The lasting impression that I obtained from this reading must not be obscured by a list of such points. This is unequivocally a book that will give many readers an insight into what is going on in the study of human morphological evolution; further, this book, introduction though it may be, is necessary reading for the original investigators themselves.

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A Heterogeneous Subject

The Genetics of Human Populations. L. L. CAVALLI-SFORZA and W. F. BODMER. Freeman, San Francisco, 1971. xviii, 966 pp., illus. $27.50. A Series of Books in Biology.

Human population genetics is a heterogeneous subject combining data and techniques from medicine, biochemistry, anthropology, demography, and statistics with those of genetics. Cavalli-Sforza and Bodmer have attempted to cover this wide area. It is a testimony to the breadth and depth of their combined knowledge that they have been able to carry it off.

This is an important book because it is the first comprehensive textbook of human population genetics. As of now it defines the field.

The book starts with a review of basic concepts of genetics—probably not necessary for most readers who are otherwise prepared for the book. It ends with two very useful appendices, one on statistical methods and the other dealing with some of the practicalities of segregation, linkage, and gene frequency analysis. Between these is material on randomly mating populations, inbreeding, assortative mating, mutation, sexual dimorphism, polymorphism, polygenic inheritance, population structure, human evolution, and eugenics. To include so many subjects in detail requires a big book (nearly 1000 pages, 4 pounds).

There is an appropriate balance of mathematical theory and empirical information. There are numerous tables and graphs, showing either actual data or numerical examples illustrating mathematical principles. The authors have clearly taken considerable pains to make the material understandable. One device is to include meticulously worked problems at the ends of most of the chapters. At the end of the book are 81 questions taken from final examinations in the medical genetics class at Stanford. If Stanford medical students master the full contents of this book along with the conventional medical wisdom of a crowded curriculum they are indeed the geniuses they are reputed to be.

The book requires no specialized knowledge not ordinarily possessed by upper level science majors or medical students. Considerable mathematics is used and this is not always easy, but it is not advanced. The more sophisticated parts of population genetics theory—for example, that dealing with stochastic processes—are largely omitted or are summarized verbally. The book is interesting to read, partly because it contains so much information from diverse sources. I found myself reading it avidly, almost like a novel. One can skim the book and is greatly aided in doing this by occasional summarizing sentences that are set off as italicized paragraphs. A proper reading, of course, involves following the algebra, and this requires pencil and paper.

The subjects are highly diverse, as is expected in a field that is still being defined. Some topics represent special interests of the authors: migration matrices, measures of genetic distance, histocompatibility and leukocyte typing, and the demography of African Pygmies. But I hasten to say that this is not overdone. In general there is a proper balance of experimental, demographic, and mathematical content.

The final chapter is entitled "Eugenics, euphenics, and human welfare." Here the authors begin to express their own views on social issues. They are anything but crusading eugenicists. They place great emphasis on the futility of phenotypic selection against rare traits and the slowness of genetic change under moderate selection for quantitative traits even when heritability is high. They also note the naiveté and racism of some of the early eugenicists. There is an extensive discussion of the heritability of intelligence and of racial differences. They argue that it is difficult, if not impossible, at present to determine whether any substantial part of the average IQ difference between Blacks and Whites is genetic. I agree. They go on to discourage further research in this area. Here I tend to disagree, and wonder if they are not overreacting to their Stanford colleague Shockley.

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The Construction of Classificatory Systems

Mathematical Taxonomy. NICHOLAS JARDINE and ROBIN SIBSON. Wiley, New York, 1971. xviii, 286 pp., illus. $15.95.

This volume constitutes the first publication in a secondary source of a considerable body of theoretical work in numerical taxonomy by Jardine and several co-workers. It will be particularly valuable as a reference text, since much of the original material was published in journals not widely read in North America.

The major theme of *Mathematical Taxonomy* is that biological numerical taxonomic methods should be chosen on the basis of their formal properties, rather than empirically. Jardine and Sibson suggest selecting methods by first specifying a set of conditions that any acceptable method must meet, then deducing which possible methods meet all the conditions. Rather than attempting a comprehensive analysis of taxonomic problems within this framework, the authors restrict their attention to two areas of taxonomic methodology: measurement of dissimilarity between pairs of OTU's (operational taxonomic units), and clustering by phenetic similarity.

Two types of measurement of dissimilarity between OTU's (considered as classes of individuals) are considered. "I-distinguishability" comprises measures of the degree of non-overlap between the (usually multivariate) probability distributions describing OTU's. "D-dissimilarity" is characterized as the gain in information realized when a class X of individuals is identified as one of A or B, given initially that X is either A or B. A generalized measure of I-distinguishability is derived, rather elegantly, from purely statistical and information-theoretic considerations. Jardine and Sibson suggest as the most desirable measure of D-dissimilarity a quantity, "K-dissimilarity," whose value between a pair of OTU's is established by summing over characters the univariate I-distinguishability terms obtained from the marginal distributions of the two OTU's. As the authors indirectly point out, this procedure yields an overall dissimilarity measure whose contribution from any one character is the same for any two non-overlapping marginal distributions. In consequence, information on the relative dissimilarities of OTU's contained in an ordinal or interval scale of a variable could be lost by the K-dissimilarity measure. In this respect, the K-dissimilarity statistic is quite different from many of the dissimilarity measures currently in use in numerical taxonomy. It is a deficiency of *Mathematical Taxonomy* that the authors provide no discussion or justification of this property of the K-dissimilarity measure.

