-trivial prohibitions of mating type, and let $0 < c \leq 1$ be fixed. Then Π_c is non-empty. (K. 259).

(Essentially, the existence of results at all in chapter 4, "Theory of Structural Numbers", constitutes a proof for a related condition with non-trivial prohibitions. This extends to the special cases discussed by White and others referenced above, where we interpret "individuals" in that theory as "all individuals with an identical geneology".)

Proof: The proof relies on the existence of fixed point(s) in the vector space of the vectors p of type distributions of males, and q of type distributions of females, under the linear transformations imposed by the functions G_{ij}^* (*). See K. 260.

Having now laid out the general framework of the problem, we go on in later chapters and sections to first critique the "usual" demographic model, then to develop our alternative. In particular, we shall present a number of different non-trivial mating systems, and then compute for each the theoretical values of c. Since we have learned from Kemperman that the stable distributions depend explicitly on c, the importance of this computation should be obvious.

It is useful to conclude with two notes. First, that if we find a fixed point vector, we have found a transformation

$$p \rightarrow p^* \text{ or } S_n \times S_n$$

for each vector p and each fixed point p^* . In general, this is defined for each k by the functions

$$(7) \quad p_k^* = \frac{1}{c} \sum_{i=1}^m \sum_{j=1}^f G_{ij}(p) f_{ijk}$$

given a particular T.

We conclude with a short observation on Kemperman's materials: to the extent we have presented them, they appear to be little more than vector space concepts applied to a special problem. This is correct, in so far as the observation is based on our summary, but is incorrect from the point of view of the succeeding sections of the original paper. The fact that the theorem quoted above references the set Π_c , and that the particular values in p_c or Π depend on selection of c and therefore on the constituents of T , emphasize this departure from purely vector-space oriented concepts.

1.2 Critique of Classical Demography

There are several relationships between the present approach of part 1.1 and classical demography, and, moreover, certain "holes" in classic theory which we hope to uncover here. However, we shall also point to a hole that we believe Kemperman has already filled, which it is not our main purpose at present to discuss at length.

Our critique of classical demography is essentially that it is limited to study of stability of age "structures", in the presence of growth in the total population. Models of zero-growth are an afterthought with respect to the main competency of demographic models to deal with age-structured phenomena. However, study of populations from the viewpoint of absolute totals, or subdivisions other than age structure, have been the main concerns of Social Anthropology.

The relative capacities of demographic computation from different kinds of initial information have been summarized by Keyfitz (1968: 183) in a handy table.

We condense the table, using the following notations:

b:	Overall birth rate	$m(a)$:	age specific birth rate
d:	Overall death rate	$\mu(a)$:	age specific death rate
r:	Growth rate	$e(a)$:	age-structure proportions
N:	Population size	$p(a)$:	stable life schedule

These values are computed or given for a particular population at a particular time. Using stable (age structure) population theory, Keyfitz points out that given particular pairs of these, we may determine all or some of the others. The pairs and what they may compute are summarized in the table below. Boxes with an I, A, or T show that the pair labeling the intersecting row and column at that part of the table determine one of three conditions:

- I: the given pair determines all others, and we may get immediately the stable results on all other variables.

TABLE 1.1 Accessible Results from Different Initial Information, Summarized from Keyfitz, 1968.

Given	By Age		Intrinsic Rates		
	p(a)	m(a)	r	d	b
c(a)	T		T	T	
p(a)		A	A	A	A
r				T	T
d					T

A: the given pair allows computation of asymptotic stability of all other variables.

T: the pair allows computation of population totals only, of variables b, r, d, and N.

Notice that from the point of view of the type of information usually available either from "general ethnography" or even from painstaking archaeology, we are happy to obtain estimates of N, and can occasionally get gross estimates of b and/or d. If records or subsequent restudy are available options, we may also get estimates of r. In rare circumstances, we can get estimates of one of the age structured variables, usually an approximation of p(a).

We can thus notice that there are two reasons why the historic isolation of demography and social anthropology has been justified: most "demographic" data is usually not available from anthropological investigation; while the weakest results from demographic theory are in treatment of the sorts of data which are available. In particular, from the demographic viewpoint, all we know uniformly in anthropological studies is the crude total population size. In the absence of age structure and growth rates, demography is of no help.

It is worth noting that there is a small body of literature dealing with what it calls "marriage theory". This literature hopes to deal with the effects of age structure by sex on such things as the availability of mates, and so on, (e.g., Keyfitz, 1968, or McFarland, 1972). This literature has been largely unsuccessful, we believe, because it has adopted the wrong model, or at least because it has modeled the problem incorrectly. We believe the "propensities" for different age groups to mate with each other are simply captured by the values p_{ij} , or at least the functions $G_{ij}(p)$, and that the fertilities of mating types are representable as the f_{ijk} values, which as fertilities over male and female age classes i, j, may have some $f_{ijk} = 0$, even for allowable (i, j) pairs. We therefore assert that the problem of

the above mentioned papers has been solved for the social theoretic case of zero growth and stationary class distributions. It has not been solved for the demographic theoretic case of non-zero growth, and stable age distribution. Because of the genetic interpretation always available for the social theoretic case, the problem has also been solved for zero growth, stationary genotype distributions (and other genetic distributions); but has not been solved for the "demographic case", as we have reviewed elsewhere (Weiss and Ballonoff, 1975), when interpreted genetically.

CHAPTER 2: KINSHIP THEORY

2.0 Introduction

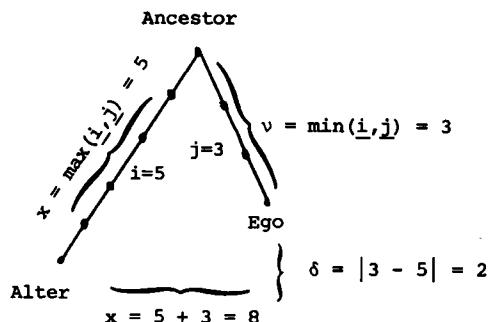
Studies in the algebra of kinship have been increasingly numerous. From a small beginning with the work of the Scottish mathematician Macfarlane (1882), the works are so numerous in the last fifteen years that we may claim the existence of a small "field" which studies the algebraic ways of describing social relationships. In genetics of course "kinship" is a name of a measure not a body of theory. However, as we will note briefly in this chapter, there are obvious relationships between the social and the genetic concepts of kinship. Sections 2.2 and following are specifically devoted to exploring new concepts for genetics based on developments given here.

The purpose of this chapter is not to review the algebra of kinship, but to present sufficient notions of kinship algebra to allow development of subsequent chapters from a common foundation. The most compact source for this purpose turns out to be two papers by Atkins (1974a, 1974b), and what follows draws from both papers.

We attempt to follow Atkins' notation literally for kinship measures, but will in general develop our own notation for other purposes.

2.1 The Fundamental Numbers

The basic problem of kinship theory, whether in social anthropology or genetics, is to study the relationship through genealogical ties of two given individuals. Following anthropological tradition, we call one of these persons "ego" and the other "alter". To define the measures of interest, consider the following diagram taken from Atkins (1974a):



Stated in ordinary language, we have six significant measures to contend with between alter and ego with respect to each common ancestor. Where j is the number of descent links from ego to the ancestor, and i from the ancestor to alter, these six measures are summarized in the following table:

Table 2.1 Summary of Definitions and Algebraic Relationships of Kinship Measures (From Atkins, 1974a, Table 2)

Measure	Definition	Range of Values	Useful Equalities
γ (Generation)	$\gamma = j - i$	$\dots, 2, 1, 0, 1, 2, \dots$	$\gamma = \sigma\delta$
σ (Generation sign)	$\sigma = \text{sgn}(j - i)$	-1, 0, 1	$\sigma = \text{sgn } \gamma$
δ (Generation removal)	$\delta = i - j $	0, 1, 2, ...	$\delta = \gamma $ $\delta = \chi - \nu = \kappa - 2\nu$
ν (Collateral removal)	$\nu = \min(i, j)$	0, 1, 2, ...	$\nu = \chi - \delta = \kappa - \chi$
χ (Canon degree)	$\chi = \max(i, j)$	0, 1, 2, ...	$\chi = \delta + \nu = \kappa - \nu$
κ (Civil degree)	$\kappa = i + j$	0, 1, 2, ...	$\kappa = \nu + \chi = \delta + 2\nu$ $= 2\chi - \delta (*)$

* from Ballonoff, 1975.

Since the measures defined in terms of the diagram are quite straightforward, there is little need to explain their "meaning" or the origin of the "useful equalities", most of which are obvious from the definitions. Atkins also gives lengthy explanation of the history of these and several other related measures.

The simplicity of these measures is more apparent than real. In fact, we hardly exploit even the simplest measures at their simplest values. For example, chapter three depends only upon the values δ , χ , and κ . In its normal development, population genetics depends only upon κ . In chapter 3 on the graph theory of marriage systems, and in chapter 4 on structural numbers, we essentially assume $\delta = 0$, and $\nu = \chi = (1/2)\kappa = i = j$. However, the methods of chapter 4 are extendable to any values, and are defined in their general sense, while in chapter 6 we indicate how to introduce less discrete conditions though retaining the theory derived from $\delta = 0$, at least for demographic purposes.

In Atkins' terminology, these six measures are referred to as "fundamental consanguineal measures". We shall retain this terminology, and also refer to them as "kinship" measures. In chapter 4, we will develop a separate theory of yet other numbers. We will refer to the numbers found in chapter 4 as "structural numbers", since they depend on the types of graphs (structures) found under specified values of kinship measures.

2.2 Genetic Uses of the Fundamental Numbers*

In population genetics, following Malecot (1969), we are concerned with the probability of identity by descent of an allele chosen at random from a locus of ego, with an allele chosen at random from the homologous locus of alter. In the special case of ego and alter being mates, we may study the inbreeding of their offspring, which is the probability that the two homologous alleles at a given loci of the offspring are identical by descent. Clearly, the inbreeding of the offspring is identical to the kinship of the parents.

Denote ego by I and alter by J; let K be the offspring of I and J; use " f_a " for the inbreeding of the common ancestor "a" of I and J; and use f_K for inbreeding of K, θ_{IJ} for the kinship of I, J. Then

$$(1) \quad f_K = \theta_{IJ} = \sum_a \left(\frac{1}{2} \right)^{\kappa_a + 1} (1 + f_a)$$

where κ_a is the civil degree relationship of I, J through ancestor a, and we sum over all common ancestors.

As is evident from reading texts on population genetic theory (e.g., Jacquard, 1974 or Crow and Kimura, 1971), a considerable amount of the abstract theory depends upon the population average values of f or of θ . Further, many empirical studies from civil records are essentially studies of distributions of values of f , which is the same as studying distributions of values of κ .

In the next sections, we note that κ is not the only way to compute f or θ .

2.3 Semicontinuous and Continuous Genealogical Measures

The "normal" methods of genealogical counting of links in pedigrees is to count the numbers of "steps" between offspring and ancestors. Thus, from a person to his grandparent, there are two "steps", or three individuals in the path, and from a person to their first cousin, there are five individuals in the path, or four connecting links.

If k is the number of persons in the path, or g the number of connecting links, then we have $k = g + 1$. Genetic relationship ρ is computed as $\rho = (\frac{1}{2})^g$ through each path (of a non-inbred ancestor) and kinship as

$$(2) \quad \theta = \left(\frac{1}{2} \right)^k = \left(\frac{1}{2} \right)^g + 1 = \frac{1}{2} \rho$$

*Readers uninterested in genetics may omit the remainder of this chapter.

In all of these measures, values of k and g are always integers, so that we may consider this method of computation as "discrete".

Now, if we look at the genealogical path between two individuals I, J through a common ancestor, we note from Ballonoff (1975) and section 2.1 that this path breaks into two parts: the path from individual I to the ancestor, and the path from the ancestor to J . Then the number g above is the sum of these two paths, and is equal to κ of the table 2.1. Also, from table 2.1, the maximum of these two paths is χ , and the difference between them, δ , we have from the above references the fact that

$$(3) \quad g = 2\chi - \delta = \kappa.$$

From Ballonoff (1975), we have the following method of computing δ in the absence of information other than χ , and the birth dates of I, J . If the difference in years of the birth dates of I, J is d_{IJ} , and the average time span between generations of the population (average age of childbearing for females) is \bar{G} , then we can estimate $\bar{\delta}_{IJ} = \frac{d_{IJ}}{\bar{G}}$ and use $\bar{\delta}_{IJ}$ as an estimate of δ for each pair I, J , with apparently reasonable results. For example, the mean computed result from the example in Ballonoff (1975) is evidently a much better estimate of the "true" ρ of a population than are estimates found from isonomy, summarized by Yasuda and Morton (1967).

In this model, although δ is discrete valued, $\bar{\delta}$ is continuous valued. For this reason, if we compute θ or ρ as in (1), but using (2) to estimate g , and estimating δ with $\bar{\delta}$, e.g.,

$$(4) \quad \theta = \frac{1}{2}\rho = \left(\frac{1}{2}\right) 2\chi - \bar{\delta} + 1$$

then we have a semi-continuous measure, dependent on the discrete valued χ and the continuous valued $\bar{\delta}$.

We may go one step further, and also estimate χ continuously by measuring the maximum difference in dates of birth of the ancestor and I , or the ancestor and J . Calling this difference D_{IJ} , and using \bar{G} as above, we get an estimate $\bar{\chi}_{IJ} = \frac{D_{IJ}}{\bar{G}}$ of χ for each pair I, J . We then estimate g as

$$(5) \quad \hat{g} = 2\left(\frac{D_{IJ}}{\bar{G}}\right) - \bar{\delta}_{IJ} = \frac{2}{\bar{G}}(D_{IJ} - d_{IJ})$$

Equation (5) gives us a completely continuously valued estimate of g , which has the unique property that we may estimate the genetic relationship of two individuals provided only that we know: both the individuals have some common ancestor(s); and, the birthdates of both individuals and of all common ancestors.

Using continuous estimates, the following problem arises: the connecting path from each common ancestor to each of individuals I and J is not always "relatively simple". Here, relatively simple means that for each ancestor A common to I and J, and for any particular path connecting I and J through A, there is no relative born later in time who also has A for an ancestor and who is an ancestor of both I and J. Obviously, if we find such an intermediate ancestor on a given path, then we must first estimate the inbreeding of that ancestor, and then compute the relationship ρ_{IJ} via the closer ancestor using

$$\rho_{IJ} = \left(\frac{1}{2}\right)^g(1+f)$$

where f is the inbreeding of the closer ancestor.

This also implies that we need to know how many paths connect each pair through each ancestor. This problem is not unique to kinship computation by continuous or semi-continuous methods. However, we have learned that there is yet another discrete valued measure embedded in computation of θ or ρ , namely the multiplicity of connection via each ancestor. In discrete and semi-continuous computation, since we compute each path separately, the multiplicity of each 1, so we are not necessarily conscious of the number of paths through each ancestor. However, in continuous computation, we are in danger of losing information by using only age structure information, unless we also discover techniques for finding multiplicity of connection.

With this background, in the following we discuss use of semi-continuous measures on a particular problem, namely modeling the prediction of amount of inbreeding to be found in artificial populations of say salmon, which have an "age structure" which is simply a proportionate mixing of generations, moving over time. The example is useful since it shows that marriage theory and in particular the branch of marriage theory dealing with kinship is in fact much more broadly applicable than simply to human populations.

2.4 Introduction to Use of Semi-Continuous Models

For each individual's parents, we may calculate the coefficient of kinship θ or of relationship $\rho = 2\theta$. The inbreeding of the individual offspring is therefore also $\frac{1}{2}\rho$ of the parents, and the inbreeding of a population is the average of the inbreeding of individuals, hence is computable from θ or ρ .

Now, for a given individual with parents I, J, the number of steps (generations) from I to a particular common ancestor is i , and from J, it is j , so $\rho = \frac{1}{2}^{i+j}(1+f_a)$ or $\theta = \frac{1}{2}\rho = \frac{1}{2}^{i+j+1}(1+f_a)$. To not worry about the "extra" +1 in the exponent, we use ρ instead of θ .

Let $\chi = \max(i, j)$, $\delta_{ij} = |i - j|$. For each matched pair in the population we can compute $\rho = \frac{1}{2} \frac{(i_a + j_a)}{a^2} (1 + f_a)$ for each ancestor a and for one or more ancestors, with inbreeding. Now, from section 2.3, we know that $\kappa = 2\chi_{IJ} - \bar{\delta}_{IJ}$ is an estimate of $i + j$. Therefore $\rho_a = \frac{1}{2} 2\chi_a - \bar{\delta}_{IJ} (1 + f_a)$ is an estimate of the relationship due to ancestor a of couple I, J. And $\rho_{IJ} = \frac{1}{2} \sum_a 2\chi_a - \bar{\delta}_{IJ} (1 + f_a)$ is an estimate of the total relationship of pair I, J.

Now consider a population divided into m classes each of males and females, and let $1 \leq i \leq m$ index these classes in the males and $1 \leq j \leq m$ index these classes in the females. Let $p_i^{(t)}$ be the proportion of males in class i at time t and let $p_j^{(t)}$ be the proportion of females in class j at time t . (Notice that we can generalize for different numbers of classes in males and females by allowing all $p_i = 0$, or $p_j = 0$ for $i \geq k$, $k < m$.)

If we are now interested in the classes of pairs of classes i, j (a male from i , female from j) we can let this proportion at time t be $p_{ij}^{(t)}$.

We may now consider the matrix $P_t = [p_{ij}^{(t)}]$ which shows the proportions of all pairs of classes at time t . Assume that every member of class i or j has the same genetic history as every other member of class i or j . That is, if an individual in class i has a particular individual ancestor at a particular degree of removal, then every other individual in class i has this same ancestor at the same degree of removal, etc.

Therefore, for each class pair (i, j) the expected genetic relationship is ρ_{ij} . And in the whole population, the average genetic relationship is, at time t

$$\bar{\rho}_t = \sum_i \sum_j p_{ij} \rho_{ij}$$

For convenience, define the matrix multiplication * which is the element by element multiplication of square matrices of the same order. If S, M, R are $n \times n$ square matrices, $S = M * R$, if and only if $[s_{ij}] = [m_{ij} r_{ij}]$ for all i, j . Clearly $M * R = R * M$, etc.

Then denoting $P_t = p_{ij}^{(t)}$, $R_t = \rho_{ij}^{(t)}$ we have

$$\bar{\rho}_t = \text{perm } P_t * R_t$$

where $\text{perm } M$, M a matrix, is the sum of all entries in the matrix.

2.5 Estimating Proportions

We must now discuss how to estimate P , how to estimate R , and their effects on $\bar{\rho}_{ij}(t)$. We have several possible cases for P and R . Looking first at P , we have several cases:

$$(i) \quad p_{ij}^{(t)} = p_i^{(t)} p_j^{(t)}$$

Or, the proportion of i, j pairs in the population is the simple product of their relative proportions in the entire population at time t ,

$$(ii) \quad p_{ij}^{(t)} = \frac{p_i^{(t)}}{\sum_w p_w^{(t)}} \cdot \frac{p_j^{(t)}}{\sum_v p_v^{(t)}}$$

where $\sum_w p_w^{(t)}$ is the total of proportions of a set of w of the classes of males,

$1 \leq w \leq m$, and class i is one of the w classes, with similar interpretation of $\sum_v p_v^{(t)}$

for females. Expression (ii) has the effect of saying the pairs form selectively from the population, but randomly within this selected set. Notice that case (i) is case (ii) with $w = v = m$;

$$(iii) \quad p_i^{(t)} \text{ and } p_j^{(t)}$$

depend on the productivity of mating types in the previous generation, so $p_{ij}^{(t)}$ is defined as a finite difference equation.

Note that these models essentially only duplicate the developments of chapter 1.

2.6 Estimating Genetic Relationship

Cases for types of ρ computations are:

CASE (I): Parental populations of i, j unrelated for all $i \neq j$. Then we simply have

$$\bar{\rho}_t = \text{perm } P_t \times R_t = \text{perm } [ER_t] * P_t = \sum_{i,j} p_{ij} \rho_{ij}$$

since for $i \neq j$, $\rho_{ij} = 0$, and E is the identity matrix. In more detail, for each $i = j$, all members of the population have the same ancestry; for $i \neq j$, ancestry is not in common. Then $\rho_{i,j} = 0$ for $i \neq j$, and

$$\bar{\rho}_t = \sum_{i,j} p_{ij}^{(t)} \rho_{ij}^{(t)} = \sum_{i,j} p_{ij}^{(t)} \sum_a \frac{1}{2} \delta_{ij}^{(t)} - \delta_{ij}^{(t)} a (1 + f_a)$$

In particular, if the common ancestors of classes i, j are their immediate parents, then $\chi_{ij} = 1$. Also, the generation difference between i and j is zero, so $\delta_{ij} = 0$,

$$\text{and } \bar{\rho}_t = \sum_{i=j} p_{ij}^{(t)} \frac{1}{a} \left(\frac{1}{2}\right)^2 (1 + f_a)$$

If there are no genealogical "complications" other than the common parents, we have

$$\bar{\rho}_t = \frac{1}{4} \sum_{i=j} p_{ij} \frac{1}{a} (1 + f_a)(t)$$

where f_a is the inbreeding of a parent of pair i, j , and the subscript (t) on $(1 + f_a)(t)$ is simply a reminder that we are talking about ancestors of pairs in generation t .

CASE (II): All classes i, j are bred from the same parental stock. Therefore, for all i, j , $p_{ij}^{(t)}$ equals a constant h , which is independent of time and of the classes or class-pairs. Then $\bar{\rho}_t = h$ perm $P = h$, so the relationship at any time is independent also of the class composition.

CASE (III): A set of each class $i = j$ of case (ii) are kept as breeders for the classes $i + 1, j + 1$. Therefore, at time t , $\chi_{ij} = i$ for $i = j$, $\chi_{ij} = \delta_{ij} + 1$ for $i \neq j$, or $\chi_{ij} = \delta_{ij} + 1$ for all i, j . We get, for each pair-type i, j

$$\rho_{ij} = \frac{1}{a} \left[\frac{2(\delta_{ij} + 1)}{2} - \frac{\delta_{ij}}{\bar{G}_t} \right] (1 + f_a)(t)$$

Concentrating on the exponent, we notice

$$2\delta_{ij} - \frac{\delta_{ij}}{\bar{G}_t} + 2 = \delta_{ij} \left(\frac{2\bar{G}_t - 1}{\bar{G}_t} \right) + 2 = \delta_{ij} \left(2 - \frac{1}{\bar{G}_t} \right) + 2$$

which we call Δ_{ij}^t for convenience. Note that for $\bar{G}_t \sim 1$, $\Delta_{ij}^{(t)} \sim \delta_{ij} + 2$; for $\bar{G}_t \sim \frac{1}{2}$, $\Delta_{ij}^{(t)} \sim 2$; for $\bar{G}_t \ll \frac{1}{2}$, or δ_{ij} "small", $\Delta_{ij}^{(t)} < 2$. Also, recall that in general, δ_{ij} is a small integer such as 0, 1, 2, 3, 4.

Looking at the inbreeding of each pair's parents, we can notice that the inbreeding f_a of the ancestors of a particular pair will, in fact, be defined by a recurrence: the parents of $\{(i, j) \mid i = j\}$ are precisely the pair $(i - 1, j - 1)$, or at least the inbreeding is the same, so that f_a here becomes

$$\theta_{i-1, j-1} = \frac{1}{2} \rho_{i-2, j-2} = \frac{1}{a} \left(\frac{1}{2} \right)^{(\Delta_{i-2, j-2}^{(t)} + 1)} \left(1 + f_{a_{i-2, j-2}} \right)$$

For diagonal entries in R, we have entry

$$(i, i) = \frac{1}{2} \Delta_{i,i}^{(t)} (1 + \frac{1}{2} \rho_{i-2, i-2})^{(2)} = \frac{1}{2} \Delta_{i,i}^{(t)} (1 + \frac{1}{2} \rho_{i-2, i-2})$$

Now, $\Delta_{ii}^{(t)} = \delta_{ii}^{(t)} (2 - \frac{1}{G_t}) + 2$, and since $\delta_{ii} = 0$ for all i , all t , $\Delta_{ii}^{(t)} = 2$.

The diagonal entries look like $\rho_{i,i} = \frac{1}{2} + \frac{1}{4} \rho_{i-2, i-2}$

The arbitrary entry looks like $\rho_{i,j}^{(t)} = \frac{1}{2} \Delta_{i,j}^{(t)} (1 + \frac{1}{2} \rho_{\max(i,j), \max(i,j)})^{(2)}$
 $= \frac{1}{2} \Delta_{i,j}^{(t)} - 1 + \frac{1}{2} \Delta_{i,j}^{(t)} \rho_{\max(i,j)-2, \max(i,j)-2}^{(t-2)}$

Using, for simplicity, $h_t = (2 - \frac{1}{G_t})$, we have

$$\Delta_{ij}^{(t)} = \delta_{ij}^{(t)} h_t + 2$$

$$\Delta_{ij}^{(t)} - 1 = \delta_{ij}^{(t)} h_t + 1$$

and $\rho_{ij}^{(t)} = \frac{1}{2} \delta_{ij}^{(t)} h_t + 1 + \frac{1}{2} \delta_{ij}^{(t)} h_t + 2 \rho_{\max(i,j)-2, \max(i,j)-2}^{(t-2)}$

$$j = 0 \quad 1 \quad 2 \quad 3 \quad 4 \quad 5 \quad 6$$

The matrix of δ_{ij} is: $i = 0$	$\begin{array}{ccccccc} 0 & 1 & 2 & 3 & 4 & 5 & 6 \\ 1 & 1 & 0 & 1 & 2 & 3 & 4 & 5 \\ 2 & 2 & 1 & 0 & 1 & 2 & 3 & 4 \\ 3 & 3 & 2 & 1 & 0 & 1 & 2 & 3 \\ 4 & 4 & 3 & 2 & 1 & 0 & 1 & 2 \\ 5 & 5 & 4 & 3 & 2 & 1 & 0 & 1 \\ 6 & 6 & 5 & 4 & 3 & 2 & 1 & 0 \end{array}$
---	--

which is simply generational removal (see table 2.1) and the Matrix showing $\max(i,j) - 2$, $\max(i,j) - 2$ is:

	j = 0	1	2	3	4	5	6
i = 0	(-2, -2)	(-1, -1)	.	.	.	(3, 3)	(4, 4)
1	(-1, -1)	(-1, -1)			.	.	.
2
3
4
5	(3, 3)	(3, 3)	.
6	(4, 4)	(4, 4)

which is $\chi = 2$, from table 2.1. So the matrix $R^{(t)}$ looks like:

$$R^{(t)} = \begin{bmatrix} \frac{1}{2}^{0+h+1} + \frac{1}{2}^{0+h+3} p_{(-2,-2)}^{(t-2)} & . & . & . & \frac{1}{2}^{6+h+1} + \frac{1}{2}^{6+h+2} p_{(4,4)}^{(t-2)} \\ . & . & . & . & . \\ . & . & . & . & . \\ . & . & . & . & . \\ \frac{1}{2}^{6+h+1} + \frac{1}{2}^{6+h+2} p_{(4,4)}^{(t-2)} & . & . & . & \frac{1}{2}^{0+h+1} + \frac{1}{2}^{0+h+2} p_{(4,4)}^{(t-2)} \end{bmatrix}$$

or, $R^{(t)} = \left[\frac{1}{2}^{\delta_{ij}^{h+1}} \right] + \left[\frac{1}{2}^{\delta_{ij}^{h+2}} \right] * R^{(t-2)}.$

Essentially, everything depends on the value of h , and on the initial p for the initial population(s). If h is positive or 0, then we have a system with "regular" behavior. If h is negative, then the dynamics are unusual, first growing as δ_{ij} grows, then growing (even faster?) as $\delta_{ij} > 3$, depending on initial R , and dependent on the initial inbreeding of the initial pair, and on the "age structure" p_i, p_j of breeding pairs after that.

Notice, we do not have recursion in the proportions p_{ij} or dependence of \bar{p}_t on any values of $p_{ij}^{(t)}$ other than for the same time period t , because we assume no relationship (independence) if fertility and matrix type by "age class", providing the class exists at all in a particular time period t .

However, if we wish in this model, we can set $p_{ij}^{(t)} = p_{i-1, j-1}^{(t-1)}$ so that the entire matrix P of frequencies of classes moves over time in a regular way. In this case, the same method allows us to extend the computations as long as the stock is maintained as indicated.

CASE (IV): The proportions of matings between relatives of type $x=1, 2, \dots$ for each pair $\{i, j \mid i=j\}$ is given by a vector X of relative proportions of types (v_1, v_2, \dots, v_k) of relationship types $x=1, x=2, \dots, x=k$.

Case (IVa) $\{i, j \mid i \neq j\}$ has the same vector v of proportions of kin types.

Then for each class type i, j we must compute the relationship as the mean of the types:

$$\bar{\rho}_{ij} = \sum_k v_k \sum_{\text{all ancestors}} \left[\frac{1}{2}^{2k-\delta_{ij}} \left(1 + f_{\substack{\text{each ancestor at degreee} \\ (\max(i,j)-1, \max(i,j)-1)}} \right) \right]$$

Let us assume all initial f values are zero for now. Also, assuming there is one common ancestor, we find

$$\bar{\rho}_{ij} = \sum_k v_k \frac{1}{2}^{(2k-\delta_{ij})}$$

or, two common ancestors (both parents):

$$\bar{\rho}_{ij} = \sum_k v_k \frac{1}{2}^{(2k-\delta_{ij}-1)}$$

Case (IVb) the vector v of relative proportions of kin types (x values) differs. For example, in cases II and III above, the relative proportions of possible relatives is strongly related to or determined by the assumptions on mating system. In case II, we assumed all ancestors of type (i, j) were of a specific class.

For other cases, we must make specific computations. In these cases, we compute the matrix equation

$$\begin{aligned} R^{(t)} &= \left[\frac{1}{2}^{2x_{ij}^{(t)}} - \delta_{ij}^{(t)} \right] + \frac{1}{2} \left[\frac{1}{2}^{2x_{ij}^{(t)}} - \delta_{ij}^{(t)} \right] * R^{(t-2)} \\ &= x^{(t)} + \frac{1}{2} x^{(t)} * R^{(t-2)} \end{aligned}$$

Also, the rows below show the number return in numbers of years from time of release, the columns show population composition at a given time from $T_0^{(i)}$

$T_0^{(0)}$	$T_1^{(0)}$	$T_2^{(0)}$	$T_3^{(0)}$	$T_4^{(0)}$	$T_5^{(0)}$	$T_6^{(0)}$	\dots
$T_0^{(1)}$	$T_1^{(1)}$	$T_2^{(1)}$	$T_3^{(1)}$	$T_4^{(1)}$	$T_5^{(1)}$	$T_6^{(1)}$	\dots
$T_0^{(2)}$	$T_1^{(2)}$	$T_2^{(2)}$	$T_3^{(2)}$	$T_4^{(2)}$	$T_5^{(2)}$	$T_6^{(2)}$	\dots
$T_0^{(3)}$	$T_1^{(3)}$	$T_2^{(3)}$	$T_3^{(3)}$	$T_4^{(3)}$	$T_5^{(3)}$	$T_6^{(3)}$	\dots
$T_0^{(4)}$	$T_1^{(4)}$	$T_2^{(4)}$					\dots
$T_0^{(5)}$	$T_1^{(5)}$						\dots
$T_0^{(6)}$							\dots

release at
time i , and
 $T_j^{(i)}$, $j > 0$
later returns in
periods j units
from i .

2.7 Proportions of Wild Types

Suppose that in addition to the classes $1 \leq i \leq m$, $1 \leq j \leq m$ there are classes $i=0$, $j=0$ of individuals which are not produced by the same source as the other classes i , j . In other words, a set of "wild" types unrelated to the classes i , j .

Then, for any pair (i,j) , $i \neq 0$, $j \neq 0$, we have the same computations as above. For any pairs $(0,j)$, $(i,0)$, $i \neq 0$, $j \neq 0$, the genetic relationship must be zero, since there are no common ancestors. Likewise, all $(0,0)$ pairs have no history in common with i , j , but there may be an amount of w of genetic relationship ($\frac{1}{2}w = \bar{f}_0^{(t)}$). If the proportions of the classes are

$$p_t = [p_{ij}^{(t)}] \text{ for } i, j \text{ pairs}$$

$$p_{0,j}^{(t)} = [p_{0j}^{(t)}] \text{ for } 0, j \text{ pairs}$$

$$p_{i,0}^{(t)} = [p_{i0}^{(t)}] \text{ for } i, 0 \text{ pairs}$$

$$p_{0,0}^{(t)} = [s^{(t)}] \text{ for } 0, 0 \text{ pairs}$$

We can also treat 0 as the lower index of i and j and look at the new $(m+1) \times (m+1)$ matrices P , R , but we can set a clearer picture by setting $q_{ij} + q_{0j} + q_{i0} + q_{00} = 1$ where q is the proportion of the total represented population in the matrix of the same subscript. We could make these q 's into matrices by use of multiplication to study each element independently. The same analysis as follows would then hold for each element independently and the final average value will be the average for all elements.

