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MATHEMATICAL DEMOGRAPHY OF SOCIAL SYSTEMS, II

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The population characteristics of a cultural system may be derived from an algebraic description of its rules of composition. After summarizing prior results, extension of the technique to lineage organized systems is presented, followed with three examples. The appendix gives tables which underlie the methods of this paper and of earlier work.

1. INTRODUCTION

The purpose of the mathematical theory of cultural structures is to create a deductive theory which embodies assumptions of cultural descriptive science, and from these predicts the observed properties of human cultures. Such a theory should be capable of predicting the range of possible observations, the conditions under which each could be observed, and the properties each must have under particular conditions.

The statistical assumptions upon which previous work [1],[4],[6],[7], was based (individual uniqueness, role identity) require the use of a statistical mechanics based on properties of the Stirling Number of the Second Kind, rather than on the physical-theoretical mechanics based on the Stirling Number of the First Kind(1),(2).

The existing mathematical theory is most extensively developed for "kin-based marriage rules". However, I deliberately imply that the same general method of construction may apply to other forms of social interaction "rules" for which less extensive empirical or theoretical foundation may now exist. I therefore express the following summary of results to date in general terms with the caution that the statements have only been demonstrated in depth for marriage rules.

1.1. The rules of a given social system induce the existence of particular social forms which constrain the possible relationships observed in that system.(3)

Result 1.1 has been argued primarily from group theoretical representations, and related techniques. The thrust of this work has been that a particular restriction on social bonds require (or, prohibit) representation of social relationships by a particular (mathematical) group. I refer to the order of this unique group as the structural number of the rule [17],[6].

1.2. The rules of a particular system imply the possible sets of population statistics which may be associated with the system.(4)

There is a very simple mathematical form which connects result 1.1 and result 1.2. If s denotes the structural number of a system, n_s the average family size (number of offspring per reproducing female surviving to reproductive age, per generation) and p_s the proportion of the adult population ascribable as "married" by according to the rules, then at zero growth a rule with structural number s determines unique values n_s and p_s such that

$$n_s p_s = 2 \quad (1)$$

This result is a very simple form of result 1.3, below.

1.3. Structural theories give statistical results for "pure systems" in their equilibrium state [7].

This can be seen from the following tautological equation:

$$e^{r(t)\,T} = \frac{1}{2}\, n(t)\; p(t) \quad (2)$$

where r(t) may be considered a kind of growth rate of a particular system in year t, n(t) the cultural-theoretical average family size in year t, p(t) the cultural-theoretical proportion of reproducing adults in year t, and T the generation interval in years. If r(t) = 0 then (for finite, non-zero T) $e^{r(t)T} = 1$, and

$$n(t)\; p(t) = 2 \quad (3)$$

If, further, this system is acting according to a rule with structural number s (and no other rules) then $n(t) = n_s$, $p(t) = p_s$.

1.4. Social change (i.e., change in the particular mix of rules) is itself a cause of population growth [7].

If, several rules are used simultaneously at time t in proportions described by the probability row vector of degree of use coefficients, v(t), then equation (2) must be rewritten as

$$e^{r(t)T} = v(t)\; Pv(t)' \quad (4)$$

where

$$P = \frac{1}{2}\begin{bmatrix} n_1p_1 & \cdots & n_1p_k \\ \vdots & & \vdots \\ n_kp_1 & \cdots & n_kp_k \end{bmatrix} \qquad (5)$$

and where the subscripts index rules with different structural numbers and elements $v_i(t)$ in $v(t)$ show the degree of use of each. Since $v(t)$ is a probability vector, the product $v(t)Pv(t)' > 2$ whenever any two of the $v(t)$ are not equal to 1 (recall that $v_i(t) \geq 0$ and $\sum_i v_i(t) = 1$).

