

CHAPTER **10**

Present Problems and Some Future Prospects

10.1. THE ACCOMPLISHMENTS OF NUMERICAL TAXONOMY TO DATE

It is not easy to evaluate the accomplishments of numerical taxonomy to date without a detailed knowledge of the organisms studied, and the range of these is too wide for us to present a competent critique of all the studies. The results in microbiology have been reviewed by Sneath (1962), and fields other than biological systematics are discussed in Section 10.6. The findings presented below are arranged in systematic order (Section 10.1.1) and by the type of problem to which they furnish an answer (Section 10.1.2).

10.1.1. Published applications of numerical taxonomy to different groups of organisms

So far there have been relatively few studies which employ numerical taxonomic methods of the kind we feel are necessary. In listing those of which we are aware at the time of writing, it is impressive to note the number of people who have independently undertaken such studies in the last few years and to see the wide range of organisms for which numerical methods have been successfully used.

In zoology, numerical taxonomy has been applied to the study of bees (Michener and Sokal, 1957; Sokal and Michener, 1958; Sokal, 1958; Rohlf and Sokal, 1961; and Rohlf and Sokal, 1962). These studies on 97 species of the *Hoplitis* complex (four genera of the family Megachilidae) have illustrated a number of points; the affinities and dendrograms were in good agreement with the previous orthodox taxonomy of the group, and in addition they gave interesting new information on the finer structure of the taxonomic hierarchy and on the systematic position of a number of aberrant species. Rohlf (1962) studied 48 species of the mosquito genus *Aedes*, developing a classification resembling those established by recent studies of the group. Ehrlich (1961c) studied butterflies (*Euphydras* species) and examined the correspondence between affinities based on characters from different parts of the body and also the relation between phenetic status and geographic location. A brief report has appeared on numerical taxonomy applied to man (Cain and Harrison, 1960a). Sokal (unpublished) has reanalyzed the data by Haltenorth (1937) on skulls of 8 species of cats. These data await suitable publication. Little (1963) has recently completed a numerical taxonomic study of the boring sponge genus *Cliona*, in which 103 species were clustered on the basis of 36 characters. The classification resulting from this work seemed to agree well with modern ideas on this group.

In botany numerical taxonomy has been applied to rice (*Oryza* species) by Morishima and Oka (1960), who found reasonable agreement with orthodox taxonomy and with genetic data, and to manioc plants (Rogers, in IBM, 1959; and Rogers and Tanimoto, 1960). Soria and Heiser (1961) studied species of *Solanum* and found rather close agreement with the earlier taxonomy and also some agreement with the relations as judged by the ease of hybridization between the species. Hamann (1961), in a numerical taxonomic study of the thirteen families of the "Farinosae" of Engler together with four other monocotyledonous families, found the resulting similarity coefficients agreeing well with newer opinions on relationships of these families (see Section 10.1.2.2).

These methods have also been applied in paleontology to fossil fish (Sneath, 1961) but only as an illustrative example.

In bacteria the methods are used more widely. Some studies have included a wide range of bacteria from different orders (e.g., Sneath and Cowan, 1958), and the methods seemed as successful as when applied to strains within one species. Several atypical forms, such as the plague bacillus, were correctly classified as judged by later and more

detailed evidence on their position. Brisbane and Rovira (1961) have made a similar study of soil bacteria, but they used fewer characters and obtained less clear-cut results.

A great simplification of the confused taxonomy of the actinomycetes, particularly species of *Streptomyces*, together with some interesting correlations with the antibiotics they produce, is resulting from the work of Silvestri and his colleagues (Gilardi et al., 1960; Hill et al., 1961; Silvestri et al., 1962). Similar assistance has been given in the taxonomy of cocci (Hill, 1959; Pohja, 1960; Blondeau, 1961; Colobert and Blondeau, 1962), *Pasteurella* (Talbot and Sneath, 1960) and the pseudomonads (Liston, 1960; Liston and Colwell, 1960; Shewan, Hobbs, and Hodgkiss, 1960; Thornley, 1960; Colwell and Liston, 1961a, b, c, d; Rhodes, 1961; Lysenko, 1961). In some of these instances these workers were also able to distinguish subgroups within rather homogeneous collections of strains. In other instances the existing arrangements of species into genera were largely confirmed. A detailed study of one genus, *Chromobacterium*, was made by Sneath (1957b), and very good correspondence was found with the previous grouping of strains into "species" and with serological data (Sneath and Buckland, 1959; Sneath, 1960). Results on another genus, *Bacillus* (Sneath, 1962), were also fairly consistent with other data. Cheeseman and Berridge (1959) employed a restricted set of chemical attributes in a study of *Lactobacillus*, in which agreement with the current taxonomy was not very close; however, the current taxonomy of this genus is not very satisfactory (see Sneath, 1962).

The application of these methods to viruses (Andrewes and Sneath, 1958; Sneath, 1962) has shown that groups are formed which are very similar, with one exception, to those recognized and named informally by virologists, although the data are not yet sufficient to build a meaningful hierarchy for the groups. The application of numerical taxonomy to entities on the uncertain borderland between living organisms, genes, and chemical compounds is a severe test, and the results are therefore encouraging.

10.1.2. Assistance of numerical methods in some taxonomic problems

10.1.2.1. Concordance between numerical taxonomic studies and established taxonomies

The study of Michener and Sokal (1957) on bees showed quite good agreement with the established taxonomy. Morishima and Oka (1960)

and Soria and Heiser (1961) likewise found good agreement with the established taxonomies of *Oryza* and *Solanum*, respectively. For example, the five species of the "Sativa" group of *Oryza* were clustered together, and the aberrant *O. subulata* was well separated from them. However, *O. granulata* did not occur in a separate section (as in the earlier taxonomy) but was part of the "Sativa" complex.

In bacteria the earlier taxonomies are widely recognized as often unsatisfactory, so that concordance with them is not an important issue. Nevertheless, most studies have shown reasonable agreement (for example, Hill, 1959; Liston, 1960; Sneath, 1962).

10.1.2.2. *The naturalness of taxa*

The testing of the naturalness of higher ranks is closely related to the question of agreement with previous taxonomies, but in addition it may involve transfer of major subgroups from one group to another. Michener and Sokal (1957), for example, found that most of the earlier subgenera were "natural," but the genera *Hoplitis* and *Proteriades* underwent some change by the transfer of two subgenera from the former to the latter.

Hamann (1961) found that the thirteen monocotyledonous families of the "Farinosae" of Engler were an unnatural assemblage. He regrouped them into four orders on the basis of a numerical taxonomic study. The Thurniaceae were placed in the order Juncales; the Pontederiaceae, Cyanastraceae, and Philydraceae were placed in the order Liliales; the Bromeliaceae were separated as an order Bromeliales; and the remaining families formed the Commelinales (divided into four suborders). It is not clear why Hamann did not take the logical steps of including the Cyperaceae in the Juncales, the Gramineae with the Restionineae, and adding the Bromeliaceae to the Liliales, as indicated by the affinity values he obtained. Possibly the number of features was not adequate for a thorough revision of the group, and the affinities do show some unusual properties when subjected to cluster analysis (Section 7.3.2.6).

In bacteria a number of studies have confirmed that many of the recognized genera are natural, such as *Pseudomonas*, *Aeromonas*, *Xanthomonas* (Liston, 1960; Thornley, 1960; Colwell and Liston, 1961c; Rhodes, 1961), while other genera, such as *Vibrio*, are very heterogeneous, as had been suspected (Colwell and Liston, 1961b). Among the higher groups certain families and orders were found to form natural taxa, such as, the Actinomycetales (Sneath and Cowan, 1958).

A pervasive problem in bacteriology is the initial grouping of individual strains into taxa of low rank, conventionally regarded as species.

