BACKGROUND

Measurement in Anthropology

Human skeletal and dental remains continue to provide the most direct evidence for examining the biology of past populations (Larsen, 1997, 2002). Quantitative (i.e., metric) as well as more qualitative (i.e., nonmetric or discrete) aspects of human biological variation remain central to studies in physical anthropology since its inception. Measurement of living (anthropometry) and skeletal remains (osteometry and craniometry), and the methods for analyzing this category of variation represent one of the discipline’s most notable contributions to science.

Much of this early attention to measurement and description in physical anthropology focused on investigations of human population structure and past biological relationships, including the assignment of unknown specimens to known reference groups. As was typical of the discipline as a whole during this formative period, these early studies of population history were associated frequently with the now outdated concept of racial typing and classification. After this formative period, there have been major refinements in biological evolutionary theory and the methods for analyzing quantitative data, refinements that now provide a solid foundation for understanding the history of human groups and biological relatedness among groups, past and present.

Biological Distance Studies

Although the focus of interest in skeletal biology has now greatly expanded to include studies of health and well-being, diet, physical activity, paleodemography, violence, and trauma of past populations, interests in determining biological relatedness or ancestry, today referred to as biological distance (or biodistance) (Buikstra et al., 1990), continue to attract attention in physical anthropology, bioarchaeology, and forensic anthropology.

Since metric (and nonmetric) aspects of skeletal and dental form and structure (i.e., morphology) have a genetic basis, these categories of variation provide valuable information about past genetic relationships. Groups that share more metric and nonmetric features in common are considered to be more closely related than groups not sharing these same features (Larsen, 2002). Analysis of morphological and, in particular, quantitative traits thus provides an indirect reflection of genetic variation within and between human groups. Several sophisticated models have
been developed specifically that allow the genetic analysis of quantitative traits (e.g., Konigsberg, 1990, 2000; Konigsberg and Blanero, 1993; Relethford, 1994, 2001, 2002; Relethford and Blanero, 1990; Relethford and Harpending, 1994, 1995; Rogers, 1986; Rogers and Harpending, 1983; William-Blanero and Blanero, 1992).

Although biodistance analyses have typically used both metric (i.e., continuous linear measurements and indices) and nonmetric (i.e., discontinuous or quasi-continuous traits) categories of data, the multivariate techniques discussed in this chapter are more amenable to the analysis of continuous or metric data rather than nonmetric data. (For a discussion of nonmetric traits, see Saunders and Rainey, this volume). Furthermore, because of the popularity of the skull in investigating population structure and past relationships, the applications selected to illustrate these methods will be based on multivariate analyses of cranio metric data. In addition to studies that focus on methodological issues and the genetic analysis of cranio metric data, the literature provides many examples of analytical applications of biodistance studies (e.g., Hemphill, 1998; Howells, 1973, 1989, 1995; Jantz and Owsley, 2001; Pietrusewsky, 1990a, 1994, 1997, 2004, 2005; Powell and Neves, 1999; Relethford and Lees, 1982; Sculli, 1990; Sokal et al., 1987; Steele and Powell, 1993; Stefan and Chapman, 2003; Stefan, 2004, Varela and Cocilovo 2002; and many others).

Landmark Measurements and Alternative Data

Traditionally, the variables used in metric analyses have been simple distances and angles (linear dimensions) defined by cranio metric landmarks. These variables are measured directly on the specimen using handheld calipers. Recent alternatives to landmark measurements include coordinate points (Dean, 1995), surface contouring (e.g., moire fringe patterns), holography, methods that capture images through the use of digitizing pads, video-based systems, and three-dimensional imaging techniques such as those used in geometric morphometric studies (Adams et al., 2002; Bookstein, 1991; Rohlf, 1998). This chapter will focus exclusively on the application of multivariate statistical procedures using traditional cranio metric landmark data. Richtsmeier et al. (2002) have recently reviewed comparable methods for analyzing three-dimensional landmark coordinate data in morphometric analyses. Although these technical developments in recording three-dimensional objects are becoming more common, traditional measurement methods are still practical for geographically dispersed study samples and provide the foundation for student instruction.