We have:

$$\bar{\rho}_t = q_{i,j} p_{i,j}^{(t)} * R_{i,j}^{(t)} + q_{0,j} p_{0,j}^{(t)} * R_{0,j}^{(t)} + q_{i,0} p_{i,0}^{(t)} * R_{i,0}^{(t)} + q_{0,0} p_{0,0}^{(t)} * R_{0,0}^{(t)}$$

Notice that since $R_{0,j}^{(t)} = R_{j,0}^{(t)} = [0]$, we can eliminate two terms, but since $q_{i,j} + q_{0,0} \neq 0$ in general, we can say little about the total relationship if we assume $R_{0,0}^{(t)} \neq 0$. If we can compute values for $q_{0,i}$, $q_{i,0}$, $q_{0,0}$ then direct computations are possible. Otherwise, if we assume $R_{0,0}^{(t)} = [0]$, then $q_{0,i}^{(t)} + q_{i,0}^{(t)} + q_{0,0}^{(t)} = q^{(t)}$ and $q_{i,j}^{(t)} = 1 - q^{(t)}$. In this case, we may set

$$\hat{\rho}_t = \bar{\rho}_t (1 - q^{(t)}) + q^{(t)} \cdot 0 = \bar{\rho}_t (1 - q^{(t)}).$$

The total relationship is reduced by the product $q^{(t)} \bar{\rho}_t$. If we assume we have correctly computer $\bar{\rho}_t$ from (i,j) information we may then estimate the proportion $q^{(t)}$ of matings with wild types and between wild types, hence the proportion $1 - q^{(t)}$ of matings between "factory produced" types:

- (1) providing we can estimate $\hat{\rho}_t$ from other evidence (e.g., biochemical studies of the population), or
- (2) if a direct estimate of $q^{(t)}$ can be made from catch proportions and a specific assumption on proportions of mating types.

$$\text{In case (1): } q^{(t)} = \frac{\bar{\rho}_t - \hat{\rho}_t}{\bar{\rho}_t}$$

In case (2): estimate $q_{i,0}$, $q_{0,j}$ and $q_{0,0}$ by the specific assumptions, then compute $q^{(t)}$ as above.

In the case where we treat each component separately, so that the q 's become matrices $Q_{0,i}$, etc., we have:

$$\begin{aligned} \hat{\rho}_t &= \text{perm} \left[Q_{i,j}^{(t)} * p_{i,j}^{(t)} * R_{i,j}^{(t)} \right] + \text{perm} \left[Q_{0,j}^{(t)} * p_{0,j}^{(t)} * R_{0,j}^{(t)} \right] + \\ &\quad \text{perm} \left[Q_{i,0}^{(t)} * p_{i,0}^{(t)} * R_{i,0}^{(t)} \right] + \text{perm} \left[Q_{0,0}^{(t)} * p_{0,0}^{(t)} * R_{0,0}^{(t)} \right] \end{aligned}$$

One estimate of $q^{(t)}$ is then

$$q^{(t)} = \text{perm} Q_{0,j}^{(t)} p_{0,j}^{(t)} + \text{perm} Q_{i,0}^{(t)} p_{i,0}^{(t)} + \text{perm} Q_{0,0}^{(t)} p_{0,0}^{(t)}.$$

We then estimate θ_t from the exterior source, and compute

$$q^{(t)} = \frac{\text{perm } Q_{i,j}^{(t)} P_{i,j}^{(t)} R_{i,j}^{(t)} - \delta_t}{\text{perm } Q_{i,j}^{(t)} P_{i,j}^{(t)} R_{i,j}^{(t)}}$$

Note that the fact that we are using ρ and not θ or f is irrelevant, since as is clear in these last two expressions, the proportionality constants ρ , f , θ , will all cancel out of the estimation equations for $q^{(t)}$.

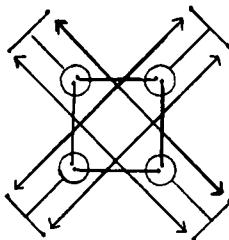
These equations therefore allow computations of $q^{(t)}$ from prior knowledge of computations in the earlier sections.

CHAPTER 3: GRAPHS AND OPERATORS OF MARRIAGE THEORY
(co-author, sections 3.1 and following: Thomas Duchamp)*

One of the better developed areas of social theoretic mathematics is the use of graphs and relations to describe actual relations among individuals in particular populations. In this chapter, we give specific formulations of the use of graphs and operators to describe particular networks, and to relate these problems to other related problems, such as the prediction of possible future networks from given present states, or to the particular interpretation of various possible measures on the operators themselves or on functions of the operators. We present a summary of the origins in the existing literature of our formalism, then the formalism itself.

Two of the most basic ideas may be traced to Sewall Wright. One of these is the already well known technique of path analysis, which postulates a network of people connected by lines representing descent links, and then gives methods of calculating degree of relatedness along these various descent paths (Wright, 1968). Wright first completed this work early in the century, along with a second important calculation. In a paper in 1921, he showed that the maintenance of a particular system of inbreeding could be associated with a smallest number of people required in each generation to maintain the system. To do this, Wright assumed a rather ideal case of two offspring to each mating, and that these were always one male and one female. These restrictions allowed him to calculate, for example, that where marriage (i.e., mating) to first cousins is prohibited, at least eight people are required in each generation (Wright, 1921).

Using a slight variant of the ordinary diagramming technique, this may be shown as:



* This paper is an expanded version of the paper "Foundations of Marriage Theory" given by the authors at the 1971 meetings of the American Association of Physical Anthropologists, Boston, Massachusetts. The underlying logic and its potential relation to the Dirac notation was originally outlined in the doctoral dissertation of P. A. Ballonoff, but developed into the present form only in co-operation with T. Duchamp while both were at Southern Illinois University. See also, Duchamp and Ballonoff (1974).

In this picture, we use a dot "•" to represent a person, whether male or female, a line between two dots "—" to show that the two are siblings, a circle around two dots to show a "marriage" between them, and a sibling line with a vertical insert into a marriage circle to show descent from a marriage. The double pointed arrows show available partners across the diagonal of the square are available to each other.

We call the number of "distinct families" (groups of persons connected by the same sibling link) required in each generation to maintain the stability of the rule, the structural number (also minimal stability number) for that system. (See chapter 4 for details of this topic.) It is very useful to find such a diagram for each marriage system one wishes to study. Indeed, this is very close to or identical to the procedure already followed by many ethnographers and ethnologists. For example, R. T. Zuidema has constructed precisely such a system, with seven sides and from four to five layers of generation depth, in order to discuss the lineage system of Incan Peru, and to analyze similarities to North American clan systems (Zuidema, 1964, 1965); E. A. Cook has presented similar arguments for the Manga of New Guinea (1967, 1969); and B. Ruheman has shown similar properties of the classic Australian systems (1945). Another property of these same diagrams is that one may study them more easily as patterns of cycles and chains of an abstract mathematical system. F. B. Livingstone (1969) and C. Levi-Strauss (1967, Chapter 15; 1969) have both indicated this should be a profitable attack.

Next, it has long since been pointed out that related properties of marriage systems may be represented as group operators of various sorts. Andre Weil presented the needed demonstration in the appendix to the 1949 edition of Levi-Strauss (1969) referenced above, subsequently being reprinted in H. White (1963). This later book was also important for its axiomatization of kinship systems, and its mapping of such systems onto role trees suitable for later analysis. In our representation, we also use operators to represent the properties of marriage systems. The notations and methods of analysis we suggest are very similar to those adopted by Maruyama and Yasuda (1970), and by Maruyama (1970), but we have modified this approach by use of a notation similar to that found in Hall and Collins (1971). Use of this notation will provide a very free mathematical framework in which to work, since in the present case, it implies acceptance of the use of Euclidian spaces, easily generalized to Hilbert spaces, as the proper mathematical space for treatment of problems of marriage theory. In such spaces, one may define and calculate long term averages, as well as carry out certain algebraic operations.

3.1 Summary of Notation

To make these ideas available to anthropology, we have adopted the "Dirac notation" of "bra" $\langle \cdot |$ and "ket" $| \cdot \rangle$ to show elements of a Euclidian space. If the basis on the space is chosen to correspond to individuals in a population, the elements may be written $\langle p_i |$ or $| p_i \rangle$. Taking the cross product of the population with itself, and writing marriage kinship rules as logical operations, one may create a square matrix of zeros and ones according to the truth value assignments peculiar to the system under study. We may thus construct self-adjoint linear operators, which might be designated:

- M_t : marriage operator in generation t
- S_t : same sex designator
- X_t : exclusion by "incest prohibition"
- C_j^i : generalized cousin operator showing j links of "depth" and i links of width
- B_t : sibling operator
- etc.

These operators allow demonstration of structural theorems with demographic content. For example, the theorem $\text{tr}(M \cdot C) = 0$ implies that a marriage rule "no one is married to a (specific) cousin" holds. The existence of such rules corresponds to the existence of stability rules like: the least number of persons per generation required to maintain first cousin exclusion in marriage is eight. These clearly correspond as well to numbers used for Wright's breeding calculations. (Chapter 4 discusses these numbers in more depth.) Using these operators, and possibly others depending on the society and the marriage rule, we can describe the "marriage history" of a society as a chain of Euclidian spaces and operators, each generation linked to the preceding one by a progeny transformation:

$$H_0 \xrightarrow{P_0} \dots H_t \xrightarrow{P_t} H_{t+1} \longrightarrow \dots$$

where H_0 is the Euclidian space of the zeroth generation, P_0 the progeny operator from H_0 to H_1 , etc. We define, N , to be a link in the chain

$$N_t = \left\{ \begin{array}{ccc} H_t & \xrightarrow{P_t} & H_{t+1} \\ & B_t & \\ H_t & \xrightarrow{} & H_t \\ & M_t & \\ H_t & \xrightarrow{} & H_t \\ & (i_c^j)_t & \\ H_t & \xrightarrow{} & H_t \end{array} \right\}$$

where it is understood that the operators B_t , etc. are on $H_t \times H_t$. Then the marriage rule, birth rates, mortality rates, etc., will determine a set of transition probabilities, $\langle N | N_o \rangle$ being the probability that a society described by network N_o will be described by network N in one generation.

We may then define $\langle N | N_o \rangle_t$ as the probability that a society described by N_o will be described by N in t generations. Letting U be the set of all networks, the expression $\langle | N_o \rangle_t$ defines a probability measure on U . Suppose $f: U \rightarrow R$ is a function from U to the real numbers. Then f can be considered as a random variable on the probability space $(U, \langle | N_o \rangle_t)$ and

$$\hat{f}_{N_o}(t) = \int f(N) \langle N | N_o \rangle_t$$

will be the expected value of f in n generations after N_o . In particular, we define for $N \in U$

$r(N)$	= population of N
$E(N)$	= average ties of N
$\bar{E}_g(N)$	= average genetic ties of N
$\bar{E}_m(N)$	= average marriage-sibling ties of N
etc.	

The expectation values of these functions can be useful. For example, $\hat{r}_{N_o}(t)$ is the expected population in t generations after N_o . $\hat{\bar{E}}_{gN_o}(t)$ is the average genetic ties n generations after N_o . We note that this is related to the expected average inbreeding coefficient. We may also write more general expressions for inbreeding in a generation and the existence of cycles, as in equations (1).

3.2 Detailed Foundations

Consider a society that uses a given marriage rule (see chapters 3 and 4 for two different definitions of "marriage rule") and which is such that generations may be assumed discrete. We will show how to represent the marriage theory (hereafter termed "history") of the society in terms of linear transformations of a real Euclidean space. Note that in chapter 4 is provided a more compact summary of an application of the following.

FUNDAMENTAL DEFINITIONS

Definition 1: Let \mathbb{R} be the real numbers and let

$$H = \bigoplus_{i=1}^k \mathbb{R}_i \quad \mathbb{R}_i = \mathbb{R}, i = 1, 2, \dots,$$

where k is at least as large as the population size, and usually much larger, but finite and H is a finite dimensional vector space over \mathbb{R} . We define an inner product on H by

$$\langle A | B \rangle = \sum_{i=1}^k a_i b_i$$

where

$$|A\rangle = \sum_{i=1}^k a_i \quad a_i \in \mathbb{R}_i$$

$$|B\rangle = \sum_{i=1}^k b_i \quad b_i \in \mathbb{R}_i$$

These two bottom sums are formal sums and not sums of real numbers, whereas the first sum is a numerical sum. This inner product is clearly a complete, positive definite, bilinear form on H . We stipulate that all Euclidean spaces used will be isomorphic to H , unless otherwise specified.

Definition 2: A set $N \subseteq H$ will be called an orthonormal base (or simply a basis) for H if

i) For all $|a\rangle, |b\rangle \in N$, $\langle a | b \rangle = \begin{cases} 1 & \text{if } |a\rangle = |b\rangle \\ 0 & \text{if } |a\rangle \neq |b\rangle \end{cases}$

ii) Any vector in H can be written in a unique way as a linear combination of a finite number of elements of N .

(This definition is more restrictive than the usual definition of orthonormal basis as used in analysis.)

Definition 3: A function $F: H \rightarrow K$, where H and K are Euclidean spaces, is called a linear transformation if for all $|v\rangle, |u\rangle \in H$ and $a, b \in \mathbb{R}$,

$$F(a|v\rangle + b|u\rangle) = aF|v\rangle + bF|u\rangle.$$

If $H = K$, then we call F a linear operator (or simply an operator) on H .

Definition 4: An operator $P:H \rightarrow H$ is called a projection operator if P is the identity on a subspace of H and zero on the orthogonal complement of this subspace.

Equivalently, $P^2 = P$, which is symbolized by the commutative diagram:

$$\begin{array}{ccc} H & \xrightarrow{P} & H \\ & \searrow P & \downarrow P \\ & H & \end{array}$$

Definition 5: Let N be an orthonormal base of H and $F:H \rightarrow H$ an operator on H . The trace of F (symbolized by $\text{tr}(F)$) is

$$\text{tr}(F) = \sum_{|a\rangle \in N} \langle a | F | a \rangle$$

The trace of an operator is independent of the orthonormal basis chosen.

Definition 6: Let H be a Euclidean space, P a projection operator and $F:H \rightarrow H$ an operator on H . F is called a P -operator if we have:

$$\begin{array}{ccc} H & \xrightarrow{F} & H \\ \uparrow P & \swarrow F & \downarrow P \\ H & \xrightarrow{F} & H \end{array}$$

that is, the range of F is in the range of P and F is zero on the orthogonal complement.

We may now apply the above to real people and relations between them. Let

$$G_0 = \{p_1^0, p_2^0, \dots, p_{\text{pop}_0}^0\}$$

$$G_1 = \{p_1^1, p_2^1, \dots, p_{\text{pop}_1}^1\}$$

.

.

$$G_n = \{p_1^n, p_2^n, \dots, p_{\text{pop}_n}^n\}$$

The elements of G_i correspond to members of the i^{th} generation. pop_i^t = total population of the i^{th} generation.

Let H_t be a Euclidean space and let

$$N_t \{ |p_1^t\rangle, |p_2^t\rangle, \dots, |p_{pop_t}^t\rangle, |p_{pop_t+1}^t\rangle, \dots \}$$

be a basis for H_t . Let $\pi_t: H_t \rightarrow H_t$ be the projection operator defined by:

$$\pi_t : |p_j^t\rangle \mapsto \begin{cases} |p_j^t\rangle & \text{if } 1 \leq j \leq pop_t \\ |0\rangle & \text{if } pop_t < j \end{cases}$$

Any vector in the range of π_t , say $|v\rangle = \sum_{j=1}^{pop_t} a_j |p_j^t\rangle$

corresponds to the subset of G_t : $v = \{p_j^t \in G_t \mid a_j \neq 0\}$

the magnitude of a_j serves as a measure of the stress laid on the j^{th} individual.

For example $|v_1\rangle = |p_1^t\rangle + 4|p_2^t\rangle$

stresses p_2^t whereas $|v_2\rangle = 2|p_1^t\rangle + |p_2^t\rangle$

stresses p_1^t although both $|v_1\rangle$ and $|v_2\rangle$ represent the same subset of G_t . Note that by using only 0 and 1 as weights, and interpreting "+" as a set theoretic sum, we obtain an expression describing the elements of a particular set.

We now give an interpretation of π_t -operators on H_t . Let $R: H_t \rightarrow H_t$ be a π_n -operator, we define a relation R on G_t by:

$$\forall a, b \in G_t, aRb \Leftrightarrow \langle a | R | b \rangle \neq 0.$$

The magnitude of $\langle a | R | b \rangle$ gives the "strength" of the relation R between a and b .

We may work the other way and define a π_i -operator on H_t given a relation R on G_t : Define $R: H_t \rightarrow H_t$ by

$$R : |p_j^t\rangle \mapsto \sum_{i=1}^{pop_t} r_{ji} |p_i^t\rangle$$

$$r_{ji} = \begin{cases} 1 & \text{if } p_j^t R p_i^t \\ 0 & \text{otherwise} \end{cases} \quad | \leq j \leq pop_t$$

$$R : |p_j^t\rangle \mapsto |0\rangle, j > pop_t.$$

By allowing the a_{ij} 's to differ from 1 and 0, we can incorporate the idea of strength of a relation in our operator R .

3.3 Operators of Marriage Theory

(i) Basic Operators:

In this section, we consider some of the relations that are necessary in marriage theory. Consider G_t . We note several important relations on G_i .

- i) $B_t : H_t \times H_t \rightarrow H_t$
 $aB_t b \equiv a \text{ and } b \text{ are siblings}$
- ii) $M_t : H_t \times H_t \rightarrow H_t$
 $aM_t b \equiv a \text{ is married to } b$
- iii) $C_t : H_t \times H_t \rightarrow H_t$
 $aC_t b \equiv a \text{ is a first cousin of } b$
- iv) $C_t^x : H_t \times H_t \rightarrow H_t$
 $aC_t^x b \equiv a \text{ is a cross-first cousin of } b$
- v) $C_t'' : H_t \times H_t \rightarrow H_t$
 $aC_t'' b \equiv a \text{ is a parallel-first cousin of } b$
- vi) $S_t : H_t \times H_t \rightarrow H_t$
 $aS_t b \equiv a \text{ is of same sex as } b$

where $a, b \in G_i$. Following the last section, we have corresponding to i) - vi), the following operators:

i) $B_t : H_t \rightarrow H_t$

$$|p_i^t\rangle \mapsto \sum_{j=1}^{\text{pop}_t} b_{ij} |p_j^t\rangle, \quad b_{ij} = \begin{cases} 1, & \text{if } p_i^t B_t p_j^t \\ 0, & \text{if not } i \leq \text{pop}_t \end{cases}$$

$$|p_i^t\rangle \mapsto |0\rangle, \quad i > \text{pop}_t$$

ii) $M_t : H_t \rightarrow H_t$

$$|p_i^t\rangle \mapsto \sum_{j=1}^{\text{pop}_t} m_{ij} |p_j^t\rangle, \quad m_{ij} = \begin{cases} 1, & \text{if } p_i^t M_t p_j^t \\ 0, & \text{if not } i \leq \text{pop}_t \end{cases}$$

$$|p_i^t\rangle \mapsto |0\rangle, \quad i > \text{pop}_t$$

.

vi) $S_t : H_t \rightarrow H_t$

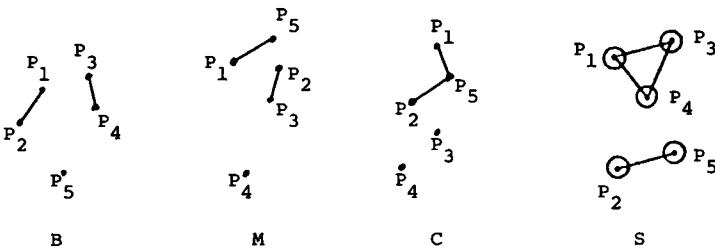
$$|p_i^t\rangle \mapsto \sum_{j=1}^{\text{pop}_t} s_{ij} |p_j^t\rangle, \quad s_{ij} = \begin{cases} 1, & \text{if } p_i^t S_t p_j^t \\ 0, & \text{if not } i \leq \text{pop}_t \end{cases}$$

$$|p_i^t\rangle \mapsto |0\rangle, \quad i > \text{pop}_t$$

These are sufficient to describe the "American System" and many others, however, particular marriage systems could require more or even a different set of operators

In this event, one could proceed in a way similar to what follows. Note that given a specific history, these relations are defined empirically. However, we also note that the "kinship logic" of a particular system also restricts which empirical relations may be possible. Our system is capable both of describing empirical networks and making computations on them, and also of creating and studying properties of synthetic or theoretical systems.

We now give an example of how to construct some of the above operators given a particular situation: Suppose $G = \{p_1, p_2, p_3, p_4, p_5\}$ and we had relations corresponding to these graphs:



Then

$$\begin{aligned} [b_{ij}] &= \begin{bmatrix} 0 & 1 & 0 & 0 & 0 \\ 1 & 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 1 & 0 \\ 0 & 0 & 1 & 0 & 1 \\ 0 & 0 & 0 & 0 & 0 \end{bmatrix} & [m_{ij}] &= \begin{bmatrix} 0 & 0 & 0 & 0 & 1 \\ 0 & 0 & 1 & 0 & 0 \\ 0 & 1 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 & 0 \\ 1 & 0 & 0 & 0 & 0 \end{bmatrix} \\ [c_{ij}] &= \begin{bmatrix} 0 & 0 & 0 & 0 & 1 \\ 0 & 0 & 0 & 0 & 1 \\ 0 & 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 & 0 \\ 1 & 1 & 0 & 0 & 0 \end{bmatrix} & [s_{ij}] &= \begin{bmatrix} 1 & 0 & 1 & 1 & 0 \\ 0 & 1 & 0 & 0 & 1 \\ 1 & 0 & 1 & 1 & 0 \\ 1 & 0 & 1 & 1 & 0 \\ 0 & 1 & 0 & 0 & 1 \end{bmatrix} \end{aligned}$$

From these matrices, we may compute the values of the operators for any vector. For example, let $|a\rangle = |p_1\rangle + |p_3\rangle$, then

$$B|a\rangle = B|p_1\rangle + B|p_3\rangle = |p_2\rangle + |p_4\rangle$$

$$M|a\rangle = M|p_1\rangle + M|p_3\rangle = |p_5\rangle + |p_2\rangle$$

$$C|a\rangle = C|p_1\rangle + C|p_3\rangle = |p_5\rangle + |0\rangle = |p_5\rangle$$

$$\begin{aligned} S|a\rangle &= S|p_1\rangle + S|p_3\rangle = |p_1\rangle + |p_3\rangle + |p_4\rangle + |p_3\rangle + |p_4\rangle \\ &= |p_1\rangle + 2|p_3\rangle + 2|p_4\rangle \end{aligned}$$

(ii) Some Theorems

The following theorems follow immediately from the nature of relations i) - vi).

Theorem 1: For $t = 0, 1, 2, 3$.

$$\begin{array}{ccc} \begin{array}{c} H_t / \text{Ker}(B_t + \pi_t) \\ \downarrow \zeta_n \\ H_t \\ \xrightarrow{C_t} H_t \end{array} & \begin{array}{c} H_t / \text{Ker}(B_t + \pi_t) \\ \downarrow \zeta_n \\ H_t \\ \xrightarrow{C''_t} H_t \end{array} & \begin{array}{c} H_t / \text{Ker}(B_t + \pi_t) \\ \downarrow \zeta_n \\ H_t \\ \xrightarrow{C^X_t} H_t \end{array} \end{array}$$

where $\text{Ker}(B_t + \pi_t) = \{ |v\rangle \in H_t : (B_t + \pi_t)|v\rangle = 0\}$ and ζ_t is the natural map onto the quotient space. Notice that dimension $(H_t / \text{Ker}(B_t + \pi_t))$ = number of distinct families in G.

Theorem 2: For $t = 0, 1, 2, \dots$, $C_t = C_t^X + C_t''$.

Theorem 3: For $t = 0, 1, 2, \dots$, $B_t M_t C_t, C_t^X, C_t'', S_t$ are self adjoint operators.

Theorem 4: For $t = 0, 1, 2, \dots$, $F \in \{B_t, M_t, C_t, C_t^X, C_t''\}$, $\text{tr}(F) = 0$.

Theorem 5: For $t = 0, 1, 2, \dots$, and Axioms corresponding to marriage rules A1 to A5 of the next chapter.

$$\text{Axiom 1)} \iff \text{tr}(M_t) = 0.$$

$$\text{Axiom 2)} \iff \text{tr}(M_t \cdot B_t) = \text{tr}(M_t) = 0.$$

$$\text{Axiom 3)} \iff \text{tr}(M_t \cdot C_t'') = \text{tr}(M_t \cdot B_t) = \text{tr}(M_t) = 0.$$

$$\text{Axiom 4)} \iff \text{tr}(M_t \cdot C_t^X) = \text{tr}(M_t \cdot B_t) = \text{tr}(M_t) = 0.$$

$$\text{Axiom 5)} \iff \text{tr}(M_t \cdot C_t) = \text{tr}(M_t \cdot B_t) = \text{tr}(M_t) = 0.$$

(Note: $\text{tr}(M_t \cdot C_t) = 0 \implies \text{tr}(M_t \cdot C_t'') = \text{tr}(M_t \cdot C_t^X) = 0$.)

These theorems on zero trace of particular operators under particular marriage rules suggests the existence of a theory which studies non-zero trace operators or products and powers of operators. In fact, non-zero traces correspond to the existence of cycles and chains of various length of individuals connected through the operators (or products or powers of operators) whose traces are taken. In the present example, the results simply hold from the fact that a particular marriage rule is followed in a given case.

(iii) Progeny Transformation

We now present a transformation relating people in one generation to their children in the next.

Definition 7: For $t = 0, 1, 2, \dots$, the i^{th} progeny transformation is a map
 $\text{Prog}_t : H_t \rightarrow H_{t+1}$

$$|p_j^t\rangle \mapsto \sum_{k=1}^{\text{pop}_{t+1}} p_{jk}|p_k^{t+1}\rangle, \quad 1 \leq j \leq \text{pop}_t$$

$$p_{jk} = \begin{cases} 1, & \text{if } p_j^t \text{ is a parent of } p_k^{t+1} \\ 0, & \text{otherwise} \end{cases}$$

$$|p_j^t\rangle \mapsto |0 \text{ if } j > \text{pop}_t$$

Since Prog_t is zero outside the image of π_t and has image in the image of π_{t+1} , we have:

Theorem 7: For $t = 0, 1, 2, \dots$,

$$\begin{array}{ccc} H_t & \xrightarrow{\text{Prog}_t} & H_{t+1} \\ \pi_t \downarrow & \searrow & \downarrow \pi_{t+1} \\ H_t & \xrightarrow{\text{Prog}_t} & H_{t+1} \end{array}$$

Theorem 8: If marriage is monogamous, then for $t = 0, 1, 2, \dots$, we have:

$$\begin{array}{ccc} H_t & \xrightarrow{\zeta_t} & H_t / \text{Ker}(M_t + \pi_t) \\ & \searrow & \downarrow \\ H_t & \xrightarrow{\text{Prog}_t} & H_{t+1} \end{array}$$

where $\text{Ker}(M_t + \pi_t) = \{|a\rangle \in H_t : (M_t + \pi_t)|a\rangle = 0\}$ and ζ_t is the natural map.

Theorem 9: For $t = 0, 1, 2, \dots$,

$$\langle p_j^{t+1} | B_{t+1} | p_k^{t+1} \rangle \neq 0 \implies$$

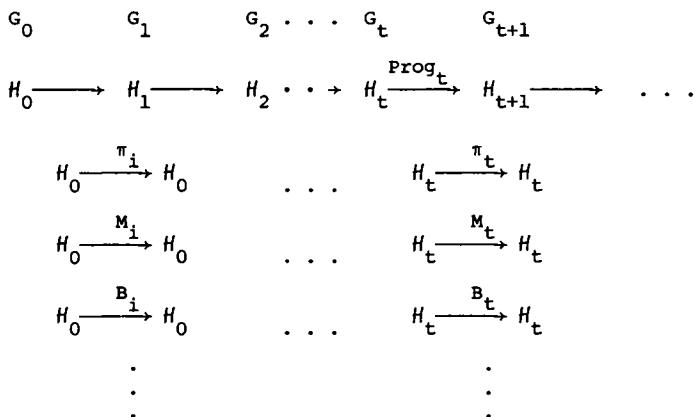
$$\text{Prog}_h^t | p_j^{h+1} \rangle = \text{Prog}_h^t | p_k^{h+1} \rangle$$

Notice that the operator Prog_t here can be constructed from the descent maps of the next chapter. Similarly, pop_t is simply the size of the set G_t , which the operators M , B , S here correspond to the partitions M , B , S of the next chapter, and G , the set of people of a given generation remains the same concept. We use "P" here for an arbitrary descent transformation, and Prog_t for the specific transformation from t to $t+1$. Note that P is also a projection. A similar looseness occurs

by using N in parts to refer to a specific network, and sometimes to refer to all networks isomorphic to the specific network. The context is generally clear for networks, but see section 4.3 for a clearer treatment of the difference between networks and isomorphism classes of networks.

(iv) Marriage History

We now have the apparatus to describe the history of a society. For each generation, G_t , we have a Euclidean space H_t , an orthonormal basis N_t , a projection operator π_t , several operators: M_t , B_t , C_t , S_t , etc., (the exact operators in the list depending on the marriage system under consideration) and a progeny transformation, Prog_t . We also have the conditions the operators must satisfy to be compatible with reality (some of these conditions are given in the previous theorems). Thus, we have schematically:



A diagram as above corresponds to a specific history of a society. This cannot be predicted. However, probably diagrams can be found and their probabilities calculated. This is what we seek to do in what follows.

3.4 Relation Strength

In sections 3.2 and 3.3, we found out how to represent relationships as linear transformations. In this section, we develop some operators which measure the strength of the marriage rule. This measure is useful in an analysis of the genetics and economics of a society.

In this section, B , M and P denote the sibling, marriage and progeny operators on a generation. Also we suppress subscripts as generation numbers needed in formulas

will be obvious from context. Also, we may assume an infinite history for a society by augmenting the diagram so that for $t < 0$, the history is empty. We always are referring to the case in what follows unless otherwise specified. We assume that we are working in particular generation with finite population size g .

(i) Generalized Cousin Operator

Definition 10: Let (H, N, π) , (H', N', π') , and (H'', N'', π'') be three objects in the set of all triples (Euclidean spaces, possible networks, populations of individuals), with $N = \{|p_1\rangle, |p_2\rangle, \dots\}$, The same for N' and N'' except with primes; with $\pi: |p_i\rangle \mapsto |p_i\rangle \quad 1 \leq i \leq g$

$$|p_i\rangle \mapsto |o\rangle \quad g < i$$

and the same for π' and π'' with g' and g'' in place of g . Let $F: H \rightarrow H'$, $G: H' \rightarrow H''$ be two linear transformations defined by the matrices: $F = [f_{ij}]_{g' \times g}$, $G = [g_{ij}]_{g'' \times g}$, where $f_{ij} \geq 0$, $g_{ij} \geq 0$ for all i, j . Then define $G \circ F$ by:

$$G \circ F: H \longrightarrow H''$$

$$|p_i\rangle \mapsto \sum_{j=1}^{g''} a_{ij} |p_j''\rangle$$

$$\text{where } a_{ij} = \begin{cases} 1 \text{ if } p_j'' |G \circ F| p_i \rangle \neq 0 \\ 0 \text{ otherwise} \end{cases}$$

where $G \circ F$ is composition of functions. In the following, all multiplications of operators will be *-multiplication.

Theorem: If all operators are as in Definition 10, then * is associative.

Note: Denote $\underbrace{G \circ G \circ \dots \circ G}_{k\text{-times}}$ by G^* , and denote the transformation of an operator P by P^T .