There is often doubt whether strains bearing one specific name comprise one reasonably homogeneous taxon. Most of the numerical taxonomic studies in bacteriology deal in part with this problem. Sneath (1957b) made a thorough comparison of many strains of two species of *Chromobacterium* and found that they fell into the expected two groups, which were sharply separated from one another, as clearly shown by models (Lysenko and Sneath, 1959). Studies by Hill (1959), Pohja (1960), Talbot and Sneath (1960), and Blondeau (1961) showed that many of the earlier groupings were natural, though some were not. Silvestri et al. (1962), however, found one or two instances of variant strains which were not placed very close to their known parents, and one or two instances of bacteria which seemed to be seriously misplaced. These were only a small minority of the strains studied. Viruses fell into the groups generally recognized by virologists, with one notable exception, the pox viruses (Sneath, 1962), but the confidence bands in this study were quite broad because of the few characters available. Zарapkin (1939) noted good agreement between phenetic relationship and the recognized different geographic races of the coccinellid, *Epilachna*. Ehrlich (1961c), however, found that geographic variants of certain butterflies were not always concordant with established species groupings. Little (1963) was able to recover three species of the sponge genus *Cliona* when clustering 47 individual specimens.

Numerical taxonomy has been used to look for clusters within diffuse assemblages of very similar strains of bacteria and to get some idea of how distinct these clusters were. In addition to the papers cited above, the following studies were directed toward this: indistinct clusters were found in a species of *Streptococcus* by Defayolle and Colobert (1962); Rhodes (1961) was unable to find any distinct clusters in a collection of strains of *Pseudomonas*, which had earlier been found to be very homogeneous; and Brisbane and Rovira (1961) found somewhat indistinct divisions in a large collection of soil bacteria of several genera, perhaps because they employed rather few characters. Since there is considerable uncertainty about the extent to which bacteria form sharp groups and how far they merge together into an indistinct "spectrum" of intermediate forms (Cowan, 1955), these studies are of some importance in this field.

Bojalil and Cerbón (1961), Cerbón and Bojalil (1961), and Bojalil, Cerbón, and Trujillo (1962) discovered in the genus *Mycobacterium* some new taxa which had previously not been recognized. Pohja (1960), Blondeau (1961), and Colobert and Blondeau (1962) also found new

and unnamed groups of cocci by numerical taxonomic analysis. Colwell and Liston (1961a, c) reported new subgroups within the genus *Xanthomonas*. As a consequence of their study on bees, Michener and Sokal (1957) established a new subgenus, *Isosmia*.

Numerical taxonomy has helped various workers to decide the "proper" taxonomic position of certain curious and puzzling organisms. In bees, Michener and Sokal (1957) were able to place satisfactorily several "difficult" species. Sneath and Cowan (1958) were able to classify satisfactorily *Jensenia*, *Corynebacterium pyogenes*, and the plague bacillus, which had puzzled taxonomists. Colwell and Liston (1961c, d) obtained interesting information on the aberrant plant pathogens, *Pseudomonas solanacearum* and *Xanthomonas stewarti*. Gilardi et al. (1960) were able to place satisfactorily several curious strains of actinomycetes.

Michener and Sokal (1957) and Morishima and Oka (1960) noted that the dendrograms obtained by numerical taxonomy gave increased discrimination between the forms they studied. This has the same effect as introducing rank categories intermediate between those usually employed and named. It seems to us that the phenon nomenclature is well suited for labeling such categories. In contrast, several bacteriological studies have led to a considerable simplification of taxonomies which had previously been confused, both at low ranks (for example, Blondeau, 1961) and medium ranks (for example, Hill, 1959; Thornley, 1960; Colwell and Liston, 1961a, c; Silvestri et al., 1962).

10.1.2.3. *Concordance of numerical taxonomies with other properties of the organism*

This problem has been mainly studied in bacteria. The host range of bacteriophages is closely associated with genetic similarity and ease of hybridization. Numerical taxonomic work to date agrees fairly well with bacteriophage studies (Sneath, 1963). The recent work on bacterial cell walls gives much the same generic groupings as numerical methods (see Cummins and Harris, 1956, 1958; Sneath and Cowan, 1958), which in some instances are not the same as the traditional taxa.

An important practical use of numerical taxonomy would be to allow one to predict the finding of new antibiotics in new streptomycetes. This might be possible if the clusters of streptomycetes were correlated with the class of antibiotic they produced. Little has yet been published in this connection, but the work of Silvestri et al. (1962) seems promising. Some correspondence was noted by Talbot and Sneath (1960) between the phenetics and the pathogenicity of the hemorrhagic septicemia bacil-

lus (*Pasteurella septica*). They noted that all the strains from cats and from internal lesions in humans had high affinities with one another (unlike many of the strains from dogs), which suggested that most human internal infections involving the organism probably originate in cats.

10.1.2.4. *The stability of numerical taxonomies*

It is clearly too early to say much about the stability of taxonomies obtained by numerical methods. Comparisons of analyses on the same groups of microorganisms by different workers or using different sets of characters indicate that the taxonomies will probably be quite stable (compare the classifications of Liston, 1960, and Colwell and Liston, 1961b, with those of Shewan et al., 1960, Thornley, 1960, and Rhodes, 1961; also compare Hill, 1959, with Pohja, 1960; and Sneath, 1957b, with Sneath and Cowan, 1958).

One of the attractive properties of taxonomies based on large numbers of characters is their robustness under different statistical treatments. By this we mean that a given body of data, when analyzed by different similarity coefficients or by different cluster analyses, or both, usually yields remarkably similar dendrograms and hierarchies. This is undergoing intensive testing at the moment, but a few published findings may be cited. Sokal and Michener (1958) obtained very similar dendrograms from several different methods of cluster analysis. There is close agreement between association coefficients using negative matches and those which do not, as well as between cluster analyses by the weighted variable-group methods of Sokal and Michener (1958), the method of Rogers and Tanimoto (1960), and that of Sneath (1957b) (see Gilardi et al., 1960; Hill et al., 1961; and Silvestri et al., 1962). Sneath (1961) found very similar relative affinities, using the MCD of Cain and Harrison (1958) and correlation coefficients. Comparisons of a number of different statistics and methods are given by Sokal and Michener (1958), Sokal and Rohlf (1962), and Rohlf and Sokal (1962). Agreement between taxonomies based on these statistics is quite good.

10.2. CRITICISMS OF NUMERICAL TAXONOMY

In presenting numerical taxonomy to the scientific public at meetings as well as in print we have met with repeated criticism based on a variety of grounds. Much of this has been constructive criticism which has been gratefully received and has led to modifications and, we hope, to improvements of our views. Other criticism is often based on a mis-

understanding of our position. Many of the controversial issues have already been presented at appropriate places throughout the book. We have collected below various other criticisms not adequately discussed in earlier chapters. They are divided into those objecting to our philosophy or procedures on the basis of fundamental biological principles, those criticisms of numerical taxonomy based on considerations of convenience and practicality, and those comments deploring the advent of quantification and automation in taxonomy.

10.2.1. **Objections on fundamental biological principles**

One frequently voiced objection has been well stated by Hennig (1950) in a discussion actually antedating the recent development of numerical taxonomy. He argues that phenomena in the various disciplines subsumed under the general heading of systematics (taxonomy, ecology, zoogeography, behavior, and so on) can be unified only by the principle of descent with modification, as expressed by the phylogeny of the group. The validity of this viewpoint is self-evident. Hence, Hennig reasons that any taxonomy must be based on this unifying principle, and therefore phylogeny must be considered the primary principle of classification. We would agree with all but the last conclusion. Evolution is indeed an all-explanatory principle. It cannot, however, be used in classificatory procedures, since we mostly do not know (and in many cases cannot know) its true course.

The approach of numerical taxonomy has been called anti-evolutionary. It seems hardly necessary to disavow such attitudes, because of our own interest in evolution and our employment of evolutionary modes of thought. Only the principles and processes of classification are restricted to phenetic evidence, not the entire field of systematics.

It has been said that biological classifications have special characteristics which distinguish them from classifications of inanimate objects. Assuming that vitalistic principles are not invoked when such a statement is made, we can only believe that this assertion refers to the historical dimension of biological organisms—their phylogeny. However, even inanimate objects such as automobiles or nuts, bolts, and screws show evidence of their historical development, as discussed elsewhere. There appears to be no difference between empirical, phenetic classifications of living organisms and those of inanimate objects except that the hierarchies arrived at in classifications of inanimate objects do not necessarily reflect the course of descent with modification. Those who

would now reverse this argument and say that because empirical, phenetic classification can be applied to inanimate objects it must not be applied to living objects seem to us to find a mystique in the latter, which unless demonstrated and defined would not warrant consideration.