Justification for Continued Use of Metric Data

Several convincing arguments have been made supporting the use of measurements, especially cranio metry, as sources of taxonomic information (see, e.g., Howells, 1973, 1989, 1995; Van Vark and Howells, 1984). The precision and repeatability of measurements, the conservative nature of continuous variation, the direct link with the past, and the demonstration of a heritability component for this category of biological variation (e.g., Devor, 1987; Sjøvold, 1984) provide the theoretical foundation for metric analysis. Isolation by distance models indicates a strong correlation between genetic and cranio metric results that also suggests that cranio metric variation (or at least the multivariate patterns of among-group variation they produce) is, on average, selectively neutral (González-José et al., 2004; Relethford, 2002; Roseman, 2004; Roseman and Weaver, 2004). Perhaps the most important reason, from a statistical and mathematical point of view, is the continuous (and correlated) nature of measurements, which makes them well suited for applying multivariate statistical procedures.

Despite the development of mathematical theory, which underlies multivariate statistical methods, in the early decades of this century,
the analysis of metric data using these procedures was slow to gain widespread usage. Much of the initial reluctance can be attributed to the often extensive and tedious computations involved. A variety of historical, political, and scientific reasons, in the mid-twentieth century, diverted attention away from the study of skulls, including the use of measurements, to other areas of interest in the field (Lahr, 1996:xv). General applications of these methods had to wait for the appearance of mainframe computers, commencing in the late 1960s and early 1970s, and then personal computers that have become available only since then. The use of these methods continues to the present.

The focus of this chapter will be the analysis of metric, or quantitative, data using multivariate statistical procedures, methods that have emerged as the most appropriate and advanced for investigating metric data. Although the methods to be discussed are based on complex and sometimes intimidating mathematical statistical theory, this discussion will be largely nontechnical and devoid of mathematical formulas and detailed statistical discourse. Although familiarity with such theory facilitates the use of these methods, this chapter will focus on the application and interpretation of results primarily generated by computer statistical packages, a strategy that will hopefully encourage students and others to use these methods. The use of multivariate statistics in skeletal biology, including biodistance analyses, has been reviewed by Buikstra et al. (1990). More recently, Larsen (1997, 2002) and Wright and Yoder (2003) have provided summaries and syntheses of specific studies in skeletal biology that make extensive use of biodistance measures using metric as well as nonmetric data. Several publications further summarize the use of multivariate statistics and biodistance studies in biological anthropology (e.g., Feldesman, 1997; Larsen, 1997; Van Vark, 1985, 1995; Van Vark and Howells 1984; Van Vark and Schaafsma, 1992).

**METRIC ANALYSIS: UNIVARIATE METHODS**

The use of measurements in physical anthropology and skeletal biology has a long history. Cranial morphology, including craniometry, has been an integral part of this long history. The ubiquitous cranial index and the attendant labels, *brachycranic, dolichocranic*, and *mesocranic*, which were used to express cranial vault shape, are synonymous with early physical anthropology and its attempt to reconstruct human racial history. As W.W. Howells (in Lahr, 1996:viii) has stated:

> When Anders Retzius, a century and a half ago, invented the cranial index, he gave us an answer for which there was no question.

These early, often very industrious, efforts in physical anthropology, now regarded as exercises in typological racial classification, resulted in massive compilations of descriptive information on human populations, which including their use as classificatory devices are now of uncertain value. Individuals, or their skeletal remains, were assigned (typed) to groups on the basis of several observable qualitative and/or quantitative features. The approach was largely visual where combinations of observed features determined group membership. More mathematically based approaches to this problem followed a good deal later.

Given this early concern with quantification, it is not surprising that the fields of physical anthropology and mathematical statistics have shared, at least in their formative stages, a mutually beneficial relationship (Howells, 1984). Early statisticians, such as Karl Pearson, used measurements recorded in skulls and people to develop new statistical procedures. These earliest analytical methods were predominantly restricted to descriptive, or univariate, statistics such as measures of central tendency, dispersion, and variance, the statistics of measurements, not individuals, or populations (Howells, 1969:312). Although comparisons between populations
might proceed one measurement at a time, or possibly two at a time as in the case of an index or bivariate plot, the statistics of populations and the treatment of individual specimens in the context of their parent population had to await the introduction of multivariate statistical procedures by Hotelling (1933), Fisher (1936), Mahalanobis (1936), Rao (1948, 1952), and Mahalanobis et al. (1949), among others, beginning in the third decade of the twentieth century.