Definition 11: Consider the diagram below. Assume we are in a particular generation j , say the t^{th} generation with population size g . We define operators on H_t :

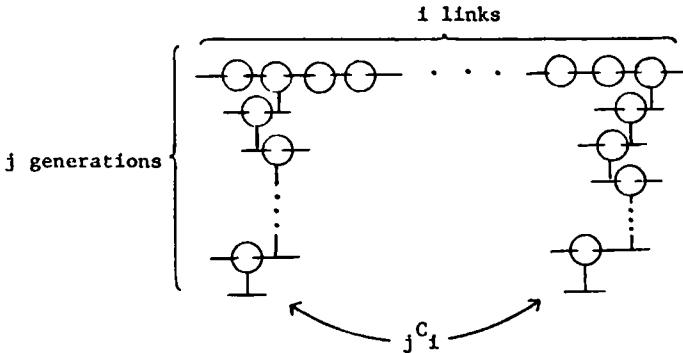
$$j C_0 = (P^{j*}) * (B) * (P^T)^{j*} \quad 1 \leq j \leq \infty$$

$$j C_i = (P^{j*}) * (B + M)^{i*} * (P^T)^{j*} \quad 0 \leq j \leq \infty$$

$$1 \leq i$$

Note that if $j > q$, then $j C_i = 0$.

We call these operators "generalized cousin operators". When it becomes necessary to show generation numbers, we write ${}_j C_i^q$ (q = generation number). The relations described by the ${}_j C_i$ are illustrated by the following diagram:



Thus, ${}_1 C_1$ is the "first cousin operator", ${}_2 C_1$ is the "second cousin operator".

Note: Since $P^T * P \neq 1$, we do not have ${}_K C_S * {}_K C_T = {}_K C_{S+T}$.

The set $E = \{ {}_i C_j \}$ describes paths that genes could follow as well as some measure of economic and political ties. We now seek a measure of the strength of relational ties between individuals ("bond strength").

Definition 12: Let $E = aI + bB + cM + c_m E_m + c_p E_p + c'E'$

where c_m, c_p, c' are real numbers ≥ 0 , and

$$E_m = \sum_{k=1}^{\infty} (1/2k) {}_0 C_k, \quad E_g = \sum_{k=1}^{\infty} \left(\frac{1}{2^{2k+1}}\right) {}_j C_1, \quad E' = \sum_{\substack{k=1 \\ k=2}}^{\infty} \left(\frac{1}{2^{2j+k-1}}\right) {}_i C_j$$

These operators show that E_g , the usual counting function for measuring probability of identity by descent, can be simply stated as an analytic form using the previous definitions; and that other particular networks of relations among individuals may be stated and computed with various weights. In the present case, we pick 1/2 to specified powers as the weight to emphasize correspondence to genetic theoretic probabilities, but other weights for E_m , may also be selected.

Given two subsets of a generation $\{|p_{i_1}\rangle, |p_{i_2}\rangle, \dots, |p_{i_r}\rangle\}$ and $\{|p_{j_1}\rangle, |p_{j_2}\rangle, \dots, |p_{j_s}\rangle\}$ we can define the average bond strength between individuals in these two sets. Let $|p_{i_1} \dots p_{i_r}\rangle = \sum_{k=1}^r |p_{i_k}\rangle$ and $|p_{j_1} \dots p_{j_s}\rangle = \sum_{k=1}^s |p_{j_k}\rangle$. Then

$$\frac{\langle p_{i_1} \dots p_{i_r} | E | p_{j_1} \dots p_{j_s} \rangle}{\langle p_{i_1} \dots p_{i_r} | p_{i_1} \dots p_{i_r} \rangle \langle p_{j_1} \dots p_{j_s} | p_{j_1} \dots p_{j_s} \rangle}$$

is a measure. By $|E|$ we mean:

$$\frac{\langle p_1 \dots p_g | E | p_1 \dots p_g \rangle}{(\langle p_1 \dots p_g | p_1 \dots p_g \rangle)^2}$$

where g is the total population size.

3.5 Probabilistic Formulation

In section 3.2 we showed how the marriage history of a society can be represented by a diagrammatic sequence of operators, which in fact is a statement of the history of a society. Starting with the initial state, an infinite number of diagrams are possible, each corresponding to a particular history. However, some diagrams are more probable than others. What we wish to do is discuss the formulation of probabilities of different possible histories.

Consider a population $G = \{p_1, \dots, p_g\}$ of g people, represented as a space H with basis $N = \{|p_1\rangle, \dots, |p_g\rangle, \dots\}$ and projection operators $\pi: H \rightarrow H$. Let $B: H \rightarrow H$ be the sibling operator. In a society which has a marriage rule which specifies whom a person cannot marry (or equivalently, whom a person can marry) as a set of people which are in one or more particular relations to that person we may characterize the marriage rule as follows: there is a set of π -operators $E = \{R^1, \dots, R^k\}$ on H . The marriage operator $M: H \rightarrow H$ must satisfy the condition " $\langle p_i | M | p_j \rangle = 1$ " (that is, p_i may marry p_j) only if $\langle p_i | F | p_j \rangle = 0$ for all $F \in E$. (Or, p_i is not related to p_j by any of the relations represented by E .) This may be stated in terms of an "exclusion operator".

Definition 13: Let E be as above, $X: H \rightarrow H$ is an operator defined for $|p_i\rangle \in N$ by:

$$1 \leq i \leq g \quad X|p_i\rangle = \sum_{j=1}^n e_{ij}|p_j\rangle$$

$$e_{ij} = \begin{cases} 1 & \text{if there is an } F \in E \text{ such that} \\ & \langle p_j | F | p_i \rangle \neq 0. \\ 0 & \text{otherwise.} \end{cases}$$

$$g < i \quad X|p_i\rangle = |0\rangle$$

The marriage rule may be stated as follows: $\text{tr}(X \cdot M) = 0$
for any admissible marriage operator.

Note that the operators which compose to form the exclusion operator are precisely those representing classes of relations which the marriage states as prohibited. Note also that any rule, whether stated initially in a proscriptive or prescriptive form, may be translated into a statement of which types of relations are prohibited as partners, and which are not. The composition used here is to combine by a logical "or" all those operators representing excluded classes under a given rule.

We assume that all marriages in a generation take place sequentially in a relatively short span of time, that monogamy is practiced, and that marriages continue until all persons marry that can without violating the marriage rule. With the assumption the reader will note that the set of allowable marriage sequences is in 1-1 correspondence with the following set, labeled $XM(g)$:

Definition 14: Let X be the exclusion operator on a population of size g as described above. Let $s = \text{greatest integer } \leq g/2$. Then $XM(n)$ is the set of s -triples of $g \times g$ matrices of "0's" and "1's" such that $(M_1, M_2, \dots, M_s) \in XM(g)$ if and only if the following hold:

- i) M_i is symmetric and has zero's along the diagonal for $1 \leq i \leq s$.
- ii) There is at most one "1" in every row of M_i for $1 \leq i \leq s$. (This is the monogamy assumption.)
- iii) If we consider X as an $g \times g$ matrix (or M_i as an operator) the diagonal of the matrix $X \cdot M_i$ (or the trace of the operator $X \cdot M_i$) is zero for $1 \leq i \leq s$. (This is the marriage rule.)
- iv) The number of "1's" in M_i is equal to the number of "1's" in M_{i+1} or the number of "1's" in $M_{i+1} - 2$.
- v) If (the number of "1's" in M_i) = (the number of "1's" in M_{i+1}), then $M_i = M_{i+1}$ for $1 \leq i \leq s - 1$.
- vi) If M_i is the first matrix in (M_1, \dots, M_s) such that $M_i = M_{i+1}$. Then if M' is any $g \times g$ matrix with a "1" in the j, k position, if M_i has a "1" in the j, k position, and if M' has a "1" in a position where M_i does not have a "1", then M' violates i), ii), or iii). (This states that all people that can marry do so.) We call $XM(g)$ the "marriage space of X ".

We now define a probability measure on $XM(g)$:

Definition 15: PX is the probability measure on $XM(g)$ defined by:

$$\forall A \in XM(g) \quad PX(A) = \frac{1}{|XM(g)|}$$

$$\forall S \subseteq XM(g) \quad PX(S) = \sum_{A \in S} PX(A).$$

where $|XM(g)|$ is the number of elements in $XM(g)$. This is the measure gotten if all possible marriage sequences are assumed equally likely. This is not exactly true in general, especially when a segment of the population for some reason has priorities over the rest in choice of marriage partners (for example, rulers of society). Also, there will be sections of the population considered less desirable than others. At this stage in our research, we are content with the above measure which in many cases is close to reality, and which can always be altered should it prove inadequate.

Consider now a population of n people on which are imposed two marriage rules, X and X' . These rules will in general restrict the marriage sequences differently. We may compare X and X' in several ways, some of which will be presented later. For the present, we consider the entropy functions as defined by Shannon and Weaver (1964).

Definition 16: Let $XM(g)$ be a marriage space and PX the probability measure on it. The entropy of PX , written $H(PX)$, is defined by:

$$H(PX) = -\sum_{A \in XM(g)} PX(A) \log_2(PX(A)).$$

This function simplifies when PX is defined as above:

$$H(PX) = \log_2 |(XM(g))|.$$

Essentially $H(PX)$ is a measure of the constraint placed on the population by the marriage rule: the smaller the $H(PX)$, the more constraint. We may now compare X and X' by computing $H(PX)$ and $H(PX')$. One should note that the exclusion operator is not only a function of the marriage rule, but also of the particular state of the society, hence so is H . For example, a population of 10 unrelated people has a high entropy under first cousin exclusion, but a population of 10 first cousins has a zero entropy.

One author of this chapter (P.A.B.) believes that "entropy" measures to base 2 are not the correct functions. Instead, measures to the base of the population size are more meaningful, and can allow "entropy" to either increase or decrease as a more accurate summary statement of the amount of structure on a population.

However, P.A.B. also believes that entropy measures in either form would be less useful than a theory of "distances" between populations defined in terms of the various possible traces of operators. In such a case, the probabilities used in the "entropy" formulation might also enter as weights, but in a way more useful to the comparison of concrete networks and the evolution of possible networks.

(ii) Progeny

Suppose now that the people of generation G have married in a particular sequence: $(M_1, M_2, \dots, M_s) = A$ consisting of q marriages. Let $\{m_1, m_2, \dots, m_q\} = C_q$ be the set of couples in order of marriage. We are interested in the progeny of these couples. Suppose m_i has $f_1(m_i)$ males and $f_2(m_i)$ females. Then we have a function:

$$f: \{m_1, \dots, m_q\} \rightarrow \mathbb{Z}^+ \times \mathbb{Z}^+$$

$$m_i \xrightarrow{\text{---}} (f_1(m_i), f_2(m_i))$$

where $\mathbb{Z}^+ \times \mathbb{Z}^+$ is the set of pairs of non-negative integers. We can consider f as a function from $\{1, 2, \dots, q\}$, if we remember the order of marriage. Thus, the set of all functions $f: \{1, 2, 3, \dots, q\} \rightarrow \mathbb{Z}^+ \times \mathbb{Z}^+$ corresponds to the set of all possible birth distributions of the couples. The progeny operator: Prog (labeled P) is always to be understood as a direct sum:

$$\text{Prog} = P_m \oplus P_f$$

$$P_m = \text{male progeny}, \quad P_f = \text{female progeny}$$

with components P_m and P_f known. Thus, Prog is really two operators, a male part and a female part.

Definition 17: Let $B_q = \{f: \{1, 2, \dots, q\} \rightarrow \mathbb{Z}^+ \times \mathbb{Z}^+\}$. For $f \in B_q$, let f_1, f_2 , and \bar{f} be defined by

$$f(i) = (f_1(i), f_2(i)), \quad 1 \leq i \leq q$$

$$\bar{f}(i) = f_1(i) + f_2(i).$$

Now let $\bar{P}(g)$, $g \in \mathbb{Z}^+$, be the probability that a couple will have exactly k children which grow up to mature and reproduce. Let P_1 be the probability that a particular child will be a male and $P_2 = 1 - P_1$ the probability that it will be a female.

Then we have a probability measure on B_q :

Definition 18: PB_q is the probability measure on B_q defined by:

$$\text{For } f \in B_q \quad PB_q(f) = \prod_{i=1}^q \bar{P}(f(i)) \cdot \frac{\bar{P}(f(i))}{\bar{P}_1(f_1(i))} P_1^{f_1(i)} q P_2^{f_2(i)}$$

Note: If \bar{P} is assumed to be Poisson with mean λ we get

$$PB_q(f) = \frac{e^{-q\lambda} (\lambda P_1)^{\bar{n}_{f_1}} (\lambda P_2)^{\bar{n}_{f_2}}}{\prod_{i=1}^q (f_1(i)!) (f_2(i)!)}$$

where $\bar{n}_{f_1} = \sum_{i=1}^q f_1(i)$, $\bar{n}_{f_2} = \sum_{i=1}^q f_2(i)$.

By defining PB_q in this way, we can account for the death rate, birth defects, and the like which affect the size of the portion of the actual population which is capable of reproduction. This we call the "breeding population". Thus, if there are 50 people in a population and half are non-reproductive, we say the "breeding population" is 25. (Note that this is "approximately" the "effective population size" of population genetic theory.)

(iii) Case of Several Generations

What has been said about the marriage history of a society can be represented by a list, for each generation of all the functions and operators in that generation together with the properties:

- a) π_t composed with any of the other operators is that operator.
- b) all operators are symmetric.
- c) X_t is defined in terms of the R_t^i as above.
- d) E_t is defined as in section 3.4 in terms of π_t , B_t , M_t and the $i_j C_j$'s.
- e) $O_j^C = (B + M)$.

The above analysis leads to an abstract definition of a generation as an ordered tuple:

$$N_t = (H_t, N_t, \pi_t, B_t, M_t, P_t, E_t, X_t, R_t^1, R_t^2, \dots, R_t^r, \{i_j C_j\}).$$

Satisfying a), b), c), d), e) when N_t is a basis compatible with π_t as in section 3.2. All other conditions imposed by the physical meanings of the operators (e.g., $\text{tr}M_t = 0$, $\text{tr}(M_t \cdot X_t) = 0$, etc.) are also assumed.

Let \mathcal{U} be the set of all such tuples. What we seek is an answer to the question: "Suppose $N_0 \in \mathcal{U}$ is a generation, what is the probability that the progeny of N_0 marry and reproduce to produce generation $N \in \mathcal{U}$?"

Definition 19: Let $N_0, N \in \mathcal{U}$, denote by $\langle N | N_0 \rangle$ the above probability. Then we have a probability measure on \mathcal{U} : $\langle * | N_0 \rangle : \mathcal{U} \rightarrow \mathbb{R}$

$$N \mapsto \langle N | N_0 \rangle$$

We call this the probability of N_0 producing N in one generation.

Definition 20: Let $\langle * | N_0 \rangle$ be as above, then $\langle * | N_0 \rangle_t : \mathcal{U} \rightarrow \mathbb{R}$ is a probability measure on \mathcal{U} defined by

$$\langle N | N_0 \rangle_t = \sum_{\substack{\text{all } (t+1)\text{-tuples } \\ (N_0, \dots, N_n) \in \mathcal{U} \\ N_0 = N_0, N_n = N}} \prod_{i=1}^t \langle N_i | N_{i-1} \rangle$$

We call this the probability of N_0 producing N in t -generations.

Note: $\langle | N_0 \rangle = \langle | N_0 \rangle_1$.

We now proceed to characterize the calculation of $\langle | N_0 \rangle$:

Let $N_0 = (N_0, H_0, \pi_0, B_0, M_0, P_0, E_0, X_0, R'_0, \dots, R_0, \{C_j^0\})$

$$N = (H, N, \pi, B, M, P, E, X, R', \dots, R^z, \{C_j\})$$

There are several conditions that N must meet for a transition from N_0 to N to even be possible. These conditions all follow from the definition of the operators and are easily seen to be necessary:

$$a') B + \pi = P * P^{-1}$$

$$b') i+1 C_j = P * C_j * P^{-1} \quad i = 1, 2, 3, \dots \quad j = 1, 2, 3, \dots$$

$$c') P \pi_0 = P$$

d') Since X, R', \dots, R^z depend only on N_0 (as stated elsewhere in this chapter), they must agree with N_0 (the exact statement of how to determine this agreement depends on the particular marriage rule used).

If any of these conditions is not met, $\langle N | N_0 \rangle = 0$. If these are met, then once M and P are found, N is completely determined. Let $r = \dim_m(P_0) =$ number of progeny of N_0 , then we have a measure PX_0 on $X_0^M(r)$, the space of possible marriage

outcomes. Given a marriage outcome:

$$A = (M_1, M_2, \dots, M_s), \quad (s = \text{greatest integer } \leq r/2)$$

consisting of n_A marriages, we have a probability measure PB_{n_A} on the space of progeny outcomes, B_{n_A} . Given a pair (A, f) , $A \in X_0^M(t)$, $f \in B_{n_A}$, M and P are determined. Thus, the probability of getting M and P which we label $P(M, P)$ is

$$P(M, P) = \sum_{\substack{\text{sum over} \\ \text{all } (A, B) \text{ which} \\ \text{produce } (M, P)}} P_{X_0}(A) PB_{n_A}(f)$$

But we now have $\langle N | N_0 \rangle = q(N_1 N_0) \times P(M, P)$

where $q(N_1 N_0) = \begin{cases} 1 & \text{if } a', b', c' \text{ and } d' \text{ are met} \\ 0 & \text{if not.} \end{cases}$

(iv) Random Variables

Now that we have a set of probability measure on U , $\{\langle * | N_0 \rangle_t | N_0 \in U, t = 1, 2, 3, \dots\}$ we can begin an analysis of how a marriage system affects the history of a society. This is done in terms of random variables defined on U .

We conclude the chapter by summarizing some useful random variables on U . Let $N = (H, N, \pi, B, M, P, E, X, R', \dots, R^\zeta, \{C_i\}) \in U$:

- i) $r(N) = \dim(I_m^P)$ = number of progeny of N .
- ii) $\bar{E}(N) = \langle E \rangle$ = average tie of N (see Section 3.3).
- iii) $\bar{E}_m(N) = \langle E_m \rangle$ = average marriage sibling ties.
- iv) $\bar{E}_p(N) = \langle E_p \rangle$ = average genetic ties.
- v) $\bar{E}_s(N) = \text{tr}(E)/r(N)$ = average self-ties.

Given $N_0 \in U$ we can use those random variables to find their expected values after t -generations:

Definition 22: Let $N_0 \in U$, then define:

- i) $N_0 \langle r \rangle_t = u^t r(N) \langle N | N_0 \rangle_t$
- ii) $N_0 \langle \bar{E} \rangle_t = u^t \bar{E}(N) \langle N | N_0 \rangle_t$
- iii) $N_0 \langle \bar{E}_m \rangle_t = u^t \bar{E}_m(N) \langle N | N_0 \rangle_t$
- iv) $N_0 \langle \bar{E}_p \rangle_t = u^t \bar{E}_p(N) \langle N | N_0 \rangle_t$
- v) $N_0 \langle \bar{E}_s \rangle_t = u^t \bar{E}_s(N) \langle N | N_0 \rangle_t$

These expectation values define functions as follows:

Definition 23: Let $\mathbb{Z}^+ = \{1, 2, 3, \dots\}$

$$\text{i) } r : U \times \mathbb{Z}^+ \longrightarrow R$$

$$(N_0, t) \longmapsto N_0 \langle r \rangle_t$$

$$\text{ii) } \bar{E} : U \times \mathbb{Z}^+ \longrightarrow R$$

$$(N_0, t) \longmapsto N_0 \langle \bar{E} \rangle_t$$

$$\text{iii) } \bar{E}_m : U \times \mathbb{Z}^+ \longrightarrow R$$

$$(N_0, t) \longmapsto N_0 \langle \bar{E}_m \rangle_t$$

$$\text{iv) } \bar{E}_p : U \times \mathbb{Z}^+ \longrightarrow R$$

$$(N_0, t) \longmapsto N_0 \langle \bar{E}_p \rangle_t$$

$$\text{v) } \bar{E}_s : U \times \mathbb{Z}^+ \longrightarrow R$$

$$(N_0, t) \longmapsto N_0 \langle \bar{E}_s \rangle_t$$

These functions serve as predictions of the path a society is likely to take from an initial state.

CHAPTER 4: THEORY OF STRUCTURAL NUMBERS

4.0 Introduction

In theoretical chemistry, we can roughly distinguish two broad areas of work: the theory of atomic structure which tells which are the possible elements and how they may relate to one another; and structure determination, in which one studies exactly which structure(s) exists in a particular case. In some sense, this entire manuscript is about the first problem: which structures are possible, and what would be the properties of the various possible "pure elements"

In their "purest form" elements are often found in crystals with definite regular structure, and this chapter lays the foundations for the study of the "crystal structure" of mating systems. From this point of view, the last chapter laid the ground work for description of any "compound" structure, whether it is a "simple crystal", a "chain molecule", or any mixture. The following chapters begin the discussion of what are the statistical properties of systems composed of the "pure materials" but not necessarily in their crystalline state. Thus, in the present chapter, we have as results, generally nice simple diagrams, graphs, and numbers whose appearance is deceptively simple. In the following chapters, we learn how these simple numbers, which are properties of marriage rules and not of populations, can predict statistics which are properties of populations following the rules.

This chapter is the actual "first" so far as theoretical developments are concerned: We develop the theory of structural numbers in detail. The reader may wish to see introductory sections of chapter 6.4 for a very short summary of the present developments or for a list of further examples of the rules discussed here.

4.1 Definitions

DEFINITION 4.1: A generation G is a set of elements p, q, \dots called individuals. A configuration C is a triple (B, M, S) such that:

- i) B is a partition of G ;
- ii) M is a collection of two element subsets of G ;
- iii) There are subsets of G labeled m and f such that $|m \cap f| = 0$ and $m \cup f = G$ and S is the partition of G imposed by these labelings.
- iv) $|m \cap M| = 1$ and $|f \cap M| = 1$ for all $M \in M$.

In anthropological applications, G ; is interpreted as a population of people of a particular "generation", whose parents (by Definition 4.2 below) are members of

the previous generation and whose descendants are of the following. Thus, generations are "discrete". The partition \underline{B} sorts individuals into sets of siblings who are descendants of the same parents. \underline{M} is a monogamous "marriage" or "mating" relation between individuals of different sexes. Sequential marriages, etc. are not encompassed by these definitions.

DEFINITION 4.2: A descent relation d from a generation \underline{G} with a configuration \underline{C} to a generation \underline{G}' with configuration \underline{C}' is a map $d: \underline{B}' \rightarrow \underline{M}$, which is 1-1 into \underline{M} and such that the inverse map is 1-1, from a subset of \underline{M} onto \underline{B}'

An infinite sequence of generations $\underline{G}^{(n)}$ is a sequence $\dots, \underline{G}^{(n)}, \underline{G}^{(n+1)}, \dots$ of generations together with configurations $\dots, \underline{G}^{(n)}, \underline{C}^{(n+1)}, \dots$ and together with descent maps $d^{(n)}: \underline{B}^{(n+1)} \rightarrow \underline{M}^{(n)}$.

A finite sequence of generations is a sequence $\underline{G}^{(n)}, \underline{G}^{(n+1)}, \dots, \underline{G}^{(n+k)}$ of generations together with configurations $\underline{C}^{(n)}, \underline{C}^{(n+1)}, \dots, \underline{C}^{(n+k)}$ and together with descent maps $d^{(i)}: \underline{B}^{(i+1)} \rightarrow \underline{M}^{(i)}, 1 \leq i \leq k$.

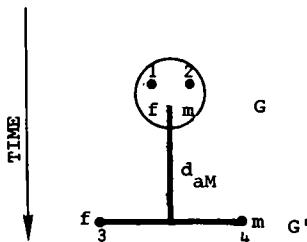
Notice that while a of \underline{B}' is mapped to some distinct element M of \underline{M} , there may be elements of \underline{M} which have no members of \underline{B}' mapped to them.

Notational Convenience:

"Let $\underline{G}^{(n)}$ be a generation in a sequence of generations" will be used to mean: "Let $\dots, \underline{G}^{(n)}, \underline{G}^{(n+1)}, \dots$ be an (infinite) sequence of generations with configurations $\dots, \underline{C}^{(n)}, \underline{C}^{(n+1)}, \dots$, and maps $\dots, d^{(n)}: \underline{B}^{(n+1)} \rightarrow \underline{M}^{(n)}, \dots$, for all n and let $\underline{G}^{(n)}$ be a generation in this sequence."

Note that under certain circumstances, the existence of a finite sequence permits construction of an infinite sequence of generations. For this reason, "sequence of generations" will mean "infinite sequence of generations" unless otherwise stated. A theorem on cyclic sequence construction is presented later.

Notation is developed for displaying these pairs $(\underline{G}, \underline{G}')$ in a graphic manner. Use a dot ".." to represent individuals $\epsilon \underline{G}$ and use a labeled dot ".m" or ".f" to show that the individual p represented by the dot is either pef or pem, respectively. A line between dots (labeled or unlabeled dots) will show equivalence mod \underline{B} for individuals in \underline{G} , and mod \underline{B}' for individuals in \underline{G}' . A circle around two dots shows equivalence mod \underline{M} or mod \underline{M}' respectively. Lines and circles may be labeled. On occasion, a line will be allowed to branch, to include more than two individuals mod \underline{B} , etc. A line with no dot at the end, from inside a circle to a line with dots, or to a single dot, shows a particular descent map element.

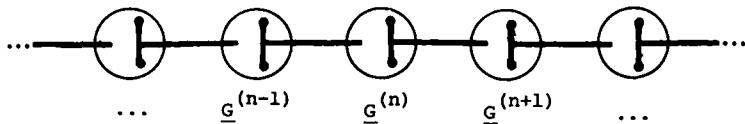


In this diagram, the pictorial representation depicts the following sets:

$\underline{G} = \{1, 2\}$; $\underline{B} = \{(1), (2)\}$; $\underline{G} = \{1, 2\}$; $\underline{B} = \{(1), (2)\}$; $\underline{M} = \{M\} = \{\{1, 2\}\}$; $\underline{S} = m f = \{\{2\} \{1\}\}$; $\underline{G}' = \{3, 4\}$; $\underline{B}' = \{a\} = \{\{3, 4\}\}$; $\underline{M}' = \emptyset$; $\underline{S}' = \{m \cup f\} = \{\{4\} \cup \{3\}\}$; $d = \{d_{aM}\}$. Thus, \underline{G}' is a generation with configuration $\underline{C}' = \{\underline{M}', \underline{B}', \underline{S}'\}$. The elements of \underline{M}' , \underline{B}' and \underline{S}' are enumerated above. Individuals 1 and 2 of \underline{G}' are the ancestors of 3 and 4 in \underline{G} , which has configuration $C = \{\underline{M}, \underline{B}, \underline{S}\}$ whose elements are also enumerated above. Note $d(a) = M$.

In addition, an arrow with two shafts will be used between drawings which show marriage structure on a generation which previously had no indicated marriages, while a single shafted arrow will be used to show application of descent maps from an existing generation to a "new" generation. (See theorems 4.4 and 4.5 for examples.)

Note that because of definitions 4.1 and 4.2, every generation in a sequence of generations has at least the following minimal statistics: $|M^{(n)}| \geq 1$, $|B^{(n)}| \geq 1$, $|\underline{G}^{(n)}| \geq 2$, $|m^{(n)}| \geq 1$, $|f^{(n)}| \geq 1$, for all n . If a particular sequence had only these statistics, it could be illustrated as follows:



DEFINITION 4.3: If \underline{G} and \underline{G}' are a pair of generations with configurations \underline{C} and \underline{C}' respectively, and $d: \underline{B}' \rightarrow \underline{M}$ is a descent map from \underline{B}' to \underline{M} , and $d(a) = M$, and $p \in a$ and $q \in M$, then q is a parent of p , and p is an offspring of q .

Let $\underline{G}^{(n)}$ be a generation in a (finite or infinite) sequence of generations. Let $p \in \underline{G}^{(n)}$ and suppose $\underline{G}^{(m)}$ is another generation in this sequence and $m < n$, and $q \in \underline{G}^{(m)}$. A descent chain from q to p exists if there exists a sequence $q^{(m)}, q^{(m+1)}, \dots, q^{(n)}$ such that $q^{(n)} \in \underline{G}^{(n)}$ is an offspring of $q^{(i-1)} \in \underline{G}^{(i-1)}$, $q^{(i-2)}$ is a parent of $q^{(i-1)}$, $\dots, q^{(m)}$ is a parent of $q^{(m+1)}$, and $p = q^{(n)}$ and $q = q^{(m)}$.

If there exists a descent chain from q to p , then q is an ancestor of p , and p is a descendant of q .

Note that if q is a parent of p , then q is also an ancestor of p ; if p is an offspring of q , then p is also a descendant of q . Note also that for a pair of generations $(\underline{G}, \underline{G}')$ with configurations $(\underline{C}, \underline{C}')$ and a descent map $d: \underline{B}' \rightarrow \underline{M}$, if $d(a) = M$, then there exist, for each $p \in a$, two distinct elements of $q \in M$, each of which is an ancestor of p .

DEFINITION 4.4: Suppose $\underline{G}^{(n)}$ is a generation in a sequence of generations, and suppose $a \in \underline{B}^{(n)}$ and $b \in \underline{B}^{(n)}$ and $p \in a$ and $q \in b$. Let $\underline{G}^{(m)}$ be some other generation in the sequence such that $m < n$, and let $j = n-m$. Then p and q are j-removed if there exists $p' \in \underline{G}^{(m)}$ such that both p and q are each descended from p' . (See section 2.1.)

If p and q are j -removed, write $R^j(p, q)$.

Note: $p \approx q \text{ mod } \underline{B}$ if $R^1(p, q)$.

Definition 4.4 allows discussion of "descent relations" that extend "backward" over several generations, while definition 4.5 below allows discussion of relations which extend "across" a single generation.

DEFINITION 4.5: Suppose $\underline{G}^{(n)}$ is a generation in a sequence of generations, and suppose $p \in \underline{G}^{(n)}$ and $q \in \underline{G}^{(n)}$ and $p \in a \in \underline{B}^{(n)}$ and $q \in b \in \underline{B}^{(n)}$ and $d(a) = M_a \in \underline{M}^{(n-1)}$ and $d(b) = M_b \in \underline{M}^{(n-1)}$.

If $M_a = M_b$ then $a = b$ and $p \approx q \text{ mod } \underline{B}^{(n)}$. Call this condition " p and q are 0-linked", written $L^0(p, q)$.

If $M_a \neq M_b$ then $a \neq b$. Suppose $p' \in M_a$ and $q' \in M_b$ are ancestors of p and q respectively, and $q' \approx p' \text{ mod } \underline{B}^{(n)}$. Then p and q are 1-linked, or first linked, written $L^1(p, q)$. If $p' \neq q' \text{ mod } \underline{B}^{(n)}$ but there exist $r' \approx p' \text{ mod } \underline{B}^{(n)}$ and $t' \approx q' \text{ mod } \underline{B}^{(n)}$ and $r' \approx t' \text{ mod } \underline{M}^{(n)}$, then p and q are 2-linked.

Similarly, if p and q are not i -linked for all $i < j$, but a series of $j + 1$ distinct B -equivalence classes linked by j distinct M -equivalence classes, then p and q are j -linked, written $L^j(p,q)$.

The particular sequence of B -sets linked through M -sets of $\underline{G}^{(n-1)}$ from p' to q' , inclusive, forms a chain of $j + 1$ B -sets, and a chain of j M -sets.

Remark: The following is easily proved:

Theorem: (Simply extended removal)

Suppose $\underline{G}^{(n)}$ is a generation in a sequence of generations, and assume p and $p \in \underline{G}^{(n)}$ and $R^j(p,q)$. Then $R^{j+1}(p,q)$ for any positive integer n .

Motivation for the next definition should be apparent, except to note that the distinction of several types of isomorphism is necessitated by the structure imposed by definition 4.1.

DEFINITION 4.6: Suppose \underline{G} and \underline{G}' are two generations with configurations \underline{C} and \underline{C}' respectively, and suppose there exists a 1-1 onto map $f: \underline{G} \rightarrow \underline{G}'$.

Then \underline{C} and \underline{C}' are B -isomorphic iff for $p \in \underline{G}$ and $q \in \underline{G}$, if $p \approx q \pmod{B}$ then $f(p) \approx f(q) \pmod{B'}$.

\underline{C} and \underline{C}' are M -isomorphic iff for $p \in \underline{G}$ and $q \in \underline{G}$ are $p \approx q \pmod{M}$ then $f(p) \approx f(q) \pmod{M'}$.

\underline{C} and \underline{C}' are S -isomorphic iff if $p \in \underline{G}$ and $q \in \underline{G}$ and $p \approx q \pmod{S}$ then $f(p) \approx f(q) \pmod{S'}$.