It has been charged that the methods of numerical taxonomy are typological (Inger, 1958; Simpson, 1961). By this is surely meant that the procedures employed are allied to the now largely discredited views of typology and idealistic morphology. Sokal (1962b) has shown in an extensive review of this subject that the term typology as used in taxonomy implies procedures and philosophies of diverse meanings. While some aspects of typology are untenable in the context of modern biological theory (especially those related to Platonic idealism), others are reasonable and defensible in the light of present-day knowledge. Simpson's (1961) statement that typological theory is inextricably linked with philosophical idealism is not correct. Simpson himself has pointed out the empirical nature of some of the newer typological approaches and has stated that there is no necessary connection between the idealistic point of view and an empirical but nonphylogenetic method. Bloch (1956), in an extensive philosophical study of the nature of systematics, finds that it is not necessary to consider all nonphylogenetically oriented morphology and taxonomy as idealistic.

Simpson (1961, p. 50) also criticizes typology to the effect that "the concept of distinct and static patterns cannot meaningfully be applied to real groups of organisms, which are parts of an evolutionary continuum and which are always highly variable." It seems to us that these statements confuse the dynamism of evolution with the essentially static nature of the resemblances and differences on the basis of which we perceive evolutionary changes and their results in a group of organisms. To deny the validity of a static approach to classification is in effect to deny the validity of the bulk of the taxonomic work in existence today. The legitimacy of the coexistence of static classifications alongside the phylogenetic ones has been recognized by such eminent taxonomists as Hennig (1950) and Michener (1957). Typology is unacceptable when contaminated with idealistic, metaphysical concepts or when restricted only to morphological evidence and based on few characters. But when (1) it represents an empirical summation of the information available on a given taxon without phylogenetic value judgment of these characters, and (2) when it is performed on the basis of numerous characters of many kinds rather than few of a single kind, typology can serve as a yardstick of resemblance between taxa. This yardstick, when properly

quantified, should yield important information on the results of evolutionary processes. It is the aim of numerical taxonomy to furnish such a yardstick. Problems of noncorrespondence between phenetic and phyletic relationships have been adequately discussed in Chapters 2 and 8.

Many people have criticized the Adansonian principle of allocating equal weight to all characters. We have already adequately covered this topic in earlier sections. Statements to the effect that one character may be much more useful in classifying a group of organisms than ten other characters are based on confusion between construction of taxa and identification of individuals. Unless and until a consistent, logically defensible system for weighting characters can be provided, weighting must remain equal. When such a weighting scheme has been devised, it is likely that the analysis would still be done on a computer, employing the logic furnished by the taxonomist.

In a recent paper Kiriakoff (1962) has criticized the neo-Adansonian school, though regrettably this was written before he had an opportunity to see the most recent papers on the theory of numerical taxonomy. It is interesting to see that he agrees with us on three points: (1) that most current systematic work is crypto-typological; (2) that similarity and blood relationship do not necessarily agree; (3) that the details of phylogeny cannot be known with certainty. On some points, however, he is under a misconception about numerical taxonomy. First, the work of Verheyen (which Kiriakoff cites as an argument against equal weighting) was not a numerical taxonomic study of the kind we advocate. Second, Kiriakoff writes: "I feel quite certain that any neo-Adansonian would classify two very different organisms together *if he had the positive evidence of their recent common ascendance* [his italics]. In failing to do so, he would expose himself to the loss of his scientific standing." We have clearly stated the very opposite in this book (see also, Sneath, 1961). Third, he states that numerical taxonomy is unable to use such factors as time and space, which is incorrect (see Sections 5.4.4, 8.2.2, 8.2.4). We do not think that Kiriakoff offers any constructive suggestions for an alternative method of taxonomy.

10.2.2. Considerations of convenience and practicality

There are numerous statements in the literature (for example, Hennig, 1950) that phenetic relations can in principle never be measured, or that at least the present techniques are inadequate for this. We believe, however, that taxonomists have always estimated phenetic relations intuitively.

tively and that the methods of numerical taxonomy are in general adequate for estimating them objectively. We are unaware of serious criticisms of the methodologies of coding and processing taxonomic information.

Persons skeptical of the method may claim that it takes too much work to describe such a large number of characters in a large group and then process it by procedures which are expensive and possibly time-consuming. Why is all this necessary when by previous methods, based on few characters and the intuitive assessment of resemblance, one could achieve reasonable taxonomies? We have pointed out in Chapter 2 why good taxonomies have been established by *repeated* revisions using earlier methods. Numerical taxonomy aims to reach a position of comparable stability *immediately*. This would clearly be of importance in little-studied groups. Even in the best worked out groups, relationships among the taxa are vague because they have not been quantified; in less studied groups such relationships are altogether missing. It is therefore inaccurate to say that the work done by the computer can be duplicated by taxonomists working on a few characters. On the contrary, computer processing should be superior to that done by the average taxonomist.

Gilmour (1961b), in discussing the mathematical approach to taxonomy, notes that it may help to decide between disputed classifications, but he warns against two dangers. The first is that the increased precision may not be worth the labor involved and may involve changes in nomenclature and consequent loss of stability in classification. We believe that the increased precision will be valuable and will require little extra effort. The confirmation of previous classifications will increase our confidence in systematics; the changes in previous classifications will lead to better ones. There is in any event much instability in nomenclature, and to insist on stability where major taxonomic revisions are proposed would deny biologists the possibility of improving their taxonomies, whether the improvements come from numerical, orthodox, or other studies.

The second danger, that one may imagine that one is achieving some sort of "objective reality," is well taken. This danger is indeed pertinent from a philosophic point of view. We do not claim that numerical taxonomies are "objective realities"; the fact that a number of slightly differing taxonomies may be obtained by different statistical methods is clear evidence that they are not. Nevertheless, having defined precisely what is pertinent to biological classification and what are the best statistics for achieving a given end, we can obtain taxonomies which

fulfill the needs for which they are devised, in the same way that we can agree that the arithmetic mean is a valid measure of the central tendency of a frequency distribution, for a given purpose we have in mind.

With respect to the agreement between the results of numerical taxonomic work and previous taxonomies, we unfortunately become involved in a "damned-if-you-do" and "damned-if-you-don't" type of argument. If a classification by numerical taxonomy yields results similar to those previously shown by orthodox methods, it is argued that numerical taxonomy is unnecessary since the results are after all similar. If, on the other hand, numerical taxonomy yields radically different results, then the new method is "clearly wrong," because the results differ from the established ones, which "obviously" must be right. We believe this dilemma can be solved only by consistently basing classifications on numerical techniques.

Taxonomists may believe it is difficult to find 100 characters in their material; however, it is possible to find many more characters than have in the past been used for taxonomic work. This is certainly true in external morphology but clearly even more so when internal morphological, histological, cytological, histochemical, and similar characters are considered. An abundance of the classical type of morphological characters have been demonstrated in well-studied groups where they had hitherto been overlooked, as, for example, by Ehrlich (1961a), who described a great number of internal morphological characters in butterflies; by Rohlf (1962), who found a large number of previously undescribed characters on the legs of the well-known mosquito genus *Aedes*; and by Haltenorth (1937), who recorded 86 characters from only the skulls of cats, not even considering the teeth. Thus, lack of characters is due most probably to lack of appropriate methods of discovering these characters and to the taxonomists' satisfaction, that a few are enough. The term character is often used by taxonomists in the sense of a feature differentiating one group from another in a given classification. Accordingly, variation in features within an accepted taxon is often considered as trivial by taxonomists and not recorded. Conversely, characters that do agree with an accepted classification are also ignored by some because they do not "add" to the present taxonomy.

The arguments that computational facilities are not available or that the techniques are too intricate are not realistic. There should be little difficulty today in obtaining computer facilities. Almost every university and many government institutions where active research is carried out have a computer installation. Taxonomists in government service or

museums or research institutes can, if they wish, have access to these computers, frequently at very reasonable rates, if not gratis. It should be emphasized here that one need not be a master statistician or computer programmer in order to practice numerical taxonomy.