MULTIVARIATE STATISTICAL PROCEDURES

Multivariate statistical procedures comprise a family of related mathematical procedures that allow the simultaneous analysis of multiple variables (i.e., measurements or nonmetric traits) recorded in individuals or objects from one or more groups. More rigorous definitions require that all variables must be random and interrelated and that their different effects cannot be interpreted individually in a meaningful way (Hair et al., 2006:4). Multivariate statistical procedures are exceptionally well suited for investigating interrelationships among the variables, examining group differences, and making other inferences of the variables and groups selected.

By definition, measurements, which represent distance or quantity, have continuous distributions and phenotypes. Statistically, metric traits (e.g., maximum cranial length) can take any value within a range of a scale whose values change smoothly or continuously rather than abruptly. By contrast, nonmetric or discrete traits have discontinuous (qualitative) phenotypes that are expressed by a certain finite, usually small, number of values (or character states) that do not transition smoothly from one value or character state to the next. The distinction between these two kinds of data, continuous and discontinuous, is important in selecting the appropriate multivariate statistical procedure.

Another important concept in multivariate analysis is the variate, here defined as a linear combination of weighted variables represented by a single value. These variates are generated by a specific multivariate statistical procedure such as discriminant analysis or factor analysis.

Some multivariate techniques may be considered extensions of univariate techniques; others, like factor analysis, discriminant analysis, and generalized distance, require more complicated statistical procedures that resolve the entire data matrix requiring the use of matrix algebra. The data for a single group usually take the form of a data matrix consisting of N rows of observations (number of individuals) and P variables (number of measurements), which are arranged in columns. Reading the rows, an individual becomes a vector of its scores on P traits, whereas the vector of measurements is read by examining the scores for N individuals in the columns. The mean vector (or centroid) is the mean of each variable. Univariate statistical techniques are concerned with mean vectors and variance, whereas multivariate statistics must consider the entire matrix of numbers, which is a procedure that requires a consideration of covariance (and correlation) of each possible pair of variables in the matrix.

The primary purpose of multivariate analysis is to investigate relationships among the transformed variables. By reducing the information contained in the original measurements to a smaller number of uncorrelated (orthogonal) variables, or scales, multivariate procedures overcame one of the greatest obstacles posed in earlier attempts to devise a distance statistic [e.g., Pearson’s Coefficient of Racial Likeness (Pearson, 1926) and Penrose’s Size and Shape statistic (Penrose, 1954)], namely that of correcting for the correlation among measurements and the repeated influence of size in individual measurements. Finally, these secondary, transformed, variables allowed individuals and/or populations to be located in multivariate space. The mathematical basis of multivariate statistical methods relies on the matrices of variation and covariation. These methods allow
individual specimens to become vectors of their measurements that, in turn, allow them to be located in multivariate space defined by the newly created transformed variables. This appropriateness of multivariate analyses in handling populations is succinctly stated by Howells (1973:3–4):

Methods of multivariate analysis...allow a skull to be treated as a unit, i.e., as a configuration of the information contained in all its measurements. Next, they allow populations to be treated as configurations of such units, taking account of their variation in shape because they in turn are handled as whole configurations of individual dimensions. Finally, the relations and differences between all the populations being considered are set forth in terms of their several individual multivariate ranges of variation. Thus it is possible to see the range of the whole species in such complete and objective informational terms. That is the importance of multivariate statistics: they fit the model of populations looked on not as centroids or means, but as swarms of the varying individuals who compose them; and the differentiation of these swarms from one another constitutes a statement of the degree and nature of the difference between the populations. Although the information is ultimately limited by the measurements selected to describe the skull, their relationships and their relative taxonomic significance are not otherwise biased by the worker.