This also implies:

1.4'. Single systems using mixed rules will be at positive growth rates if their "population policies" account only for the equilibrium effects of the rules used singly; or equivalently,

1.4". Populations which attempt zero growth with respect to each of the rules they use, to the degree to which they use that rule, will attain positive growth rates whenever the rules in use do not all have the same structural number.

1.5. When a social system shifts between rules, the greater the difference in complexity of the rules, the greater the amount of growth which results [7].

Consider rules with structural numbers i and j. Let $x = |p_i - p_j|$ and $p = \min(p_i, p_j)$. The total of all interaction terms between i and j in the matrix P becomes

$$\text{total interaction} = 2 + \frac{x^2}{p^2 + px} \qquad (6)$$

For given p, this value increases for increased x; that is the larger the absolute difference between respective p_s values, the greater the resulting growth from change.

1.6. Population planning may not ignore the social rules of behavior [7].

The conclusion is obvious from the above points.

1.7. The particular time sequence of the degree of use of rules determines the historical demography of a system [7].

The particular sequence of $v(t)$ vectors describing the changing mix of rules used over time of a given system completely determine the amount of growth computed by equation (4). This results from 1.2 which in turn implies that the matrix P of equation (5) is a constant matrix, whose entries do not change with time; they depend only on the particular rules in use in the relevant portion of history of the system.

1.7'. The total passage time which the system spends using more than one rule is directly related to the total resulting growth.

1.7". The number and particular set of rules available therefore bounds the minimum possible growth attained and also bounds the possible sets of histories which may be observed.

1.8. The longer is the generation interval, for given social rules, the lower will be the yearly growth rate.

This is obvious from equation (2), since T is (from considerations given so far) independent of other variables, while the total value $e^{r(t)T}$ depends on $v(t)$ and P (i.e., on social considerations). A deeper reason and more complete interpretation is given in [7].

1.9. The "age-structure" of the population is not an explicit part of this formulation. Therefore, these results are not "demographic" as that term is normally understood.

2. THEORY OF LINEAGE ORGANIZATIONS

Recent papers such as [11],[14] place the presumption of distinctness of fields of study in considerable question. In particular, from the discussions of Hirshleifer(5), an integrated theory would be based on family or other kin-based associations; it would have a necessary connection to population viability; and have an equilibrium process analysis using reproductive ratio. The present work support the views of [14] in that the essential descriptions of kinship and marriage form may be considered as legal prescriptions (or, proscriptions), and may be considered a theory of risk. (See appendix to [7]).

In the mathematical theory of social anthropology, a major problem is representing the structures of kinship and marriage which occur in human cultural systems, and to find the statistics associated with a population behaving according to a given "marriage rule". The underlying structure assumed is a set, denoted by G which we call a generation and upon which we call a generation and upon which there may be defined a number of relations such as: if a and b are offspring of the same parents, write $aBb = 1$, and otherwise put $aBb = 0$. By such techniques a variety of different relations may be defined on G; call the collection of these the configuration of G. This configuration is empirically defined, but even so some of the relations (operations) found in it may have useful properties. For example, the relation B just mentioned is a partition of G. Also, it is often useful to keep in mind that for any given operation, we may define a corresponding matrix operator in an appropriate Boolean algebra.

Now define a lineage organization of G as a mapping

$$\Lambda : G \rightarrow G/\Lambda$$

such that for all $a,b \in G$, if $a \equiv b \bmod B$ than $\Lambda(a) = \Lambda(b)$. From [15] we get immediately the major result which is that given a particular partition B with $|G/B| = \beta$ and $|G/\Lambda| = \lambda$ that the number of ways of forming distinct lineage organizations is given by the Stirling Number of the Second Kind for placement of β objects into λ cells such that none is empty.(6)

Define an i-th order lineage organization as the i-th mapping in a sequence of mappings of the form

$$\Lambda_0 : G \to G/B$$
$$\Lambda_1 : G/B \to G/\Lambda_1$$
$$\vdots$$
$$\Lambda_r : G/\Lambda_{r-1} \to G/\Lambda_r .$$

Thus B represents the zeroth order mapping, and all others are lineage organizations each of which preserves the lower ordered mappings. Call such a system an r-layered lineage organization; thus the ith-ordered lineage organization is also the i-th layer of the r-layered system. The result on use of Stirling Numbers of the Second Kind obviously also extends to each layer of an r-layered lineage organization.