10.2.3. Objections to the quantification and automation of the taxonomic process (the "Man versus Machine" controversy)

At meetings of taxonomists where these ideas have been presented, the question has often been raised, openly or implicitly, whether techniques such as numerical taxonomy will not result in computers taking over the work of the taxonomist. At this stage of the development of computers and of numerical taxonomy, it is, of course, too early to forecast the relative roles of automated equipment and taxonomist by the end of this century. However, interesting thoughts about the symbiotic relations between scientists and computers have recently been expressed by Fein (1961) and Jahn (1961). At the moment it would appear that the job of the taxonomist will continue to be the collection of data for taxonomic research and, more importantly, evaluation both taxonomically and phylogenetically of the results of computer-processed taxonomic work. Only the estimate of similarity between taxa—tedious and difficult to perform—and the cluster analysis are done by the computer. The rest of the taxonomic task still needs the experience and judgment of the specialist in the field.

A misconception about the nature of computers is that machines can calculate and count, but not evaluate or analyze form and shape [such a comment, for example, was made by Illies (Appendix to Sokal, 1960)]. It is, of course, not correct that machines cannot evaluate or make logical decisions. These they can do if the thought processes of the taxonomist are exactly defined. The machine has the advantage of being faster than taxonomists; it is not easily influenced in an unpredictable fashion; and it can process more information simultaneously than the human mind. A major benefit of programming taxonomy for a machine is that the taxonomist has to think through the logic of the taxonomic process rather than simply follow his taxonomic "intuition."

Some colleagues have stated explicitly or at least implied that quantification is an inherently unsuitable procedure in biology, or at least in taxonomy. Kiriakoff (1962) says: "Neo-Adansonians may be right quantitatively or statistically (and even so with many qualifications); they are wrong biologically." From this it seems that he wishes to separate

quantitative and statistical approaches from so-called biological ones (whatever the latter may mean). He also implies that the classical methods of taxonomy are adequate for present-day problems. We do not agree on either point and should take this opportunity to declare firmly that, as in other sciences, quantification is a desirable goal in taxonomy. Scientific processes cannot be thoroughly formulated or understood until they are quantified, and this holds true for biology as well as for any other science.

Mayr (1959) has stated that no electric computer has so far been able to surpass in the arrangement of higher categories the integrating power of the brain of an intelligent and experienced taxonomist; he says, "in the hands of our less gifted colleagues even the best computer would produce absurd systems." The facts are quite to the contrary. Not only do we hope to have shown that numerical taxonomy will yield results superior to those obtained by orthodox taxonomic work, but especially do we feel that it will give protection against poor taxonomic practices. It will permit a check on the nature of characters chosen. If the characters studied by the taxonomist are poorly defined and erroneously recorded, the evidence will be there for his peers to judge. Furthermore, if the characters have been correctly collected, the machine procedures would produce repeatable results clearly preferable to a classification established by "one of our less gifted colleagues."

It has been said that by employing numerical taxonomy we do not rely on the experience of the taxonomist, which would ordinarily be used in weighting characters. We have been asked whether an "intelligent ignoramus"—one possessing enough intelligence to find characters, but knowing nothing of a group—could by cataloguing the characters and then passing them through the procedures of numerical taxonomy arrive at a proper classification. It seems to us that this may be possible. If that were indeed so, the premium presently put on experience might be unwarranted. We hope to be able to test this particular aspect of numerical taxonomy in the future. Yet it is also clear that experience on the part of the investigator will result in better choice and description of characters.

10.3. SOME PRACTICAL CONSIDERATIONS

10.3.1. Material for numerical taxonomic studies

At present the field in which numerical taxonomy is most useful is in the middle and lower ranks, in the study of genera and species and

perhaps of families. In bacteria, where there is great difficulty in establishing satisfactory lower taxa, it has been very useful when applied to individual strains, and there seems to be no reason why it should not be employed with individual specimens in other fields, particularly in paleontology and in some other applications mentioned below.

We believe that in the great majority of organisms it will be possible to find the necessary numbers of characters for analysis. In a few difficult groups there may be few available characters, which in itself would show that previous taxonomies must have been based on inadequate data; any improvement in the classification, therefore, must first require new methods of study.

How representative of the whole taxon should the OTU's be? It is obvious that the more representative the data, the more representative will be the results. Ideally one would study all the species of a genus and all genera of a family, and so on. Yet it is seldom that all such material is readily accessible, and it may be necessary to work with incomplete material. It will then be necessary to reanalyze the taxon with more data at a later time.

A more difficult problem is that of incomplete data for the characters in the OTU's of a study. This has already proved troublesome in studies on viruses (Sneath, 1962), where very few characters had been recorded for all the viruses under study. It is also a problem in current studies on higher categories in animals and plants. For example, the best described species of an order may never have been examined by newer techniques, while for other members of the order it may be mainly the newer data that are recorded. This commonly happens when different organisms are used as the representative of the order in different laboratories, because of availability, personal interest, and the like. It would clearly be unjustifiable to score the characters of one organism on the assumption that they are the same as these characters in another organism without checking the specimens concerned. In consequence it may be necessary to undertake extensive studies to obtain the missing data. Although this is in a formal sense a limitation of numerical taxonomy, it is equally a limitation of orthodox taxonomy, since a great many assumptions of this kind may have been unconsciously made during the description of higher ranking taxa.

We may look forward to the application of numerical taxonomy to higher ranks, such as orders and classes. The problems of choosing taxa and suitable characters will be somewhat different from those in the studies carried out to date. However, the application of numerical

taxonomy to a range of bacteria which is conventionally considered to cover several different orders has given a reasonably satisfactory result (Sneath and Cowan, 1958), and there seems no reason to assume that the extension of numerical taxonomy to the higher ranks of other kinds of organisms will involve any basically different principles.

We discussed in Sections 5.1 and 5.8 the choice of entities intended to represent heterogeneous taxonomic groups, and there is no need to repeat this except to point out that one exemplar, however typical, cannot exhibit the range of variation of the whole taxon. Systematists must therefore choose sufficient exemplars to serve the purpose they have in mind. The choice of characters when studying the higher ranks is likely to be more difficult. It is at first sight not easy to know how we could select features for the comparison of an insect with an echinoderm. Much of the difficulty will lie in knowing whether it is legitimate to employ features which seem to have no relevance to one of the forms. Would it, for example, be allowable to mark the echinoderm as "wings absent," or should it be scored as "this feature does not apply?" We believe that the absence of wings is indeed a perfectly valid taxonomic difference between a winged insect and an echinoderm. It may be more debatable whether absence of wings in two echinoderms should score as a similarity in a study in which winged animals are also included. In other words, the validity of negative comparisons may be more doubtful as we analyze more widely differing creatures. Yet even in extreme cases like the one given above we can find some characters to serve for numerical studies—for instance, the composition of the integument, the form of symmetry, the forms of digestive organs, the composition of the tissue fluids, and so on. We may be forced to omit many features because of uncertainty on whether they can validly be considered "the same" in the two forms, even employing the concepts of operational homology (see Section 5.3.4). When we choose a less extreme example, such as a bird compared to a mammal, we can at once find a large range of characters for use, such as form of erythrocytes, structure of the heart and great vessels, form of the parts of the brain, and many others. We must only be on our guard against choosing solely those features which have been selected to prove a preconceived point or which have been accepted by tradition as significant, for to do so would bias the analysis from the start. This statement should not be interpreted to mean that no previously recognized characters can be employed. The study by Michener and Sokal (1957) was based entirely on previously recognized characters. However, previous taxonomic treatments of the same groups

had each made use of comparatively few characters, the sets of characters used differing from one study to the next; and for no one species had bee taxonomists ever employed anywhere near the number of characters which Michener and Sokal used.

10.3.2. Techniques of numerical analysis

Until the advent of electronic computers, numerical analysis of taxonomic data, if they were abundant, was quite impracticable. This is no longer true. Computers now are widely available, and several centers are able to process material for taxonomists who are at a distance from such facilities. The cost is small, far smaller than that of either hand computation or traditional rumination and revision, if the real cost of maintaining departments of systematics is considered.