These refinements in technique have made multivariate methods theoretically the most soundly based for analyzing metric variation. The procedures adopted depend on the questions being asked, but traditionally, differences (or distances) between human groups and classification (grouping analysis) have been the two principal concerns in physical anthropology. Skeletal biologists have addressed similar issues, usually from an archaeological and/or bioarchaeological perspective, including studies that investigate the processes of evolution (selection, drift, gene flow, and the effects of geography), and whether differences in population structure can be attributed to internal versus external (i.e., introduced) influences. Other studies in skeletal biology have been designed to examine more specific issues such as the identification of population (ethnic) boundaries, postmarital residence patterns, familial and kin relationships, cemetery structure, evidence for social stratification, and the presence of intrusive individuals and/or evidence of admixture with different groups (e.g., Buikstra et al., 1990; Konigsberg and Buikstra, 1995; Relethford and Blangero, 1990; Steadman, 2001; Williams-Blangero et al., 1990). Other potential uses of this family of statistical procedures include the identification of individual crania for repatriation claims and forensic applications (Ousley and Jantz, 2005; Powell and Rose, 1999; Snow et al., 1979).

ASSUMPTIONS OF MULTIVARIATE DATA

In recent years, several researchers have cautioned against the inappropriate and “blind” use of multivariate statistical procedures (e.g., Kowalski, 1972; Rhoads, 1984; Van Vark, 1976; Van Vark and van der Sman, 1982). In an attempt to prevent possible misuses of these procedures, careful scrutiny of the data and the assumptions underlying multivariate data are recommended.

All multivariate statistical procedures have a number of underlying statistical and conceptual assumptions that require evaluation if statistical inferences are to be made (e.g., Campbell, 1978; Corruccini, 1975; Hair et al., 2006; Kowalski, 1972; Krzanowski 2000; Tabachnick and Fidell, 2001; Van Vark and Pasveer, 1994). Among the assumptions, multivariate normality and equality of covariances (or within-group variances) are perhaps the most critical. Adherence to the mathematical conditions of multivariate analyses, including adequate sample sizes, however, helps alleviate most of the assumption violations.

Multivariate procedures require sufficiently large sample sizes. As a general rule, some
(e.g., Corruccini, 1975; McHenry and Corruccini, 1975) have suggested that the sample size should exceed the number of variables used. Others (e.g., Lachenbruch and Goldstein, 1979:70) suggest that there should be at least three times as many individuals for each sample as there are measurements (variables). Aside from these and other more general guidelines, there is a lack of unanimous agreement on what constitutes a "sufficiently" large sample. Howells (1973, 1989, 1995), who maintains that samples should be relatively large and comparable in size, ultimately selected 50–55 specimens of each sex in his multivariate analyses. Opinions vary on the effects of unequal sample size especially with regard to the covariance matrix. As a general precaution, however, it is advised that sample sizes be kept uniform. The techniques of statistical power analysis and sample size estimation, now part of most statistical software packages (e.g., SAS), can be used to determine how large a sample is needed for statistical judgments to be accurate and reliable.

Multivariate normality of the data is the assumption that each variable, and all linear combinations of the variables are normally distributed (Tabachnick and Fidell, 2001:72). Ideally, the distribution should be normal, but opinions vary as to the adversity of the effects of non-normal distributions in influencing the results of multivariate analyses. Maintaining equal and sufficiently large samples would seem to satisfy this condition. Reymert (1990) discusses some of the more robust techniques that control for non-normality. There are also distribution-free inferential techniques such as jackknife and bootstrap analyses, based on resampling, that do not require normally distributed data.

Perhaps the most critical assumption of the multivariate conditions is homogeneity of the covariance (variance–covariance) matrix (Campbell, 1978), which is an assumption that may never be completely satisfied (Van Vark and Schaufsma, 1992:236). If the covariance matrices of individual groups (these represent the deviation between one variable and its mean times the deviation between a second variable and its mean, etc.) are unequal, the results of multivariate analyses can be affected adversely. Maintaining large and approximately equal sample sizes should, at least on mathematical and statistical grounds, reduce the likelihood of violating the homogeneity covariance assumption.

