

CHAPTER 7: STRUCTURAL MODELS AND CORRESPONDENCE PROBLEMS

1.0 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 description + statistical treatments + theoretical theories + structural treatments + structural 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.

1.1 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 buttermilk 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 deliberate 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).

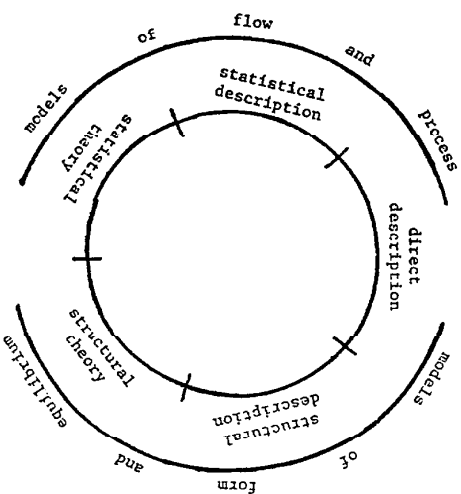
The field which most clearly exhibits the classical form of this development has been physical theory. (See Cropper, 1970, or other standard histories.) From a stage of observation of interesting phenomena in the eighteenth century and earlier, the nineteenth century saw the initial description of statistical 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 Ballouff (1974) 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 meaning 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	III
E	I	III
L	I	IV
S	Different	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 Pólya'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).

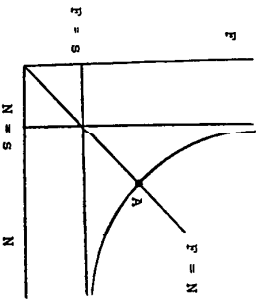
7.2 Correspondence of Marriage Theory to Production Theory

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 examples; 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 Saavy (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 approximately "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 denote 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 line 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 of "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

$$f(s) = \left\{ (F, N) : s = N - N_0, N_0 = N \left(1 - \frac{1}{F}\right) \right\}$$

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 (see 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

$$f\left(\sum w_i s_i\right) = \sum w_i f(s_i), \quad \sum w_i = 1.$$

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

$$C = r_1 N + r_2 F + b.$$

Assume n_x and n_y are determined by the "ecology and economy" of the society, and where v is just a proportionality constant. Then if $n_x = a$, then $F_x = av$. Or,

$$v = F_x / F_y n_x$$

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 $v = .72 + (.01)$ 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 isogants 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 s (demographically) clearly two offspring per couple. Where \bar{n}_g is the average family size required for equilibrium in a population strictly following a rule with structural number s , and p_g is the proportion of the population (of females) who actually reproduce, in a zero variance model, then for all s , $\bar{n}_g \cdot p_g = 2$ was a condition of the model.

However, if the "correct" proportion p_g marry, but have the average family size \bar{n}_x required to maintain the population size to account for sex ratio fluctuations, irrespective of the rule, then in general $\bar{n}_x \cdot p_g \neq 2$. In fact, for $s > 6$, $\bar{n}_x \cdot p_g < 2$, while for $s < 6$, $\bar{n}_x \cdot p_g > 2$ and only at $s = 6$ is the "demographic" condition of "random mating" also the marriage theoretic equilibrium condition.

However, when ever the basic identity $\bar{n}_x \cdot p_g = 2$ 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 "cousins"); 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}_g , the average family size for a kin-based system characterized by a rule with structural number s , or as \bar{n}_x , 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}_g ; 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

$$\bar{n}_f \cdot p_f = 2$$

$$(2) \quad \bar{n}_m \cdot p_m = 2$$

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

$$(6) \quad \bar{n}_f = \frac{p_m}{p_f} \bar{n}_m$$

while

$$(7) \quad \bar{n}_m = \frac{p_f}{p_m} \bar{n}_f$$

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 include "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} 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.

7.1 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 a priori 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,

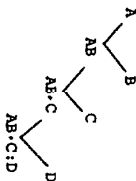
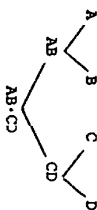
$$(AB)C \neq A(BC).$$

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 population's 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 product, 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 joins two conformal (essentially, isomorphic) shapes.

Two examples on histories of shapes with degree $\delta = 4$ are:



$$\alpha = 2, \delta - 1 = 3$$

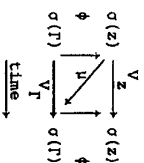
$$\alpha = 3, \delta - 1 = 3$$

It turns out that the following relations among α , δ and μ hold:

- 1) $\alpha + 1 \leq \delta \leq 2^\alpha$;
- 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) $\mu \leq 3 \cdot (2^{n_\delta - 2}) - 1$.

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

$$\begin{matrix} \phi_0 & & \\ s_z \xrightarrow{\quad} & \mu_0 & \xrightarrow{\quad} s_T \end{matrix}$$

interprets the usual Hardy Weinberg law: $x^2 = x$ (e.g., idempotency of a stable distribution).

Two authors are responsible (independently) for this idea: S. N. Bernstein (1925) and I. M. H. Esherington (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 Jordan 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.