It is, of course, inevitable that some of the statistics will have to be taken on trust. Few biologists have the interest in mathematics that would lead them to familiarity with all the arguments involved here. Nevertheless, they have a check on the statistics in their own shrewd judgments on the worth of the results. How many biologists understand all the statistical logic underlying such simple measures as the arithmetic mean and the standard deviation, which so many of them employ? With better experience it will become possible to advocate standard numerical methods which are applicable with safety to most material, and thereafter the taxonomist, if he will take this on trust, need not consider the details of the mathematics or of the computers. The basic concepts are simple enough. In the Appendix many practical points of analysis are discussed in some detail.

We may here add some comments on the likely advances in technique in the future. It seems to us that these will occur in three main ways. First, there will be better methods for assembling the crude data into a state suitable for analysis. This may take the form of automatic standardization or character coding. Even more valuable would be methods for converting drawings into matrices of character states, employing such concepts as information theory, character recognition, and automatic analysis of complex variables (for example, Rogoff, 1957). These would have the effect of "streamlining" the work by eliminating much of the laborious coding of characters and their states.

Second, the estimation of affinity and cluster analysis will become more sophisticated and more generally applicable, with increased safeguards against ridiculous results and with provision for isolation of

pertinent factors such as overall size and shape. Third, automatic processing of the affinities and dendrograms will enable diagnostic keys, discriminant functions, and tests of significance to be made as a routine, together with information on Q-R relations and even on nomenclature.

The use of machines for automatic printing of distribution maps is another development (Walters, 1954). The day when a monograph can be prepared by computer may still be far off, but the way toward this is clear. Modern data processing machinery in centers for numerical taxonomy would here come into their own.

Advantages would accrue from close cooperation between different workers in the field. The exchange of data, affinity matrices, and computer programs would facilitate this. A step in this direction is the inception of the newsletter *Taxometrics* issued by the Progetto Sistematica Actinomiceti, Istituto P. Stazzi, Via Celoria 10, Milan, Italy. A central repository where copies of the data could be deposited might prove very useful.

10.4. THE EXTRACTION OF DISCRIMINATORY FEATURES AND THE PREPARATION OF KEYS

After a numerical taxonomic analysis has been carried to the point of drawing up the hierarchy of natural taxa, it may be necessary to inspect the original tables of data in order to find those characters which are the most useful for rapid identification of the taxa. From these characters a synoptic key can readily be made. Hill (1959) and Pohja (1960) made such keys by finding the features by inspection, and Sneath (1962) used a method of extracting the features by their relative constancy within and among the taxa. They were then tabulated as the characters which best separated the main sections of the genus studied, and those which best separated the species within each section. More sophisticated methods will doubtless be needed in the future. This aspect of numerical taxonomy has been relatively neglected, and in this section we will only point out a few of the possible lines of development.

It is important to remember that these methods can only be employed after the taxa have been constructed. They cannot, as a rule, be relied upon to yield the taxa themselves, since they are generally based on monothetic division (though combined methods for cluster analysis and discrimination may be developed in the future). Two contrasting situations may occur. First, there may be some character states that sharply

distinguish two taxa; that is, they are present in all members of one taxon and absent in all members of the other. It is then only necessary to find these character states. Second, there may be no single states of this kind, but it may be possible to distinguish the taxa by using several character states which occur with different frequencies in the two taxa. This latter situation, phenetic overlapping (sometimes referred to as reticulation, as by Turrill, 1950, presumably because it has been attributed to reticulate evolution) is found in taxa that are fully polythetic (see Section 2.2). It has been studied mainly in botany (Anderson and Abbe, 1934; Anderson and Whitaker, 1934; Whitehead, 1954). Phenetic overlapping may occur extensively at lower taxonomic ranks (generic and below) but seems to be less common at higher ranks. Sharp discrimination without overlapping is produced by absolute correlation of two or more features, and one problem of cluster analysis is to find clusters that differ sharply in a few respects when there are many inconstant features present. A distinction must here be made between phenetic clusters (in which the inconstant features are treated equally with the correlated features) and the smallest groups showing character correlations. The latter are not necessarily phenetic taxa, though they may be of much taxonomic interest. The "Siamese" mutant of the domestic cat shows constant correlation of certain characters, but it is not certain that, phenetically, Siamese cats would form a phenon, since there are many other variable characters in both Siamese and other cats. The position is thus similar to that in genetic isolates; there may be several distinguishable entities within one phenetic taxon. The entities can be evaluated by the number of correlated features they possess, a field which has not yet been explored.

Similar considerations apply to groups distinguished by the "75 percent rule." The statistical difficulties of this have been discussed by Amadon (1949), Pimentel (1959), and Sokal and Rinkel (1963). More pertinent is the fact that the rule, or its variants, does not consider how to choose the characters for its application. If any variable feature is chosen it is plain, as Wilson and Brown (1953) and Pimentel (1958) have pointed out, that one may obtain from several characters a variety of different groupings which are not concordant. Such groupings may not even show two well-correlated characters.

The minimum number of characters for discrimination is easy to calculate. No more groups can be distinguished than the product of the numbers of character states. Thus three characters, two of three states and one of four states, allows at the most the distinction of

$3 \times 3 \times 4 = 36$ groups. In general, \log (number of distinguishable groups) $\leq \sum$ (log states). In practice many more characters are required than the theoretical minimum, since many do not discriminate between the taxa. A more advanced treatment of this topic is given by Ledley and Lusted (1959a).

Where there is phenetic overlapping, one needs to find for the taxa studied those characters that best discriminate taxa. For two-state characters the algebraic difference, G , between the frequencies of a given state in two taxa may be used (Sneath, 1962): the most discriminatory characters have the highest values of G (positive or negative). Non-additive scoring (see Section 5.3.6) causes difficulty in this method. The classificatory method of Lockhart and Hartman (1963) also extracts discriminatory characters, while Möller (1962) obtains in addition the probability of misidentification. Another simple statistic is the Hybrid Index (Anderson, 1936; Gay, 1960). In general the best discrimination is given by discriminant analysis (Fisher, 1936), in which each character is given a loading such that there is the least probability of misidentifying an individual taken at random. A worked example is given by Whitehead (1954). Related work is that of Rescigno and Maccacaro (1960) and Birnbaum and Maxwell (1961).

We do not propose to discuss at length the making of keys; for practical details we refer to the reader to the articles of Ainsworth (1941), Voss (1952), Metcalf (1954), Stearn (1956), and Cowan and Steel (1960). For a mathematical approach, see Maccacaro (1958). One will use where possible the features that are easiest to observe accurately, and the use of several characters at each fork may help with damaged or aberrant material.

The decision has first to be taken whether the most efficient and probably quite artificial system is to be used or whether the key is to be based on the taxonomy established by the numerical program. In the first case the steps to be taken are relatively quite simple. They consist in eliminating initially all those characters which are unsuitable for identification on the conventional specimen (which is commonly a preserved adult), such as, physiological and ethological characters. Then a methodical search is made by the machine for specific character states unique to the basic taxonomic entities in the study. The machine then works out the smallest number of characters required in order to differentiate every taxon from every other one. This would be done under a system which would permit a stage in the key to have more than two alternatives. If it is deemed desirable that each stage in the key should

have only two alternatives, the machine can be programmed to search for the character states which will differentiate the taxa. All those taxa that cannot be characterized by a single character state are identified by unique combinations of two or more character states.

When a natural key is desired it is simple to sort out and segregate the various taxa in the original data and then to determine the constant character states for each taxon. Among these constant characters we again eliminate those unsuitable for conventional specimens and then proceed as with the artificial key. The above methods may be described as rather pedestrian, but they are well suited to the type of routine and repetitive operation which electronic computers carry out. Key construction, however, is a field where more sophisticated approaches—information theory, for example—can produce more elegant and efficient procedures (see Maccacaro, 1958; Rescigno and Maccacaro, 1960; Möller, 1962; Hill and Silvestri, 1962).

