Differential Systematics

William H. Womble[1]

Department of Anthropology and Sociology, University of California, Los Angeles

CLASSIFICATION, ARBITRARY AND NATURAL

CLASSIFICATION is certainly as old as language, for categories are basic to vocabulary. In a sense it originated with reacting organisms. Even the ameba, responding differentially to a varied environment, effectively orders its own world. Surely so ancient and universal an activity, vital alike to primitive hunter and modern urbanite, should have been developed to a precise technique. Yet it is not uncommon for different students of the same phenomena to arrive at altogether incompatible taxonomies, which at times seem be evaluated more by the reputations of their authors than on their approximation to reality. Observational science still is founded on an imperfect art. Empiricism appeals to a new authoritarianism.

Taxonomy occasionally perplexes most scientists, but it persistently harasses the biologist. Consequently, he has acquired a thorough familiarity with the problem, if not a satisfactory solution of it. In presenting a new approach to systematics, we shall draw largely on life sciences for illustrative materials, although the principles to be developed are applicable to other fields as well.

Biologic classification pivots on the species concept—or concepts, since there are several. According to Mayr (*1*): "Species are groups of actually or potentially interbreeding natural populations, which are reproductively isolated from other such groups." Although relevant only to contemporary, sexually reproducing forms, this definition, based on breeding patterns as found in nature, possesses clear theoretical advantages. The practice of distinguishing species by degree of morphological difference is purely arbitrary, and the test of hybrid sterility lumps together many diverse types that normally intermingle without interbreeding, or produce hybrids inadequate to natural competition. In Mayr's biologic interpretation, species are genetically interacting universes. In their response to differing selective environments, or their divergence through genetic drift or mutation, they develop distinguishing traits, any of which may serve as diagnostics. Yet, essentially, it is not the differences, but the mechanisms facilitating them, that are definitive. Through their reproduction habits and potentials, contemporary sexual species are natural, self-defining classes.

Larger taxonomic units are highly arbitrary. To be sure, if we examine a phylogenic tree, we note that any two species are related through a common stem or limb or crotch. But for what time span does this connection indicate the same genus? The same family? The same order? Splitters and lumpers engage in a continuous war of nerves over questions that are purely matters of definition. The phylogenic tree in itself constitutes the clearest and most exact supraspecific systematic.

Successional classification appears even more confused and confusing. Through geologic time, the same lineage changes in species, in genus, in family. If new forms customarily originate through single macromutations, then the traditional systematic is correct in principle. But if, as seems more probable, evolution usually proceeds through the slow grinding of the mills of selection on countless micromutations, then we must conclude that phylogenetic taxonomy reveals more concerning the accidents of paleontological discovery than of the realities of genetic change.

The data never seem adequate for a clear sequential systematic, but with respect to the subspecific taxonomy of contemporary species, especially the racial classification of man, much information has been collected, and more is available; yet the situation is equally chaotic. Neighboring populations of the same species ordinarily are distinguishable only by small differentials in a great many hereditary traits. Numerous authorities, employing different diagnostics, or diverse racial ranges in the same diagnostics, have produced competing taxonomies with little in common but their arbitrariness.

The embarrassment of both successional and subspecific classification is due, in part at least, to deficiencies inherent in a logic of classes. Discrete entities may be practically self-defining, but continuous variables, in space or in time, resist internal partition. The student of evolution in particular is hampered by the limitations of categorical reason, for dynamic processes must be sought, not in the differentiated, but in the differentiating.

VARIETY DIFFERENTIATION

Nature is the first systematist and the only unassailable authority. If other taxonomists have the effrontery to rework her notes, it is only because the detailed complexities in which she records them are beyond ready human comprehension. Yet anyone attempting a simpler approximation to reality may well study the methods by which the fussy old lady works out her varieties.

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Consider a species occupying a continuous range. Assume that, at some given time, a few populations exhibit a trait expression or gene frequency greater or less than the species mean (Fig. 1*a*). If hybridization were the only genetic process in operation, the exchange of genes between adjacent groups would, in time, erode these features of the trait topography and equalize population averages (Figs. 1*b, c, d*). Paradoxical though it seems, sexual reproduction, responsible for most individual differences through chance gene combinations, also promotes a spatial homogeneity analogous to physical entropy.