For some purposes it will be useful to have a more specialized vocabulary covering patrilineal and matrilineal systems, and I provide the following rather simple extensions of the above definitions. Use m to denote the set of all males in G and f to denote the set of all females in G. Let $B_m = B \cap m$ and let $B_f = B \cap f$. A patrilineal lineage organization is a mapping $\Pi : G \to G/\Pi$ such that if $a \simeq b \bmod B_m$ then $\Pi(a) = \Pi(b)$. A matrilineal lineage organization is a mapping $\Gamma : G \to G/\Gamma$ such that if $a \simeq b \bmod B_f$ then $\Gamma(a) = \Gamma(b)$. A strong patrilineal lineage organization is a mapping $\Pi_\sigma : G \to G/\Pi_\sigma$ such that if either $a \in m$ or $b \in m$ or both and $a \cong b \bmod B$ then $\Pi_\sigma(a) = \Pi_\sigma(b)$. Make a similar definition for strong matrilineal lineage organization Γ_σ.

The concepts of r-layered lineage organization easily extend to these four types of lineage organizations. Note that any given lineage organization cannot be both strong matrilineal and strong partilineal unless these two are identical. Thus for given G found empirically, the types of lineage organizations possible are: lineage organization; matrilineal lineage organization; patrilineal lineage organization; simultaneous matrilineal and patrilineal lineage organizations which may differ; strong matrilineal; strong patrilineal. The case of identity of strong matri- and patrilineal lineage organizations is the same as having neither prefix, hence is the same as a lineage organization.

Let M denote the relation of "marriage" found in the configuration of G. Let $\{\Lambda\}_i$ $i = 1,\ldots,r$ be an r-layered lineage organiżation of a generation G. A lineage organized marriage rule is a set of statements from the following list:

(1) for some Λ_i, $a \cong b \bmod M$ if and only if $a \cong b \bmod M/\Lambda_i$;
(2) for some Λ_i, $a \cong b \bmod M$ if and only if $a \ncong b \bmod M/\Lambda_i$;
(3) non-contradictory combinations of statements of form (1) or form (2).

Statements of form (1) require lineage exogamy at the i-th layer while statements of form (2) require lineage endogamy at the i-th layer. Note that if a system is endogamous at the i-th layer then it is endogamous at all higher numbered layers, while if it is exogamous at the i-th layer, then it is exogamous at all lower numbered layers. Also note that one of the possible lineage organizations of a given set G with given partition B is that which preserves descent groups. For example, the first layer may be that which groups all B-equivalent subsets of G into sets of individuals who are "first cousins" of each other, through a given ancestral line. Therefore, some kin-based marriage rules are special cases of lineage organizations.(7)

I introduce a non-mathematical vocabulary for classifying the amount of structure a system may have. This vocabulary will label a system as Sequence I, Sequence II, etc. according to how many layers of grouping are required to describe adequately an empirical system.

In a typical case we wish to predict the following numbers shown in a diagrammatic Sequence III.

total size of offspring group		total number of households		total number of lineages		total number of phratries
	→		→		→	