If \underline{C} and \underline{C}' are B -, M - and S - isomorphic, then they are completely isomorphic, or simply isomorphic.

The sign " $=$ " will be used between isomorphic configurations (completely isomorphic configurations), the signs " \underline{B} ", " \underline{M} ", and " \underline{S} " will be used between B -, M - and S - isomorphic configurations, respectively. If $\underline{G} = \underline{G}'$, then $\underline{G}' = \underline{G}$. If $\underline{G} = \underline{G}' = \underline{G}''$ then $\underline{G}'' = \underline{G}$. If $\underline{G} \underline{B} \underline{G}'$ then $\underline{G}' \underline{B} \underline{G}$, and if $\underline{G}^B \underline{G}' \underline{G}''$ then $\underline{G}^B \underline{G}''$, and similarly for S - and M - ismorphisms.

DEFINITION 4.7: Suppose $\underline{G}^{(n)}$ is a generation in a sequence of generations, and $p \in \underline{G}^{(n)}$ and $q \in \underline{G}^{(n)}$ and $p' \approx q' \pmod{\underline{B}^{(n)}}$. (Let p' and q' be ancestors in $\underline{G}^{(n-1)}$ of p and q respectively.)

Then if $p' \approx q' \pmod{\underline{S}^{(n-1)}}$ then p and q are parallel linked. If $p' \not\approx q' \pmod{\underline{S}^{(n-1)}}$ then p and q are cross linked. Notate this " $\text{cross } L^1(p,q)$ " and " $\text{parallel } L^1(p,q)$ " respectively.

DEFINITION 4.8: Suppose $\underline{G}^{(n)}$ is a generation in a sequence of generations. A marriage rule $A\#$, where "#" is a number, is satisfied in the sequence $\{\underline{G}^{(n)}\}$ (or, the sequence $\{\underline{G}^{(n)}\}$ satisfies A) if whenever $p, q \in \underline{G}^{(n)}$ for all $\underline{G}^{(n)} \in \{\underline{G}^{(n)}\}$ and $p \neq q \pmod{\underline{M}^{(n)}}$, then $A\#$ is true, provided $A\#$ is a conjunction of statements drawn from this list:

- (1) for some positive integer i , $R^i(p,q)$
- (2) for some positive integer i , not $R^i(p,q)$
- (3) for some positive integer i , $L^i(p,q)$
- (4) for some positive integer i , not $L^i(p,q)$
- (5) there exist ancestors p' and q' of p and q respectively in $\underline{G}^{(n-i)}$, and for some positive integer i , cross $L^1(p',q')$
- (6) there exist ancestors p' and q' of p and q respectively in $\underline{G}^{(n-i)}$, and for some positive integer i , not cross $L^1(p',q')$
- (7) there exist ancestors p' and q' of p and q respectively in $\underline{G}^{(n-i)}$, and for some positive integer i , parallel $L^1(p',q')$
- (8) there exist ancestors p' and q' of p and q respectively in $\underline{G}^{(n-i)}$, and for some positive integer i , not parallel $L^1(p',q')$

A variety of marriage rules with possible English language interpretations are presented below. Note that while the rules are unique, the interpretations may not be unique. Further examples are given in chapter 7.

Rule Name	Rule	Interpretation
A1	None	"Random", sexual mating
A2	(2)1	"Sibling exclusion"
A3	(2)1, (6)1	"Cross cousin exclusion"
A4	(2)1, (8)1	"Parallel cousin exclusion"
A5	(2)1, (4)1	"First cousin exclusion"
A6	(2)1, (1)2	"Double first cousins"

"Contradictory" marriage rules which require both $R^i(p,q)$ and not $R^i(p,q)$, or which require both $L^i(p,q)$ and not $L^i(p,q)$ for the same value or values of i are clearly not satisfied by any sequence of generations.

DEFINITION 4.9: A stable configuration of period k , or simply a k -stable configuration, is a configuration $\underline{C}^{(n)}$ such that there exists a finite sequence $\underline{C}^{(n)}, \dots, \underline{C}^{(n+k)}$ and $\underline{C}^{(n)} = \underline{C}^{(n+k)}$, and such that if $\underline{C}'^{(n)}, \dots, \underline{C}'^{(n+i)}$ is another sequence with $\underline{C}'^{(n)} = \underline{C}'^{(n+i)}$, then $k = i$.

Theorem: (cyclic sequence construction)

Suppose a sequence of generations is k-stable, such that $\underline{C}^{(n)} = \underline{C}^{(n+k)}$. Then there exists an infinite sequence $\dots, \underline{C}_v^{(k)}, \dots, \underline{C}_v^{(k+1)}, \dots$ such that $\underline{C}_v^{(i)} = \underline{C}_v^{(i+k)}$ for all i.

4.2 Developments

THEOREM 4.1: Let $\dots, \underline{G}^{(n)}, \dots$ be a sequence which satisfies A2. Then for all n, $|\underline{G}^{(n-1)}| \geq 4$, $|\underline{B}^{(n-1)}| \geq 2$, $|\underline{M}^{(n-1)}| \geq 2$, $|\underline{m}^{(n-1)}| \geq 2$, $|\underline{f}^{(n-1)}| \geq 2$.

Proof: Let p and q be elements of $\underline{G}^{(n)}$ such and $p \approx q \bmod \underline{M}^{(n)}$. Let $a \in \underline{B}^{(n)}$ and $b \in \underline{B}^{(n)}$ pea and qsb. By hypothesis (A2) $d(a) \neq d(b)$, hence $a \neq b$.

Therefore $|\underline{M}^{(n-1)}| \geq 2$, $|\underline{G}^{(n-1)}| \geq 4$, $|\underline{B}^{(n-1)}| \geq 2$ since each individual in each M-set must be from different B-sets, and $|\underline{m}^{(n-1)}| \geq 2$, $|\underline{f}^{(n-1)}| \geq 2$ from definition 1.

Q.E.D.

Theorems 4.2 and 4.3 follow immediately from theorem A.

THEOREM 4.2: Let $\dots, \underline{G}^{(n)}, \dots$ be a sequence of generations which satisfies A6. Then: $|\underline{G}^{(n)}| \geq 4$, $|\underline{B}^{(n)}| \geq 2$, $|\underline{M}^{(n)}| \geq 2$ for all n.

THEOREM 4.3: Let $\dots, \underline{G}^{(n)}, \dots$ be a generation in a sequence of generations which satisfies A2, then for each n there exists at least one $p' = \underline{G}^{(n-1)}$ and one $q' \in \underline{G}^{(n-1)}$, $p' \neq q'$, such that $L^1(p', q')$.

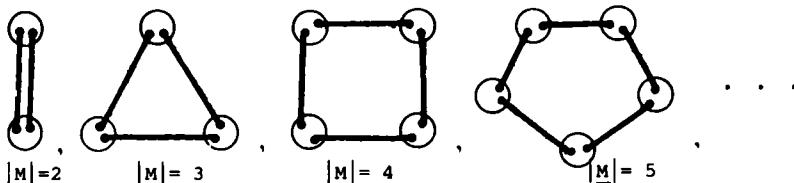
Proof: In the proof of theorem 4.1, let $p' \in M'$ be an ancestor of p and $q' \in M''$ be an ancestor of q. Note that $p' \approx q'$ is then prohibited by theorem A' and by the prohibition of $R^1(p, q)$ by A2.

Q.E.D.

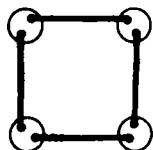
Note that while theorems 4.1, 4.2, and 4.3 specify conditions which must at least be true for viable sequences under marriage rules, they do not guarantee that any structure exists which satisfies these conditions, nor do they specify particular structures.

DEFINITION 4.10: All those configurations which are isomorphic to one another form an isomorphism class.

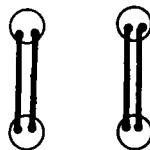
A configurational element is one of the following isomorphism classes:



Notice that an isomorphism class can be unambiguously represented up to an isomorphism of the S-labels, by display of a member of the class. Note also that in the configurations below, both have $|M| = 4$, but one consists of a single configurational element, while the other consists of the union of two configurational elements each of which has $|M| = 2$. If an isomorphism class is named "M#", where # is



M4
FIGURE I

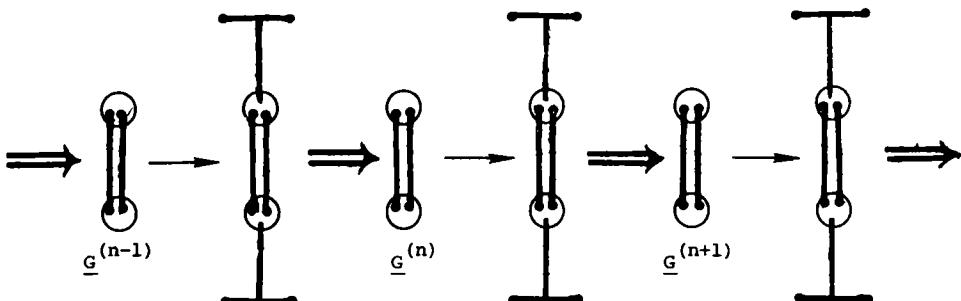


2(M2)
FIGURE II

the number of M-sets in the class, then figure I above consists of the single configurational element M4, while figure II is the union of two M2 configurational elements. This may unambiguously be notated "2(M2)", describing a single generation \underline{G} whose configuration $\underline{C} = (\underline{M}, \underline{B}, \underline{S})$ is the union of two separate configurations $C_1 = (M_1, B_1, S_1)$, $C_2 = (M_2, B_2, S_2)$, i.e., $M = M_1 \cup M_2$, $B = B_1 \cup B_2$, $f = f_1 \cup f_2$, $m = m_1 \cup m_2$.

Sequences may be uniquely named if all configurations are isomorphic to a given configuration. For example, a sequence which has $\underline{C}^{(n)} = M2$ for all n may be called $(n)\{\underline{C}^{(n)} = M2\}$. This is suggestive of similar notations for cyclic repetitions of configurations, but these will not be exploited here.

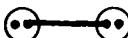
THEOREM 4.4: The sequence $(n)\{\underline{C}^{(n)} = M2\}$ which has $\underline{C}^{(n)} = M2$ for all n satisfies



theorem C with equalities in place of inequalities, and any other sequence which thus satisfies theorem C is isomorphic to $(n)\{\underline{C}^{(n)} = M2\}$.

Proof: By inspection, $\{n\} \{C^{(n)} = M2\}$ has $|M^{(n)}| = 4$, $|B^{(n)}| = 2$, $|G^{(n)}| = 4$ for all n .

To show all other sequences with this property must be isomorphic to $\{n\} \{C^{(n)} = M2\}$, consider the two examples below:

CLASS I 

CLASS II 

Since each M-class by definition 1 must have $|M| = 2$, these are the only two configurations other than M2 which have $|M| = 2$ and also have $|G| = 4$. Class I has $|B| = 4$, while class II has $|B| = 3$. Since M2 has $|B| = 2$, the theorem is shown.

Q.E.D.

Note that because of definition 4.5, theorem 4.4 implies theorem 4.4'.

THEOREM 4.4': The sequence $\{n\} \{C^{(n)} = M2\}$ satisfies A2, and satisfies theorem 4.2 with equalities in place of inequalities, and any other sequence satisfying theorem 4.2 with equalities in place of inequalities is isomorphic to $\{n\} \{C^{(n)} = M2\}$.

THEOREM 4.5: Suppose $G^{(n)}$ is a generation in a sequence of generations which satisfies A5. Then $|B^{(n-1)}| \geq 4$ for all n .

Proof: Let $p, q \in G^{(n)}$. Then not $R^1(p, q)$ implies distinct descent chains, from ancestors in $G^{(n-1)}$, hence $|M^{(n-1)}| > 2$. Let p' and q' in $G^{(n-1)}$ be ancestors of p or q respectively. Then not $L^1(p, q)$ implies $p' \neq q' \pmod{B^{(n-1)}}$. Since each M-set in $M^{(n-1)}$ has 2 individuals, and none are equivalent $\pmod{B^{(n-1)}}$, $|B^{(n-1)}| \geq 4$.

THEOREM 4.5': Suppose $G^{(n)}$ is a generation in a sequence of generations which satisfies A5. Then $|G^{(n)}| \geq 8$, $|B^{(n)}| \geq 4$, $|M^{(n)}| \geq 4$ for all n .

Proof: Apply theorem 4.5 to $G^{(n)}$ and to $G^{(n+1)}$, finding respectively that $|B^{(n-1)}| \geq 4$ and $|B^{(n)}| \geq 4$. Since $|B^{(n-1)}| \geq 4$ and descent maps are 1-1, $|M^{(n)}| \geq 4$ (since $|M^{(n)}| \geq |B^{(n-1)}|$). And since $|G^{(n)}| \geq 2|M^{(n)}|$, $|G^{(n)}| \geq 8$.

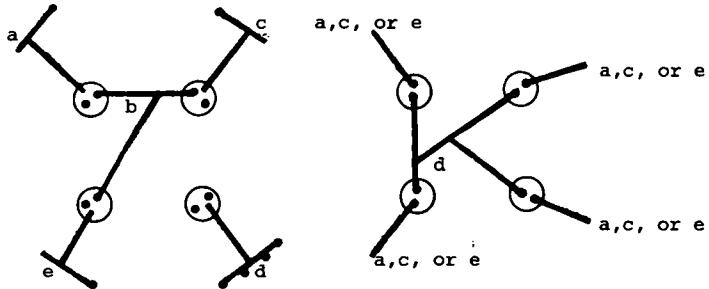
Q.E.D.

THEOREM 4.6: There exists a sequence of generations which satisfies A5, satisfies theorem 4.5' with equalities in place of inequalities, and is k-stable for $k = 1$.

Proof: The sequence is $\{n\} \{C^{(n)} = 2(M2)\}$.

THEOREM 4.6': (equipartition from A5) Any configuration $C^{(n)}$ in a sequence which satisfies A5 and theorem 4.5' with equalities in place of inequalities must have $|b_i| = 2$ for all $b_i \in B^{(n)}$, and for all n .

Proof: To show equipartition, note that if there is one B-set b with $|b| = 3$ in a generation. Then three of the M-sets will have 1-linked elements in the next generation. Because of $L^1(p,q)$ prohibition, these three can only marry from the fourth, but in the succeeding generation, all will be 1-linked (illustrated below).



The same illustration shows the consequences of $|b| = 4$ are that L^1 -prohibition prevents all marriages. Note that $|b| = 5$ is prohibited, since $8 - 5 = 3$, hence only 3 M-sets at most may be completed, in violation of $|\underline{M}^{(n)}| = 4$. Similarly for b-sets of sizes 6, 7, or 8, while if any B-set is size 1, then some other B-set is size ≥ 3 ; ($|\underline{B}| = 0$ is meaningless).

Q.E.D.

Call the minimal numbers $|\underline{B}^{(i)}| = \beta_i$, $|\underline{M}^{(i)}| = \mu_i$, and $|\underline{G}^{(i)}| = \gamma_i$ thus discovered structural numbers of A.

Note: Inferences from later generations to earlier ones in a sequence can only be made through ancestors, which are members of M-sets, or to individuals linked to ancestors, which are also members of M-sets. Therefore, all individuals in a step of a minimal representation are members of M-sets. The following is obviously true.

THEOREM 4.7: Suppose A is a k-stable marriage rule with $k = 1$ and with minimal representation @. If $\underline{C}^{(n)}$ is a step in @ and $|\underline{B}^{(n)}| = \beta_n$, $|\underline{M}^{(n)}| = \mu_n$ and $|\underline{G}^{(n)}| = \gamma_n$ then there exist numbers β , μ , and γ where γ is even, such that for all n, $\beta = \beta_n$, $\gamma = \gamma_n$, $\mu = \mu_n$ and $|\underline{m}_n| = |\underline{f}_n| = \mu = 1/2\gamma$ and $1 \leq \beta \leq \mu$.

CONJECTURE 4.7': For all $k \geq 1$, theorem 4.7 still holds.

CONJECTURE 4.7": $\beta = \mu$ in every minimal representation.

CONJECTURE 4.7''': Every step in a minimal representation is partitioned into $\beta = s$ equal B-sets of size 2.

A likely method to prove these conjectures would be to generalize the technique of the preceding examples.

If the reader is now convinced that these numbers are "too small" to be meaningful, it is suggested that he turn to chapter 7 where the 1970 U.S. census is predicted from the simple fact that the "average" U.S. structural number is 4.

4.3 Summary of the Theory of Structural Numbers*

What we have done here is to construct a theory which has certain properties, known in advance from empirical studies of "reality", but which perhaps also does more than simply predict known "facts". Here is what we know: Many different "types" of marriage rules exist; these rules may be expressed in terms of "kin" types, which may also differ by society; rules may be efficiently drawn on two and three dimensional diagrams, which appear to have group theoretical properties and characteristic numbers. In addition to this, we suspect that the efficient diagrams are "smaller" than actual population sizes, but the size of the diagram should have some relation to the actual size of population, and to evolutionary properties of the population. Later chapters construct models having the desired statistical properties.

Basic Definitions

DEFINITION 1: A generation \underline{G} is a set of elements p, q, \dots called individuals. A configuration C is a triple $(\underline{B}, \underline{M}, \underline{S})$ such that: (i) \underline{B} is a partition of \underline{G} ; (ii) \underline{M} is a collection of two element subsets of \underline{G} ; (iii) There are subsets of \underline{G} labeled m and f such that $|m \cap f| = 0$ and $\{m \cup f\} = \{\underline{G}\}$ and \underline{S} is the partition of \underline{G} imposed by these labelings; (iv) $|m \cap M| = 1$ and $|f \cap M| = 1$ for all $M \in \underline{M}$.

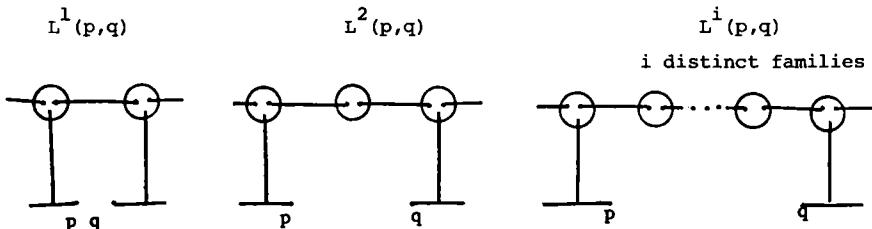
Thus, my model has discrete generations, and monogamy in the structure which illustrates a rule. The sets " M " are married pairs, m, f the sets of males and females respectively. Relations between generations will be called descent maps. These will go from sibling groups (B -sets, or "distinct families") of one generation, to M -sets of parents in a previous generation.

DEFINITION 2: A descent relation d from a generation \underline{G} with a configuration \underline{C} to a generation \underline{G}' with configuration \underline{C}' is a map $d: \underline{B} \rightarrow \underline{M}$, which is 1-1 into \underline{M} and such that the inverse map is 1-1, from a subset of \underline{M} onto \underline{B}' . A sequence of generations $\{\underline{G}^{(n)}\}$ is a sequence of generations $\dots, \underline{G}^{(n)}, \dots$, with configurations $\dots, \underline{C}^{(n)}, \dots$ and descent maps $\dots, d^{(n)}: \underline{B}^{(n+1)} \rightarrow \underline{M}^{(n)}, \dots$.

The terms "parent", "offspring", and "ancestor" will have the obvious meanings, then we can denote " p and q are i -removed" by $R^i(p, q)$. Likewise, if p and q are

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"first cousins", then $L^1(p,q)$; if they are linked through "first cousins of first cousins", then $L^2(p,q)$; and likewise, for $L^i(p,q)$. (See illustration.)

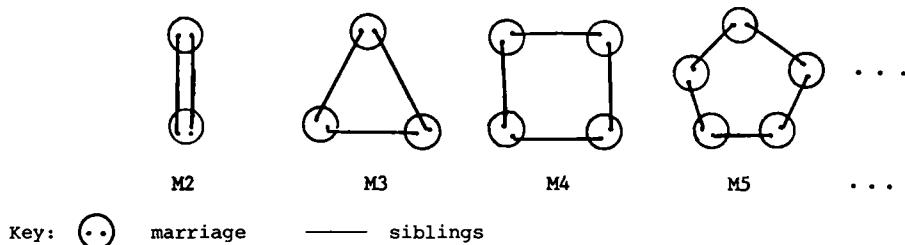


Notice that if $L^1(p,q)$ then $R^2(p,q)$, and if $R^i(p,q)$ then $R^{i+n}(p,q)$ for all integers $n \geq 1$.

It is now possible to define a marriage rule as a conjunction of statements from this list: (1) for some positive integer i , $R^i(p,q)$, and/or; (2) for some positive integer i , not $R^i(p,q)$, and/or; (3) for some positive integer i , $L^i(p,q)$, and/or; (4) for some positive integer i , not $L^i(p,q)$. It is easily possible to extend this list to include cross and parallel cousins of various degrees of removal, but (1) through (4) provide a sufficient notion for summary purposes. Thus, the combination $\{(2) i = 1, (4) i = 1\} = A$ gives a single rule: "brother-sister marriages and first cousin marriages are not possible."

A marriage rule will be called k-stable, if in a sequence $\{\underline{G}^{(n)}\}$, every generation satisfies A , and $\underline{C}^{(n)} = \underline{C}^{(n+k)}$ ($\text{the } n^{\text{th}}$ and $(n+k)^{\text{th}}$ configurations are isomorphic) and k is the smallest integer value for which this is true. Since there may be several different k -stable sequences (with the same k value) for any particular marriage rule A , we can specify further that a minimal representation of a marriage rule A has smallest k , and also smallest B , M , m , f and G sizes. These will be called structural numbers, and since it can be shown that in a minimal representation, there exists a unique number s such that $s = |M| = |m| = |f| = 1/2|G| \geq |B|$, call s the (unique) structural number of the marriage rule.

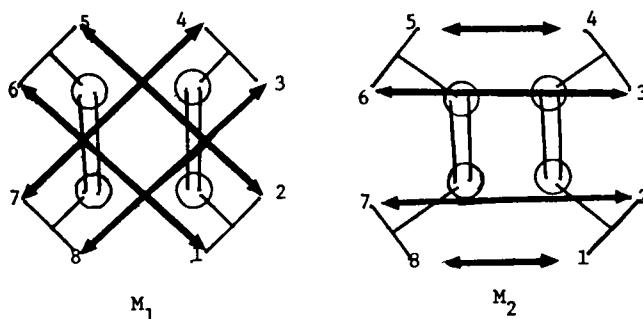
Finally, the state T_C of a configuration C is the set of all configurations isomorphic to C . The state set T_A of a sequence satisfying A is the set of states of configurations in the sequence. A special class of states are the configurational elements (denoted " $M\#$ ", according to $\#$ = the number of M -sets in the element). Configurational elements are the "cyclic" configurations shown below:



Thus, if one knows $s = 4$ for a particular minimal configuration C , both $C = M4$ or $C = 2(M2)$ may be possible in the absence of other knowledge.

It is possible to make a simple correspondence between a matrix of zeros and ones, and the relations $R^i(p,q)$, $L^i(p,q)$, marriage (M), sibling (B), and "same sex" (S). In particular, if $R^i(p,q)$ is a relation, then R^i is the corresponding matrix, if $L^i(p,q)$ is a relation, then L^i is the matrix, and denote the matrixes of the relations M, B, S, etc. by the letters themselves. Define the composition relation " \oplus " as the element by element computation of a logical "or" (i.e., $0 \oplus 0 = 0$, $1 \oplus 0 = 1$, $0 \oplus 1 = 1$, $1 \oplus 1 = 1$). Thus, if

$$\text{or, } X = \begin{bmatrix} 1 & 1 & 1 & 1 & 1 & 0 & 1 & 0 \\ 1 & 1 & 1 & 1 & 0 & 1 & 0 & 1 \\ 1 & 1 & 1 & 1 & 1 & 0 & 1 & 0 \\ 1 & 1 & 1 & 1 & 1 & 0 & 1 & 0 \\ 1 & 0 & 1 & 0 & 1 & 1 & 1 & 1 \\ 0 & 1 & 0 & 1 & 1 & 1 & 1 & 1 \\ 1 & 0 & 1 & 0 & 1 & 1 & 1 & 1 \\ 0 & 1 & 0 & 1 & 1 & 1 & 1 & 1 \end{bmatrix} \quad M = \begin{bmatrix} 0 & 0 & 0 & 0 & 0 & 1 & 0 & 1 \\ 0 & 0 & 0 & 0 & 1 & 0 & 1 & 0 \\ 0 & 0 & 0 & 0 & 0 & 1 & 0 & 1 \\ 0 & 0 & 0 & 0 & 1 & 0 & 1 & 0 \\ 0 & 1 & 0 & 1 & 0 & 0 & 0 & 0 \\ 1 & 0 & 1 & 0 & 0 & 0 & 0 & 0 \\ 0 & 1 & 0 & 1 & 0 & 0 & 0 & 0 \\ 1 & 0 & 1 & 0 & 0 & 0 & 0 & 0 \end{bmatrix}$$



The matrix M is the complement of X . M shows the possible marriages under A5, for the configuration illustrated. Where there is a single "1" entry in each row, this is the same " M " used earlier. As can be seen, there are two apparent choices of partner for each individual in this case. For example, the "1" in positions 6 and 8 of row 1 show that 1 can mate with either 6 or 8. (Notice that all of these matrixes are symmetric.) However, only two sets of choices produce 1-stable sequences. These two are shown below as M_1 and M_2 . The reader may wish to verify that any other matrix M is either not premitted in a sequence satisfying A5, or creates M_4 , which is 2-stable. Both M_1 and M_2 below create $2(M_2)$, which is 1-stable, hence in the sequence.

$$M_1 = \begin{bmatrix} 0 & 0 & 0 & 0 & 0 & 1 & 0 & 0 \\ 0 & 0 & 0 & 0 & 1 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 & 0 & 0 & 0 & 1 \\ 0 & 0 & 0 & 0 & 0 & 0 & 1 & 0 \\ 0 & 1 & 0 & 0 & 0 & 0 & 0 & 0 \\ 1 & 0 & 0 & 0 & 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 1 & 0 & 0 & 0 & 0 \\ 0 & 0 & 1 & 0 & 0 & 0 & 0 & 0 \end{bmatrix} \quad M_2 = \begin{bmatrix} 0 & 0 & 0 & 0 & 0 & 0 & 0 & 1 \\ 0 & 0 & 0 & 0 & 0 & 0 & 1 & 0 \\ 0 & 0 & 0 & 0 & 0 & 1 & 0 & 0 \\ 0 & 0 & 0 & 0 & 1 & 0 & 0 & 0 \\ 0 & 0 & 0 & 1 & 0 & 0 & 0 & 0 \\ 0 & 0 & 1 & 0 & 0 & 0 & 0 & 0 \\ 0 & 0 & 1 & 0 & 0 & 0 & 0 & 0 \\ 1 & 0 & 0 & 0 & 0 & 0 & 0 & 0 \end{bmatrix}$$

$$B = \begin{bmatrix} b_{11} & b_{12} \\ b_{21} & b_{22} \end{bmatrix} = \begin{bmatrix} 0 & 1 \\ 1 & 0 \end{bmatrix} \quad \text{and} \quad S = \begin{bmatrix} s_{11} & s_{12} \\ s_{21} & s_{22} \end{bmatrix} = \begin{bmatrix} 1 & 0 \\ 0 & 0 \end{bmatrix} \quad \text{then}$$

$$S \circ B = \begin{bmatrix} b_{11} + s_{11} & b_{12} + s_{12} \\ b_{21} + s_{21} & b_{22} + s_{22} \end{bmatrix} = \begin{bmatrix} 1 + 0 & 0 + 1 \\ 0 + 1 & 1 + 0 \end{bmatrix} = \begin{bmatrix} 1 & 1 \\ 1 & 1 \end{bmatrix}$$

Using R with no superscript to denote an arbitrary relation, we may define the mating exclusion rule X of any population as

$$X = \sum_{j=1} c_j R_j$$

where j indexes all possible relations R , and if a particular relation R_j is part of the exclusion rule, then $c_j = 1$, otherwise $c_j = 0$, and always $c_s = 1$ for S = the same sex operator. (Definitions thus far follow chapter 3.)

The rule (2) $i = 1$, (4) $i = 1$ (to give it a name, call this rule "A5") has the exclusion operator:

$$X_{A5} = S \oplus R^1 \oplus L^1.$$

Since A5 has $s = 4$, X is a matrix of order $|\underline{G}| = 2s = 8$. Following the "canonical rules" of always placing odd numbers as males, and even as females (which works since $m = f = 1/2|\underline{G}|$ and $|\underline{G}| = 2s$ is even) and always positioning siblings next to each other, the exclusion matrix under A5 showing a minimal configuration is:

$$X = \begin{bmatrix} 1 & 0 & 1 & 0 & 1 & 0 & 1 & 0 \\ 0 & 1 & 0 & 1 & 0 & 1 & 0 & 1 \\ 1 & 0 & 1 & 0 & 1 & 0 & 1 & 0 \\ 0 & 1 & 0 & 1 & 0 & 1 & 0 & 1 \\ 1 & 0 & 1 & 0 & 1 & 0 & 1 & 0 \\ 0 & 1 & 0 & 1 & 0 & 1 & 0 & 1 \\ 1 & 0 & 1 & 0 & 1 & 0 & 1 & 0 \\ 0 & 1 & 0 & 1 & 0 & 1 & 0 & 1 \end{bmatrix} \oplus \begin{bmatrix} 1 & 1 & 0 & 0 & 0 & 0 & 0 & 0 \\ 1 & 1 & 0 & 0 & 0 & 0 & 0 & 0 \\ 0 & 0 & 1 & 1 & 0 & 0 & 0 & 0 \\ 0 & 0 & 1 & 1 & 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 & 1 & 1 & 0 & 0 \\ 0 & 0 & 0 & 0 & 1 & 1 & 0 & 0 \\ 0 & 0 & 0 & 0 & 0 & 1 & 1 & 0 \\ 0 & 0 & 0 & 0 & 0 & 1 & 1 & 0 \end{bmatrix} \oplus \begin{bmatrix} 0 & 0 & 1 & 1 & 0 & 0 & 0 & 0 \\ 0 & 0 & 1 & 1 & 0 & 0 & 0 & 0 \\ 1 & 1 & 0 & 0 & 0 & 0 & 0 & 0 \\ 1 & 1 & 0 & 0 & 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 & 0 & 1 & 1 & 0 \\ 0 & 0 & 0 & 0 & 0 & 1 & 1 & 0 \\ 0 & 0 & 0 & 0 & 1 & 1 & 0 & 0 \\ 0 & 0 & 0 & 0 & 1 & 1 & 0 & 0 \end{bmatrix}$$

$S \qquad \qquad \qquad R^1 \qquad \qquad \qquad L^1$

Notice that either M_1 or M_2 is a permutation matrix of the first $2s$ integers $\{1, 2, \dots, 2s\}$, or in this case the integers $1, 2, 3, 4, 5, 6, 7, 8$. We can thus recognize the following result:

If A is marriage rule with l -stable minimal representation and structural number s , and $\underline{C}^{(n)}$ is the minimal configuration of A , then there is a marriage matrix M_i of A which transforms $\underline{C}^{(n)}$ into an isomorphic image $\underline{C}^{(n+1)}$ of itself, and M_i is a $2s$ by $2s$ permutation matrix.

From this, each marriage matrix M_i is therefore uniquely representable as a permutation

$$M_i = \begin{pmatrix} a_1, a_2, \dots, a_{2s} \\ b_1, b_2, \dots, b_{2s} \end{pmatrix} \qquad a_i, b_i, i = \{1, 2, \dots, 2s\}$$

Notice, however, that not every one of the $(2s)$ ways of permuting $2s$ integers is a possible permutation (possible marriage matrix). Even ignoring the marriage rules, the restriction $m = f = 1/2|\underline{G}| = s$ means there are only s possible entries for each row, and by symmetry, only s rows to independently permute.

DEFINITION 3: An almost minimal sequence under a k -stable marriage rule A is a sequence $\{\underline{G}^{(n)}\}$ such that for all $\underline{G}^{(n)} \in \{\underline{G}^{(n)}\}$, $|\underline{B}^{(n)}| = |\underline{M}^{(n)}| = |\underline{f}^{(n)}| = |\underline{m}^{(n)}| = 1/2|\underline{G}^{(n)}| = s$.