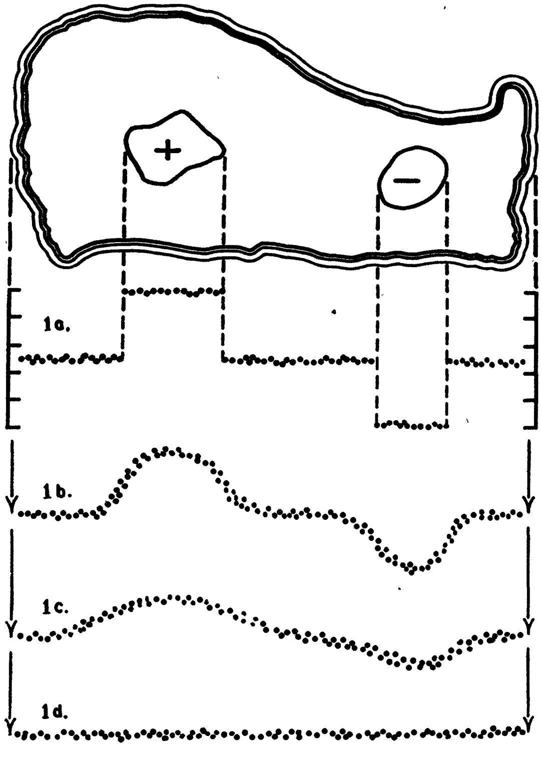

FIG. 1. In sexual species with continuous distributions, gene flow alone would eventually level all geographic distinctions.

Inasmuch as species do continue to show geographic variation, some force or forces counter to hybridization must be effective, both for establishing regional differences, and for maintaining them in dynamic equilibrium with gene flow. Differential mutation rates do not provide an adequate answer, for the rate differences themselves require explanation. Although successful new mutations establish flow fronts through the range of a species, such distinctions, unless fixed by other processes, are, in the long-term view, necessarily transitory.

Genetic drift may account for local differences while isolating mechanisms are effective, but these variations should randomize over any considerable area, and in any case they are swamped out with the reestablishment of gene flow. Only where large isolates are long maintained, or small groups migrate and subsequently populate broad territories, does it seem probable that drift is operative in major variety formation.

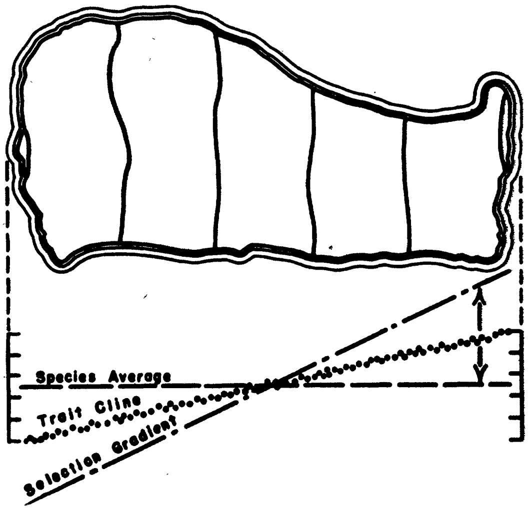

FIG. 2. Differential selection establishes regional variations and maintains them against erosion by gene flow.

Selection remains—not in the sense of a generalized force driving living organisms to a hypothesized future perfection, but as a specific mechanism for local adaptation to a differentiated environment. Consider a variable trait, quantifiable by metric, index, or gene frequency. If selection alone were operative, in time every local population would approximate that average trait expression most successful at its locus. A schematic plane, covering the species range and passing through the local values of maximum adaptation, has been defined as the *selection gradient.*

With a gradient of uniform slope (Fig. 2) the trait expression is caught in a tension between selection, drawing it toward local adaptive values, and gene flow, tending to reduce the species to spatial uniformity. The resultant trait cline may be a function of several variables, such as slope of the selection gradient, effectiveness of selection, numbers of gene

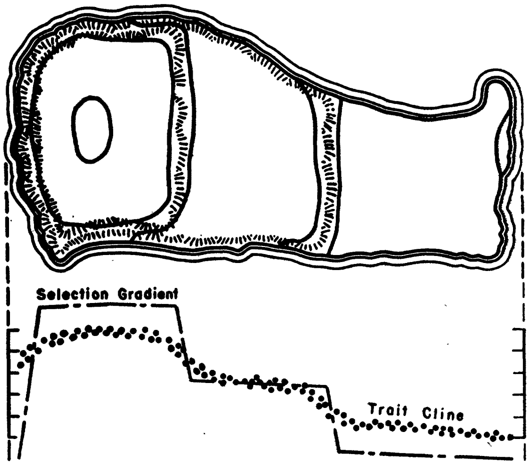

FIG. 3. Sharp environmental distinctions produce stepped selection gradients, which generate stepped trait clines.

loci and alleles involved and their relative dominance, inherent variability of the trait, mutation rates, and—of particular significance for this discussion—the relation between the geographic extent of the species range and the rate of gene flow across it. Rapid gene exchange and small ranges result in geographic homogeneity. Slow flow over broad and diverse areas favors regional differentiation.