To attain a concrete prediction up we must therefore first determine the total size of the pre-reproductive age population. Call this N_1, enter the table and predict up to a particular value we can call L_1, which is a prediction of the number of "households". Set $L_1 = N_2$ and predict up from N_2 to L_2 which is a prediction of the number of "lineages" given N_2 "households". Next, predict up to number of "phratries", L_3, by allowing $L_2 = N_3$ and predicting up again from N_3; and so forth for higher levels when present:

offspring "household" "lineages" "phratries"

$$N_1 \to L_1 \quad = \quad N_2 \to L_2 \quad = \quad N_3 \to L_3 \ldots\ldots$$

Note that the predicted average family size is simply N_1/L_1. The total group size of a monogamous system with stable mated pairs would be $N_1 + 2L_1$ plus an allowance for unmated individuals in the adult generation computed as $(1 - 2L_1/N_1)N_1 = N_1 - 2L_1$. Adding these two estimates gives the simple result that in a monogamous system the total population size of adults plus offspring is approximately $2N_1$ at equilibrium. This estimate makes no allowance for either surviving post reproductive individuals, which would raise the total, or for pre and post reproductive mortality, which would lower the total size. This result also implies that two time variables completely determine the reasonably possible age structures for any population at equilibrium: the age at puberty, and the average period in years of reproductive capacity of [illegible] theoretical statistics for [illegible] We may also [illegible] is the theoretical average higher level [illegible] per lineage; etc. Thus we number of ho[illegible] study of prediction down. may now learn [illegible] effect is not quite a simple which due to [illegible] reversal of prediction up. For each L value at which we enter the table, there results a greatest N value N^g and a least N value N^ℓ, and also all N values between N^ℓ and N^g are associated with the particular L value uniquely. An examination of the sample table of the appendix will show this.

Therefore assume say a Sequence III system (a 4-layered system) and construct the fan down:

offspring households lineages phratries

$$N_1^g \leftarrow L_1^g = N_2^g \leftarrow L_2^g = N_3^g \leftarrow L_3$$
$$N_1^\ell \leftarrow L_1^\ell = N_2^\ell \leftarrow L_2^\ell = N_3^\ell \leftarrow L_3$$

In this case we need two pieces of information to make a prediction: the system ideology which provides the sequence number, and the number of unites in the highest level of organization. For this number, L_3, predict an upper and lower bound for the lower ranks of N and L values by continunig to predict towards the largest N value in each lower level from the previous L^g, and towards the smallest value at each level from the previous L^ℓ.

In computing the average population statistics, rather than a unique value we get instead a range of possible values. For example:

upper bound for average family size = $N_1^g/L_1^g = n_g$

lower bound for average family size = $N_1^\ell/L_1^\ell = n_\ell$

Also we get an estimate of the proportion of socially ascribed, or "married", reproductive females (and/or males depending on the ideology expressed) with the respective

upper bound value = $2L_1^\ell/N_1^\ell = p_\ell$

lower bound value = $2L_1^g/N_1^g = p_g$.

Notice that because of the behavior of N and L in the table, the roles of upper and lower bound reverse for the n's and p's, but it is still true that both $n_\ell p_\ell = 2$ and $n_g p_g$ as required.

3. EMPIRICAL EXAMPLES

The thesis of the present section is that it is possible to predict "the demography" (i.e., the particular set of jointly occurring population average measures) of a particular cultural system from an ethnographic description of its marriage rules. The demography thus computed is independent of the generation interval in years of the system; it may constrain the possible age-structured birth and death schedules compatable with the ethnography but does not predict them.

There are three examples: of a Sequence I system, the Birhor as described in [19]; and two Sequence II systems, the Hopi as described by [13]; and the Kashmiri Pandit described in [12]. The Birhor statistics illustrate the prediction of average value statistics rather than total group size statistics for band size. From [19] page 79, the average number of persons per band is 26.8; households per band 6.0; persons per household 4.49; ratio of single to married undifferentiated by age, as ratio of single/total population .502; ratio of married males/total males .469; ratio of married females/total females .530 of resident 22 bands.

Assume a Sequence I system maintaining 6 households. Placing $L_1 = 6$, N_1 ranges from 13 to 15 and average family size as from 2.16 to 2.50, being closer to 2.50 for a relatively more endogamous system. If a household consists of a male and a female plus offspring, the theoretical estimate of household size is from 4.16 to 4.50. An estimate of total group size is obtained by doubling the estimate of offspring group size, giving $2N_1$ from 26 to 30 per local group. Only the p value is not closely predicted, but there is also no evidence on whether the population is growing.