Create the matrix T_{M_A} on $T_A \times T_A$ with all entries zero unless at the r_j^{th} entry (the row state T_r , to the column state T_j) a descent map exists in some sequence from a configuration in state T_j to a configuration in state T_r . This follows from the fact that no sequence is possible unless there is some non-zero entry, and each non-zero entry shows an equally possible descent map in that row. In the row of state T_r there are only u_r such entries. Let the value of each entry

in a row be $= 1/u_r$. Then the fixed points of T_{M_A} show the proportion times spent in each possible state, in all possible almost minimal sequences. If we were to construct sequences where "probability" and "possibility" were not related in this simple way, then the entries in T_{M_A} would not be $1/u_r$, but the fixed points of T_{M_A} would still be the "average distributions" of states of A.

As an example, we find the fixed points of the state transition matrix of the almost minimal sequences under A5. The only two states which may occur in such sequences are M4 and 2(M2). From M4, only 2(M2) may follow, while 2(M2) may precede either M4 or itself. The state transition matrix is, therefore,

$$T_{M_{A5}} = \begin{bmatrix} M4 & 2(M2) \\ 0 & 1 \\ 1/2 & 1/2 \end{bmatrix} \quad \begin{matrix} M4 \\ 2(M2) \end{matrix}$$

Let $a_1 + a_2 = 1$ so that (a_1, a_2) is a probability vector, and we must solve

$$(a_1, a_2) T_{M_{A5}} = (a_1, a_2)$$

to find the fixed points of $T_{M_{A5}}$. It is easily seen that $a_1/a_2 = 1/2$, so $a_1 = 1/3$, $a_2 = 2/3$, and, therefore, the fixed point proportions are 1/3 in state M4, and 2/3 in state 2(M2). Note that $T_{M_{A2}}$ is the 1×1 unit matrix [1].

DEFINITION 3': Consider the state set T_A of 1-stable rule A. Define the set of a-almost minimal sequences of a marriage rule A with structural number s, as the set $T_{A,a}$ of all sequences satisfying A, and such that for each generation for any configuration in a state of $2s \leq |G| \leq 2(s+a)$, where a is a non-negative number. Note that 0-almost minimal is almost minimal.

That is, if $a = 0$, $T_{A,0}$ is the set of almost minimal sequences of A in the sense of the earlier definition 3, and also note that for all a, and all $\underline{G} \in \{\underline{G}^{(n)}\} \in T_{A,a}, 2(s+a) \leq |\underline{G}|$.

Also note that a may be any non-negative number, not just an integer, which is useful in constructing a more statistically meaningful theory. The restriction to positive numbers is not really needed, since the meaning of "minimal sequence" is that $|T_{A,-a}| = 0$ for $|-a| \leq s$, and if $|G| < s$ at any generation in a sequence, then the sequence is terminal, but not necessarily empty. The range $-2 \leq a < 0$ allows study of behavior "near extinction" of sequences, which is not the present purpose.

CHAPTER 5: ELEMENTARY PROBABILISTIC MARRIAGE THEORY

5.0 Introduction

The arguments presented so far have all been "structural", or in the vocabulary of some, "deterministic". In the author's view, "deterministic" is a highly improper description since one need not pretend a system ever followed a rule to study the structure or structures which would allow the rule to function. Indeed, as soon as we discuss anything other than 1-stable minimal systems, the apparent determinism quickly evaporates.

Marriage theory is therefore not a deterministic theory, but neither is it "probabilistic" or "stochastic" as we have so far viewed it. Nonetheless, there are very important problems of empirical interpretation which appear to demand these approaches. In this and the next chapter, I have arbitrarily isolated two sorts of non-deterministic models: those which resemble sampling with a fixed probability (probabilistic models in the present chapter); and those which may have an underlying probabilistic foundation but appear to be more easily modeled by some other technique ("stochastic model", in chapter 6). What we are essentially after in this chapter is a means to estimate with a probability the "viability" of a population with particular population statistics and particular network structure.

5.1 Family Sizes

The most important and obvious non-deterministic problem in marriage theory is family size. The minimality condition used so far implies that a population observed over several generations is minimally stable if the size in any later generation is equal to or greater than the size of the first generation, but no bigger than it needs to survive. This allows us to write a simple equation which holds in minimal or nearly minimal surviving sequences (or, for that matter, any surviving sequence).

$$(1) \quad |\underline{G}^{(t)}| \geq |\underline{G}^{(t-1)}|$$

From (1), we can find a new equation. Let $f_i^{(t)}$ be the frequency of family size i occurring in the t^{th} generation. Since $\sum_{i=1}^{\infty} f_i^{(t)} = 1$, then

$$(2a) \quad \sum_{i=1}^{\infty} i f_i^{(t)}$$

is the average family size of the t^{th} generation and

$$(2b) \quad \sum_{i=1}^{\infty} i f_i^{(t-1)}$$

is the average family size of the $t-1^{\text{th}}$ generation.

One may reason that the number of individuals produced in a generation n is the number of marriages in the previous generation $|M^{(t-1)}|$, times the proportion of "fertile" marriages h_{t-1} , times the average family size of that generation. However, if we assume that each generation forms as many marriages as possible, then the number of marriages is simply the population size $|G^{(t-1)}|$ times the minimum of the proportion m of males or f of females ($m + f = 1$) and we lose no generality by denoting this minimum by m . Therefore, we can write

$$(3) \quad |G^{(t)}| = h_{t-1} m_{t-1} |G^{(t-1)}| \sum_{i=1}^{\infty} i f_i^{(t-1)}.$$

Dividing by $|G^{(t-1)}|$ we get

$$(4) \quad \frac{|G^{(t)}|}{|G^{(t-1)}|} = h_{t-1} \cdot m_{t-1} \cdot \sum_{i=1}^{\infty} i f_i^{(t-1)}.$$

Now, equation (1) implies

$$(5a) \quad \frac{|G^{(t)}|}{|G^{(t-1)}|} \geq 1$$

holds in turn only if (5b) holds:

$$(5b) \quad \sum_{i=1}^{\infty} i f_i^{(t-1)} \geq \frac{1}{h_{t-1} \cdot m_{t-1}}$$

Equation (5b) is interesting for a variety of reasons. First, it is expressed completely in terms of information available on a well done genealogy of a living population at a given time. Second, both sides are independently measurable, so that values may be meaningfully calculated. Third, because it is calculable, it provides a direct means of testing at least one implication: those societies in which equation (5b) does not hold, should also not be minimal, or should be undergoing some transformation (such as migration) which maintains the existing system in spite of the apparent lack of population.

But most important for present purposes, it leads directly to recognition that average family sizes in evolving sequences need not be, and in general are not, the ideal 2 persons per family. Indeed, this only occurs when $h = 1$, and $m = 1/2$, which of course are the conditions of minimal structural stability found in chapter 4. In general, $h < 1$, and $m \neq 1/2$. We wish to study the effects of variations in one or the other of these parameters. (Note that h may relate in some cases to c of chapter 1.)

5.2 Sex Ratio

One of the main reasons that the average family size is not two persons per family even in an equilibrium condition is that the numbers of males and females in an arbitrary population are not equal. The present section, which was worked out by Mr. Duchamp, provides a means of estimating the increased family size implied.

Let n be the total number of population pairs in the generation, and $E(N)$ the expected difference between number of males and females in a population of size N . Use j to index possible values of this difference, and p and q for the probabilities of males and females respectively. The formula for $E(N)$ is then given by:

$$E(n) = \sum_{j=0}^n |N - 2j| \binom{N}{j} p^{N-j} q^j$$

In the expression, $\binom{N}{j}$ is the combinatorial $\binom{N}{j} = \frac{N!}{j!(N-j)!}$

which may be approximated by the appropriate gamma function

$$\binom{N}{j} = \frac{\Gamma(N+1)}{\Gamma(j+1) \Gamma(N-j+1)}$$

which was used to calculate table 5.1. Because there are small errors as the number of combinations becomes larger, due to approximations in the computer, the values past $80 = N$ are not included. Every tenth value is shown only to give an idea of the general behavior of the function, which continues to decline. The table assumes $m = f = 1/2$ in calculating expectations.

The average family size in table 5.1 is estimated from

$$\frac{2}{1 - E(N)/N}$$

since $\frac{E(N)}{N}$ is the proportion lost per generation from an absolute loss of $E(N)$ in a population of size N . Entries in the table are the population size N , expected loss $E(N)$, incremental loss $\Delta E(N)$, incremental proportion $\frac{\Delta E(N)}{\Delta N}$, and the family size needed for equilibrium. Incremental family size is computed as:

$$\frac{\Delta E(N)}{\Delta N} = \frac{E(N) - E(N-2)}{N - (N-2)}$$

Values from table 5.1 will be used again in later chapters.

TABLE 5.1: EQUILIBRIUM FAMILY SIZE FOR SEX RATIO 1/2 IN POPULATIONS OF SIZE N

N	E(N)	$\Delta E(N)$	$\frac{2}{1 - E(N)/N}$ Equilibrium average family size
Population size			
2	1.000	1.000	4.000
4	1.500	0.500	3.200
6	1.875	0.375	2.909
8	2.187	0.312	2.752
10	2.460	0.273	2.652
12	2.707	0.246	2.582
14	2.932	0.225	2.529
16	3.142	0.209	2.488
18	3.338	0.196	2.455
20	3.523	0.185	2.427
22	3.700	0.176	2.404
24	3.868	0.168	2.384
26	4.029	0.161	2.366
28	4.184	0.155	2.351
30	4.334	0.149	2.337
32	4.478	0.144	2.325
34	4.618	0.140	2.314
36	4.754	0.135	2.304
38	4.886	0.132	2.295
40	5.014	0.128	2.286
42	5.140	0.125	2.278
44	5.262	0.122	2.271
46	5.382	0.119	2.265
48	5.499	0.117	2.258
50	5.613	0.114	2.253
60	6.154	0.104	2.228
70	6.652	0.096	2.210
80	7.114	0.090	2.195
90	7.547	0.084	2.183
100	7.958	0.082	2.172
110	8.345	0.073	2.164
120	8.720	0.074	2.156
130	9.079	0.070	2.150
140	9.422	0.067	2.144
150	9.755	0.066	2.139
160	10.078	0.066	2.134
170	10.387	0.059	2.130
180	10.690	0.060	2.126
190	10.984	0.058	2.122
200	11.269	0.056	2.119
210	11.548	0.056	2.116
220	11.822	0.054	2.113
230	12.089	0.053	2.111
240	12.345	0.051	2.108
250	12.601	0.047	2.106

5.3 Survival Chances I

In this section we will develop a formula specific to circular mating systems. We define s as the length of a cycle, family size as n , sex distribution $p_m + p_f = 1$, and probability of survival P_s for a cycle of length s . We further assume that each distinct family must produce both males and females in order to participate in the mating exchanges. I am aware that this approach ignores many combinatorial difficulties, but hope that those with better skills in the field may improve upon my work.

We proceed as follows. For offspring family size n , the probability of all members being males is \underline{m}^n and of all members being females is \underline{f}^n . The probability of each of the s reproducing units being neither all male nor all female is thus

$$(1 - \underline{m}^n - \underline{f}^n)$$

for all s families to be so, P_s becomes:

$$P_s = (1 - (\underline{m}^n + \underline{f}^n))^s$$

and for $\underline{m} = \underline{f} = 1/2$,

$$P_s = (1 - 1/2^{(n-1)})^s$$

Thus for family size $n = 1$, the system has no chance of survival, while for large family size, the chances are much higher, depending on the values of s .

The following are a few examples. With family size 2 and cycle length 3,

$$P_3 = (1 - 1/2)^3 = 1/2^3 = 1/8$$

while with length 5,

$$P_5 = (1 - 1/2)^5 = 1/2^5 = 1/32$$

With family size 3, and cycle length 4, the above formula gives survival probability $(3/4)^4$, while with lengths 3 and 5, the probabilities are respectively $(3/4)^3$ and $(3/4)^5$.

A group of this sort may well want to maximize its survival chances. In the present model, there are only two ways to do this: decrease the cycle length, or increase the family size (or both). To allow s to change for a fixed probability of survival, adjustments in n are required, and may be found from the following. With known values of p_s , n_o and s_o , and a particular new value of s_1 , the formula for n can be found from:

$$P_{s_o} = (1 - 1/2^{n_o-1})s_o = (1 - 1/2^{n_1-1})s_1 = P_{s_1}$$

By taking logs and rearrangement, we get:

$$n_1 = \frac{\log (1 - [1 - 1/2^{n_o-1}] \frac{s_o}{s_1})}{\log 1/2} + 1$$

for constant probability as structure size changes.

Taking as an example $n_o = 2$, $s_o = 2$, and $s_1 = 4$, this formula gives $n_1 = 2.74$. If this data point were graphed, it would be easily seen to lie between the curves for family sizes 2 and 3. The formula generates a whole "family" of related curves, one for each value of average family size, so the particular point is simply in one of the many possible curves.

An analogous expression tells how to change the stability number in order to reduce the family size needed for stability. This time we must presume s_o , n_o and n_1 are known, and that $n_1 < n_o$. We start from the same equality as in the last section, but by very simple taking of logs and division, find:

$$s_1 = \frac{s_o \log (1 - 1/2^{n_o-1})}{\log (1 - 1/2^{n_1-1})}$$

Reversing the example of the last section, for $n_o = 2.74$, $n_1 = 2.0$, and $s_o = 4$, we find that $s_1 = 2$ is a suitable solution.

We may thus calculate the chance of survival given values of family size and structural description, and given the values from which these have been adjusted, or to which they will be changed. We can calculate the effect of various changes providing the probability is fixed. We now wish to calculate the needed family size n to maintain a marriage rule near its structural minimum, for a specified probability of survival. Taking the log of the general formula for P_1 given at the start of the section, we get

$$n = \frac{\log (1 - P_1^{1/s})}{\log (1/2)} + 1$$

As an example, take $s = 4$, and the survival chances .5, .75, .9:

for $P_s = .5$,	$n = 3.6$
$P_s = .75$,	$n = 4.7$
$P_s = .9$,	$n = 6.3$

5.4 Survival Chances II

To analyze survival probability, one must ask "survival of what". To answer this, I shall begin with an unproved but provable statement: a very large number of the conceivable marriage systems can be represented by pairs of sibships in "sister exchange". Using s as the structural number of a given rule, this means that for even numbered structural numbers, one need only analyze the probability that all of the $s/2 = w$ pairings survive, for 1-stable $w(M2)$ minimal configurations.

For each of the w pairs, if the family size is 2, the possible sex distributions are (m,m) , (m,f) , (f,f) , which occur if the sex proportions are $\underline{m} + \underline{f} = 1$, with frequencies $(\underline{m}^2, 2m\underline{f}, \underline{f}^2)$. Construction a table of the possible combinations to calculate frequencies of each type of pairing, it is apparent that only the back diagonal entries are "fully viable" for most systems.

	\underline{m}^2	$2m\underline{f}$	\underline{f}^2
$(m,m) \quad m^2$	m^4	$2m^3\underline{f}$	$m^2\underline{f}^2$
$(f,m) \quad 2mf$	$2m^3\underline{f}$	$2m^2\underline{f}^2$	$2m\underline{f}^3$
$(f,f) \quad f^2$	f^2m^2	$2m\underline{f}^3$	\underline{f}^4

The entries " \underline{m}^4 " and " \underline{f}^4 " are clearly not viable in any system, since this pairing of sibships is all of one or the other sex, with the indicated frequency.

Similarly, entries such as $2\underline{m}^2\underline{f}$ and $2m\underline{f}^3$ show "partially viable" systems, since on the average only one pair of individuals from the four may mate, and two persons of the same sex will be left mateless. (This assumption of monogamy is required by the definitions of chapter 4. However, see section 7.3 for how to relax this assumption.) It is thus apparent that the fully non-viable portion of pairing with average family size \bar{n} is $2(\underline{m}^{2\bar{n}} + \underline{f}^{2\bar{n}})$, or if $\underline{m} = \underline{f} = 1/2$,

$$(1) \quad v = 2(1/2)^{2\bar{n}} = 1/2^{2\bar{n}-1}.$$

Similarly, there are four "partial-survival" terms in v_p or where sex ratios are equal

$$(2) \quad v_p = \bar{n}(1/2)^{2\bar{n}-2}.$$

The corresponding survival probabilities become

$$(3) \quad \begin{aligned} s_1 &= (1 - v)^w \\ s_2 &= (1 - v - v_p)^w, \end{aligned}$$

and the equilibrium replacement per individual thus is $1/S_1$ and $1/S_2$, respectively, or $2/S_1$, $2/S_2$ for replacement family size per successfully mated pair of individuals.

Computation of S_1 , S_2 , $1/S_1$, $1/S_2$ for $w = 1, 2, \dots, 20$ (structural numbers 2, 4, ..., 40) for family sizes 2 through 10 in increments of .2 was carried out by computer. Table 5.2 (see end of this chapter) for $w = 1, 2, \dots, 10$ shows typical patterns. S_1 starts at low values, but "quickly", usually by $\bar{n} \leq 4.0$, reaches a 90% or higher S_1 survival, and that while S_2 may require astonishingly large replacement per person at small values, $1/S_2$ also drops to seemingly reasonable levels with smallish \bar{n} .

Results of these computations will be summarized in chapter 6. However, note that the results obtained by a Stirling number technique in the next chapter could just as well result from picking a fixed survival probability, and finding the associated family sizes for each.

5.5 Preliminary Probabilities of Cycles

In this section, we will begin to discuss the statistics which need to be developed for a more complete theory of internal population structure (i.e. linkages found in genealogical histories). In previous sections, we derived the condition that the average distinct family size in an offspring generation must be greater than or equal to the inverse of the product of the proportion of reproducing matings times the proportion of males in the population. However, we already know that no system will survive using a marriage rule if the system has fewer people in it than are required by the structural numbers. Hence, a closely related probability is that of finding a chain large enough to be minimal, or to find the minimal cycle existant at a given time, if any. (I point out that material in this section was worked out with the cooperation of Mr. Duchamp.)

The problem discussed here is the probability of being able to have a chain of length k given: k = families of 2 siblings each with the probability of male = m , and the probability of female = f , subject to condition that male cannot marry male and female cannot marry female. We will use "d.f" to mean "distinct family" (each B-set is a distinct family). Note that we are operating under minimal structural conditions of 1) monogamy; 2) two offspring per family; 3) identifiable and discrete generations; 4) survival to reproduction of all births; 5) marriage within generations but not between them; 6) all available people will marry and reproduce if possible. We seek the probability that the sex distribution of the members of the distinct families will allow marriage which produces a "chain" of length k .

Label the families: 1, 2, 3, 4, . . . , k. These numbers correspond to segments of the chain. We can represent a particular chain by the following illustration:

$$\begin{matrix} (\text{m}, \text{f}) & (\text{m}, \text{f}) & (\text{m}, \text{m}) & (\text{f}, \text{f}) & (\text{m}, \text{f}) & \dots & (\text{m}, \text{m}) & (\text{f}, \text{f}) & (\text{m}, \text{f}) & \dots & (\text{f}, \text{f}) & (\text{m}, \text{f}) & (\text{m}, \text{f}) \\ 1 & 2 & 3 & 4 & 5 & & i-1 & i & i+1 & & k-2 & k-1 & k \end{matrix}$$

By the way, this notation can be easily elaborated "chemical" style by using subscripts for repeated elements, and dots between closed cycles:

$$2(M2) = \{2(\text{mf})_2; 2[(\text{mm})(\text{ff})_2]; (\text{mf})_2 \cdot (\text{mm})(\text{ff})\}$$

An admissible chain is one in which: a) the number of links of form (m,m) occurring = the number of links with (f,f) occurring; b) the first part of the first entry (in this example: m) is of opposite sex as the last part of the last entry (in this example: f); c) the second part of k^{th} entry must be different from the first part of $(k+1)^{\text{th}}$ entry; d) in between any two (m,m) terms must occur an (f,f) term; e) in between any two (f,f) terms must occur an (m,m) term; (note that d and e imply a). Therefore, the placement of the m,m terms and f,f terms completely determine the chain.

Let: $P_{\text{mm}} = \text{probability of 2 males in the same family (e.g., sibship),}$

$P_{\text{ff}} = \text{probability of 2 females in the same family,}$

$P_{\text{mf}} = \text{probability of a male and a female in the same family.}$

We can classify all chains according to the number of (m,m) terms or the number of (f,f) terms. A particular chain having $n(m,m)$ terms has probability

$$P_n^k = (P_{\text{mm}}^n) P_{\text{ff}}^n (P_{\text{mf}}^{1-2n})$$

of occurring.

However, we can argue that the distribution of such elements will not affect the ability to form cycles, since the probability of creating a chain of length n in a population of $2n$ is simply the probability of finding n males and n females in the population. This follows from the restrictive assumption of 2 people per distinct family, and the need to link distinct families through a male to a female in each marriage pair. Hence the formula giving the probabilities is:

$$P(n) = C_n^{2n} f^n m^n.$$

For the value $P(n)$ the probability thus calculated is:

$n = 1$.500
2	.375
3	.312
4	.258
5	.207
6	.163
7	.126
8	.094

This data assumes $f = m = 1/2$.

This shows that cycles of lengths greater than five are relatively unlikely to occur, and that lengths of eight or more are very unlikely, for family size two. The formula used to calculate this curve is also a special case in another sense, which will be presented now in more general form. The special case presumes that the cycle length K and number of males in the population are equal. Using p = probability of a male, and q = probability of a female offspring, the distribution of possible offspring pairs is given by the binomial distribution $l = (m + f)^{2n}$, where n is the number of families, each having two offspring per family. In addition, $|m| + |f| = 2n$, since there are as many total male plus female offspring as there are families. We can calculate the following probability of being able to get the maximum possible chain of length $k = P(k)$, which is:

$$P(k) = \sum_{j=k}^{2n-k} \binom{2n}{j} m^{2n-j} f^j$$

providing $k \leq n$. However, the possibility of a chain of exactly length k is

$$P_e(k) = \binom{2n}{k} m^k f^{2n-k} + \binom{2n}{2n-k} m^{2n-k} f^k$$

Therefore, $2n - m \leq k$ or $2n - k \geq m$, and $k \leq m \leq 2n - k$ which implies $k \leq 2n - j \leq 2n - k$. The formula used above is the special case of this when $k = n$.

5.6 The Number of First Cousins

One of the more apparently simple questions in an intuitive approach to anthropology is to ask how many first cousins a person can have, given a marriage system. And indeed, the diagrams used so far make the answer appear quite simple. But as one moves from the elementary diagrams, the complexity increases quickly. The following material gives an example of this, by proceeding from the simple diagrams and the formulas based on them to more involved considerations. The result is a formula for the average expected number of first cousins in a population of an arbitrary composition of cycles and chains of arbitrary length. Such formula leads to notion of equivalence of systems whose structures are vastly different when seen

as genealogies. In particular, it implies that a generation with arbitrary internal structure may in some cases be equivalent to a simple circular system of given length (that is, to one of the configurational elements M_i). This emphasizes the potential importance of a theory of cycle structure in future developments.

If we carry out sample calculations on the simple configurational diagrams with two persons per distinct family, as in minimal systems, the average number of first cousins per person in a chain of length n is $4 \frac{n-2}{n-1}$. As can be seen, in an infinite chain, the ratio approaches 4, so that a very long chain and a very long cycle may be equivalent for statistical purposes.

This leads to the interesting observation that we may identify a chain of specified length which is statistically similar to an arbitrary composition of cycles and chains in the population, so long as one knows the average number of first cousins in the system. Where z is the average number of first cousins, $z = 4 \frac{n-2}{n-1}$ implies that this equivalent length is $n = \frac{z-8}{z-4}$. Both by plotting a few points, the reader can discover that this number grows from $n = 2$ at $z = 0$, to $n = 50$ for $z = 3.99$, and that as z approaches 4.0, n very quickly grows into large values! Note that in a cycle, the number of families n is also the length of the cycle.

TABLE 5.2a SURVIVAL PROBABILITIES FOR $w = 1, \dots, 10; s = 2, 4, \dots, 20$. $w = 1$

\bar{n}	$1/s_1$	s_1	$1/s_2$	s_2
2.0	1.142	0.874	2.666	0.374
2.2	1.104	0.905	2.047	0.488
2.4	1.077	0.928	1.713	0.583
2.6	1.057	0.945	1.509	0.662
2.8	1.043	0.958	1.373	0.727
3.0	1.032	0.968	1.280	0.781
3.2	1.024	0.976	1.212	0.824
3.4	1.018	0.982	1.162	0.860
3.6	1.013	0.986	1.125	0.884
3.8	1.010	0.989	1.097	0.911
4.0	1.007	0.992	1.075	0.929
4.2	1.006	0.994	1.058	0.944
4.4	1.004	0.995	1.046	0.956
4.6	1.003	0.996	1.035	0.965
4.8	1.002	0.997	1.028	0.972
5.0	1.002	0.998	1.022	0.978
5.2	1.001	0.998	1.017	0.983
5.4	1.001	0.998	1.013	0.986
5.6	1.000	0.999	1.010	0.989
5.8	1.000	0.999	1.008	0.991
6.0	1.000	0.999	1.006	0.993

 $w = 2$

2.0	1.306	0.765	7.111	0.140
2.2	1.220	0.819	4.191	0.238
2.4	1.160	0.861	2.936	0.340
2.6	1.118	0.894	2.277	0.439
2.8	1.087	0.919	1.887	0.529
3.0	1.065	0.938	1.638	0.610
3.2	1.049	0.953	1.470	0.680
3.4	1.036	0.964	1.352	0.739
3.6	1.027	0.972	1.266	0.789
3.8	1.020	0.979	1.204	0.830
4.0	1.015	0.984	1.157	0.864
4.2	1.011	0.988	1.121	0.891
4.4	1.009	0.991	1.094	0.913
4.6	1.006	0.993	1.073	0.931
4.8	1.005	0.994	1.057	0.946
5.0	1.003	0.996	1.004	0.957
5.2	1.003	0.997	1.034	0.966
5.4	1.002	0.997	1.027	0.973
5.6	1.001	0.998	1.021	0.979
5.8	1.001	0.998	1.016	0.983
6.0	1.001	0.999	1.012	0.987

\bar{n}	$1/s_1$	s_1	$1/s_2$	s_2
$w = 3$				
2.0	1.492	0.669	18.963	0.052
2.2	1.347	0.741	8.581	0.116
2.4	1.250	0.799	5.031	0.198
2.6	1.182	0.845	3.436	0.290
2.8	1.134	0.881	2.593	0.385
3.0	1.099	0.909	2.097	0.476
3.2	1.074	0.930	1.782	0.560
3.4	1.055	0.947	1.572	0.636
3.6	1.041	0.959	1.425	0.701
3.8	1.031	0.969	1.321	0.756
4.0	1.023	0.976	1.244	0.803
4.2	1.018	0.982	1.187	0.842
4.4	1.013	0.986	1.144	0.873
4.6	1.010	0.989	1.111	0.899
4.8	1.007	0.992	1.086	0.920
5.0	1.005	0.994	1.067	0.936
5.2	1.004	0.995	1.052	0.950
5.4	1.003	0.996	1.040	0.960
5.6	1.002	0.997	1.031	0.969
5.8	1.001	0.998	1.024	0.975
6.0	1.001	0.998	1.019	0.981
$w = 4$				
2.0	1.706	0.586	50.567	0.019
2.2	1.489	0.671	17.568	0.056
2.4	1.347	0.742	8.620	0.115
2.6	1.250	0.799	5.186	0.192
2.8	1.183	0.844	3.563	0.280
3.0	1.135	0.880	2.684	0.372
3.2	1.100	0.908	2.161	0.462
3.4	1.075	0.930	1.828	0.547
3.6	1.056	0.946	1.604	0.623
3.8	1.042	0.959	1.449	0.689
4.0	1.031	0.969	1.338	0.747
4.2	1.024	0.976	1.257	0.795
4.4	1.018	0.982	1.197	0.835
4.6	1.013	0.986	1.151	0.868
4.8	1.010	0.989	1.117	0.895
5.0	1.007	0.992	1.090	0.916
5.2	1.005	0.994	1.070	0.934
5.4	1.004	0.995	1.054	0.948
5.6	1.003	0.996	1.042	0.959
5.8	1.002	0.997	1.033	0.967
6.0	1.002	0.998	1.025	0.974

\bar{n}	$1/s_1$	s_1	$1/s_2$	s_2
$w = 5$				
2.0	1.949	0.512	134.847	0.007
2.2	1.644	0.607	35.968	0.027
2.4	1.451	0.689	14.771	0.067
2.6	1.322	0.755	7.826	0.127
2.8	1.234	0.810	4.895	0.204
3.0	1.172	0.853	3.436	0.291
3.2	1.127	0.887	2.620	0.381
3.4	1.094	0.913	2.125	0.470
3.6	1.070	0.933	1.806	0.553
3.8	1.053	0.949	1.590	0.628
4.0	1.040	0.961	1.439	0.694
4.2	1.030	0.970	1.331	0.751
4.4	1.022	0.977	1.252	0.798
4.6	1.017	0.983	1.193	0.838
4.8	1.013	0.987	1.148	0.870
5.0	1.009	0.990	1.114	0.897
5.2	1.007	0.992	1.088	0.918
5.4	1.005	0.994	1.068	0.935
5.6	1.004	0.995	1.053	0.949
5.8	1.003	0.996	1.041	0.960
6.0	1.002	0.997	1.032	0.968
$w = 6$				
2.0	2.228	9.448	359.594	0.002
2.2	1.816	9.550	73.638	0.013
2.4	1.563	0.639	25.311	0.039
2.6	1.398	0.714	11.810	0.084
2.8	1.287	0.776	6.725	0.148
3.0	1.209	0.826	4.398	0.227
3.2	1.154	0.866	3.177	0.314
3.4	1.114	0.897	2.471	0.404
3.6	1.085	0.921	2.033	0.491
3.8	1.064	0.939	1.745	0.572
4.0	1.048	0.954	1.548	0.645
4.2	1.036	0.964	1.410	0.709
4.4	1.027	0.973	1.309	0.763
4.6	1.020	0.979	1.235	0.809
4.8	1.015	0.984	1.180	0.846
5.0	1.011	0.988	1.139	0.877
5.2	1.008	0.991	1.107	0.902
5.4	1.006	0.993	1.083	0.923
5.6	1.005	0.994	1.064	0.939
5.8	1.003	0.996	1.050	0.952
6.0	1.002	0.997	1.038	0.962

\bar{n}	$1/s_1$	s_1	$1/s_2$	s_2
$w = 7$				
2.0	2.546	0.392	958.917	0.001
2.2	2.007	0.498	150.760	0.006
2.4	1.684	0.593	43.371	0.023
2.6	1.479	0.675	17.822	0.056
2.8	1.342	0.744	9.240	0.108
3.0	1.248	0.800	5.629	0.177
3.2	1.182	0.845	3.852	0.259
3.4	1.135	0.880	2.874	0.347
3.6	1.100	0.908	2.288	0.436
3.8	1.075	0.930	1.915	0.522
4.0	1.056	0.946	1.665	0.600
4.2	1.042	0.959	1.493	0.669
4.4	1.032	0.969	1.370	0.729
4.6	1.024	0.976	1.280	0.781
4.8	1.018	0.982	1.214	0.823
5.0	1.013	0.986	1.164	0.858
5.2	1.010	0.989	1.126	0.887
5.4	1.007	0.992	1.097	0.910
5.6	1.006	0.994	1.075	0.929
5.8	1.004	0.995	1.058	0.944
6.0	1.003	0.996	1.045	0.956
$w = 8$				
2.0	2.910	0.343	2,557.114	0.000
2.2	2.217	0.451	308.653	0.003
2.4	1.814	0.551	74.318	0.013
2.6	1.564	0.639	26.894	0.037
2.8	1.400	0.714	12.695	0.078
3.0	1.289	0.775	7.205	0.138
3.2	1.211	0.825	4.671	0.214
3.4	1.155	0.865	3.342	0.299
3.6	1.115	0.896	2.575	0.388
3.8	1.086	0.920	2.101	0.475
4.0	1.064	0.939	1.791	0.558
4.2	1.048	0.953	1.581	0.632
4.4	1.036	0.964	1.433	0.697
4.6	1.027	0.973	1.326	0.753
4.8	1.020	0.979	1.248	0.801
5.0	1.015	0.984	1.189	0.840
5.2	1.011	0.988	1.145	0.872
5.4	1.009	0.991	1.112	0.898
5.6	1.006	0.993	1.087	0.919
5.8	1.005	0.994	1.067	0.936
6.0	1.003	0.996	1.052	0.950

\bar{n}	$1/s_1$	s_1	$1/s_2$	s_2
$w = 9$				
2.0	3.326	0.300	6,818.968	0.000
2.2	2.449	0.408	631.909	0.001
2.4	1.955	0.511	127.345	0.007
2.6	1.654	0.604	40.585	0.024
2.8	1.460	0.684	17.442	0.057
3.0	1.330	0.751	9.223	0.108
3.2	1.240	0.805	5.664	0.176
3.4	1.177	0.849	3.886	0.257
3.6	1.131	0.884	2.899	0.344
3.8	1.097	0.910	2.306	0.433
4.0	1.073	0.931	1.927	0.518
4.2	1.054	0.947	1.674	0.597
4.4	1.041	0.960	1.498	0.667
4.6	1.031	0.969	1.374	0.727
4.8	1.023	0.977	1.283	0.779
5.0	1.017	0.982	1.215	0.822
5.2	1.013	0.986	1.165	0.857
5.4	1.010	0.989	1.127	0.886
5.6	1.007	0.992	1.098	0.910
5.8	1.005	0.994	1.076	0.929
6.0	1.004	0.995	1.059	0.944
$w = 10$				
2.0	3.801	0.263	18,183.921	0.000
2.2	2.705	0.396	2,293.716	0.000
2.4	2.106	0.474	218.207	0.004
2.6	1.749	0.571	61.246	0.016
2.8	1.523	0.656	23.964	0.041
3.0	1.373	0.727	11.805	0.084
3.2	1.270	0.786	6.867	0.145
3.4	1.198	0.834	4.518	0.221
3.6	1.146	0.872	3.263	0.306
3.8	1.109	0.901	2.530	0.395
4.0	1.081	0.924	2.073	0.482
4.2	1.061	0.942	1.772	0.564
4.4	1.046	0.956	1.567	0.637
4.6	1.034	0.966	1.423	0.702
4.8	1.026	0.974	1.319	0.758
5.0	1.019	0.980	1.242	0.804
5.2	1.014	0.985	1.185	0.843
5.4	1.011	0.988	1.142	0.875
5.6	1.008	0.991	1.109	0.900
5.8	1.006	0.993	1.084	0.921
6.0	1.004	0.995	1.065	0.938

TABLE 5.2b SUMMARY STATISTICS OF \bar{n} VALUES
FOR $w = 1$

n	V	V_p	S	$V+V_p+S$
2.0	0.125	0.500	0.374	1.000
2.2	0.094	0.416	0.488	1.000
2.4	0.071	0.344	0.583	1.000
2.6	0.054	0.282	0.662	1.000
2.8	0.041	0.230	0.727	1.000
3.0	0.031	0.187	0.781	1.000
3.2	0.023	0.151	0.824	1.000
3.4	0.017	0.122	0.860	1.000
3.6	0.013	0.097	0.888	1.000
3.8	0.010	0.078	0.911	1.000
4.0	0.007	0.062	0.929	1.000
4.2	0.005	0.049	0.944	0.999
4.4	0.004	0.039	0.956	0.999
4.6	0.003	0.031	0.965	1.000
4.8	0.002	0.024	0.972	1.000
5.0	0.001	0.019	0.978	1.000
5.2	0.001	0.015	0.983	0.999
5.4	0.001	0.012	0.986	1.000
5.6	0.000	0.009	0.989	0.999
5.8	0.000	0.007	0.991	1.000
6.0	0.000	0.005	0.993	0.999
6.2	0.000	0.004	0.995	0.999
6.4	0.000	0.003	0.996	0.999
6.6	0.000	0.002	0.996	1.000
6.8	0.000	0.002	0.997	0.999
7.0	0.000	0.001	0.998	0.999
7.2	0.000	0.001	0.998	0.999
7.4	0.000	0.001	0.998	1.000
7.6	0.000	0.000	0.999	1.000

CHAPTER 6: ELEMENTS OF DISTRIBUTIONAL MARRIAGE THEORY

6.0 Introduction

Since Graunt (1662) demographers, historical demographers, and economists have noted a shift in human fertility and mortality trends, apparently in association with the development of industrialization and urbanization. Broad characteristics of this trend appear to be declining fertility with increasing density, increased mobility, reduction of the network of family ties, and increasing instability of social units in general (Ryder 1959, Keyfitz 1972, etc.). Attempts to associate these trends with various economic or psychological "causes" have been made (e.g., Easterlin 1968) but all share a common characteristic: inability to simultaneously account for past experience and to successfully anticipate future demographic conditions. This past experience includes such facts as the near universal existence of actual fertility at levels well below the intrinsic rate of which humans are capable. Past and present inability of prediction by the usual techniques were early demonstrated by Pearl (1939) whose "upper asymptote" for human population levels have long since been passed. More recent techniques (such as Meadows 1972) while more exciting are based on the same rate process already proven insufficient for population policy.