Fairly smooth clines, varying with some aspect of the environment, are reported. Tongue lengths of European honey bees have been expressed as a linear function of latitude, whereas the relative size of their wax glands seems to vary with temperature (*2*). Within half a century of their introduction, the size of English sparrows in the interior United States differentiated with respect to climatic zones, the larger birds being favorably selected in areas of rigorous winters (*3*).

Numerous traits in many species, however, show stepped clines. One explanation is a similar and even more pronounced stepping in the selection gradient (Fig. 3). Thus, abrupt changes in ground color over large territories, in conjunction with flying predators, are highly effective in differentiating the coat color of rodents; but smaller areas of distinctive soils may not establish local types because of population infiltrations from surrounding regions (*4, 5*).

Stepped clines are also possible with constant selection gradients (Fig. 4*a*). If, in consequence of relatively sparse population or hindrances to communication, zones of reduced gene flow intersect the species range, the spatial genetic structuring of groups between the obstructions approaches that for distinct species. Since effective geographic extension is reduced relative to the rate of gene exchange, the trait clines are locally flattened. Inasmuch as the diminished genetic interaction between provinces exerts little influence for the maintenance of species unity, trait averages of the partial isolates approach local values of the selection gradient. Consequently, the clines must steepen through the barrier zones, which constitute the weakest threads in the genetic fabric. Should geographic isolation become complete, clines would show discontinuous steps (Fig. 4*b*). Regional trait expressions, completely freed from species ties, would find equilibrium at maximum adaptive values.

When barriers are removed, gene flow may re-establish species continuity, first producing stepped trait clines, and later even gradients. Or an insular group, through loss of variability, overspecialization, or failure to keep pace with evolution in other areas, may be eliminated in the ensuing intertype competition. If, however, during geographic isolation, biologic isolating mechanisms (such as hybrid sterility, changes in mating season or courtship patterns, etc.) develop between the separated groups, then the removal of geographic barriers does not result in effective hybridization. Each type may be so well adapted to its home environment that the others cannot displace it, although in the territory of each there are often local areas best suited to its competitors. Consequently, the ranges of such groups may overlap, yet the types remain distinct, thus demonstrating complete speciation (Fig. 4*c*).

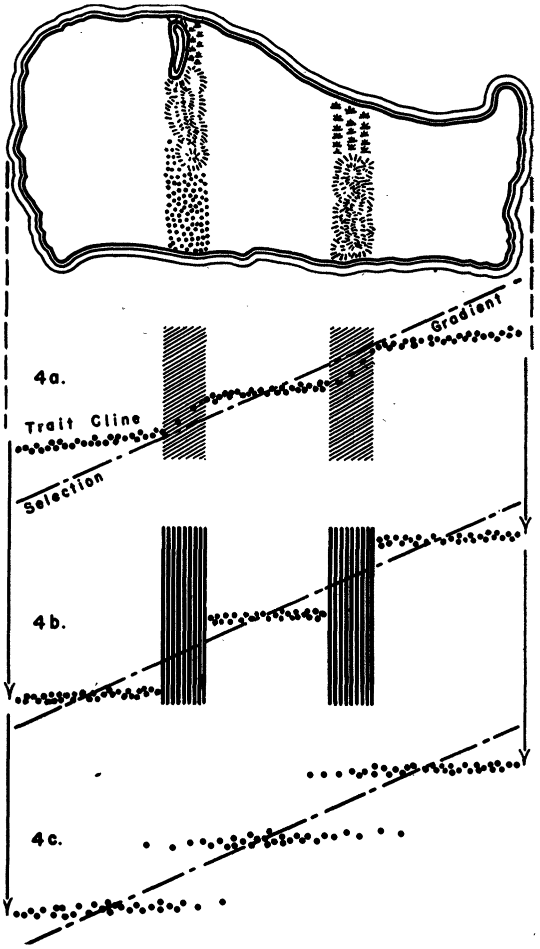

FIG. 4. The role of differential gene flow in variety and species formation: 4*a*, Zones of relatively reduced gene flow may produce stepped trait distributions, even with selection gradients of constant slope. 4*b*, Complete isolation results in discontinuous stepped clines with easily recognizable varieties. 4*c*, If biologic isolating mechanisms develop before the removal of physical barriers, former varieties may interpenetrate each other's ranges without hybridizing, demonstrating speciation.