The Sequence II example is the Moenkopi Hopi people as described by [13]. The lowest level kin-based unit is a woman plus her offspring; then the lineage as a grouping of related women; then the clan as a grouping of related lineages. Households do not always correspond with these kin units in a simple way, since there has been an apparent increase over time in the apparent number of nuclear households (those with a male plus female plus offspring). The author of [13] estimates 60% as an upper limit for this type residence as a percentage of all households. Demographic data range from a population of 182 in 1910, to 592 in 1962, with steady growth. The number of clans resident were reported as: 1906 - 10 clans; 1937 - 14 clans; 1948 - 15 clans; 1962 - 14 clans.

Clan number thus appears to be stable at 14 while the population is growing as roughly 2% per year. By prediction down from the clan number, the predicted values are given in table 1.

TABLE 1. Computations and predictions of various demographic values for Moenkopi Pueblo.

Observed Clan Number	Intermediate $N_2 = L_1$ values		Predictions: N	n	p	2N
10	min	25	83	3.32	.60	166
	max	28	99	3.54	.57	198
14	min	39	146	3.74	.53	292
	max	42	164	3.90	.51	329
15	min	43	165	3.83	.51	330
	max	46	183	3.98	.51	366

For the 1906 value of 10 clans the predicted range of values of 2N is 166 to 198, while the observed size is 182. Migrations post 1906 then raise the clan number to 14 by 1937, at which time the reported population size is 409, while the theoretical (2N) equilibrium size range is 292 to 398. By 1962, the reported size is 592, approximately twice the size needed for a stable exogamous community with clan number 14.

The study does not claim to accurately report the completed family size (n). The theoretical ($\bar{p}$) value is .60 for 10 clans, and .51 to .53 for 14 clans in a Sequence II System. No observed proportion of reproductive females is given, but the distribution of household types shows that nuclear families, plus bilateral extended families, plus matrilineal households represent 78.3% of all households, each of which may be taken to correspond to a reproducing female. This may be taken as a crude index of the proportion of reproducing females. It is larger than the theoretical estimated range of .51 to .60. Thus if the true proportion of reproductive females is p = .78 instead of p = .5 to .6 as required by the theory, then the system could only remain in equilibrium if the empirical family size dropped to around 2.2 or so, from the theoretical values of closer to 3.5. Otherwise we expect some growth, as is reported.

Consistency of theory with observed data is reinforced by the fact that Moenkopi Pueblo was both politically, and residentially divided into two approximately equal sized sub units, each at approximately the lower range of the total theoretical population size needed to maintain a Sequence II system of 14 highest level units.

The second example of a Sequence II system is a Kashmiri Pandit population [12]. The sampled area is a pairing of two closely linked but not (yet) independently functioning communities, Utrassu and Umanagri, composed of exogamous patrilineally organized households, divided so that Utrassu has 11 different patrilines and Umanagri has 14. Using prediction down in each case, I compute:

number of patrilines → upper limit number of households → upper limit town population of offspring

number of patrilines → lower limit number of households → lower limit town population of offspring

These computations are summarized in Table 2 using values read out of the theoretical tables. Estimates are also obtained for upper and lower bounds of the actual population size, which both cases fall in the predicted range!

TABLE 2. Computation of Theoretical Values of n, p and of Population Size Using Technique of "Prediction Down"

	UTRASSU		UMANAGRI	
	Lower	Upper	Lower	Upper
Empirical number of lineages	11		14	
Theoretical numbers of Households	29	31	39	42
Theoretical Offspring Population Size = N	101	113	146	164
Theoretical n	3.45	3.65	3.74	3.90
Theoretical p	.57	.55	.53	.51
Theoretical 2N	202	226	292	328
Empirical Village Size	214		308	

4. CONCLUSION

This paper and its earlier companion [7] provide the foundations for an effective theory of cultural organization. This theory is based on a logical or algebraic description of the cultural rules, such as found in part 2 here or in [5] or in [6] chapter 4. From this description, characteristic numbers which describe the size of an idealized structure are derived.