For this reason, we must look for a new approach, and the history of physical science in this century tells us where. Consider the condition of physical science about 1900 (cf. Jammer 1966, Cropper 1970, etc.): numerous physical phenomena were known on a statistical level; "heat" for example could be measured and correlated with other "system variables"; radiation could be produced by application of other means of energy, but in what amounts and why?, etc. While developments such as that of statistical mechanics by Gibbs were brilliant steps, it was not until the development of quantum theory that physics was able to relate simultaneously both the known statistical properties of various materials and potential properties of new materials.

Quantum mechanics, as a structural theory, has several characteristics important for the present discussion. First, it uses the mathematics of group theory to predict the possible configurational arrangements of molecules, based on the symmetry properties of atoms. Secondly, it relies on properties of the group theoretical representation to devise operators with statistical predictive ability. Thirdly, using these properties, it is able to predict the possible states in which an atomic system may exist, and their characteristic properties. As an example of the importance of these techniques, consider the approach of Frejka (1973) to the study of

demographic equilibrium. Like nearly all demographically oriented authors, equilibrium occurs when "births" balance "deaths" with appropriate adjustments for age structure, reporting problems, etc. of "developed" or "underdeveloped" countries. Nonetheless, how are we to know at precisely what family size to balance "birth" and "death"? Just as in chemical systems, the energetic bond for stable molecules differs for different chemical structures, so in social theory, stable family size (or equilibrium family size) may differ according to the social structure.

6.1 A Basic Statistic

Consider a society maintaining L arbitrary "families" (where "family" here simply means biological reproduction unit at the level above the individual). Assume this society has a marriage rule which has structural number s , and that the ideology of the society interprets the units to which "s" applies as the same units which are called "families" in the last sentence. Since s is the structural minimum, but L is empirical, clearly, $s \leq L$, and intuitively one suspects the strict inequality must hold. If there are N unique individuals born per generation, and all and only L families are kept, then these N individuals must be distributed such that none of the L families is empty. The standard computation for the number of ways N distinct objects can be placed into L indistinguishable cells is the Stirling Number of the Second Kind, which has been calculated in a table (Andrews and von Foerster, 1965). We use this since structural theorems do not care about names of females, only total numbers.

Note that for any N value, $1 \leq L \leq N$ is possible, but which of these shall actually occur? If the problem is posed as meeting "unknown circumstances" with the greatest number of possible opportunities (greatest variability of individual traits), then this maximum variability should occur with the L value for a given N which has the highest number combinations of possible placements. Calling this "max L " for "maximum L value, given N ", a table was constructed showing max L for $N \leq 242$. The authors of the simulation found it necessary to stop at 242, since the order of magnitude of the number of combinations at max L , $N = 242$ was $\sim 10^{350}$.

It is useful here to briefly examine the distribution of the number of combinations of placement of N objects into $1 \leq L \leq N$ cells by this statistic. For $L = 1$, there is only one way to place all N into the single family. Likewise, for $L = N$, there is only one indistinguishable placement. On the other hand, even for small N , the peak number of combinations for placement into $1 < L < N$ cells has easily $> 10^{100}$ number of different ways of occurring. In fact, for $N = 90$, the maximum number of placements is $\sim 10^{100}$, which occurs at $L = 26$. (Even for $N = 20$,

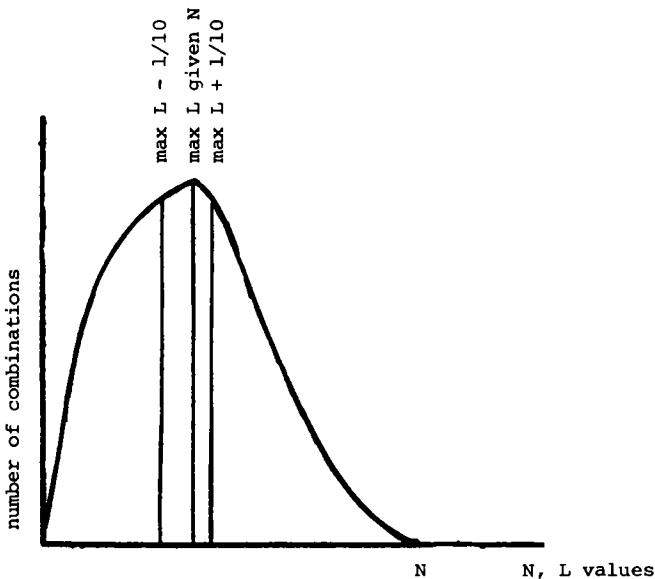


DIAGRAM 6.1

which is a small population, the maximum number of combinations occurs at $L = 10$, and has $\sim 10^{13}$ different possibilities!). If one examines the L value which occurs at $\pm 1/10$ the maximum number of combinations, one discovers values which are about $\pm 10\%$ of L . This means that the distribution of the number of combinations of placements is very flat in the region of $\text{max } L$, but very steep from the region of $\pm 10\%$ of the maximum to the lower axis values at $L = 1$ and $L = N$.

This provides a second reason for picking $\text{max } L$ as the "correct" prediction: $\text{max } L$ and values close to $\text{max } L$ ("close" means up to 10 times fewer ways of occurring) include almost the entire mass of the possible distributions which may occur at all!

Thus, if we treat these values as expectations over a large number of trials, this statistic has several implications. First, (dropping the "max" from $\text{max } L$, but remembering that $L = \text{max } L$) $N/L = \text{average "family size"}$. Next, since there must at equilibrium be the equivalent of one female reproducing "fully" per reproduction unit, $L/N = \text{the proportion which must be female reproducers from the whole population}$, and with $\underline{m} = \underline{f} = 1/2$, $2L/N$ gives the proportion of the female population which

which must be engaged in full-time reproduction, defined as each producing the N/L offspring per generation while $1 - \frac{2L}{N}$ produce no offspring. These values are summarized in Table 6.1 (see end of chapter 6) for $1 \leq N \leq 240$. This was as high as the number of combinations at max L would permit computation.

Since the table stops at $240 = N$, it is interesting to attempt to fit a curve, or several curves to the (N, L) pairs. Unfortunately, using the standard UCLA Bio-med polynomial regression program, a single curve does not suitably fit the entire curve. For the entire curve, the best fit regression is

$$L = 1.63 + .322N - (.633 \times 10^{-3})N^2 + (.113 \times 10^{-5})N^3$$

which, unfortunately, is explosive for larger N , and since $N < L$ is impossible, the equation is unsuitable. The second degree equation

$$L = 1.35 + .338N - (.711 \times 10^{-3})N^2$$

for $1 \leq N \leq 95$ is focused in the wrong direction, as is

$$L = 5.41 + .242N - (.966 \times 10^{-5})N^2$$

for $100 \leq N \leq 242$. However, using only the last 50 values,

$$L = 9.80 + .199N$$

is a good linear equation, and the only one which appears valid for "large" N . Using this estimator, the handy asymptotic ratio $\frac{L}{N} = .20$ occurs as N gets large, but finite. This implies that the largest family size ever required by a social system is $\bar{n} \sim 5$, but it also implies that the family size increases with N , while simultaneously $\frac{2L}{N}$ decreases with N , from > 1.0 at the smallest values, to $.40$ at large values. This corresponds to the notion that in small societies $\frac{2L}{N} \sim 1$, so that every woman is almost fully engaged in reproduction, while in large societies only $.40$ of the women need be so engaged, provided each turns out 5 offspring.

These results will be further interpreted below. Also note that for $N \leq 8$, $\frac{2L}{N} > 1$ for all cases except these pairs: $(N = 4, L = 2)$, $(N = 6, L = 3)$, $(N = 8, L = 4)$, and, therefore, for populations whose empirical size is N , no other pairs at these small values are physically possible in this model, since they require more reproduction capacity than exists in the population. This is consistent with the purely structural arguments of chapter 4: these are the only cases where $s = L = 1/2N$.

The existence of local maxima of $\frac{2L}{N}$ after each increment of L , and local minima before each increment, should not be ignored. The existence of this discontinuity may be interpreted as a structural flaw forcing continued population growth!

Each time the total population increases by one "family" (L increases by one unit) we also have increasing total N . By "spreading reproductive burden", by inching down the average family size, we discover that structural reasons require a slight increase in the number of families, which accumulate in this model as a discontinuity which incidentally also raises the average family size needed for equilibrium.

One should pay special attention to the fact that we have just computed the value $(1-c)$ of chapter 1: the value $\frac{2L}{N}$ is precisely the stable proportion of mated persons in the population. Further, the value $\frac{1}{1-c} = \frac{N}{2L}$ is the average number of offspring per individual needed to replace the population. Note that $\frac{2L}{N} \cdot \frac{N}{2L} = 1$ appears trivial, but we shall see in chapter 7 that it is a very productive tautology.

6.2 Analytical Model

Recall that in the last section we were concerned with equilibrium replacement of number of "families", considered as one equivalent fully reproducing female per family. Suppose there are N families per generation, and that there are F females. Let the chance that a particular birth occurs in a particular family be $\frac{1}{N}$, hence $\frac{N-1}{N}$ that it does not occur in that family. Note that if N_0 families have no female offspring, we must have

$$(4) \quad s \leq N - N_0 .$$

Noticing that $\left(\frac{N-1}{N}\right)^F$ is the probability that with F births, none is female, and

$$(5) \quad N_0 = N \left(\frac{N-1}{N}\right)^F$$

is the proportion of families which do not reproduce females. This is a permissible calculation since $\left(\frac{N-1}{N}\right)^F$ may also be seen as the $F = i$ term in the binomial expansion

$$\binom{F}{i} p^i q^{F-i}$$

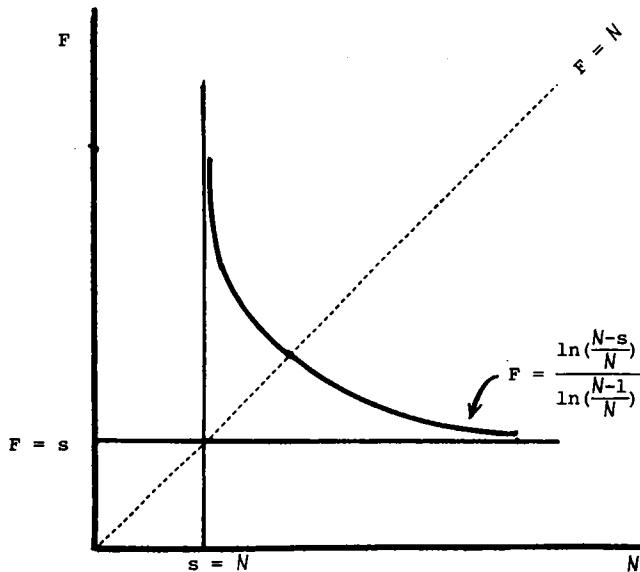
with $p = \left(\frac{N-1}{N}\right)^F$, $q = 1 - p$.

It is now possible to derive one direct relationship between s , F , and N , at the equilibrium values of $F = L$ (that is, one fully reproducing female per biological unit). This is done by placing an equality in (4) and solving for F , which gives

$$(6) \quad F = \frac{\ln\left(\frac{N-s}{N}\right)}{\ln\left(\frac{N-1}{N}\right)}$$

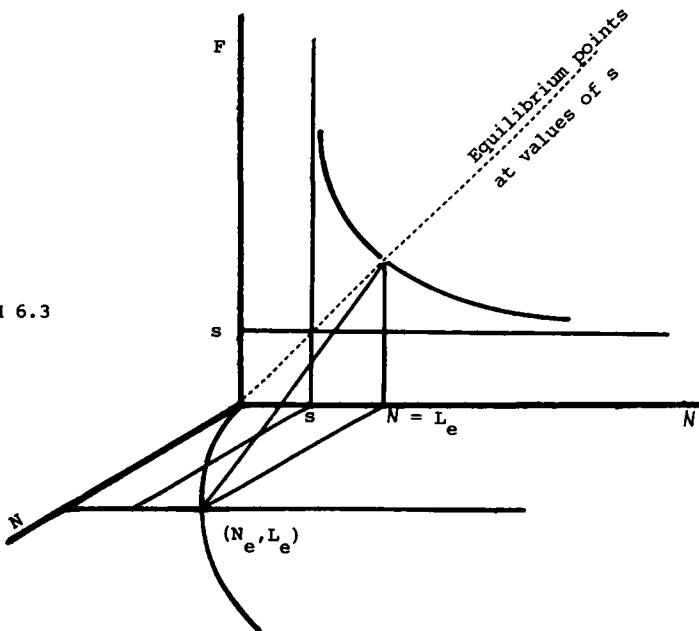
Note that (6) graphs as shown in Diagram 6.2 with the equilibrium values of each s on the 45° line through the origin, and with $F = s$, $n = s$ as vertical and horizontal asymptotes.

DIAGRAM 6.2



In diagram 6.3, we get an expanded view of the relationship between F , N , L , s , and

DIAGRAM 6.3



It is also interesting to note that

$$\frac{dF}{dN} = \frac{\frac{s}{(N-s)} \ln\left(\frac{N-1}{N}\right) - \frac{1}{(N-1)} \ln\left(\frac{N-s}{N}\right)}{\ln\left\{\left(\frac{N-1}{N}\right)\right\}^2}$$

Treating s and N as inputs, by numerical iteration, the equilibrium values of $1 \leq s \leq 31$ were found, and are reported for $s \leq 18$ in the column " $N = F$ " of Table 6.2. This same iteration discovered that for all points of $F_e = L$ equilibrium,

$$\left. \frac{dF}{dN} \right|_{F_e} = -.72$$

and only for $s \leq 4$ did this derivative stray from the .71 - .73 range, and then only by $\sim .01$.

Another remarkable result appeared from the simulation: $F_e = L$ is closely approximated for the simulated range by a simple linear equation:

$$F_e = .23 + 1.56s$$

which may be verified by examining the " $F - s$ " column of Table 6.2. This means as well that by simple substitution into the estimation equations for $\max L$ from N , given above, that simple quadratic and linear predictions of N and N from s result. These numerical extensions would thus have limited utility. Please note that a more hierarchical model is under preparation to account for large N , which model bears certain strong resemblances to the present model.

The variety of notation in this section requires some explanation. Essentially, the problem of this section is to study the conditions which allow maintenance of a system which "appears to be in equilibrium" while maintaining a given marriage rule. We are seeking the statistics that are associated with this appearance. Thus, the values F , L and N are not the same number, and the resulting solution of apparent equilibrium can only occur when these three different variables have the same value. Note that F is the number of "actively reproducing females", assumed to appear as one each to each of a stable number of families; N is the number of families which appear to have a reproducing female; L is the number of families which maximize the Stirling Number statistic. Thus, once we have solved equation (6) (numerically) to find values of $F = N$ which satisfy (6) for given s , we are then able to predict a value of L associated with s by assuming $F = L$. Please note also that the objective of these calculations is calculations of average value statistics that are associated with the appearance of maintaining a rule

TABLE 6.2: VALUES OF s AND ASSOCIATED STATISTICS

(1)	(2)	(3)	(4)	(5)	(6)	(7)	(8)	(9)	(10)	(11)	(12)
s	$L=R_e$	$2L/N$	S_1	$2/S_1$	S_2	$2/S_2$	N	\bar{n}_e	F_{e-s}	r	
1											
2	2.8	1.00	.874	2.29	.375	5.33	4	2.00	4.00	.8	~.30
3	4.4	1.00	-	-	-	-	8	2.00	2.65	1.4	.406
4	6.0	0.92	.800	2.50	.200	10.00	13	2.12	2.55	2.0	.450
5	7.6	0.82	-	-	-	-	17	2.43	2.45	2.6	.450
6	9.2	0.82	.810	2.46	.230	8.70	22	2.44	2.40	3.2	.459
7	10.8	0.74	-	-	-	-	27	2.70	2.35	3.8	.447
8	12.3	0.73	.845	2.36	.280	7.12	33	2.75	2.32	4.3	.453
9	13.9	0.68	-	-	-	-	38	2.92	2.29	4.9	.438
10	15.5	0.68	.830	2.40	.290	6.70	44	2.93	2.27	5.5	.436
11	17.1	0.66	-	-	-	-	51	3.00	2.25	6.1	.425
12	18.7	0.63	.840	2.38	.280	7.14	57	3.17	2.23	6.7	.423
13	20.3	0.63	-	-	-	-	64	3.20	2.22	7.3	.417
14	21.8	0.61	.845	2.36	.259	7.72	69	3.29	2.21	7.8	.411
15	23.4	0.60	-	-	-	-	76	3.30	2.20	8.4	-
16	25.0	0.60	.825	2.42	.214	9.34	83	3.32	2.19	9.1	-
17	26.6	0.58	-	-	-	-	96	3.42	2.17	9.6	-
18	28.2	0.58	-	-	-	-	99	3.42	2.17	10.2	-

Note: Values in this table were done by numerical iteration by techniques discussed in the text. Values entered as a "-" were not amenable to estimation by the chosen technique.

with given structural number. All the variables F , L and N are no more than intermediate steps in the computation of the values found in Table 6.2. Please refer to columns 2, 3, 8 and 9 for numerical results of computations in this section.

6.3 Comparison of Statistical Results

The various statistics described in earlier sections may now be compared, along with two other statistics of interest. Table 6.2 summarizes the important values. In column (1) are s values from 1 - 18, representing potential configurations including almost any known empirically. Column (2) shows the equilibrium values $F_e = L$ found from the analytic model by numerical iteration, assuming one "equivalent reproducing female" per fully reproducing family. In column (3) are the required proportions of reproducing females for stability under the stochastic model, at the point $F_e = L$. This is precisely the c value of chapter 1, given a marriage rule. Columns (4) and (6) respectively give P_1 and P_2 for $\bar{n} = N/F_e$ from chapter 5 while (8) gives the N/F_e average family size for equilibrium under the stochastic model, and (5) and (7) give average family sizes under the two probability models of the last chapter. Column (10) gives average family sizes for equilibrium where only accidental unbalances in sex ratio are considered, also from chapter 5. Finally, column (11) gives the $F_e - s$ values discussed in 6.2, and column (12) gives values of r , an empirical constant to be discussed below.

Especially note here the apparent constancy of $S_1 \sim .82$, (and of $S_2 \sim .25$) with corresponding approximate average family size ~ 2.4 (columns (4) to (7)). This stability from the probability model is not reflected in the stochastic approximation of the analytic equilibrium (column (9)), which has an average family size increasing from 2.00 to 3.42 as s goes to 18, and in fact goes on to 5.00 for large s . However, there is a relationship between the probability model and the stochastic, found by comparing the family sizes of the stochastic-analytic model to "random-mating", of column (10), for given s in the analytic model. These values graph as shown in Diagram 6.4, and the point of intersection is $2.44 = \bar{n} \sim N/F_e$.

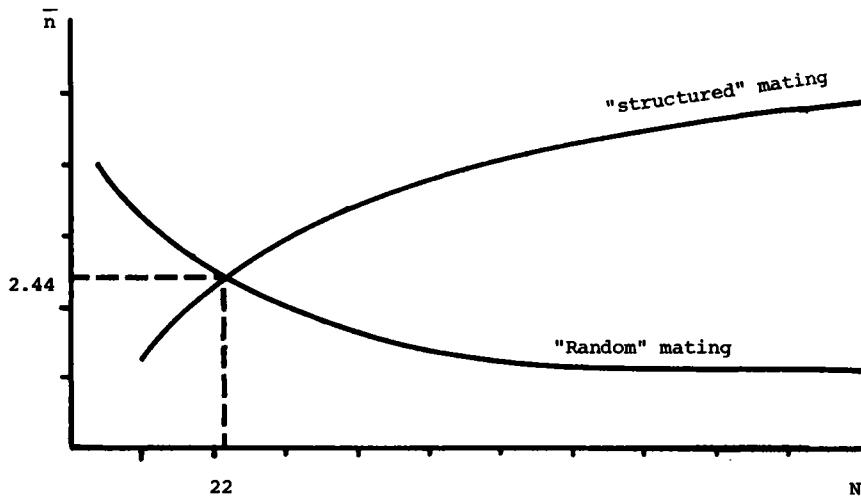
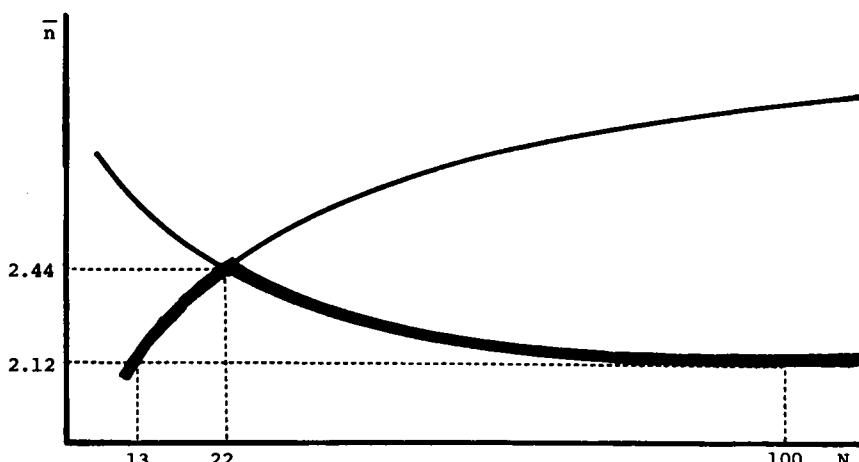


DIAGRAM 6.4



"Least Effort" Structure Prediction for Values of Population Sizes is shown in heavy black. Values of $n = 2.0$ are physically impossible. (Not to scale. See tables 5.1 and 6.2.)

DIAGRAM 6.5

Diagram 6.5 then illustrates the implied empirical prediction for the range of possible marriage structures as N increases, under the assumption that a system will be as efficient as possible with its investment in population size. Note that for generation cohort size $N \leq 22$, the system will attempt to attain the highest structural number possible, but since all such systems are underpopulated relative to sex ratio requirement, these systems will be highly unstable. Once past $N = 22$, it is no longer necessary to force family size up and improve stability by increasing the structural number. In the range $22 \leq N \leq 100$, most any system with structural numbers $s \leq 6$ might be found, but the larger numbers are certainly not compatible with $\bar{n} \sim 2.11$ for $N \geq 100$. Indeed, only $s = 4$ is compatible with maintaining sufficient population size to account for sex-ratio disproportion for "medium" to "large" size N .

Thus, in "metropolitan" societies, one would expect to find rules no more complicated than "first cousin exclusion", while in small societies, more complicated systems are necessary for survival. In very small systems, only a limited number of combinations of numbers of families with numbers of offspring are physically possible, hence one would expect the most rigid rules, such as those Australian systems with group theoretical properties, to occur in smallish populations. Such rigid rules, from Table 6.1, can only have 4, 6, 8, and perhaps 10 as the number of "lineages" or basic reproduction units, and these must be regulated by structural numbers $s \leq 6$. For all systems, the proportion of females engaged in reproduction is fairly high, being above .8, even for large systems using $s \sim 4$.

But there are other and equally startling implications: If a system is operating at equilibrium, with average size of interacting unit small, and "modern transportation", etc., suddenly makes greater migration possible, then with no change in marriage practices, or no modification in health techniques, the fact that the relevant N for sex equilibrium is now larger means that \bar{n} for sex equilibrium is smaller, and sudden growth will result from the old marriage practices.

The model also implies that average family size is not regulated by total system size (U.S. population total is irrelevant to the equilibrium family size!). Rather, the neighborhood size is the determinant of local average family size, and the national average is simply an average of these local unit sizes. This average will always be greater, by a meaningfully large amount, than the equilibrium predicted for the whole system as a single unit.

As a final note, I point out that, using the empirical constant r found in table 6.2,

$$s = -\sqrt{rNdN} = L(N - L) - \frac{r}{2} N^2 .$$

I conclude the section by posing the problem of the empirical meaning of r . Should a reader wish to work on this problem, or attempt to derive the expression rigorously, I point out that although

$$-\int rLdL = C - \frac{r}{2} L^2$$

that $C \sim L(N - L)$

is by no means a constant for all N . It is therefore certainly an open question whether the integral is legitimate at all, but at least it is an interesting possibility.

6.4 Basic Demographic Properties

The purpose of the present section is to summarize the important statistics of these several papers, and to compute several new statistics. It is hoped that the present article will present these statistics in a form that will allow other researchers to apply them in particular cases. In addition, a short exploration of the genetic effects of a restricted class of systems is presented.

The first concept necessary is that of structural number of a kin based marriage rule. While a technical definition is provided in chapter 4, for present purposes, the structural number of a marriage rule is the least number of marriages per generation which must be used to represent the application of a rule in the genealogy of an ideal population following the rule. Examples are given in table 6.3.

Note that several rules may have the same structural number. One does not intuitively expect that all such systems will have the same population statistics, and in fact two sets of statistics are developed. One set will depend on the value \bar{n}_r , which is defined as the average family size needed for replacement (stable population size) in a population mating "at random" (ignoring the marriage rule, whatever claims are made socially). Variations in \bar{n}_r therefore result only from fluctuations in sex ratio due to probability of male or female birth. Since the relative size in expected difference of numbers and females is relatively larger in a small population, \bar{n}_r is size dependent.

The second set of statistics will be related to the value \bar{n}_s , which is defined as the average family size needed for equilibrium (stable population) in a population strictly following the stated rule. Values of \bar{n}_r and \bar{n}_s were computed and discussed in chapter 6 and are summarized here in table 6.4, columns (4) and (5) for structural numbers $s = 2$ to $s = 10$.

Table 6.3 Some simple rules and their structural numbers (all rules assume sibling exclusion).

Rule	Structural Number
Forced first cousin marriage, no lineage exclusion	2
"Four section system"	2
First cousin marriage closest allowed (or preferred)	2
Prohibition of parallel cousins, cross cousins allowed (or required, or preferred)	2
Prohibition of cross cousins, parallel cousins allowed (or required, or preferred)	2
First cousin marriage closest allowed, matri- or patri-lineage exclusion	3
Forced first cousin marriage, either matri- or patri-lineage exclusion	3
Prohibition of all first cousins	4
Required (preferred) marriage to sixth degree relative of same generation	4

Table 6.4 Structural numbers and associated average population statistics
(Summary of table 6.2)

(1) s	(2) N	(3) P	(4) \bar{n}_s	(5) \bar{n}_r	(6) E_s
2	4	1.00	2.00	4.00	-100.0
3	8	1.00	2.00	2.65	- 32.5
4	13	.92	2.18	2.55	- 20.3
5	17	.82	2.43	2.45	- 00.8
6	22	.82	2.44	2.40	01.7
7	27	.74	2.70	2.35	14.9
8	33	.73	2.75	2.32	18.5
9	38	.68	2.92	2.29	27.5
10	44	.68	2.93	2.27	29.1

Other values in table 6.4 are: the minimal population size (e.g., number of reproductively active persons) per generation needed to maintain a rule with that structural number, in column (2), from chapter 6; the proportion of females in the population who must reproduce at this average family size, in column (3), also from chapter 6; the relative difference in \bar{n}_r , \bar{n}_s values at the given number in column (6), from E_s , defined as

$$E_s = \frac{\bar{n}_r - \bar{n}_s}{\min(\bar{n}_r, \bar{n}_s)} \cdot 100$$

The first use to which we may put these statistics involves uses of table 6.4. I will first show that if individuals reproduce as if maintaining only their own local unit, that the reproductive burden of females is independent of the empirical population size. Let W be the empirical population size, and let n be the average family size (completed family size surviving to reproductive age per female). Then W/n is the number of "equivalent" reproducing females if each produced exactly n offspring. Let x be the proportion of females in the population, so that xW is the number of females. Then the relative reproductive burden per female is $(W/n) / (xW) = (1/nx)$ which is independent of the empirical population size. Values in column (3) of table 6.4 assume $x = .5$ and $n = \bar{n}_s$. Note that we may simultaneously interpret $1/xn$ as the burden per female of reproducing family size n , if evenly proportioned over all females; but also, as the proportion of females who must reproduce exactly n offspring if $1 - 1/xn$ reproduce exactly zero offspring.