If factors of lesser evolutionary importance are ignored, the formation and maintenance of geographic varieties in sexually reproducing animal forms are resultants of the interplay of gene flow and local selection. A regional adaptive differential (past or present) would seem to be the first requisite to a consistent regional trait differential. Thus selection, so effective in eliminating deviants from local natural populations, also is the prime mover of geographic variation. This is the obverse of our previous paradox concerning the role of sexual reproduction in promoting spatial homogeneity while producing individual differences. Uniform gene flow partially obscures the effects of pronounced features of the selection gradients on the trait clines; but if gene exchange is itself

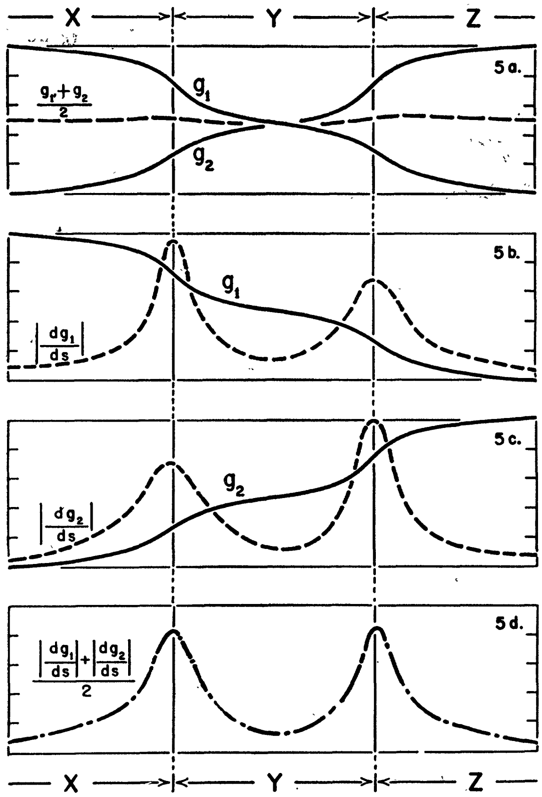

FIG. 5. Profiles demonstrating the synthesis of multiple variable traits into a composite derivative: *5a,* Traits g_1 and g_2 show clines of opposite slope. Averaging them only confuses the picture of the evident varieties *X, Y* and *Z*. *5b,* The absolute value of the derivative of g_1 is determined from the slope of its cline. *5c,* The derivative for g_2 is similarly developed. *5d,* The two derivatives (and those for any other traits as well) are averaged as a composite derivative. Peak values divide the varieties.

regionally differentiated, this pattern is stamped on clines generated by other processes.

COMPOSITION OF MULTIPLE VARIABLES

As with specific, so with subspecific differentiation the more basic evolutionary reality lies, not in trait values in themselves, but in the genetic structure of which they are symptomatic. The species, constituting a universe of gene interaction, is seldom, if ever, homogeneous through time and space. Normally, various sized clumpings of nearly like populations are separated by stress zones or transition periods of differing extent and intensity. It must be the task of any adequate "natural" systematic to assay this structure, not only with respect to the spatial and temporal loci of similarities and differences, but also as to their relative degrees.

Huxley (*6*) has pointed out that species with a single reported varying characteristic, distributed in a continuous, uniform gradient, may be described as occupying a cline between the terminal populations. If the cline is stepped, one may designate geographic varieties, their boundaries falling in zones of steepest slope, although a more accurate definition is provided by the cline profile or, still better, a map with isophenes or isogenes drawn through loci of equal trait expression.

Three or four differing characteristics might be grasped in this manner without confusion, but well-studied species show too many variations to readily keep them all in mind at once. Our problem is to synthesize any number of such continuous variables into a single composite that shall closely approximate the natural differentiation of the total heredity. To facilitate comparisons, we recalculate the values of each trait to a scale from zero to one, representing the minimum and maximum population averages within the species for each measurement, index, and gene frequency employed in the analysis. For simplicity, we first consider in profile the clines for only two traits, g_1 and g_2, defining three evident varieties: *X, Y,* and *Z* (Fig. 5*a*). The mean value $\frac{g_1+g_2}{2}$ seems more to conceal than to reveal these distinctions. However, both the generalized effect of the intraspecific differentiation of gene flow on all trait distributions and the indirect action of selection gradients on the total genetic balance of the organism establish a common tendency for clines to steepen in the same zones. Therefore, even with gradients inclined in opposite directions, there is a good probability that the high and low absolute values of their slopes will coincide in geographic locus (Figs. 5*b, c*). Consequently, it is reasonable to average them as a mean derivation:

$$\frac{\left|\frac{dg_1}{ds}\right| + \left|\frac{dg_2}{ds}\right|}{2}.$$

As may be observed (Fig. 5*d*), peaks of this curve effectively bound the geographic varieties.

Of course, any number of trait derivatives may be so combined into a composite. If desired, a weighting factor *w* may be applied to each cline slope before summation, provided it is also represented in the denominator:

$$\frac{\sum\limits_{n} w_i \left|\frac{dg_i}{ds}\right|}{\sum\limits_{n} w_i}.$$

Although this introduces arbitrary judgments as to the relative importance of the traits (which might, for example, be based on estimates of the numbers of gene loci involved in their expressions), the resultant weighted average slope may more closely approximate the genetic reality than if the equally arbitrary assumption of trait equality is implicitly accepted. Because of sampling problems, it is preferable to exclude rare traits and those with little normal variability from the analysis. Otherwise, the more gene frequencies and truly independent biometric measurements and indices included in the development of the composite derivative, the greater is the probability that the latter will closely approximate the change with distance of the total genetic reality.