However daunting these assumptions may appear, potential users, including those with little or no background in mathematics and/or statistics, should not be unduly dissuaded from applying these methods. Statistical tests for normality and equivalence of covariances, and their remedies, are available in most multivariate statistical packages. Choosing samples with care, maintaining equal and large sample sizes, careful scrutiny of the data, and the possible pre-selection of variables using discriminant analysis as prescribed by some (Van Vark and Schaufsma, 1992), help to avoid violating these underlying assumptions.

**CLASSIC MULTIVARIATE STATISTICAL METHODS**

The statistical procedures most commonly used by skeletal biologists and physical anthropologists include factor analysis, principal components analysis, discriminant function analysis, and generalized distance. The latter two multivariate procedures are designed to handle two or more groups, whereas principal components analysis, factor analysis, and related techniques are for investigating underlying patterns in a single group. Various clustering methods, and multidimensional scaling techniques, provide a useful means of visualizing the results of multivariate procedures. Some of the newest approaches include the use of digitizing nodes to produce three-dimensional images as well as other uses of coordinate geometry that generate a multitude of measurements in place of the traditional caliper-generated ones.
Principal Components and Factor Analysis

Factor analysis and related procedures such as principal components analysis (PCA), by focusing on the interrelationship (covariation) among a large number of variables of a single sample, seek to identify common underlying patterns of variation through an inspection of their shared underlying factors, or axes. Unlike discriminant function analysis, PCA does not employ any criterion for maximizing differences among the groups. Individual specimens can be scored or located on these new axes or factors. Examples that use factor analysis and PCA in physical anthropology include studies by Howells (1957, 1972, 1973) and Brown (1973).

Discriminant Function (Canonical) Analysis

The major purpose of discriminant analysis is to maximize differences between two groups. The mathematical basis (Goldstein and Dillon, 1978) for this procedure is to weight and combine, in a linear manner, two or more discriminating variables in such a way that the intercorrelations of the variables are considered and the ratio of between-group variance to the within-group (total) variance is maximized (Tatsuoka, 1970). This concept can then be extended to include more than two groups; in which case, the procedure is commonly referred to as multiple discriminant function, or canonical variate, analysis. The resulting transformed variables, known as discriminant functions, or canonical variates, possess the important property of being orthogonal (uncorrelated, or independent). Individuals and/or groups can then be placed in a multidimensional space, thus providing a means of visualizing these interrelationships. The total number of functions is one less than the number of groups entered or one less than the original number of measurements if that is less. Typically, the first few transformed variables account for the preponderance of the variation among groups. The remaining functions, usually ranked in decreasing importance, are responsible for the residual variation. Although originally designed to assign an unknown specimen to one or more groups, discriminant analysis is now widely used as a measure of group separation (Campbell, 1978).

The original measurements selected in computing the linear classification functions can be chosen in a stepwise manner (stepwise discriminant function analysis) such that, at each step, the measurement that adds the most to the separation of the groups is entered into the discriminant function in advance of the others (Dixon and Brown, 1979:711). The technique also identifies which of the measurements (variables) are most responsible for the observed differentiation. Another utilitarian aspect of the latter procedure is that it allows for the selection of a subset of measurements for use in subsequent distance analyses (Heathcote, 1994; Rightmire, 1970). In the applications presented in this chapter, the interpretation of the discriminant functions and the patterns of group separation is based on an inspection of standardized canonical, or discriminant, coefficients.

At the end of the stepping process, each specimen is classified into one of the original groups based on the several discriminant scores it receives. The probability of group membership can be evaluated mathematically through the calculation of posterior probabilities and/or typicality probabilities. Posterior probabilities assume that the unknown specimens belongs to one of the groups included in the function, whereas typicality probabilities evaluate how likely the unknown belongs to any, or none, of the groups based on the average variability of all the groups in the analysis (Tatsuoka, 1971:228–232; Van Vark and Schaafsma, 1992:244–246). The results are presented in the form of a classification matrix. The classification results provide an additional check on how well the groups are, or are not, differentiated from one another as well as provide a general guide for assessing the homogeneity or heterogeneity of each group. Most major computer packages provide cross-validation procedures (e.g., jackknife methods) to check
discriminant results and the probability that an individual belonging to a specified group has been misclassified. To ensure that the results are externally as well as internally valid, the final stage of discriminant analysis typically involves the validation of the discriminant function—results. One such technique, as will be demonstrated in the examples in this chapter, is the jackknife classification method in which the discriminant function is reestimated on multiple subsets of the original samples. In these examples, each case is reclassified into a group (its own or any other one included in the analysis) according to the classification functions computed from all data except the individual case being classified.