The implication of independence of reproductive burden of females of empirical population size is quite important. It allows us to use the statistics associated with a marriage rule in any population following the rule. However, in populations whose empirical per generation size is close to the minimum given in table 6.4, column (2), it will also appear as if we have predicted the population size as well. This occurred for example in Ballonoff (1973) for Apache and Hopi systems, while part II here predicts U.S. growth rate with no reference to empirical population size. However, where \bar{n}_r values are used, we must know the (distribution of) isolate sizes to predict growth rates.

In the present paper, we present tables of two additional statistics which may be calculated from values in table 6.4. These are the gross fertility (number of births per year per 1000 females ever married) and the marriage rate (number of marriages per year per 1000 females). Both statistics are calculated at equilibrium, defined as the condition where the total offspring group size, distributed over a fraction $p = 1/xn$ of the female population of reproductive age, have family size n .

Table 6.5 Gross fertility for structural numbers $s = 1, \dots, 10$ and generation intervals of 20, 21, ..., 30 years.

s	Inverse of generation interval (years)						1/29	1/30
	1/20	1/21	1/22	1/23	1/24	1/25		
2	280.00	266.67	254.55	243.48	233.33	244.00	215.38	207.41
3	145.75	138.81	132.50	126.74	121.46	116.60	112.12	107.96
4	117.69	112.09	106.99	102.34	98.08	94.15	90.53	87.18
5	109.53	104.31	99.57	95.24	91.27	87.62	84.25	81.13
6	100.36	95.58	91.24	82.27	83.64	80.29	77.20	74.34
7	94.00	89.52	85.45	81.74	78.33	75.20	72.31	69.63
8	85.77	81.69	77.97	74.58	71.47	68.62	65.98	63.53
9	83.77	79.78	76.15	72.84	69.80	67.01	64.44	62.05
10	79.97	76.16	72.70	69.54	66.64	63.97	61.51	59.23

It is clearly true that once we know the gross fertility, that other fertility statistics may be calculated (e.g., number of female births per 1000 females is $(1/x)G.F.$ at equilibrium, and so on).

The gross fertility (G.F.) per 1000 females ever married, behaving as if according to a marriage rule, is found by this formula:

$$G.F. = n p I (1000)$$

where n is average family size (either \bar{n}_r or \bar{n}_s); p is the proportion of "equivalent females" reproducing at this size (table 6.4, column (3)); I is the inverse of the generation interval in years; and 1000 is the adjustment factor to convert the value $n p I$ to a number per 1000. Notice that regardless of whether we chose \bar{n}_r or \bar{n}_s , that we must use p as given by \bar{n}_s , since this is the value which relates to social network density, and in particular to number of "nodes" in any such social network. In general, in the present work, I do not study this aspect mathematically, but must retain an awareness of it to attain the needed results.

Table 6.5 shows gross fertility where $n = \bar{n}_r$, and is used below to predict U.S. fertility rates. Note that if $s = 4$ is taken as an estimate of "the" structural number of "the" U.S. marriage rule of first cousin exclusion, that the row corresponding to $s = 4$ in table 6.5 gives almost an exact prediction of the range of variation of gross fertility in the U.S. for the last 50 years (DeJong, 1968).

In table 6.6, we calculate the value of G.F. for $n = \bar{n}_s$. Substitution into the formula for gross fertility shows that, for $n = \bar{n}_s$,

$$G.F. = \bar{n}_s \cdot \frac{1}{\bar{n}_s x} \cdot I \cdot 1000 = 2000 I, \text{ for } x = .5$$

The coefficient 2000 results from the fact that if $x = .5$, $1/x = 2$, and this assumption was used in estimating p values. What is most significant about this expression is that gross fertility, when calculated for fertility required to maintain a specific marriage rule, is in fact independent of what that marriage actually is.

Notice that these values are almost exactly those of gross fertility for ($s = 6$, $n = \bar{n}_r$), which occurs since $s = 6$ is the approximate intersection of the \bar{n}_r and \bar{n}_s curves.

In terms of fertility, a population can do better, apparently, by claiming a complicated rule ($s > 6$) but actually mating at random. This however is only true if only the demographic parameter of family size is considered. If one notes that $\bar{n}_r < \bar{n}_s$ for $s > 6$, then the denisty of the connected kin network required to stabilize the empirical mating system (measured as the proportionate distribution of

Table 6.6 Gross fertility at $n = \bar{n}_s$.

I	1/20	1/21	1/22	1/23	1/24	1/25	1/26	1/27	1/28	1/29	1/30
G.F.	100	95.2	90.9	87.0	83.3	80.0	76.9	74.0	71.4	69.0	66.7

Table 6.7 Survival probabilities for different rules at minimal equilibrium family size, from chapter 5, table 5.2a, at the family size found in table 6.4, column (4).

<u>s</u> =	2	4	6	8	10
P =	.87	.82	.80	.81	.81

cycles in a graph) will not be maintained. In fact, from the crude formulas in chapter 5, we can see that as family size decreases, the probability of maintaining this network decreases. Therefore, to maintain a fixed empirical network as well as demographic stability, a system must attempt to maintain the family sizes required by the rule, giving values in the $n = \bar{n}_s$ table above. Table 6.7 summarizes survival probabilities at different family sizes for selected structural numbers.

The conclusions thus appear to be that for $s < 6$, a population would "prefer" to mate at random if it could do so to minimize gross fertility, but unfortunately $\bar{n}_r > \bar{n}_s$ at these values, and also the proportion of females who must reproduce is high. However, since $\bar{n}_r > \bar{n}_s$, the network of family ties is clearly at least as dense as wanted for stability of the network (if not too dense!). The choice in populations using an $s < 5$ is therefore either strict adherence to the rules and maintenance of low family size, but high proportions of females mating; or else loose adherence to the rules and high \bar{n}_r family size, with corresponding high growth. For $s \geq 6$, great reduction in family size may only accompany "poor connections" in the kin network.

We may calculate the per generation actual growth rate that would accompany attempting equilibrium of the kin network at \bar{n}_s , and ignoring demographic equilibrium (\bar{n}_r).

Table 6.8 Expected yearly marriage rates per 1000 females at stability, with sex ratio = .5 using
 P values in Table 6.4.

S	Generation interval (years)						
	20	21	22	23	24	25	26
2	70.0	66.7	63.5	60.9	58.3	56.0	53.8
3	55.0	52.3	50.0	47.8	45.8	44.0	42.3
4	46.2	44.0	43.0	40.1	38.5	37.0	35.5
5	44.7	42.5	40.6	38.9	37.3	35.8	34.4
6	41.8	39.8	38.0	36.4	34.8	33.4	32.2
7	40.0	38.1	36.4	34.7	33.3	32.0	30.8
8	37.0	35.2	33.6	32.1	30.8	29.6	28.4
9	36.6	34.8	33.2	31.8	30.5	29.2	28.1
10	35.2	33.6	32.0	30.1	29.4	28.2	27.1

This is essentially the same for $s \geq 6$ as calculating E_s . E_s gives the relative growth resulting from using \bar{n}_s over \bar{n}_r values where \bar{n}_r is lower. Negative signs simply show $\bar{n}_s < \bar{n}_r$, but should be interpreted as the positive relative growth if \bar{n}_r values are attempted in this range. Note that where E_s is negative, growth results essentially from the fact that if strict control of family size is not practiced, then too many females are getting "married" ($p \approx 1.0$), whereas if E_s is positive, growth can result from the case where an attempt is made to maintain the density of social networks required by \bar{n}_s values, and this is true in spite of the fact that p values decline as s rises. The difficulty is that from the perspective of the individual or family, the immediate social net depends on the female portion of \bar{n}_s and on a fraction p of these continuing the needed patterns, while demographically only a family of size $\bar{n}_r < \bar{n}_s$ will do, but then the proportion $p \cdot \bar{n}_r$ is too small.

Also notice that where E_s is negative ($s \leq 5$) that a population might do much better by choosing to strictly regulate sex ratio and number of offspring at birth, hence to use table 6.6 rather than table 6.5. Also, notice that if a population with large per generation isolate sizes were to determine from this table its most efficient possible structural number, it would pick $s = 4$. (We define "most efficient" to mean that $\bar{n}_r \leq \bar{n}_s$, and $|\bar{n}_r - \bar{n}_s|$ is minimized, so growth is minimized, where \bar{n}_r is specific to the isolate size, and \bar{n}_s is specific to the rule. The optimal case is $\bar{n}_r = \bar{n}_s$, since this implies both demographic stability and social network stability.) This is so since $s = 3$ and $s = 2$ have infeasible \bar{n}_s (that is there is no finite population for which $\bar{n}_r \leq \bar{n}_s$), whereas for per generation group sizes of 80 to 100, $\bar{n}_r \approx \bar{n}_{s=4}$, and $\bar{n}_r < \bar{n}_{s=4}$ above 100 per generation. For larger structural numbers, there will be simultaneous demographic and network growth for much smaller per generation group sizes, and network collapse at $\bar{n}_r < \bar{n}_s$.

This may be one reason why systems with very large population sizes often appear to have $s = 4$, but would also explain why systems with more complicated marriage rules ($s \approx 7, 8, 9$, etc.) also appear to have larger family sizes, or why such systems might not respond well to "family planning" programs based on \bar{n}_r stability.

An ideal family planning program would calculate the \bar{n}_s for the given rule, then find the per generation population size for which $\bar{n}_r = \bar{n}_s$. Population policy could then ignore family size, on the argument that people would have only as many children as needed to maintain their social networks. Instead, policy would relate to maintenance of "isolates" of the proper size, or at least to knowing what the actual causes of growth are.

The final demographic statistic we wish to present here is the equilibrium marriage rates per 1000 females per year, which is simply $M.R. = (.5/x)pI(1000)$. This is given in table 6.8, where $x = .5$. Note again from the line $s = 4$ that we have the proper order of magnitude for U.S. national statistics of the 1970 census, when the population was close to zero growth. We discuss this prediction in the remainder of this section.

In fact, we discuss the general prediction of large aggregate data from the preceding tables. We do this specifically to counter the argument that we only have a theory of the minimal case. However, for an example of treatment of a population near its own minimal values, see Ballonoff (1973), which treats the case of the Western Apache. Notice that for small aggregates, the probability of failure (see chapter 5) is so significant that in fact the behavior of systems close to minimum is not precisely determined by the minimal values, but by some structural value above the minimum. Only in large aggregates is it possible to actually attain minimal population statistics without high risk of total system failure.

Let us assume as is frequently the case in U.S. data that a particular region has the civil law and actual practice of forbidding marriage to siblings and first cousins, and allows all other marriages within the generation (we temporarily ignore cross-generational marriages). Assume we have found an isolate (probably rural) with a per generation group size of 80 persons (these represent the "reproductively active" population, excluding those below marriage age, and above reproductive age). Then the expected equilibrium average completed family size is 2.18 for ever married females; the expected percentage ever married females who actually reproduce is .92; therefore, the actually observed average completed family size should be $\frac{1}{.92}$ (2.10) = 2.28.

If we now account for the reproductive interval (generation time) we can predict the gross fertility (per 1,000 females per year) of such isolates. (table 6.5, line $s = 4$) shows that the following holds under the stated assumptions:

Generation Interval (Years)	20	21	22	23	24	25	26	27	28	29	30
Expected Equilibrium Gross Fertility	117	112	106	102	98	94	90	87	84	81	78

Thus, expected gross fertility, if the generation interval is 25 years, is 94 per 1,000 females per year.

DeJong (1968) showed that gross fertility of the U.S. fluctuated between values 78 and 113 in the years 1930 to 1970. These are approximately the low estimate (30 year span) and high estimate (21 year generation span) if the nation had

a uniform marriage pattern as described and only generation times were changing. This same study (DeJong 1968) also noted that many isolates in Appalachia had higher "fertililities" early in the period, and lower "fertililities" later. This result is also mathematically predicted by this chapter. In English, the argument is that if relative isolation of communities breaks down, then the relative size of endogamous units would be expected to increase. Since average family size is predicted to decrease as the endogamous population size increases for fixed structural number reverting from \bar{n}_s to \bar{n}_r values, the gross fertility should also decrease. Thus, the end of historic isolation in Appalachia is sufficient to predict decreased fertility.

Assume now that the observed completed family size (adjusted as above) for some census tract is 2.8, and the predicted as above is 2.4. We therefore expect a combined growth and/or out migration as $\frac{2.8 - 2.4}{2.4} = \frac{.4}{2.4}$ or 16 percent relative to the expected equilibrium value. This supposed "rural" area could thus "export" about 13 people per "generation", and retain its same size if completed family size is 2.80. This technique will allow computation of total expected migration and/or growth (immigration and/or decline) relative to each base period projection for each summary unit. Also, notice that by summation of these values for all areas which show net excess family size compared to areas which show net insufficient size, an estimate by region and/or nation can be made as to whether or not the total observed change in size can be accounted for by domestic processes alone.

Using the 1970 census, the average for all states of number of children ever born to ever married females is 2.62. If all isolates were small so that 2.40 is our equilibrium, then the expected growth per generation is 9.6 percent. If we use 2.28 as equilibrium (assuming all isolates are large) the growth rate is 14.6 percent per generation. On a per year basis, these rates are approximately .73 percent per year (large isolates) and .48 percent per year (small isolates) assuming a 20 year generation interval and ignoring compound growth effects.

6.5 Implication of the Preceding

I begin with a caution: Readers who believe that this work or this style of work represents a "new departure in anthropology" should be aware that the author does not share this view. It is the most common occurrence that an individual anthropologist, after working on a "people" or a problem, gains an insight peculiarly his own. This insight then becomes a plague: the rest of life is a battle to make others understand, accept, or even consider and reject the idea. In writing this work, I have revised the theoretical foundations four or five times. If I can not now make my insights intelligible, then it is not for failure of effort. As an

anthropologist rather than a mathematician, I have defined my work as discovering the structural foundations of my subject, demonstrating to some reasonable degree that the mathematical imaginings reflect "ethnographic reality", and indicating possible productive lines of mathematical research. A competent mathematician can now discover alleys and corners much more quickly than I can.

The first necessary issue is that of organization of "role trees", and mutual comparability of role trees between different "societies". Anthropology has, in the past, made two broad sweeps at this problem: the "cognitive" approach, which has focused on linguistic type structures and organization of cultural materials in forms amenable to linguistic analysis; and the "structural" approach, which has dealt with more abstract classifications relying primarily on totemistic and kin based logical systems.

By careful examination of the kinship operators used in this work, it should become apparent that these two approaches are not incompatible. Providing we do not confuse mentalistic interpretation with comparison of linguistic structure, then I believe there is hope of progress on several fronts. When the mathematical kinship theorists of the last decade carry out their composition operations, they are in fact doing something very similar or identical to the composition of operators used in chapter 3 to define the "exclusion matrix" of a marriage rule. The boundary between the "kinship" (and "cognitive") approaches and "marriage theory" (or "totemic") approaches is precisely the difference between studying the individual kin operators and their applicability to a particular society, and studying the possible effects on a generation or a sequence of generations of various combinations of "kin" matrices into the exclusion matrix of some particular marriage rule. The first is a highly empirical problem, while the second is empirical but also much more capable of abstract treatments. If the reader is surprised with the simplicity of marriage theory, the author is far more surprised that it has not already been widely recognized as a single coherent area of study.

The theory not only provides a means of unifying the frameworks of these intertwined areas of study, it can also have the capability of refining the proper application of a non-mathematical description. Considerable progress could also be made by study of the cycle distributions produced by various marriage rules, in their minimal and other forms. As is hinted at by matrix developments, it is possible to generate numerous distributions of theoretical ties under many rules, study the sequences of states (and state transitions) possible at or above the size of the minimal structure of a rule, and produce an *a priori* theory of sampled marriage systems, parametrized by the marriage rule and population size alone. This theory

would allow probabilistic statement of how likely it is that a particular collected genealogical history could have come from the sequence of one marriage rule or from another. Development is already to a point where probability statements can be made about future generations' configurations, knowing only the marriage rule and the population sizes of interest. The principal weakness of the operator approach for this problem is that it has not yet integrated demographic measures of fertility, etc. into its formulation.

By looking at the minimal structures appropriate to different marriage rules we also now have a means of studying, for at least a narrow class of problems, the affects of changing the axiom systems that "govern" social behavior. In this case, the "axioms" are the marriage rules themselves. We are in the nice position that we now know what needs to be studied. By comparing the graph theoretical structures of marriage rules, one can discover which changes of rules are feasible, which are more difficult, and which are impossible in a given population size, with a given genealogical history. We also appear to have a system which meets one of the criteria requested by Claude Levi-Strauss: by changing only a small part of our axiom system, we can get additional models of the same type. By "type" here, I mean both that we can get models of marriage systems in general, and that we can find classes of similar rules, with similar generational structures. When one considers that the full possibilities of mathematical groups for this problem have not yet even been completely explored, it is staggering to realize that the number of possible marriage rules may not even be countable, and that we have in the present work only the barest hints of the possible relations of rules to their minimal structures, to mathematical groups, or to demographic and genetic theory.

In constructing the theory, I have on the other hand tried to stay close to the dictum of Frederic Barth, that we should try to generate forms, and not simply make homologies. For example, it is well known that there is a homology between semigroups and kinship terminologies. Of itself, this fact has not lead anywhere. Far more useful to kinship theory would be an abstract system which produced as a theoretical outcome mathematical objects which could be interpreted as kin-terminologies. (See papers in Ballonoff 1974c for papers on this line.) In addition, it is certainly time that mathematical anthropology stopped repeating itself. The semi-group and relational algebra style interpretation of kinship has been known since 1882 (Macfarlane). A future historian of English language anthropology must certainly ask why the field has steadfastly refused not only to recognize the existence of this prominently placed article, but why it has persistently ignored all approaches which differ from it in any substantial way.

The above criticism is certainly not universal, nor directed at personalities. It would be to the advantage of all if certain key articles were viewed simultaneously. In addition to references found elsewhere in the text, the excellent contributions of Stephen Tyler, Paul Kay, Haldane and Jayakar, and John Atkins should all be looked at. Each has moved the frontier a small amount — together it is a large expansion.

Marriage theory is far from a complete theory of anthropological demography, but nonetheless is a start in that direction. This is evident in several places in the text. In the materials on matrices, I have pointed out that we can find a theoretical connection between the population size, and the amount of "free choice" allowed by a rule. For different rules, given a particular history and population size, the choices may be quite different, and can not always be easily discovered by study of population size alone.

Much more powerful, at present, is state transition theory. The value of this development for predicting histories has been noted above, but the utility for connecting demographic to structural measures should be emphasized. The particular distributions of cycles of a generation depends very heavily on the actual marriages which occur in that generation, and the sequence of vectors of cycle lengths for each generation which describe a particular history are therefore strongly related to the number and fertility of the actual marriages. Indeed, implicit in the construction of the needed matrices for any predictions of future genealogical patterns is some assumption about fertility patterns.

The reader should carefully note that minimal structures are rare indeed if we are concerned with the empirical reality they depict. However, this does not mean that the structures are not relevant to reality — on the contrary, they are an excellent point of departure — but it does mean that one must be very careful in noticing what the structures do and do not describe. A great deal of the beauty of the structures themselves follows from the very simple theorems of chapter 4. The pictures do not claim that every family in the universe must have two offspring, for example, but they do say that this is a correct way of efficiently depicting the operations of marriage rules. (In particular, note that there is no place where the claim is made that all family pairs in every minimal structure consist of a male and a female!)

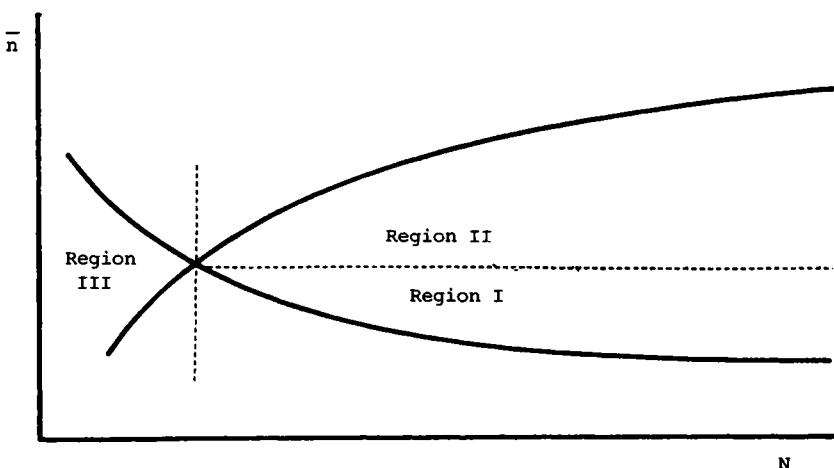
On the other hand, the very simple minimal structures do indeed differ from each other, and it is more important to realize that 3 as a number is 50 percent larger than the number 2, than to muse about how small a system with those structural numbers are compared to "reality". An atom is small compared to a sheet of

material containing millions of the same atoms, but the properties of the atoms are still important to the properties of the whole material.

I do not argue that we can now ignore statistical studies, but I do argue that we should no longer ignore structural studies. This is not only because of the poetic beauty of the structures, but because the structures themselves are incredibly revealing of the potential range of statistics which may be discovered. Diagram 6.4 and its interpretation are the single most important page in this work. Even if its interpretation turns out to be wrong, the mere fact that it is possible to construct a demographic prediction from a totally structural argument (indeed from nothing more than the structural numbers!) should certainly give pause to those who in the past have dismissed structuralist approaches.

This is a very important point, and I would like to review again the interpretation given this graph, which is duplicated below, but subdivided into regions for the purpose of the present discussion. Look first at region I. I have claimed that the family sizes implied by the furthest right region of the curve are only compatible with the smallest structural numbers, and in particular with structural number 4. Since we do not seem to observe prescriptive rules in the largest populations,

DIAGRAM 6.6



it is certainly consistent to interpret this section of the curve as predicting the observed proscriptive rules of many metropolitan societies. But there is also a correlation predicted by the shape of the curve: there should be a small negative coefficient of regression between average family size and total population size, of the basic neighborhood units. Dr. David Martin (private communication) carried out

an analysis of the family size and population density of the ten densest census tracts in the United States, and discovered a coefficient of regression on the order of 0.1. This result strongly suggests that if we can isolate the relationship between endogamy rates and group size, and then re-do the correlation, that a correlation of the predicted size should result.

If we look at region II, the discussion of this chapter suggests that this region will not occur, or if it does, then there is certainly a restrictive marriage rule (with structural number above 6). The necessary empirical study should, therefore, look at systems which involve large numbers of named lineages, resident in fixed locations, with marriage rules based on these lineages (as in areas of India); it should look at phratry and clan systems such as those of the Zuni; it should look at hierarchical or clan exogamy systems wherever they are found. Since a proper study of this topic could easily be more massive than the theoretical background, I am not prepared to claim a correspondence exists in this region, but preliminary indications are that correspondence is good, and that one may use the Stirling Number of the Second Kind not only to predict from total population per generation to number of families, but from number of families to number of units on higher levels. Looking, for example, at the Old Oraibi populations (Titiev, 1943), the family sizes and number of lineages before and after the split into two groups are as the Stirling statistics would predict them to be, assuming that the "social system" was attempting to maintain 8 or 9 phratries. In the case of at least one body of suitable recorded Indian statistics, the predictions were at the lower edge of the reasonable. However, the principal difficulty with study in this region of the curve is not the availability of data, but the availability of adequate theory. I have several times indicated that the present work in its present form is not yet a theory of lineage organization. Although it is not necessary to interpret the individuals" of my basic sets as particular people, the consequences of changing this interpretation are not easy to discover.

In region III, we have perhaps the most interesting case. We are led to make the following predictions: because of the extreme consequences of disproportion in sex ratio which differ from the structural minimums, one could expect to find rigidly defined and rigidly enforced rules. Where this rigidity is absent, then one would expect to find very unstable systems, due to the fact that the "random mating" curve produces a higher average family size than does the curve for more structured systems. Such region III systems would either be constantly spawning small migrant communities which leave it, or constantly reorganizing itself into smaller groups than appear to occur by birth, or both. I submit that the classic Australian

systems are examples of the rigid type, while the Amazon Basin provides ethnographic examples of the unstable type. (One reason why I avoid more concrete observations is that I have defined my task as constructing a theory, and indicating what is needed for a proof. Anthropology has seldom experienced purely theoretical developments. A proper test will require time, good data on genealogical histories of many particular systems, and imagination in minimizing computational difficulties.)

The above areas are not the only ones where demographic connections of the present theory to other work may be found. The "integral" equation at the end of section 6.2 might usefully be compared to the generally accepted work of population models. In making this study, one would compare the terms in my "structural integral" to the terms and parameters of the more accepted demographic theory. Likewise, a comparison of the present matrix methods to those used by other authors in social anthropology or population genetics would be very useful.

In most earlier versions of this work, I included a chapter or more on the philosophical or mathematical relationships between marriage theory and quantum mechanics. In the present version, there was even a stronger temptation to supplement with comparisons of our apparently every important Stirling Number of the Second Kind to forms of statistical mechanics. Certainly such discussions, using large words in difficult sentences, would be in the current of modern writings. There are several reasons why this discussion is not included. One of these is that it is unclear whether further progress can be made on the basis of speculation. However, it might be very useful to explore certain mathematical possibilities suggested by "wave" representations which result from group theoretical properties of minimal structures, or by the angular properties suggested by analogy between marriage circles to chemical bonds. Possibly by working from both these insights, one could develop a form of "fourier analysis" which decomposes an arbitrary generation into "angular components" parametrized by the structural numbers. An approach to this particular problem is developed in chapter 5, where it is suggested that arbitrary chains of linkages within a generation might be considered equivalent to a particular circular configuration of specifiable circumference. Since these are the very configurational elements which can be shown to form a "basis space" for the states of marriage systems, a second approach is state space theory. It is certainly of more than simple amusement that it is possible to suggest how to complete the circle from statistics to structure and back in a completely analytic way.

Thus, while quantum mechanics may have proved a personal guide in searching ideas, it is certainly premature to claim anything more than broad comparisons. Indeed, this work represents a compromise between the clear need in modern anthropology

for unencumbered theoretical work, and the liking of all anthropologists for speculation, but with sufficient substance that further developments in the same direction are possible.

TABLE 6.1:
 VALUE OF L WHICH MAXIMIZES STIRLING NUMBERS OF THE
 SECOND KIND, AND RELATED STATISTICS*

N	L	L/N	2L/N	N/L
1	1	1.0000	2.0000	1.0000
2	2	1.0000	2.0000	1.0000
3	2	0.6667	1.3333	1.5000
4	2	0.5000	1.0000	2.0000
5	3	0.6000	1.2000	1.6667
6	3	0.5000	1.0000	2.0000
7	4	0.5714	1.1429	1.7500
8	4	0.5000	1.0000	2.0000
9	4	0.4444	0.8889	2.2500
10	5	0.5000	1.0000	2.0000
11	5	0.4545	0.9091	2.2000
12	5	0.4167	0.8333	2.4000
13	6	0.4615	0.9231	2.1667
14	6	0.4286	0.8571	2.3333
15	6	0.4000	0.8000	2.5000
16	7	0.4375	0.8750	2.2857
17	7	0.4118	0.8235	2.4286
18	7	0.3889	0.7778	2.5714
19	8	0.4211	0.8421	2.3750
20	8	0.4000	0.8000	2.5000
21	8	0.3810	0.7619	2.6250
22	9	0.4091	0.8182	2.4444
23	9	0.3913	0.7826	2.5556
24	9	0.3750	0.7500	2.6667
25	10	0.4000	0.8000	2.5000
26	10	0.3846	0.7692	2.6000
27	10	0.3704	0.7407	2.7000
28	10	0.3571	0.7143	2.8000
29	11	0.3793	0.7586	2.6364
30	11	0.3667	0.7333	2.7273
31	11	0.3548	0.7097	2.8182
32	12	0.3750	0.7500	2.6667
33	12	0.3636	0.7273	2.7500
34	12	0.3529	0.7059	2.8333
35	12	0.3429	0.6857	2.9167
36	13	0.3611	0.7222	2.7692
37	13	0.3514	0.7027	2.8462
38	13	0.3421	0.6842	2.9231
39	14	0.3590	0.7179	2.7857
40	14	0.3500	0.7000	2.8571
41	14	0.3415	0.6829	2.9286
42	14	0.3333	0.6667	3.0000

N	L	L/N	2L/N	N/L
43	15	0.3488	0.6977	2.8667
44	15	0.3409	0.6818	2.9333
45	15	0.3333	0.6667	3.0000
46	15	0.3261	0.6522	3.0667
47	16	0.3404	0.6809	2.9375
48	16	0.3333	0.6667	3.0000
49	16	0.3265	0.6531	3.0625
50	16	0.3200	0.6400	3.1250
51	17	0.3333	0.6667	3.0000
52	17	0.3269	0.6538	3.0588
53	17	0.3208	0.6415	3.1176
54	17	0.3148	0.6296	3.1765
55	18	0.3273	0.6545	3.0556
56	18	0.3214	0.6429	3.1111
57	18	0.3158	0.6316	3.1667
58	18	0.3103	0.6207	3.2222
59	19	0.3220	0.6441	3.1053
60	19	0.3167	0.6333	3.1579
61	19	0.3115	0.6230	3.2105
62	19	0.3065	0.6129	3.2632
63	20	0.3175	0.6349	3.1500
64	20	0.3125	0.6250	3.2000
65	20	0.3077	0.6154	3.2500
66	20	0.3030	0.6061	3.3000
67	21	0.3134	0.6269	3.1905
68	21	0.3088	0.6176	3.2381
69	21	0.3043	0.6087	3.2857
70	21	0.3000	0.6000	3.3333
71	22	0.3099	0.6197	3.2273
72	22	0.3056	0.6111	3.2727
73	22	0.3014	0.6027	3.3182
74	22	0.2973	0.5946	3.3636
75	23	0.3067	0.6133	3.2609
76	23	0.3026	0.6053	3.3043
77	23	0.2987	0.5974	3.3478
78	23	0.2949	0.5897	3.3913
79	24	0.3038	0.6076	3.2917
80	24	0.3000	0.6000	3.3333
81	24	0.2963	0.5926	3.3750
82	24	0.2927	0.5854	3.4167
83	25	0.3012	0.6024	3.3200
84	25	0.2976	0.5952	3.3600
85	25	0.2941	0.5882	3.4000
86	25	0.2907	0.5814	3.4400
87	25	0.2874	0.5747	3.4800
88	26	0.2955	0.5909	3.3846
89	26	0.2921	0.5843	3.4231
90	26	0.2889	0.5778	3.4615
91	26	0.2857	0.5714	3.5000
92	27	0.2935	0.5870	3.4074

N	L	L/N	2L/N	N/L
93	27	0.2903	0.5806	3.4444
94	27	0.2872	0.5745	3.4815
95	27	0.2842	0.5684	3.5185
96	28	0.2917	0.5833	3.4286
97	28	0.2887	0.5773	3.4643
98	28	0.2857	0.5714	3.5000
99	28	0.2828	0.5657	3.5357
100	29	0.2900	0.5800	3.4483
101	29	0.2871	0.5743	3.4828
102	29	0.2843	0.5686	3.5172
103	29	0.2816	0.5631	3.5517
104	29	0.2788	0.5577	3.5862
105	30	0.2857	0.5714	3.5000
106	30	0.2830	0.5660	3.5333
107	30	0.2804	0.5607	3.5667
108	30	0.2778	0.5556	3.6000
109	31	0.2844	0.5688	3.5161
110	31	0.2818	0.5636	3.5484
111	31	0.2793	0.5586	3.5806
112	31	0.2768	0.5536	3.6129
113	31	0.2743	0.5487	3.6452
114	32	0.2807	0.5614	3.5625
115	32	0.2783	0.5565	3.5938
116	32	0.2759	0.5517	3.6250
117	32	0.2735	0.5470	3.6563
118	33	0.2797	0.5593	3.5758
119	33	0.2773	0.5546	3.6061
120	33	0.2750	0.5500	3.6364
121	33	0.2727	0.5455	3.6667
122	33	0.2705	0.5410	3.6970
123	34	0.2764	0.5528	3.6176
124	34	0.2742	0.5484	3.6471
125	34	0.2720	0.5440	3.6765
126	34	0.2698	0.5397	3.7059
127	35	0.2756	0.5512	3.6286
128	35	0.2734	0.5469	3.6571
129	35	0.2713	0.5426	3.6857
130	35	0.2692	0.5385	3.7143
131	35	0.2672	0.5344	3.7429
132	36	0.2727	0.5455	3.6667
133	36	0.2707	0.5414	3.6944
134	36	0.2687	0.5373	3.7222
135	36	0.2667	0.5333	3.7500
136	36	0.2647	0.5294	3.7778
137	37	0.2701	0.5401	3.7027
138	37	0.2681	9.5362	3.7297
139	37	0.2662	0.5324	3.7568
140	37	0.2643	0.5286	3.7838
141	38	0.2695	0.5390	3.7105