A profile analysis is adequate for shoreline and river organisms, but most species are found in area distributions. It is advisable, therefore, to develop techniques applicable to geographic space. As previously noted, each variable is related to a scale from zero to one. Values for each trait are separately plotted as isogenes or isophenes. Since the vertical contour interval Δg_i is known, and at any point M the minimum horizontal distance between adjacent contours Δs may be scaled from the map, the former may be divided by the latter to define the maximum slope of a straight line through the point and the two contours. With reasonably close intervals and no abrupt changes in gradient, this sufficiently approximates the maximum slope of the trait topography at M (Fig. 6*a*). Distance is measured in kilometers. A multiplication constant of 10,000 produces more convenient values for mapping widespread species:

$$\left|\frac{dg_i}{ds}\right|_M \doteq \frac{\Delta g_i}{\Delta s} \underset{\text{def}}{=} \frac{10{,}000 \times \text{trait difference}}{\text{distance in kilometers}}.$$

These calculations are not difficult, but they may be dispensed with in practice. The maximum slope at any point on a trait topography can be approximated directly from a reciprocal scale laid along the shortest line between adjacent contours (Fig. 6*b*). Such a scale may be constructed by multiplying the contour interval by 10,000 and dividing the product by the values of the map kilometer scale (Fig. 6*c*).

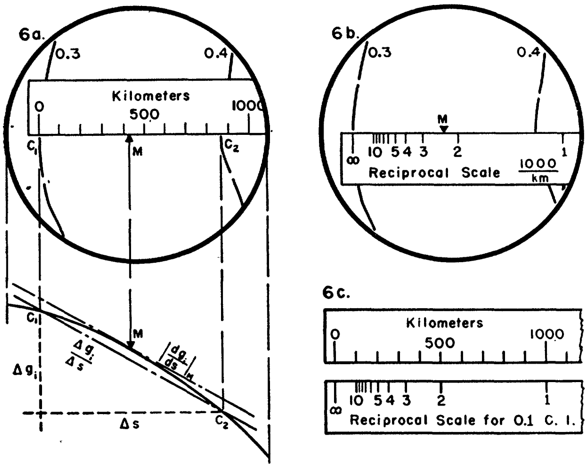

FIG. 6. Approximation of trait derivatives from contoured distributions: 6*a*, The contour interval Δg_i is given, and the space interval Δs may be scaled from the map. $\frac{\Delta g_i}{\Delta s}$ usually approximates $\frac{dg_i}{ds}$ at the midpoint M. Trait values scale from zero to one. Distance is measured in kilometers. 6*b*, The slope of a trait topography may be read directly from a reciprocal scale. 6*c*, Relation of reciprocal scale to map kilometer scale and contour interval.

Now all tools necessary for the composition of multiple variables in area distributions are at hand. From a contour map of any gene frequency or phenotypic expression (Fig. 7*a*) slopes at convenient map coordinates are read from the reciprocal scale. Results are plotted as isoclines of the trait derivative (Fig. 7*b*). For each of any number of other traits (Fig. 7*c*) derivatives are similarly developed (Fig. 7*d*). Isocline values for each trait are now multiplied by its appropriate weighting factor. At each suitable locus, all the weighted trait derivatives are summed and divided by the sum of the weighting factors. Finally, these values are plotted as isoclines of a composite derivative (Fig. 7*e*). This we define as the systemic function *Syf*:

$$Syf \underset{\text{def}}{=} \frac{\sum_n w_i \left|\frac{dg_i}{ds}\right|}{\sum_n w_i}.$$

The systemic function measures the weighted average change with distance of the trait clines. To the degree these are representative of all differentials in the species, the composite approximates the spatial variation of the totality. Ridge lines in the topography of this function indicate zones of relative disjunction, and so mark natural boundaries for the geographic varieties. Although the subspecific groups are not determined by diagnostics but by average rates of change for any number of variables, once defined they may be characterized in terms of trait averages. For uniformity, mean values for populations in the lower one half, by area, of each valley or basin in the systemic topography are accepted as typifying their groups.

Although we have determined the boundaries of subspecific units with reasonable objectivity, we still have not produced a classification. All ridges are not equally well defined. Which mark primary divisions and which secondary and tertiary? To approach the question from a different direction, in a finely detailed topography there are basins within basins of every magnitude. What area or population constitutes a variety? A subvariety? A local variant? These problems are not rooted in the reality, whose differentiations are manifest from the systemic topography. They spring from the inadequacy of taxonomy for dealing with continuous variables. Not only must a classification classify its phenomena; it must also classify its own classes—and this is often necessarily arbitrary. However, since everything a classification could reveal concerning the species structure is readily apparent from an examination of the mapped composite—and more besides—there seems little point in concerning ourselves with formal classes. We can circumvent the limitations of taxonomy by circumventing taxonomy. There is no objection to labeling conspicuous features of the topography for verbal convenience, but this is extraneous to the ordering of the reality. The systemic function *is* the systematic.