Taxonomists may feel that keys based on single characters are unsatisfactory, since damaged specimens may not yield information on the critical character. Furthermore, the person identifying a given specimen may not be certain about the interpretation of a given feature in a taxonomic key and may wish to confirm his decision by reference to a second (and even a third) characteristic. The methods outlined above would, of course, be quite adaptable to producing keys based on any number of characters, so long as differences did in fact exist between the taxa which had been erected.

10.5. THE FUTURE OF SYSTEMATICS

Ehrlich (1961b) has made some predictions on the future of systematics which he refers to as unpopular. These include the prediction that data-processing equipment will be the most important tool of the taxonomist in 1970 and that a great simplification of nomenclature will take place. These predictions may be unpopular today, though whether they will prove so in the future is another matter. Fein (1961) predicts that by 1975 at least one botany department in a large university will offer a course in the application of computer techniques to taxonomic botany. Jahn (1961), in an extraordinarily interesting paper, has discussed a number of exciting possibilities. Among these he foresees machines which do not merely retrieve information, identify specimens, or give us their synonymies but which also will tell us if we have found a new organism ("Congratulations! You have discovered a new phylum"), suggest a

suitable name, question the taxonomist's veracity, and learn by experience as new organisms are discovered and their particulars given to it. "Furthermore," Jahn says, "the goal to be achieved by intellectronics is not to copy human errors of thought, but to serve as an extension of man's intellect."

Jahn also suggests that diagnostic keys might be recorded on magnetic tape for use in computers, and "presumably these tapes would be available in suitable taxonomic units from any good biological supply house." We may even look forward to the day when the larger museums have a computer wholly employed as a machine for identification of specimens, to be fed with specified characters on punched cards. Even the isolated worker may have access to such facilities by mail or telegraphic lines. Such facilities are now available for information retrieval, abstracting services, and the like. In the systematics of thoroughly worked groups of organisms the use of these devices should not be unfeasible.

Jahn (1962) has in a recent paper advocated a rigidly logical approach to taxonomy. With large, fast computers, the universal coding of taxa, descriptions, and names may indeed become feasible. At present there are two main difficulties: (1) comprehensive, logical nomenclature and identification first require satisfactory and comprehensive taxonomies; (2) until these are available we must retain large coded descriptions for the OTU's (perhaps of a hundred decimal digits). Otherwise a later taxonomic revision might disrupt a logical nomenclature that employed ordinal, familial, generic, and species code numbers.

The flood of new data available to biologists will raise its own problems. Cain (1959c) has pointed out that the assimilation of new data is one of the main problems facing systematics today. The efficient understanding of the biological significance of the data will be a greater problem. This is clearly true of their ecological and evolutionary significance. In molecular biology and genetic fine structure this will be even more difficult. It was noted in Section 5.3.1 that the potential store of information in a mammalian nucleus is of the order of 10^{10} bits, and Jahn (1961) comments that it has been calculated that this would, if set in type, fill a thousand standard books, a feat of miniaturization far exceeding any that engineers can envisage today. The scale of this can be judged from the fact that the Library of Congress could be in theory comfortably encoded in the anther of a lily.

The natural history museum of the future will be very different from those of today. It will still contain many preserved specimens and some

type material, but far more emphasis will be given to exhibitions of biochemical properties. A central feature will be a data-processing installation. Dusty files on nomenclature will be consigned to a limbo: in their place will be a few international indices which would provide immediate access to stored taxonomic data. As to the nomenclature itself, it might be monominal (as Cain, 1959b, has suggested), with numerical additions to indicate the hierarchic relation, or it might possibly be wholly numerical.

Should there be a separate numerical taxonomy, parallel to but distinct from orthodox systematics? Some aspects of the latter, such as, nomenclature, may be relatively unconcerned with numerical methods. There is a great deal to be said for incorporating the findings of numerical taxonomy into orthodox taxonomy wherever this is possible, if only because the latter is an efficient system of information retrieval.

A more detailed essay on the future of systematics can be found in Sokal (1963).

Numerical taxonomy and genetics will together provide a bridge between the molecular and evolutionary views of biology. The first will relate genotype to phenotype and will measure the degree, rate, and direction of evolution. The second will relate the genotype to physico-chemical composition and to the mechanisms of evolution.

10.6. OTHER APPLICATIONS OF NUMERICAL TAXONOMY

The principles of numerical taxonomy can be applied to domains other than that of the classification of living organisms. Analogous methods, many of them anticipating the ones we have discussed, are already widely used in plant ecology for the study of types of vegetation, in which "taxa" such as woodland, prairie, or moorland can be distinguished and analyzed (see, for example, Sørensen, 1948; Goodall, 1953; Williams and Lambert, 1959; Harberd, 1960; and the detailed review of Dagnelie, 1960). These vegetation types may sometimes form hierarchies analogous to those in systematics. Sørensen employed both association coefficients and cluster analysis. Similar methods have been used to distinguish ecological associations of marine plankton (Williamson, 1961). Grieg-Smith (1957) and Dagnelie (1960) described many of the methods used in ecology, with a critical discussion of them. There is a growing dissatisfaction with many ecological concepts at present poorly

defined (Ehrlich and Holm, 1962). An attempt to make some of these more rigorous was made by Hutchinson (1957).

Sneath has examined the ecological data on the Hoveton Great Broad (shallow lake), kindly provided by Dr. J. M. Lambert (Lambert and Jennings, 1951), consisting of 56 quadrats scored for 73 plant species. The data consisted of a series of quadrats forming a transect across a lake, bordered by reed swamp, fen, and carr (swampy willow thickets) on either side. The similarity coefficient was S_{SM} and clustering was on single linkage of similarity values. The clustering analysis, as one would have expected, brought together reasonably well the quadrats from each vegetational association; for example, the reed swamp quadrats were, in the main, placed together, though spatially on opposite sides of the lake.

On comparing this polythetic method with the monothetic association analysis described by Williams and Lambert (1959), the following points were noted. The polythetic method was less sensitive to chance presence or absence in a quadrat of any single species. That is, in the monothetic method a quadrat may be occasionally removed from quadrats which are highly similar in overall floristic content because of the chance presence or absence of the species which served to define the monothetic group. However, if the full process of nodal analysis is carried out (Williams and Lambert, 1962), these quadrats would be normally picked out as distinct. As expected, it was often impossible with the polythetic method to find "indicator species" (single species diagnostic of the clusters of quadrats). Nevertheless the dendrograms given by the two methods were very similar in differentiating open water, fen, and reed swamp, but they showed some differences in the treatment of the carr.

Similar comparisons by the two methods of the "inverse" relations (R type analysis; the grouping of species according to the quadrats in which they occurred; see Williams and Lambert, 1961a, b) also gave generally concordant results, with findings similar to those in the "normal" analyses (Q type, discussed above).

An interesting application would be the difficult subject of the classification of soils (see Manil, 1959; Chenery, 1960). Leeper (1954) has discussed soil classification and strongly criticized those based on speculations on the origins of the soil rather than on their observed properties, a significant echo of the controversy over phylogenetic taxonomies in systematics. Hughes and Lindley (1955) applied Mahalanobis' D^2 statistic to soils but employed very few characteristics. The study of Hole and Hironaka (1960) is also related to distance.

Numerical taxonomic methods may also prove useful in investigating the degree to which the environment affects the phenotype, both as regards overall size (or its equivalent) and shape. It may also find some application in genetics, such as in blood groups or where large numbers of genes have been described for certain species and their mutants (see, for instance, Kelus and Lukaszewicz, 1953; Harland, 1936).

Ornstein (1960) has used the method of Rogers and Tanimoto (1960) in studying serum protein patterns. Numerical taxonomy could be applied to some classes of chemical substances, such as proteins, and possibly genes or their DNA sequences. Sneath is currently studying peptide structure by numerical taxonomic methods, in part along the lines suggested by Fox and Homeyer (1955). Some interesting reflections on the relation between classification and chemical structure of viruses are given by Pirie (1962).