N	L	L/N	2L/N	N/L
142	38	0.2676	0.5352	3.7368
143	38	0.2657	0.5315	3.7632
144	38	0.2639	0.5278	3.7895
145	38	0.2621	0.5241	3.8158
146	39	0.2671	0.5342	3.7436
147	39	0.2653	0.5306	3.7692
148	39	0.2635	0.5270	3.7949
149	39	0.2617	0.5235	3.8205
150	39	0.2600	0.5200	3.8462
151	39	0.2583	0.5166	3.8718
152	40	0.2632	0.5263	3.8000
153	40	0.2614	0.5229	3.8250
154	40	0.2597	0.5195	3.8500
155	41	0.2645	0.5290	3.7805
156	41	0.2628	0.5256	3.8049
157	41	0.2611	0.5223	3.8293
158	41	0.2595	0.5190	3.8537
159	41	0.2579	0.5157	3.8780
160	42	0.2625	0.5250	3.8095
161	42	0.2609	0.5217	3.8333
162	42	0.2593	0.5185	3.8571
163	42	0.2577	0.5153	3.8810
164	42	0.2561	0.5122	3.9048
165	43	0.2606	0.5121	3.8372
166	43	0.2590	0.5181	3.8605
167	43	0.2575	0.5150	3.8837
168	43	0.2560	0.5119	3.9070
169	43	0.2544	0.5089	3.9302
170	44	0.2588	0.5176	3.8636
171	44	0.2573	0.5146	3.8864
172	44	0.2558	0.5116	3.9091
173	44	0.2543	0.5087	3.9318
174	44	0.2529	0.5057	3.9545
175	45	0.2571	0.5143	3.8889
176	45	0.2557	0.5114	3.9111
177	45	0.2542	0.5085	3.9333
178	45	0.2528	0.5056	3.9556
179	46	0.2570	0.5140	3.8913
180	46	0.2556	0.5111	3.9130
181	46	0.2541	0.5083	3.9348
182	46	0.2527	0.5055	3.9565
183	46	0.2514	0.5027	3.9783
184	47	0.2554	0.5109	3.9149
185	47	0.2541	0.5081	3.9362
186	47	0.2527	0.5054	3.9574
187	47	0.2513	0.5027	3.9787
188	47	0.2500	0.5000	4.0000
189	48	0.2540	0.5079	3.9375
190	48	0.2526	0.5053	3.9583
191	48	0.2513	0.5026	3.9792

N	L	L/N	2L/N	N/L
192	48	0.2500	0.5000	4.0000
193	48	0.2487	0.4974	4.0208
194	49	0.2526	0.5052	3.9592
195	49	0.2513	0.5026	3.9796
196	49	0.2500	0.5000	4.0000
197	49	0.2487	0.4975	4.0204
198	49	0.2475	0.4949	4.0408
199	50	0.2513	0.5025	3.9800
200	50	0.2500	0.5000	4.0000
201	50	0.2488	0.4975	4.0200
202	50	0.2475	0.4950	4.0400
203	50	0.2463	0.4926	4.0600
204	51	0.2500	0.5000	4.0000
205	51	0.2488	0.4976	4.0196
206	51	0.2476	0.4951	4;0392
207	51	0.2464	0.4928	4.0588
208	51	0.2452	0.4904	4.0784
209	52	0.2488	0.4976	4.0192
210	52	0.2476	0.4952	4.0385
211	52	0.2464	0.4929	4.0577
212	52	0.2453	0.4906	4.0769
213	52	0.2441	0.4883	4.0962
214	53	0.2477	0.4953	4.0377
215	53	0.2465	0.4930	4.0566
216	53	0.2454	0.4907	4.0755
217	53	0.2442	0.4885	4.0943
218	53	0.2431	0.4862	4.1132
219	54	0.2466	0.4932	4.0556
220	54	0.2455	0.4909	4.0741
221	54	0.2443	0.4887	4.0926
222	54	0.2432	0.4865	4.1111
223	54	0.2422	0.4843	4.1296
224	55	0.2455	0.4911	4.0727
225	55	0.2444	0.4889	4.0909
226	55	0.2434	0.4867	4.1091
227	55	0.2423	0.4846	4.1273
228	55	0.2412	0.4825	4.1455
229	56	0.2445	0.4891	4.0893
230	56	0.2435	0.4870	4.1071
231	56	0.2424	0.4848	4.1250
232	56	0.2414	0.4828	4.1429
233	56	0.2403	0.4807	4.1607
234	57	0.2436	0.4872	4.1053
235	57	0.2426	0.4851	4.1228
236	57	0.2415	0.4831	4.1404
237	57	0.2405	0.4810	4.1579
238	57	0.2395	0.4790	4.1754
239	58	0.2427	0.4854	4.1207
240	58	0.2417	0.4833	4.1279

* Source for N and L, N = 1 through 95: "Table of Stirling Numbers of the Second Kind", Alex M. Andrew, Technical Report #6, Dec., 1965, EERL, Univ. of Illinois, Urbana; for N = 96-240, Unpublished simulation courtesy of H. Von Foerster, EERL, Univ. of Illinois, Urbana.

CHAPTER 7: STRUCTURAL MODELS AND CORRESPONDENCE PROBLEMS

7.0 Introduction

Over the last half century, developments of theoretical science have progressed in very similar patterns in several fields. These patterns appear to have two origins: First is the scientific mood of the period, including the availability of suitable techniques and their accessibility to workers in various disciplines. Understanding this realm requires study of when techniques were invented, the method of their transmission, the level of skills and knowledge in various disciplines, and the receptivity of a field to application and publication of new techniques. While these areas are important background, they are not the present subject.

The second origin is the order of discovery of ideas. We argue that this appears in all the fields mentioned to have been a similar pattern of development. This pattern, in its "classic" form appears to be roughly as follows:

direct → statistical → statistical → structural → structural
description treatments theories treatments theories

Note that this pattern is not meant to imply "hierarchical bettering" of theory. Each fictive "stage" exists because it appears the best way to handle problems of a field at its point of development. The techniques are used because they were hopefully most appropriate, within the available range, for the problem studied.

7.1 Basic Correspondence Problems

While physical theory is the clearest example of this sequence, a similar pattern of the first three or four stages, in that order, appears also in economics, population genetics and theoretical biology, but of these, only physics so far has an accepted structural theory. The period of direct description occurs early in a field's history, and indeed defines the field. In a crude sense, this is the period of collecting butterflies simply because they are pretty. The keenness of early descriptive workers is strongly related to the rate of progress possible in other stages.

Statistical treatments refers to a body of work or period in which the principal activity is statistical/numerical treatment of masses of data, in a deliberately searching manner. Often the hope is discovery of "significant correlations", and the frequent failure of these hopes often results from inhomogeneous data and/or inappropriate direct descriptions. The statistics of this stage are largely descriptive, with correlational/regressional/clustering techniques the most powerful available.

Statistical theories involve a new step: an axiomatic framework, over which one develops techniques for predicting observed statistics from given initial conditions, which are also statistical. E.g., given a particular set of statistics at one time, what values will (can) this set take at later times. An associated problem is the possible sets of jointly occurring statistics. This question frequently requires different techniques from purely statistical ones, since by purely statistical devices, considerable enumeration, etc., is required. Substitutes are difference equations or differential equations, whose solutions give potential stable points or distributions.

Structural treatments are in a certain sense only descriptions done mathematically. E.g., a matrix to represent a mating pattern, etc. Usually, these treatments are algebraic, though in their early stages they may be verbal or geometric in some form. Their existence is probably related to knowledge of structural mathematics. The fact that they occur relatively earlier in the histories of social theories than physical, reflects the fact that these theories began later, when structural awarenesses were greater.

Structural theories take two forms. First, "purely structural" theories essentially enumerate and describe all the possible forms of a particular type, giving useful and interesting properties of the forms. Such theories have a "pure mathematical" appearance, and have examples in particle physics and their beginnings in kinship theory. Second, in connection with well developed statistical theories, structural theories can predict either the expected statistical outcome (in some sense) or else the range of possible initial conditions of external parameters (constraints) on the statistical models. This also leads to prediction of expected values (ranges of values).

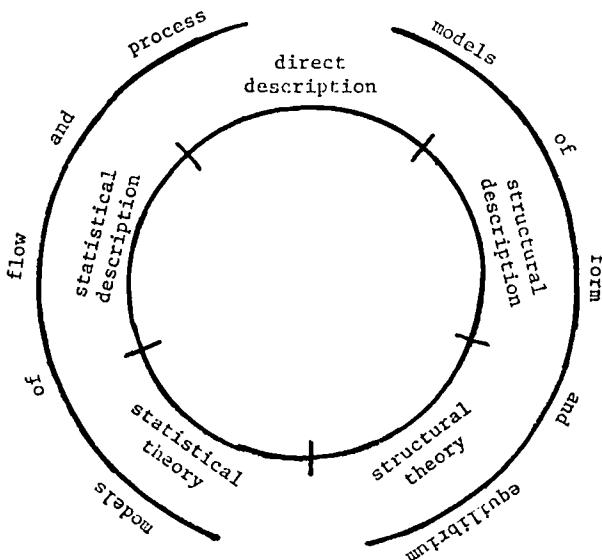
The field which most clearly exhibits the classical form of this development has been physical theory. (See Cropper, 1970, or other standard histories.) From a stage of observation of interesting phenomena in the eighteenth century and earlier, the nineteenth century saw the initial description of statistical treatments, and elements of theories of heat, etc. By the early twentieth century, true statistical theories (e.g., thermodynamics and radiation) appeared. Then, structural treatments appear, such as the Dirac notation (Dirac, 1958), which had organizing power for ideas, but no predictive power as such. Almost simultaneously quantum mechanical ideas appear, with the final flowering of predictive structural techniques, especially group theory.

Population genetics has a somewhat similar pattern, but shorter history. The early descriptive studies led to descriptive statistical work which especially filled

the English journals by the late nineteenth century. In the early twentieth century, elementary and then more advanced statistical theories appeared, most especially in the 1920's. By the 1940's, there is evidence for use of a priori structures to predict the form of results. However, no true structural theory in the full sense can yet be claimed for population genetic theory. (The introduction to Balonoff (1974a) gives a deeper treatment of this history.) In demography, descriptive statistics occur quite early, but today there are still no true structural descriptive techniques in the algebraic sense intended here. In economics, a similar situation prevails, with statistical theories at high development, but little development of structural description.

However, in the social theories, the order of development has not followed the "classical" model. The reason appears to be that since these sciences developed later historically, they also had available a greater awareness and sensitivity to structural techniques. Thus, the earliest kinship algebra in 1882 is quite nearly historically simultaneous with recognition of social anthropology as a separate field. On the other hand, even poor statistical work was not widely done until the 1940's and after. Folklore likewise produced good structural arguments before even a poor statistical work became prominent.

We can thus argue that these five "stages" of theoretical development form more a circle than a linear pattern:



Given a direct description, a field may choose either or both statistical or structural descriptions, assuming proper techniques are available at all. Theories in either realm must follow upon the existence of a suitably described domain. However, there appears to be no necessary reason why statistical description should precede structural in a field. In fact, their immediate purposes are quite different.

The meeting of statistical and structural theories occurs when structural theories begin to predict statistical values, normally the province of statistical theories. Thus, quantum chemistry predicts possible configurations of molecules, but radiation theory may be used to measure them. Correspondence problems therefore arise specifically when structural and statistical theories attempt to predict the "same" phenomena on different, and not necessarily compatible, grounds. In general, structural models are models of possible forms and their associated equilibria, while statistical models are interested in flow and process.

As an example of the interaction of available conceptual framework and ideology for their use, with what work is acceptable in a field at a particular time, we present the following simple table of bodies of possible statistics. Consider "statistics" as studying combinations and/or permutations of placements of "objects" into "cells". Both cells and objects may be alike or different, giving the following four part classification:

		OBJECTS	
		Alike	Different
C	Alike	I	III
	Different	II	IV

In cell I, all objects are like each other, all cells into which objects may be put are like each other. Therefore, the types of statistics possible here are simply counting statistics: how many objects, how many cells, how many objects per cell. This type of statistics is useful at the level of basic description, or for developing simple concepts (point potential, etc.).

In cell II, the cells are different (e.g., distinguishable), but the objects are all alike. This is the model for gas particles in a room, etc., and is the home of most physical statistical theories and the model for most social "systems" theories (see Buckley, 1968, for example). In cell III are statistics describing

diverse objects placed into identical cells, a topic with few known empirical applications. While in cell IV, we have diverse objects into diverse cells. The statistics here are potentially complicated, and are usually treated as extensions of cases I or II, or by techniques such as Polya's theorem, which allow for simplifications (discovery of isomorphism classes, etc.).

Now, which of these four cells has provided the foundation for advocacy of "quantifications" in science? Cell I is generally not a useful foundation. Cell IV is too complicated, hardly "available" to anyone at all, and filled with fancy special cases. Cell III appears "useless" *a priori*. Therefore, because experience in physical fields says it "works", and because it is presently accessible, advocates of quantification point to cell II. Unfortunately, followers of quantification use techniques of cell II everywhere, whereas they only have proven value in physical problems and aspects of biology. They are necessarily unproductive (Herbst, 1971) in social theory! However, there are good grounds for advocating the "useless" cell III as the correct statistics for social theory and we point to two applications; since they are precisely those of chapter 6, and were used to predict average population statistics both of an Apache group (Ballonoff, 1973) and of the United States census of 1970 (in this work).

7.2 Correspondence of Marriage Theory to Production Theory

To argue that social theories are now in a state comparable to the pre-stages of modern quantum theory, I shall open another line of argument. We have so far identified two critical areas of theoretical development: choice of theoretical form and its foundation, witnessed by our statistical example; correspondence between structural and statistical theories. Correspondence problems have largely arisen in physical theory, and occasionally elsewhere as diverse theories develop. I now wish to show that correspondences do exist in theories from three realms: social anthropology (marriage theory); economics (production theory); and demography (average population statistics). Such correspondences follow the path opened by Sauvy (1954).

In the present view, the correspondences draw first upon an analogy between marriage theory, whose foundations are structural, and production theory, whose basic form is statistical mechanical. The correspondence developed later between marriage theory and demography results from marriage theory as a structural theory predicting equilibrium demographic statistics for specified cultural forms. These two distinct correspondences (by analogy and by subject matter) draw upon the availability of different representations for a single idea.

Marriage theory begins with identification of a single number, called the structural number, associated with a given marriage rule (chapter 4). This number is found ethnographically, and is the number of marriages per generation needed to construct the smallest (imaginary) genealogy on which one could represent a self perpetuating population following the rule. Under strictly minimal or close to minimal conditions, where F is the number of females (more specifically, "equivalent reproducers per generation") N is the number of families, and s the structural number, the following relations hold: (1) at equilibrium, where each family is at the equilibrium size for the structural number of the rule, then $F = N$ is required for stability; (2) where N_0 is the number of families that do not reproduce out of N families, then $s \leq N - N_0$ is an interpretation of the meaning of s ; (3) $s \leq F$ and $s \leq N$ are necessary consequences. These conditions are all represented below. The approxi-

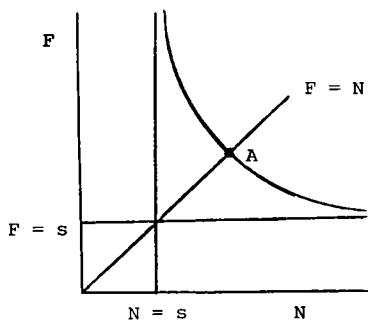
mate "hyperbolic" curve, asymptotic to $F = s$, $N = s$ is the lower envelope for points satisfying $s \leq N - N_0$. The point shown as "A" is the unique point on this envelope for which $F = N$, hence is a unique minimal equilibrium point for the given structural number s . Note that the minimal envelope is precisely the set of points satisfying $s = N - N_0$ (that is, replacing the inequality with an equality from condition (2) above). We shall de-

note this set of points as $f(s)$. Note also that we can find the derivative of $f(s)$ at the point A, and this corresponds to taking the slope of a live tangent to the minimal envelope.

We now turn briefly to economic theory, and in particular to the basic concepts of production theory. The first concept of interest is that if "isoquant", which is the locus of all combinations of two "inputs" which yield a specified level of output. In marriage theory we have a clear analogy to the lower envelope curves mentioned above. For fixed structural number s , the set $f(s)$ which gives the fixed lower bound of feasible points for the level of output is

$$f(s) = \{(F, N) : s = N - N_0, N_0 = N(1 - \frac{1}{N})\}$$

where N_0 was defined in chapter 6.



This gives the curve shown on the previous page, which has the same appearance as a single isoquant. Properties of isoquants (ref: Henderson and Quandt, 1958) are: (1) isoquants are continuous—viewed as potential average values observed in samples, $f(s)$ is also continuous; (2) isoquants cover the entire space—we can meet this condition by considering not only populations following one rule, but populations following mixes of rules. In the case of a proportion w_1 using structural number s_1 , w_2 using s_2 , with $w_1 + w_2 = 1$, we have

$$f(w_1 s_1 + w_2 s_2) = w_1 f(s_1) + w_2 f(s_2)$$

and in general

$$f(\sum_i w_i s_i) = \sum_i w_i f(s_i), \sum_i w_i = 1.$$

This requires a conception that the curves represent expected values of many similar systems, and that the weights show values of single mixed systems. These definitions also lead to the condition that the average population statistics of mixed systems are linear combinations, with the same weights, of the statistics of "pure" systems; (3) an increase of both inputs leads to an increase of output (the isoquant has no loops, etc.); and (4) the further an isoquant from the origin, the higher the level of output. Conditions (3) and (4) are similar and result from the fact that if $s_1 > s_2$, the $f(s_1)$ is to the upper right of $f(s_2)$.

Now consider an apparently "purely economic" concept, the cost constraint, which in the simplest case is

$$C = r_1 x_1 + r_2 x_2 + b$$

where b is the cost of "fixed inputs", r_1 cost of a unit of x_1 , r_2 cost per unit of x_2 . An isocost line thus defined is the amount which may be purchased for fixed amount (say C^0) of total cost, or

$$C^0 = r_1 x_1 + r_2 x_2 + b.$$

In marriage theory, we have two "inputs", N and F and at equilibrium, two simultaneous equations

$$N = F$$

and

$$C = r_N N + r_F F + b_s.$$

Assume r_N and r_F are determined by the "ecology and economy" of the society, and where v is just a proportionality constant, then if $r_N = a$, then $r_F = av$. Or, $v = r_F/r_N$.

Noting that v may be considered the rate of substitution of N for F at the optimal minimal equilibrium point (e.g., the slope of $f(s)$ at this point) we found by numerical simulation (in chapter 6) that $v = .72 \pm (.01)$ for $2 \leq s \leq 10$. (Values of v for all s were found by numerical simulation at the equilibrium conditions required above.)

It is therefore sensible to interpret the minimal functions in marriage theory as isoquants in production theory. It is also possible to expand the economic analogy. For example, by citing the demographic variables (such as average family size, etc.) as values to be chosen in an objective function, then the techniques of economic planning theory superimposed on the analytic foundations of marriage theory, give a theory of social/demographic planning.

7.3 Correspondence of Marriage Theory and Demography

We therefore now mention a second correspondence, that between marriage theory and demography. In this area, marriage theory predicts the possible forms and their associated equilibrium statistics, from purely structural criteria. On the other hand, demographic theory is principally concerned with equilibria resulting from balancing age-structured birth and death schedules. Since marriage theory essentially ignores these, one would not necessarily expect that the two theories give the same results for equilibrium average family sizes.

In fact, there are two cases, one of which is consistent, and the other inconsistent with demographic theory. Where "average family size" means "completed average family size surviving to reproduce per mating couple", at equilibrium this is (demographically) clearly two offspring per couple. Where \bar{n}_s is the average family size required for equilibrium in a population strictly following a rule with structural number s , and p_s is the proportion of the population (of females) who actually reproduce, in a zero variance model, then for all s , $\bar{n}_s \cdot p_s = 2$ was a condition of the model.

However, if the "correct" proportion p_s marry, but have the average family size \bar{n}_r required to maintain the population size to account for sex ratio fluctuations, irrespective of the rule, then in general $\bar{n}_r \cdot p_s \neq 2$. In fact, for $s > 6$, $\bar{n}_r \cdot p_s < 2$, while for $s < 6$, $\bar{n}_r \cdot p_s > 2$ and only at $s = 6$ is the "demographic" condition of "random mating" also the marriage theoretic equilibrium condition.

However, whenever the basic identity $\bar{n} \cdot p = 2$ holds, then we have some useful possibilities.

When the tables referenced above were computed for predicting equilibrium demographic statistics characteristic of particular kin-based marriage rules, these papers implicitly assumed that each society has a single such monogamous "rule", but it is well known that this does not always hold. Not all societies have "kin-based" rules (such as prohibition of a particular class of "cousin"); some societies may have more than one rule (such as different ideology for each sex); and some may be characterized by "rules" which are not explicitly kin-based, but may depend on the existence of a number of "clans" (or "lineages", etc.) whose ideology is expressed in terms of descent. In the present section we show that the previously computed statistics may also apply to these more general cases, including cases of simultaneous multiple marriage. Previous sections used the following statistics of interest here:

- \bar{n} : "average family size" (e.g., completed family size per reproducing female, surviving to reproductive age);
- p : proportion of females who reproduce per generation, at the given family size (zero variance model); and
- x : sex ratio (proportion of the total population per generation which is male).

Note that in previous sections \bar{n} was interpreted either as \bar{n}_s , the average family size for a kin-based system characterized by a rule with structural number s , or as \bar{n}_r , the average family size for a population of given size and sex ratio mating "at random". Here, when we use \bar{n} we always mean \bar{n}_s , for kin-based rules, but will introduce another interpretation for nonkin-based rules. Also note that there may be societies (such as the famous "Australian" systems) in which nonkin-based ideologies are stated as "clans", etc., but in fact are isomorphic to the cases of minimal kin-based rules. In such cases, the kin-based interpretation is adequate for demographic predictions from the previously published tables.

Table 7.1, reproduced from earlier sections, shows values of \bar{n} and p for structural numbers $s = 2$ to $s = 15$. (Then structural number of a rule is the least number of marriages per generation needed to draw a self-reproducing genealogy representing the rule.) For nonkin-based ideologies, we may read \bar{n} and p directly from the Stirling Number, table 6.1

Consider now the following identity: for a particular system at equilibrium,

$$(1) \quad \bar{n} \cdot p = 2$$

Table 7.1 Structural numbers and associated average population statistics.

s	p	\bar{n}
2	1.00	2.00
3	1.00	2.00
4	.92	2.18
5	.82	2.43
6	.82	2.44
7	.74	2.70
8	.73	2.75
9	.68	2.92
10	.68	2.93

p = proportion of females ever married reproducing at average family size

\bar{n} = equilibrium average family size

That is, the average family size times the number reproducing at this family size equals two, the number of persons in the presumably monogamous pair producing this family. Notice that this number 2 corresponds to the value used by demographers for replacement per couple, but that \bar{n} (in any of its forms used here) is independent of the birth and death schedules of the population, therefore will not correspond in general to these fertility and mortality dependent values. Roughly speaking, the present \bar{n} values are the upward adjustments from the "theoretically pure" value 2 required by the existence of a parameter p dependent on the rule itself.

Since we have defined \bar{n} and p as the family sizes and proportions respectively of females, we can be more specific and use \bar{n}_f and p_f . We can now define corresponding values for males as \bar{n}_m and p_m . Notice that although previous papers derived everything in terms of females, that the complete arguments may be recomputed, with numerically identical results, simply by appropriate insertions of a variable representing "males" instead of "females" in the equations of chapter 6.

It is still true that both

$$(2) \quad \begin{aligned} \bar{n}_f \cdot p_f &= 2 \\ \bar{n}_m \cdot p_m &= 2 \end{aligned}$$

Readers who would rather see $\bar{n}_f \cdot p_f = 1$, etc., may divide \bar{n}_f or \bar{n}_m by 2. While other adjustments, implying different assumptions on distributions of offspring to

males and females, may be considered with different effects, this one is adequate for present purposes.

If we do not concern ourselves with adjustments for empirical numbers of males and females (or assume that $x = 1/2$) then if $p_f > p_m$, we define the polygamy rate to be

$$(3) \quad P_y = \frac{p_f}{p_m}$$

while if $p_m > p_f$, we define the polygyny rate to be

$$(4) \quad P_g = \frac{p_m}{p_f}$$

Notice that although it appears as if $P_g = 1/P_y$, in general it makes no sense to discuss both "rates" simultaneously for the same system, and in any case each of several wives of a single husband (or vice versa) has one husband, not $1/P_y$ (or $1/P_g$) husbands (wives). Note that if $p_m = p_f$ then from (2)

$$(5) \quad \bar{n}_m \cdot p_m = 2 = p_f \cdot \bar{n}_f$$

we find $\bar{n}_f = \bar{n}_m$ so that in strictly monogamous (or bilaterally serially monogamous) systems, we expect the average completed family size to be the same for males and females.

However, for non-monogamous systems, we can show that these two different statistics are still compatible. From our equilibrium demographic identity (2), we find that

$$(6) \quad \bar{n}_f = \bar{n}_m \frac{p_m}{p_f}$$

while

$$(7) \quad \bar{n}_m = \bar{n}_f \frac{p_f}{p_m}$$

Now for polygamous systems, the expected number of "wives" per male is P_y , while the number of offspring per wife is \bar{n}_f , so the expected number of offspring per male is

$$(8) \quad E(m) = P_y \cdot \bar{n}_f$$

and from (3), we easily see that

$$(9) \quad E(m) = \bar{n}_m$$

The analogous result for polygynous systems,

$$(10) \quad E(f) = \bar{n}_f$$

also holds.

Assuming all the wives and offspring of a given polygamous or monogamous male form a single household, the size, H , of this household is

$$(11) \quad H = P_y + E(m)$$

which is the expected number of wives plus the expected number of children; or $H = P_y(1 + \bar{n}_f)$ which follows by simple substitutions using our demographic equilibrium identities (2).

Notice that considering monogamy as "polygamy" in which $P_y = 1$, then $H = 1 + \bar{n}_f$. We could also get this same result more directly, since in monogamy, each man has one wife and $\bar{n}_f = \bar{n}_m$ is the expected number of offspring.

Note that in all these cases, the total "household size" does not include the male nor any elderly persons, etc., who may be living with the group. However, because of the assumptions underlying the computations of statistics in tables 7.1 and 6.1, all \bar{n}_f and \bar{n}_m values used here do includ "adopted" children living with the household if they are also entitled to the "normal rights" of an offspring (i.e., who when themselves enter into reproduction, their offspring are considered no different from nonadopted "biological" offspring).

As a further note on these equations, notice that equations (6) and (7) show that, providing the ratios x , P_m and P_f are constant, any growth rate reflected in one of the two values \bar{n}_m or \bar{n}_f will also be reflected in the same percentage rate in the other.

Using tables 6.1 and 7.1 and equations (1) to (11), we may predict equilibrium demographic statistics \bar{n} and p for a huge number of possible systems, whether or not monogamous, and whether or not the males and females of the system express "marriage rules" in the same ideology. The reader has found equations extending table 7.1 to larger values in earlier sections and formulas and tables predicting gross fertility and marriage rates from \bar{n} and p in chapter 6. These later results of course need not be the same for males or for females in a given system, if the structural numbers of their respective rules differ. Also note that since these referenced tables are adjusted for generation intervals in years that they are more useful for detailed population growth (or decline) predictions than are the presently used unadjusted values of tables 6.1 and 7.1.

7.4 Structural Theory of Population Genetics

In theoretical genetics, since there is not yet a well developed structural theory, we can still identify a few areas where structural type problems contribute

to genetic thought. I point out some areas, though not necessarily in the conventional mode of presentation.

First, in the study of genetic algebras, we can find an a priori theory of which "experimental forms" are possible, that is, what are the feasible parameters for breeding systems. Second, by knowing the possible parameters of breeding experiments in terms of number of lines required, number of crosses allowed, and number of generations needed for given results, then a more complete apriori theory of the comparative costs of an experiment in various forms is possible, though not yet done on this foundation.

By way of example, we summarize from the presentation of Bertrand (1966) some work originally done by Etherington in the early 1940's. Let capital letters represent the distribution of (say) genotype frequencies in a population. A product "AB" etc. of two letters will represent the mating of a population with frequencies A with a population having frequencies B. Notice that while the product operation is commutative, since always

$$AB = BA$$

in general it is not associative, since for arbitrary A, B and C,

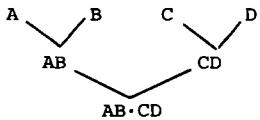
$$(AB)C \neq A(BC).$$

That is, the order in which populations are mated can usually affect the genotype frequencies of the final population.

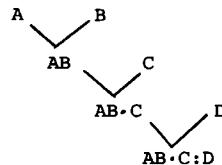
This being so, we must be concerned in genetic algebra with more detail of a populations' breeding history. In particular, Bertrand defines these parameters which describe a history in an abstract sense:

- δ : the degree of a product, or the number of factors (populations) composing the non-associative produce, or "shape"
- α : the altitude of a shape, being the number of generations in the history of the particular shape
- $\delta - 1$: the number of nodes, or branches joining products in the history
- μ : the mutability of a shape, being the number of non-equilibrating nodes, where an equilibrating node joines two conformal (essentially, isomorphic) shapes.

Two examples on histories of shapes with degree $\delta = 4$ are:



$$\alpha = 2, \delta - 1 = 3$$



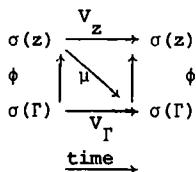
$$\alpha = 3, \delta - 1 = 3$$

It turns out that the following relations among α , δ and μ hold:

- 1) $\alpha + 1 \leq \delta \leq 2^\infty$;
- 2) $\delta \geq \mu + 2$, except where $\delta = 1$;
- 3) δ is the sum of $\mu + 1$ nonidentical powers of 2;
- 4) where n_δ is the number of terms in the expansion δ of a system of base 2, then $\mu \geq n_\delta - 1$;
- 5) $\mu \leq 3 \cdot (2^{\alpha-2}) - 1$.

These results are not too surprising when considered, but their existence is not usually noted in genetics texts, and their potential for knowing possibility of outcomes in genetic experiments not exploited. This is particularly disappointing since δ for example relates to the initial variety potentially available in the given experiment, μ relates to the symmetry with which the experiment is conducted, and α to the length of time needed to complete the result. Although these concepts are clearly important, the fact that they are inter-related deserves more attention than it has received.

Similarly, there are other areas in the organization of genetic theory which can benefit by such "algebraic" treatment. Consider the diagram below, proposed originally by Lyubich (1971):



where (loosely stated) $\sigma(z)$ is the frequency distribution of zygotes at a point in time, $\sigma(T)$ the distribution of gametes, μ the "meiosis operator", and ϕ the "fertilization operator". V_z and V_T are the evolutionary operators of these respective distributions; μ is linear, ϕ is quadratic.

This amusing commutative picture is sufficient to derive most of classical population genetic theory. For example, in stable populations, where s_z , s_T are the stable distributions and $\mu_0 = \mu/s_z$, $\phi_0 = \phi/s_T$ then

$$\begin{array}{ccc} & \phi_0 & \\ s_z & \xleftarrow{\quad} & s_T \\ & \mu_0 & \end{array}$$

interprets the usual Hardy Weinberg law: $r^2 = r$ (e.g., idempotency of a stable distribution).

Two authors are responsible (independently) for this idea: S. N. Bernstein (1925) and I. M. H. Etherington (1939, 1949). A paper by Lyubich (1971) dedicates about 40 pages to proving that from the commutativity of this little diagram and the restrictions on its operators, that genetics ought to have the form and parameters it does in fact have and use, while Bertrand (1966) derives similar results from properties of Jordon algebras (e.g., non-associative algebras with real coefficients).

7.5 Conclusions

The discussions above concentrate on identifying correspondence problems in several fields, and in developing examples of correspondences of structural to statistical theories from marriage theory and from population genetics theory. The value of recognizing differences between the structural and statistical type theories is that by knowing what results are accessible by each technique, we can know what may be expected from a particular type of theory.

Various researchers, being humans with differences in their personal insights and institutional histories, may find certain traditions of work more natural to them or more technically accessible at the moment. However, the examples of marriage theory and population genetics show us that some problems may only be accessible, indeed, may only be identified in the first place, when we cross the boundaries from developed structural and statistical theories, and require that the results of each be compatible with the other, as well as being consistent descriptions of the real world we wish to understand.

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