SYSTEMIC SPACE AND SYSTEMIC TIME

For convenience, the *systemic difference* ΔSy between two varieties $v_1 v_2$ is defined as 10,000 times their average weighted trait differences[2]:

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[2] Throughout this discussion, superscripts are designators, not powers.

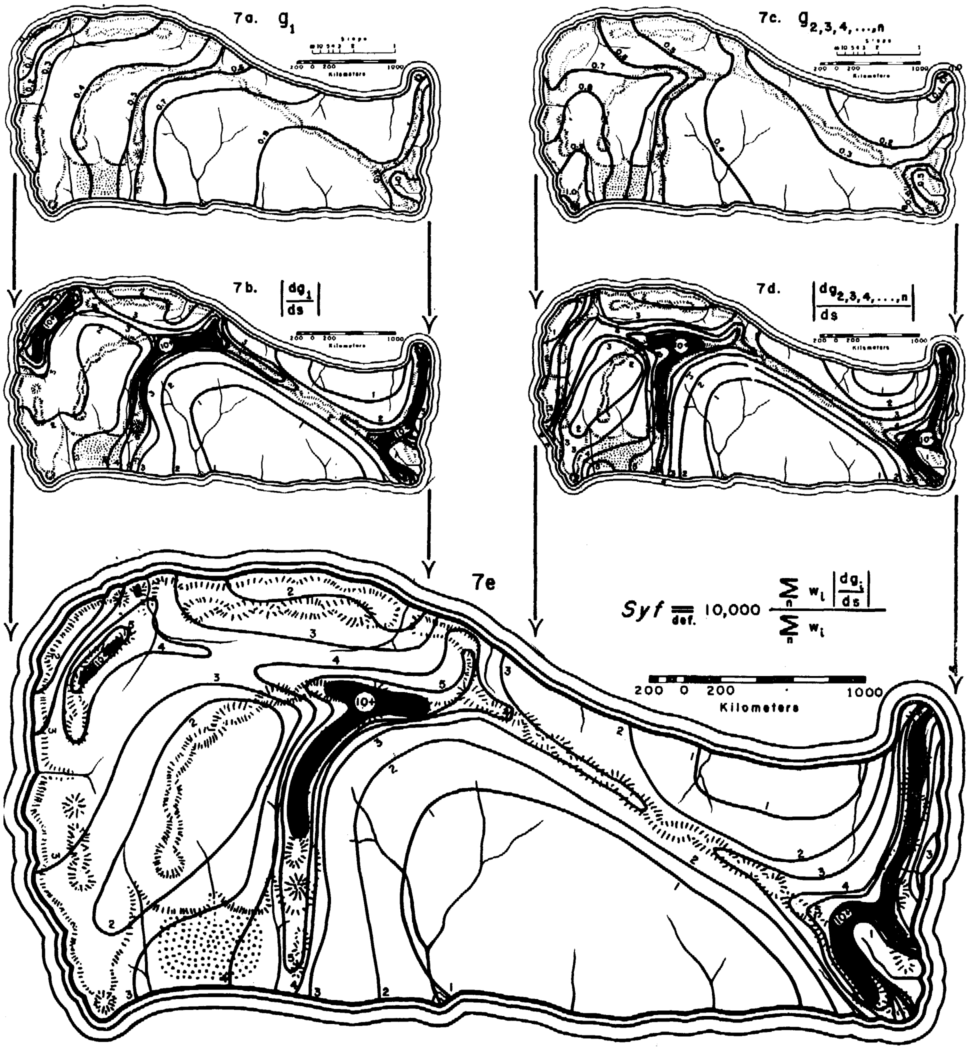

FIG. 7. Development of the systemic function: *7a*, Isogene or isophene contours are mapped for trait g_1. *7b*, The slope of the trait topography for g_1 is measured at convenient map coordinates and isoclines are drawn through points of like gradient. *7c*, Each succeeding trait $g_{2,3,4,\ldots n}$ is contoured. *7d*, Isoclines are developed for each such biometric measurement, index, and gene frequency included in the analysis. *7e*, The topography of a composite derivative is constructed by averaging the trait derivatives. (Weighting factors w_i may be employed where desirable.) This composite is defined as the systemic function *Syf*. Its ridge lines bound the geographic varieties. At any locus this variable evaluates the geographic homogeneity and heterogeneity of the species.