Some of the earliest and best known examples that use discriminant function analysis in skeletal biology are concerned with assigning an unknown individual specimen to a given reference group for determining ancestry (Giles and Elliot, 1962) and sex (Giles and Elliot, 1963). In these early examples, discriminant functions (or equations with weights for a number of measurements of an individual which are multiplied to provide a single score) are computed from the measurements of two defined groups (e.g., male and female) such that the differences between the two groups are maximized (F-ratios are maximized), whereas the deviation of individual cases from their respective means remains minimal. Once a discriminant function has been computed between two groups, an unknown specimen can be assigned to one of these groups. There have been many other applications, before and since, including, most notably, the assignment of unknown human or nonhuman primate fossils (e.g., Albrecht, 1992; Campbell, 1984; Howells, 1966; Kamminga and Wright, 1988; Powell and Neves, 1999; Rightmire, 1979; Van Vark, 1995; Wright, 1992a).

Several statistical packages, with a variety of multivariate procedures designed for mainframe and personal computers such as BMDP (Dixon, 1990a, 1990b, 1992; Dixon and Brown, 1979), SAS (1990a, 1990b), SSPS (1993, 1999a, 1999b, 1999c), SYSTAT (1992), and NTSYS (Rohlf, 1993) are now available. Other, more specialized programs written for personal computers, such as CRANID2/CRANID3 (Wright, 1992a, 1992b, 2005) and FORDISC3 (Ousley and Jantz, 2005), are also available. Complementing these are software programs that may be downloaded from websites like that of L.W. Konigsberg at http://konig.la.utk.edu/.

Similar procedures, although not accessible to the general public, have been introduced by Van der Sluis et al. (1985) and Howells (1995). The former method, POSCON, used by Van Vark and Schaafsma (1992), is similar to CRANID3 in that both use principal components analysis rather than discriminant function analysis, and the database provided by Howells (1989), to assign an unknown skull. POSCON uses Euclidean distances (explained in the next section) between the unknown skull and the group centroids for classification, whereas CRANID3 examines the Euclidean distances (space) of all the individuals of the reference groups and determines the identity of the unknown skull by reading the list of the 50 nearest individuals. Howells (1995) uses methods similar to both of these (DISPOP and POPKIN), but these are based on discriminant function analysis.

**Mahalanobis's Generalized Distance and Euclidean Distance**

Although several different distance measures are available, the most commonly used one is Euclidean distance, which can be represented geometrically (hence, the name) as the length of the hypotenuse of a right angle that is calculated by the formula: $\sqrt{(X_2-X_1)^2+(Y_2-Y_1)^2}$, where $X_1, Y_1$ and $X_2, Y_2$ represent the respective coordinates of two points plotted on two variables, X and Y. This concept may then be extended to more than two variables. Mahalanobis's distance ($D^2$) uses the squared (i.e., the sum of squared distances without taking the square root in the above formula) Euclidean distance.

Mahalanobis's generalized distance, $D^2$ (Mahalanobis, 1930, 1936; Mahalanobis et al., 1949; Rao, 1948, 1952), remains the classic, if
only realistic (Reyment et al., 1984), measure of biological distance for analyzing metric data. The immense popularity of the $D^2$ statistic as a measure of distance stems from its theoretical soundness. Generalized distance is computed by maximizing the difference between pairs of groups by maximizing the between-group variance to the pooled within-group variance. This process involves an inversion of the pooled correlation (within-group variance—covariance) matrix. The usual assumptions of equivalence of covariance matrices, normal distribution of variables, and large sample sizes are usually satisfied by pooling sample covariance matrices and avoiding small and extremely uneven sample sizes. Gower (1972), as well as Sneath and Sokal (1973), provides the mathematical basis for computing $D^2$.