The discussion of cluster analysis is quite general in that it makes no assumption regarding what measure of dissimilarity is used in the clustering. A dissimilarity coefficient (DC) is taken to be defined by any symmetric OTU × OTU matrix of non-negative, real dissimilarity values. The notion of "cluster" is formalized as a maximal collection of OTU's between any two of which an arbitrary but specified reflexive symmetric relation holds. In the special case where clusters are required to be non-overlapping, the corresponding relation is an equivalence relation. This is an extremely fruitful approach, for it is then possible to consider a phenogram (termed "dendrogram" or "numerically stratified clustering") as a monotone, continuous mapping of non-negative real numbers (the levels of the phenogram) into the collection of relations on OTU's. The level of the smallest cluster that contains both of two OTU's, A and B, can be regarded as a dissimilarity value between A and B, so that a DC is uniquely determined by a phenogram. Then any procedure which uniquely assigns a phenogram to a dissimilarity matrix can be regarded as a mapping of the set of DC's into a subset of itself.

Within this model cluster methods can be selected by imposing conditions upon the mapping of DC's into DC's. Several conditions are imposed; only two require mention. These are (i) that the result DC have elements less than or equal to the corresponding elements of the data DC and (ii) that the result DC be maximal among the set of DC's satisfying condition i. It is shown that under these restrictions the mapping from data DC's into result DC's is continuous. Jardine and Sibson point out that among hierarchic clustering methods only single linkage analysis fulfills these conditions. They provide examples of discontinuous mappings from data DC's to result DC's for complete linkage analysis and for weighted and unweighted average linkage analysis (the use of the latter two designations is the reverse of the usual meanings of these terms in the numerical taxonomic literature). Methods admitting overlapping clusters are readily considered within the model; several that satisfy conditions i and ii are described, and their properties are analyzed in some detail. The treatment of nonhierarchic clustering methods given in *Mathematical Taxonomy* is the most sophisticated available.

Jardine and Sibson succeed in selecting among clustering methods in a quite rigorous way on the basis of specified formal criteria. The details of their derivations are quite pleasing and would provide worthwhile reading for almost anyone interested in numerical taxonomy. In one respect, however, their choice of cluster analytic methods seems incompletely justified. In selecting cluster methods most appropriate for biological taxonomy the formal criteria used cannot be taken simply as axioms but must rest in turn upon some foundation of biological principle. The justification of a particular cluster method for biological taxonomy is complete only when the connection between biological principles and the formal criteria is established. Most of the formal criteria used by Jardine and Sibson are uncontroversial; their biological justification can reasonably be skipped. Criterion i, above, however, is quite controversial—yet no defense for it is given. Jardine and Sibson have in effect not presented a complete determination of biologically optimal clustering methods, but only a detailed picture of the last several steps in one possible such determination. The value of *Mathematical Taxonomy* might have been considerably enhanced had the authors derived a variety of optimal taxonomic methods corresponding to a set of alternatives to their more debatable axioms.

Mathematical Taxonomy does include, in a separate section, a considerable amount of discussion of the principles of biological classification in a numerical context. This is essentially an appendage to the more technical sections of the book. It is not a defense of the formal criteria used in selecting methods, but is rather a general discourse on the most preferable goals for biological taxonomy. The point of view is quite similar to that espoused by Sokal and Sneath in *Principles of Numerical Taxonomy*. This part of the book could be quite useful as introductory reading to the phenetic taxonomic philosophy.

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Ecological Study of Form

The Adaptive Geometry of Trees. HENRY S. HORN. Princeton University Press, Princeton, N.J., 1971. xii, 144 pp., illus. Cloth, $7.95; paper, $3.95. Monographs in Population Biology, vol. 3.

Botanists seldom give much thought to the shapes of whole plants, perhaps because the growth habit of most higher plants is a repeatedly branched system of units of variable number. It is the form of the units (leaves, flowers, roots) that provides most of the material used by descriptive botanists. The parts, however, are linked to make a more or less integrated whole, a light-trapping, gas-exchanging, water-conducting wick extended between the water and nutrients of the soil and the sunlit, desiccating environment of the air. The form of this whole may be expected to matter very much, and if adaptively critical elements in form can be isolated and measured we may expect to have a tool of great value for comparing species and understanding the working of plant communities. One of the major elements in any functional analysis of the form of plants must lie in the manner in which the canopy is displayed. This, however, is the only part of tree geometry with which this book is concerned—it is almost wholly an analysis of the effects of leaf arrangement on the trapping of light. Horn concludes that monolayers are more efficient in shade and multiple-spaced layers are more efficient in bright light. He develops this view theoretically and from field examples and then extends it to account for changes in plant succession in a text that is vividly and exuberantly written.

Much of this type of canopy analysis has been done before and in a much more sophisticated manner; reading this book is therefore rather like discovering a tribe lost to civilization that has quite independently discovered a primitive form of the internal combustion engine. Does one praise the originality or sympathize with the ignorance?