$$\Delta Sy^{v_1v_2} \underset{\text{def}}{=} 10{,}000 \frac{\sum_n w_i \left| g_i^{v_1} - g_i^{v_2} \right|}{\sum_n w_i}.$$

Adjacent groups normally are more similar than those widely separated, unless there has been mass migration. Then an intrusive population may, for some time, show closer kinship with its previous neighbors than with its new ones. To highlight such cases, deserving more detailed attention, the intervarietal systemic slope may be calculated for all pair permutations v_jv_k:

$$\frac{\Delta Sy^{v_jv_k}}{\Delta s} = 10{,}000 \frac{\sum_{i=1}^{n} w_i \left| g_i^{v_j} - g_i^{v_k} \right|}{\Delta s \sum_{i=1}^{n} w_i}.$$

Exceptionally low values indicate the probability of recent contact.

Although intertype differences and gradients are useful in some analyses, they ignore the genetic situation between the type centers. Birdsell (*7*), working with Australian aborigines, has defined genetic distance in terms of the number of isolate boundaries between any two areas. For our purposes, we prefer a more general concept that is equally applicable to continuous distributions, and that relates genetic distance inversely to effective gene flow. (Hybridization that produces offspring at an adaptive disadvantage is, of course, not fully effective. Through this mechanism, selection gradients may impress their features on flow differentiations.) However, since gene exchange can seldom be determined directly and is usually inferred from trait clines, we turn our attention to the development of a systemic space. This, except for situations complicated by mass migrations, should be a reasonably close approximation to the space of genetic interaction—although necessarily there is a time lag between genetic processes and their cumulative effects.

Systemic distance *Syd* we define as the sums of average weighted trait differences taken over successive short geographical distances Δs. Between any two points $s_1 s_2$, and with Δs approaching zero, this may be expressed as an integral of the systemic function:

$$Syd^{s_1 s_2} \underset{\text{def}}{=} \int_{s_1}^{s_2} Syf \cdot ds.$$

Graphically, this is simply the area of a profile through the systemic topography, with the space loci s_1 and s_2 as bounding verticals. Systemic distances along any line may be measured planimetrically from a profile sketch. Results will be in slope-kilometer units, which are directly comparable to the systemic difference units ΔSy previously defined. If, between any two points, every trait cline continuously increases or decreases, the systemic distance will equal the systemic difference. With any trend reversals, the distance will be the larger. Over comparative distances, $\frac{\Delta Sy}{Syd}$ provides an intimation of genetic drift, although it also is sensitive to oscillations in the selection gradients, as well as to statistical techniques and mapping practices.

And now we re-examine the topography of the systemic function (Fig. 7*e*). Not only do the ridge lines bound natural subspecific groups; they also reveal much of the genetic interaction between them. Their elevations measure the sharpness of the distinctions between provinces, whereas their profile areas evaluate the systemic distance (and approximate the genetic distance) between the types. Saddles in the ridges indicate probable routes of intergroup gene flow. Isocline values of the basins are inversely related to the cohesiveness of the varieties. In fact, at any geographic locus, the value of the systemic function *Syf* is the measure of local geographic differentiation of the species. Its reciprocal $\frac{1}{Syf}$ is an index of geographic homogeneity.

Just as systemic space may be related to physical space by summing average trait differences over short distances, so (when adequate data are available) systemic time may be related to physical time by adding average changes in the heredity over short periods. Any number of variable character expressions or gene frequencies may be plotted in time profile and their slopes determined and averaged as a composite derivative, which we define as the temporal systemic function *Syft*. The measure of systemic time *Syt* is an integral of this variable:

$$Syt^{t_1 t_2} \underset{\text{def}}{=} \int_{t_1}^{t_2} Syft \cdot dt.$$

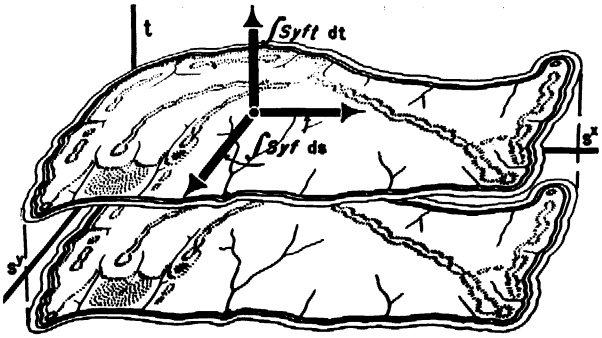

FIG. 8. By conceptualizing the systemic function as a plane of variable metric, the vertical dimension may be employed for the representation of systemic time.

Peak values indicate times of rapid evolutionary change and bound periods of longer enduring phases. (Scale values and time intervals for recording evolutionary change are still tentative. Haldane [*8*] suggests a *darwin* unit equal to an increase or decrease of size by a factor of *e* per million years—approximately 1/1000 per 1,000 years.)