Through this procedure, the original variables are transformed into a new set of variables whose correlation with the remaining variables has been removed. $D^2$ represents the summed squared difference between the transformed mean values of any two groups compared. The failure to correct for this correlation was a major flaw with earlier proposed distance statistics such as Pearson’s CRL (Pearson, 1926) and Penrose’s Size and Shape statistic (Penrose, 1947, 1954). Another attraction of generalized distance is that its values do not change if the number and kinds of measurements differ (Van Vark and Shaafsma, 1992:238).

Statistical testing of the significance of the derived distances was first introduced by Hotelling (1933). The method described in Rao (1952:245), one used by Talbot and Mulhall (1962), and later reiterated by Buranarugsa and Leach (1993:17), is the one used in the applications presented in this chapter. The quantity, \( \frac{(n_i/\bar{n}) D^2_{ij}}{n_i} \), is distributed as chi-square with \( p \) degrees of freedom \( (n_i = \text{sample size of group } i; n_j = \text{sample size of group } j; D^2_{ij} = \text{square of the generalized distance between groups } i \text{ and } j; \text{ and } p = \text{number of variables employed}. \) The nonsignificance of \( D^2 \) generally indicates that the differences are too small for detection of group differences and/or that the sample sizes are too small.

Because a single quantitative value, which measures dissimilarity between pairs of groups is obtained, another attraction of the generalized distance statistic is that various methods for clustering groups based on these values can be applied. Most computer statistical packages routinely generate Mahalanobis’s generalized distances as output in discriminant function analysis programs.

Other Multivariate Methods (Q-mode and R-mode Analyses)

Other ways of portraying relationships between individual specimens or groups include canonical plots, metric multidimensional scaling (Torgerson, 1952), and principal coordinate analysis (Gower, 1966). The latter two procedures are most often used in association with factor analysis and Q-mode principal components analysis.

Q-mode and R-mode analyses represent two related multivariate techniques, which represent the inverse of principal components analysis and related procedures. R-mode analysis focuses on relationships between variables, whereas Q-mode analysis focuses on relationships between individuals. The principal aim of Q-mode analysis is a graphical visualization of the inter-relationships between individuals of a sample and the identification of clusters (Reyment, 1990:125). Examples that apply Q-mode analysis for analyzing skeletal metric data include those of Howells (1989) and Hanihara (1996).

Alternatives to these methods include the use of Chernoff “faces” (Chernoff, 1973, 1978), Fourier transformations, and boxplots, which some researchers have adopted (e.g., Brown, 1996; Wilson, 1984). Most applications in skeletal biology, however, use distance matrices or some measure of similarity, or dissimilarity.

Finally, group means, or centroids, can be plotted for the first few canonical variates, or functions, in multiple discriminant function analysis or canonical variate analysis to
represent intergroup relationships. Although the procedures are mathematically unrelated, substantial agreement exists between tree construction procedures, which are discussed in the next section, and these other methods of representing multivariate results.

**CLUSTER ANALYSIS AND CLUSTERING ALGORITHMS**

Cluster analyses are often regarded as one group of related multivariate procedures, which differ from the other procedures discussed in this chapter in that they do not actually estimate a variate but rather use one that has already been specified (e.g., $D^2$). Again, these techniques involve the simultaneous utilization of many variables whose purpose is to group individuals (or objects) on the basis of characteristics they possess (Hair et al., 2006). The results of cluster analysis are typically depicted as a tree-like structure, or dendrogram, which has become a popular and convenient way to graphically illustrate and summarize multivariate data (Evertt and Dunn, 1992). Wilmink and Uytterschaut (1984) provide the historical and theoretical background for the use of cluster analysis in physical anthropology. Gower (1967, 1972) provides good comparisons of several methods of cluster analysis.