Although numerical taxonomy has not been employed in anthropology in the rigorous manner which we feel is essential for valid results, there is, nevertheless, a considerable body of data of some interest which was obtained by rather similar methods, notably the Coefficient of Racial Likeness. Much of the earlier work is summarized in the reviews of Bielicki (1962) and Wierciński (1962; see also, Campbell, 1962). The study of the physical anthropology of race seems to be in urgent need of studies based on characteristics of individuals rather than speculative "original" races or ill-defined populations. This is evident from a comprehensive collection of essays on race (Count, 1950), in which few authors even touch on the question of how one recognizes a race by objective criteria. It seems scarcely credible that there should still be argument over this (Bielicki, 1962; Wierciński, 1962). Possibly the same criticism applies to social anthropology (Leach, 1962).

The techniques of numerical taxonomy may also prove of use in the field of medical diagnosis. Some attempts have been made to employ computers in this field (for example, Lipkin and Hardy, 1957; Lipkin et al., 1961; Tolles et al., 1961), but they have usually met with logical problems which are taxonomic in a wide sense of that word. In particular, the validity of the disease entities (the definitions of the diseases) may be questioned, for if these should prove to be unsound the diagnostic schemes will inevitably be unsatisfactory. The construction of disease entities (that is, disease taxa based on individual cases of disease) can be made by numerical taxonomic methods, and association analysis with clustering on single linkage (as suggested by Sneath, 1957a) has

been successfully used in grouping cases of leukemia (Hayhoe, Doll, and Quaglino, report to be published). It is probable that most well-known disease entities are valid groupings, but there has been little study of this point: it is doubtful whether most of the obscure diseases have been satisfactorily classified. Possibly polythetic concepts would prove valuable here, despite the conventional emphasis on defining a disease by its etiology. Etiology, despite its great influence on treatment of diseases, may prove in medicine to be almost as unsatisfactory as phylogeny has been in biology as a general principle for defining taxa. Some clinical entities may have a varied etiology—for example, the great similarity of kinds of purulent meningitis caused by very different bacteria; conversely, one etiology may produce varied signs, symptoms, and pathology—for example, syphilis.

The construction of sound disease taxa would seem to be a necessary preliminary to full use of computers in diagnosis and prognosis. When this has been done, the correlation methods (Tolles et al., 1961) and matching methods (Lipkin et al., 1961) will prove of great value in the diagnostic process. A detailed logical study of diagnosis has been made by Ledley and Lusted (1959a, b) and Lusted (1960). The simple logical methods of Nash (1954, 1960) may also be applicable. In passing we may add that successful diagnostic techniques would seem to need provision for (1) deciding on what signs, symptoms, and diseases are pertinent (and conversely what is considered "normal" or "healthy"), (2) the satisfactory construction of disease entities, or the checking thereof, (3) the weighting of attributes for diagnosis and discrimination, (4) the questioning of the physician to confirm signs which may have been misread or overlooked, and (5) the correction of the disease entities by new data. There will be many opportunities for fruitful collaboration between those working on medical diagnosis and those working on taxonomic keys and identification methods.

We know of few applications of numerical taxonomy to fields outside biology. It may be of use in comparing and identifying rocks, for such purposes as detecting their position with regard to faults and other geological formations. It has been applied with some success to the classification of reaction facies in the study of oil-bearing strata. Whitten (1961a, b) has recently applied rather similar methods to the study of rocks. As in the studies of soils cited above, very few characteristics were studied. It should be remembered that while it is possible to compare the points of a single transect in a checkerboard of affinities, to compare

the points of an area in this way would require four dimensions. This is also true of ecological, racial, and other geographic distributions. There is considerable literature on classificatory methods in psychology.

Numerical taxonomy has recently been applied to political science in a study of legislative behavior (Professor J. G. Grumm of the University of Kansas, personal communication). It was used to classify groups of legislators into clusters, as defined by their voting patterns. Less sophisticated methods of this general kind had been used as early as 1927 by Rice and later by Beyle (1931) and Truman (1959).

The close connections between taxonomy and information theory may be seen by reading the article of Good (1958). There is a discussion not only of clumps and how to measure them (equivalent in many ways to cluster analysis) but also of John Wisdom's cow. "A cow has four legs and gives milk," but it may have three legs and may not supply milk. No one property may be essential to its "cowness." Estrin, quoted by Good, suggests information retrieval by asking for k out of n index words before selecting a document. But the group "cows" is a polythetic taxon. So are Estrin's document clusters.

Numerical taxonomy may have a part to play in problems of pattern recognition (see Unger, 1959; Stearns, 1960; Bonner, 1962). Lusted (1960) refers to this as one of the challenging problems to be found in many fields of science, such as psychometry, radiography, mapping, and recognition of handwriting. Patterns may be polythetic, and different variants of one pattern would then form phenons, which would be difficult to distinguish by monothetic methods of classification.

Other fields which come to mind where numerical taxonomy may offer assistance are archeology (Clarke, 1962), astronomy, economics, mythology, oceanography, library classification, and the identification of the literary style of different authors. It has already been used in philology (Ross, 1950). Parker-Rhodes and his colleagues are now exploring its use in language translation research (Parker-Rhodes, 1961). Methods in cultural anthropology are quite similar (Driver, 1962). A modified method was used by Sneath to solve a simple jigsaw puzzle. Almost any field dealing with polythetic groupings may find numerical taxonomy useful.

10.7. LATE REFERENCES

In a rapidly developing field, such as numerical taxonomy, bibliographies are out of date before they are even printed. In preparing this

book we have had to draw a deadline beyond which references could not be included for consideration in the general text. However, we would like to avail ourselves of the opportunity to present here references to papers which came to our attention by galley proof time. These are mostly recent publications related to numerical taxonomy. However, some of them are earlier papers which have been pointed out to us by colleagues and which we include for the sake of completeness. The publications are presented alphabetically by author in the form of an annotated bibliography.

Cavalli, L. L. 1949. Sulla correlazione media fra piú caratteri in relazione alla Biometria. *Metron*, **15**:1–16. This paper discusses Zarapkin's method of discriminating between populations and relates it to the "mean correlation coefficient," defined as the mean of the $n(n - 1)/2$ correlation coefficients between pairs of n characters. Cavalli also discusses the relation between this mean correlation coefficient and other such coefficients—as, for example, Gini's synthetic coefficient and the intraclass correlation coefficient. A reference to earlier work by Cavalli in this field is also given.

Clements, F. E. 1954. Use of cluster analysis with anthropological data. *Amer. Anthropologist*, **56**:180–199. An example of the use of Holzinger's coefficient of belonging and Tryon's cluster analysis.

Downe, A. E. R. 1963. Mosquitoes: comparative serology of four species of *Aedes* (*Ochlerotatus*). *Science*, **139**:1286–1287. The four species compared serologically in this study were also included in the numerical taxonomic study by Rohlf (1962). The serological findings show *A. communis* closely related to *A. punctor*, with *A. trichurus* related more closely to those two than is the fourth species, *A. excrucians*. These findings are duplicated by Rohlf's analysis of distance coefficients based on adults; however, his analysis of data based on adults and larvae pooled places *A. excrucians* closer to *A. communis* and *A. punctor* than to *A. trichurus* and in fact he has put *A. trichurus* in a separate species group of the subgenus *Ochlerotatus*. This is so because *A. trichurus* has several unusual larval characteristics. Thus the serology of adults is quite congruent with a numerical taxonomy of adults. It would be interesting to learn whether the serology of the larvae would be congruent with adult serology or would agree more with the rather different relations found in the numerical taxonomic study of larvae. We find here further support for the non-specificity hypothesis, in that relationships based on morphological characteristics are paralleled by relationships based on protein structure.

Driver, H. E. 1963. Survey of numerical classification in anthropology.

In Hymes, D. H. (ed.), *The Use of Computers in Anthropology*. Mouton, The Hague (in press). We have been privileged to see the manuscript copy of this article. It will be an invaluable source for persons interested in problems of numerical taxonomy as they relate to the field of anthropology, both physical and cultural.

Driver, H. E. and A. L. Kroeber. 1932. Quantitative expression of cultural relationships. *Univ. Calif. Publ. Amer. Archaeol. Ethnol.*, **31**:211-256. An early attempt to quantify cultural relationships in an attempt to make natural classifications. They discuss a number of association coefficients and show that, as a rule, these give closely concordant results.