To facilitate visualization, the spatial derivative has previously been presented as a three-dimensional topography, but it is equally valid to regard it as a non-Euclidian plane, related to a physical plane by the variable metric of "space density" provided by local values of the spatial systemic function. This makes available a third physical dimension, convenient for the representation of systemic time (Fig. 8). Additional analytic dimensions may be developed mathematically for problems involving nonassortative mating.

APPLICATIONS

Differential systematics, though originally developed for ordering well-studied, sexually reproducing species (especially man), is also applicable to other fields. Asexuals, obligatory parthenogenetic forms, and selfing hermaphrodites, lacking the species unification mechanism of gene exchange, would seem free to diversify in all directions. That such organisms still are found in only a limited number of fairly distinct types indicates either rigorous selection to well-defined ecological niches, or limited developmental possibilities, or both. The systemic functions of such forms may be developed by the same techniques employed for those of sexual species, but they require interpretation in terms of the differing genetics.

In one sense, every subspecific systematic is also a systematic of the geography and ecology, for in defining forms that *do* exist in any locality, it defines forms that *can* exist there. However, other indicators of environmental differentiation are more obvious. Ecologic balances tend to change abruptly through certain zones and periods, and to remain fairly constant over other areas and ages. Since the techniques of differential systematics may be extended to a synthesis of absolute and relative census figures for species, as well as to the averaging of any number of subspecific systematics, it should be feasible to develop a composite of composites for the evaluation of uniformity or variation in the total biota. Differentiations in purely physical factors (e.g., temperature, elevation, rainfall, etc.) may also be evaluated by this methodology, and employed either in comparison with the biologic function or integrated with it to approximate the total environmental differentiation. However, in the development of such supercomposites, subjective evaluations play an increasingly important role in choosing from among the multiude of variables the relatively few it is practical to include in an analysis.

The subtleties of human culture and the intricate relationships of its elements pose problems for which, as yet, there appears to be no adequate mathematics. However, the quantification of even the grosser variables would permit the development of a systemic function which should better define the spatial and temporal structuring of culture fields and their patterns of interaction than do any of the current culture area and culture sequence classifications.

Dialects show analogies to subspecific phenomena. Like biologic varieties, they are involved in the uneasy dynamic equilibrium of their universes of interaction. In isolation they may "speciate" as distinct languages. This methodology would seem well suited to the ordering of the many variants of dialect geography.

It is not feasible at this time to foresee all possible applications of differential systematics. Essentially, it is a development in logic rather than a specialized technique. Consequently, it may be employed in the ordering of numerous realities exhibiting multiple variations through time and space. However, significant interpretation of differing systemic functions requires that individual attention be given to the processes involved in maintaining similarities and developing differences.

In addition to whatever value this formulation may have within various fields of study, it should open new avenues for the analysis of covariation and probable interaction between phenomena now departmentalized among separate, and often mutually incomprehensible, disciplines.

Differential systematics is a methodology for synthesizing multiple measurements, indices, and frequencies into a composite variable, the *systemic function,* which, for all loci, evaluates the average change with distance of a total reality. It is applicable to the analysis of any type, number, and combination of quantifiable traits, provided only they are related as to means of variation, diffusion, and interaction.

This technique does not completely exclude arbitrary elements from the ordering of complex phenomena, but it reduces them to a minimum and makes explicit much that is often implicit in the "feeling" of an authority. The necessity for assaying numerous continuous variables, which previously has proved a liability for the development of a clear systematic, is transformed into an asset in broadening the statistical base and minimizing effects of errors in data and in judgment.

Systemic space and systemic time are introduced as conceptual tools. Also, they serve to define an analytic manifold for future developments in space-time genetic calculus.

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Technical Papers

Contaminating Bacteria in Plant Tumor Tissues[1]

William J. Robbins and Annette Hervey

Department of Botany, Columbia University, and
The New York Botanical Garden, New York

In the course of investigations on plant tumors bacterial growth was noted when a tumor (P II) believed to be bacteria-free was grown on a peptone agar. None was observed when the tumor tissue was grown on a basal medium of mineral salts, cane sugar, and three vitamins (thiamine, pyridoxine, and nicotinic acid) used for the cultivation of the tumor tissues. In fact, this tumor tissue had been cultivated in this laboratory for several years with no evidence of bacterial contamination.

As a consequence of our observation, all the tumor tissues in our collection have been examined for sterility. None had shown bacterial growth on the medium used for growing the plant tumor tissue, although under cultivation for considerable periods of time. The plant tumors examined are shown in Table 1.

A portion of each of these tissues was mashed in a small amount of sterile distilled water, streaked on slopes of AC agar, and incubated at 36° C. The AC

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