These characteristic or structural numbers (which may also be group orders for certain rules) then predict specific zero growth combinations of population measures. In [7] and in part 1 of the present paper, these zero growth numbers, when taken in certain operator formulations, lead to statements of non-zero growth associated with changes in the composition of a culture's rules.

The concrete numerical predictions of this new theory were tested in the present paper against three specific ethnographic "point in time" studies, and in [7] on a 1000 year history. In all examples, it was found that the theory interprets the literary description of the cultural system, and from this successfully predicts the population measures actually found in the empirical system.

This body of theory therefore forms part of the mathematical foundation of an empirical science: social anthropology.

FOOTNOTES

(1) Many modern texts on thermodynamics tend to treat their subject as a problem in analysis of continuous functions. Earlier works,

such as Guggenheim [10] were more cognizant of the combinatorial properties of the partition function that underlie statistical thermodynamics. Work such as Weinberg [18] page 99, which define a "Generalized thermodynamic law" in a form which potential recognizes probability foundations <u>other than</u> those needed for gas dynamics, are very rare. The more familiar view of "General Systems", such as by Bertalanffy [8] talk as if the "second law of thermodynamics" can be literally applied generally. I use the concept "<u>a</u> statistical mechanics" to imply that systems using different fundamental statistics will have different behavioral properties, leading to prediction in the sense of Weinberg.

(2) The first development of this statistic was in [6]. It was applied in [1] and in [7] and in the present paper. A more thorough development of the statistic and its meaning is under preparation as a new book by the present author.

(3) See [16], [17], [3], [6], [7].

(4) See [6], [7].

(5) See [11] pages 17 to 39 and page 50.

(6) The set of all possible lineage organizations of G form a simple, compactly generated, atomic, relatively complimented, semimodular lattice. See [9] page 96.

(7) The enumerative method of definition is crucial to development of results. See for example the development of kin-based theory in [6] chapter 4.

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TABLES OF SAMPLE STATISTICS

Properties of Stirling Number of the Second Kind at density for values of Sequences. r(t)T is the associated maximum growth or decline rate.

L_3 / -	L_2 / N_3	L_1 / N_2	- / N_1	n	p	Maximum r(t)T
SEQUENCE III						
2 →	2 →	2 →	2	2.0	1.0	
	3 →	6 →	15	2.50	.800	.223
3 →	5 →	10 →	25	2.500	.800	
	6 →	15 →	46	3.067	.652	.204
4 →	7 →	16 →	47	2.938	.681	
	9 →	24 →	82	3.417	.585	.151
5 →	10 →	25 →	83	3.320	.602	
	12 →	35 →	131	3.743	.534	.119
6 →	13 →	36 →	132	3.667	.546	
	15 →	46 →	183	3.978	.503	
SEQUENCE II						
	2 →	2 →	2	2.0	1.0	
		3 →	6	2.0	1.0	.0
	3 →	5 →	10	2.0	1.0	
		6 →	15	2.5	.800	.223
	4 →	7 →	16	2.286	.875	
		9 →	24	2.667	.750	.154
	5 →	10 →	25	2.500	.800	
		12 →	35	2.917	.686	.154
	6 →	13 →	36	2.769	.722	
		15 →	46	3.067	.652	.102
SEQUENCE I						
		2 →	2	2.0	1.0	
			4	2.0	1.0	.0
		3 →	5	1.667	1.200	
			6	2.000	1.000	.182
		4 →	7	1.750	1.143	
			9	2.250	.889	.251
		5 →	10	2.0	1.0	
			12	2.4	.833	.182
		6 →	13	2.167	.923	
			15	2.50	.800	.143