Ellegård, A. 1959. Statistical measurement of linguistic relationship. *Language*, **35**:131-156. Discusses previous work and, at some length, the significance of negatives (absence of a word or language feature). He concludes that inclusion of negative matches may be misleading in some circumstances. The inclusion of negative matches, as in *phi*, measures interdependence, or interinfluence (positive or negative), while omitting negative matches measures similarity. *Phi* = zero can indicate either no similarity at all or else no interinfluence in related languages. He concludes with some notes on significance tests, with formulas.

Floodgate, G. D. 1962. Some comments on the Adansonian taxonomic method. *International Bulletin of Bacteriological Nomenclature and Taxonomy*, **12**:171-179. Floodgate discusses the meaning of the term "feature" and reaches conclusions very similar to our own, in that he distinguishes between characters that are permissible in taxonomy from those which are not because they are redundant, invariable, or inapplicable. He also shows by an example the close agreement between several different ways of estimating similarity.

Floodgate, G. D. and P. R. Hayes. 1963. The Adansonian taxonomy of some yellow pigmented marine bacteria. *J. Gen. Microbiol.*, **30**:237-244. Another study, principally covering strains that probably belong to the genera *Flavobacterium* and *Cytophaga*, in which two main phenons and some smaller groups were found, in good concordance with other work on these bacteria.

Günther, K. 1962. Systematik und Stammesgeschichte der Tiere 1954-1959. *Fortschritte der Zoologie*, **14**:267-547. This is a useful and comprehensive summary of systematics during the years indicated. It presents a critique of the early work in numerical taxonomy but not of the more recent work.

Klimek, S. 1935. Culture element distributions. I. The structure of Californian Indian culture. *Univ. Calif. Publ. Amer. Archaeol. Ethnol.*,

35:1-70. Klimek uses a sine transformation of the four-point correlation coefficient ϕ , such that $Q_6 = \text{sine of } \frac{1}{2}\phi\pi$ radians. Illustrated by a Q type and R type analysis of the same body of data, showing correlated clusters of both tribes and of culture traits. The method seems to come from Czekanowski in 1911.

Kroeber, A. L. 1960. Statistics, Indo-European, and Taxonomy. *Language*, 36:1-21. Discusses the paper of Ellegård (see above) on classification of languages, and a number of association coefficients, with some interesting comments on biological classification and the phylogenetic problem in linguistics.

Lubischew, A. A. 1962. On the use of discriminant functions in taxonomy. *Biometrics*, 18:455-477. In this paper, and in an earlier paper in Russian, Lubischew works out a coefficient of discrimination which is a type of distance based on a single character. Lubischew's techniques are of interest also because they can be carried out with simple computational devices, including the use of nomograms.

McQuitty, L. L. We would like to draw attention to numerous papers by this author published in *Educational and Psychological Measurement* between the years 1957 and 1962. McQuitty develops a number of relatively simple methods for cluster analysis. Whether such methods can be of use in numerical taxonomy remains to be investigated.

Michener, C. D. 1964. Some future developments in taxonomy. *Systematic Zool.* (in press). This important contribution takes up several issues intimately connected with numerical taxonomy. It holds that current classifications (whether made in the traditional manner or by numerical taxonomy) are not as natural as they could be, partly because of the tradition of mutually exclusive taxa, reinforced by the present system of nomenclature in which the genus name is part of the classification and at the same time part of the name of the organism being classified. Michener recommends a system of uninominal nomenclature for which certain advantages are claimed—simplicity of rules and relatively great stability, in addition to the major one of liberating classification from the restrictions of nomenclature.

If taxonomy is to progress to best advantage on earth or be ready to provide a basis for systematic work on foreign biotas when exobiology becomes a reality, it must, of course, take advantage of instruments for automatic discovery and recording of characters and of systems for storage and retrieval of data. In connection with information retrieval systems, some suggestions are made for the development of an appropriate numbering system for organisms. There should be a unique designa-

tion for each species that incorporates nothing of the classification; the latter can be indicated by a prefixed number, subject to change as the classification changes with improved knowledge.

Emphasis is placed on the idea that even investigators as different in their approaches and objectives as numerical taxonomists and New Systematists can each contribute important information to a systematic study. Numerical taxonomy can contribute at all taxonomic levels except perhaps the highest, while contributions of New Systematics are largely limited to lower levels, especially the specific level and below.

Some of the reforms suggested by Michener require work by numbers of biologists, or discussion and action by appropriate international commissions on nomenclature, or even a costly international center for the storage and retrieval of taxonomic and related data, and such recommendations have been made by him.

Pohja, M. S. and H. G. Gyllenberg. 1962. Numerical taxonomy of micrococci of fermented meat origin. *J. Appl. Bacteriol.*, **25**:341-351. Several different statistical methods were used, including clustering by single linkage and central clustering of Rogers and Tanimoto, and the data were compared with previous numerical taxonomy of these organisms. There was close agreement between all the dendrograms. A brief reference, without details, is made to a clustering method based on the number of mismatches that is statistically significant in an association coefficient.

Proctor, J. R. and W. B. Kendrick. 1963. Unequal weighting in numerical taxonomy. *Nature*, **197**:716-717. The authors defend unequal weighting for the avowed purpose of making "form genera" (and other artificial taxa) in fungi, which they do not claim to be natural taxa (these they consider impracticable). They divide characters into primary (such as presence of some organ) and secondary—that is, characters that qualify a primary character (such as color of the organ). A primary character is given an additional weight equal to the number of secondary characters in the study that qualify it. We do not see how one can consistently distinguish primary from secondary characters. "Spores showing spines" could be a primary character, "spines (on the spores)," or a secondary one, "spores spiny." The details of scoring are not given, but one gathers that the effect will often be that of scoring inapplicable character states as being applicable. It is not clear why the authors consider a natural taxonomy to be impracticable.

Shepard, R. N. 1962. The analysis of proximities: multidimensional scaling with an unknown distance function. I and II. *Psychometrika*,

27:125–140 and 219–246. These papers describe a novel method by which the rank order of a series of some function of distances between N points in multidimensional space controls the collapse of the configuration into the smallest number of dimensions consistent with monotonicity. It has been programmed for a computer. In addition, the underlying function of distance can usually be obtained.

Smirnov, E. S. 1926. Über die Phylogenese der Kongregationen. *Biologia Generalis*, **2**:1–17. Another earlier paper on numerical taxonomy.

Smirnov, E. S. 1938. Species construction from a taxonomic point of view [in Russian, English summary], *Zoologicheskii Zhurnal*, **17**:387–418. This is an earlier paper by Smirnov which we had overlooked. In it he developed a method (“the principle of exhaustive characteristics”) for reducing the number of characters on which an evaluation of similarity is to be based. The author states that once such characters are detected and utilized, all other properties of individuals will be either tautological or will distort the real aspect of similarity. This method thus appears to be similar in aim to the use of factor analysis for removing the redundancy in character correlations which we have speculated upon earlier.

Smirnov, E. S. 1962. On the structure of a three-membered genus. In Serguiev et al. (eds.), *Problems of General Zoology and Medical Parasitology*, pp. 229–255. State Medical Publishing House, Moscow (in Russian). This paper expands the formulas of Smirnov (1960) as applied to a genus containing only three species.

Wagner, W. H., Jr. 1963. Biosystematics and taxonomic categories in lower vascular plants. *Regnum Vegetabile*, **27**:63–71. Wagner questions the validity of conventional biosystematic information in botany based on few characters thought to be important as compared with the great abundance of characters employed in numerical taxonomy for classification of plants. Attention should also be drawn to Wagner’s method for expressing phylogenetic deductions, which permits quantification of the data. An example can be found in Mickel, J. T. 1962. A monographic study of the fern genus *Anemia*, subgenus *Ceratophyllum*. *Iowa State Univ. J. Sci.*, **36**:349–482.

Williams, W. T. and M. B. Dale. 1962. Partition correlation matrices for heterogeneous quantitative data. *Nature*, **196**:602. If a data matrix such as an $n \times t$ table contains many zeros, this makes the mean to variance relationship approximate to that of a qualitative (0, 1) distribution. The authors suggest a method for partitioning the data into qualitative and quantitative elements. This indicates how the populations may be subdivided into more homogeneous subdivisions.