Although clustering is not phylogeny (Howells, 1984), dendrograms like those based on Mahalanobis’s distances, have implications for the latter and are routinely used in interpreting past relationships. The theoretical and methodological background for most of these techniques derives from classic numerical taxonomy (Sneath and Sokal, 1973). Numerical taxonomy includes quantitative (numeric) methods for grouping usually based on overall morphological (phenetic) similarity where each character, when assigned a specified numerical value, is considered to have equal weight. These methods typically allow the selection of the largest number of traits possible. Numerical, or phenetic, taxonomy represents one of the two major approaches to systematic biological classification (Levin and Foley, 2004). The other major approach to classification is phylogenetic systematics, or cladistics, in which evolutionary history is inferred from branching patterns of phylogeny that require the careful weighting of only a few traits.

The most commonly used clustering methods comprise a family of procedures known as the hierarchical (either agglomerative or divisive) clustering techniques (Sokal and Rohlf, 1995; Sneath and Sokal, 1973). Agglomerative clustering techniques commence by placing each object (or group) in a single cluster. In subsequent steps, the two most similar clusters are combined into a new (aggregate) cluster, which is a process that continues until all groups are combined into a single cluster. In the opposite clustering procedure, hierarchical divisive methods, the process begins by placing all groups into a single cluster that is then divided into two clusters that contain the most dissimilar groups. Since clusters at any stage are obtained by the combination (or division) of two clusters from the previous stage, these methods lead to a hierarchical structure for the diagram. Different options are available (e.g., single lineage, complete linkage, or group average) depending on how distance, or similarity, of the clusters is measured.

One of the most commonly used agglomerative clustering techniques is UPGMA, or the unweighted pair-group method, arithmetic average algorithm, which measures similarity as the average distance between all cases in one cluster to all cases in another. That is, the average distance between all cases in the resulting cluster is as small as possible and the distance between two clusters is taken as the average between all possible pairs of cases in the cluster. For those interested in phylogenetic tree reconstruction, this method assumes a constant rate of evolution.

An alternative clustering algorithm, the neighbor-joining (NJ) method (Saitou and Nei, 1987; Saitou et al., 1991), which was used initially to construct trees from genetic data, has also been applied to distances
derived from skeletal data. This algorithm, also known as the method of minimum evolution, is conceptually related to cluster analysis but differs from UPGMA in that it does not assume that all the lineages have diverged equal amounts, thus removing the assumption of constant rates of evolution. Recent computer simulations (Saitou and Imanishi, 1989; Saitou and Nei, 1987) have suggested that the NJ method yields more accurate trees than does the UPGMA method and thus produces a truer phylogenetic tree, at least when gene frequency data are used. The NTSYS-pc computer software program by Rohlf (1993) provides one of the most comprehensive selections of clustering algorithms of interest to skeletal biologists.

RESEARCH DESIGN

Regardless of the intrinsic problems in defining human groups, biologically and statistically, selection and definition of groups is a necessary preliminary step to data analysis. Most of the multivariate statistical procedures reviewed in this chapter require that individual specimens be assigned to groups a priori. The skeletal series encountered most frequently in skeletal biology represent aggregates of individuals found in a specified area at a given time or some subgrouping of individuals below the species level. As is often the case in skeletal biology, archaeological human remains may easily represent individuals who lived and died at different times and whose ancestral-descendant relationships are unknown. In many instances, the “skeletal series” represents a collection of skulls housed in museums documented as having been collected from a specific village, island, or region. In ideal circumstances, exact provenance of the specimens may be available, but often in these situations, completeness, preservation, and the number of specimens available is frequently problematic.

Two basic underlying theoretical assumptions in distance studies using morphological data are that morphometric similarity implies genetic similarity and that the more similar two groups are, the more closely related they must be relative to groups that exhibit greater differences. Despite the demonstration of significant heritability components for both metric and nonmetric traits, morphological traits (including measurements) are also subject to nongenetic influences. Environment and/or allometry rather than gene flow, migration, genetic drift, and other isolating factors may be responsible, or at least contribute, to the results obtained in biodistance analysis. Despite these reservations, general consensus exists (see, e.g., Van Vark and Schaafsma, 1992:241) that biological relatedness as measured by biological distances based on metric data reflects genetic similarity. Konigsberg and Ousley’s (1995) finding of a correlation between anthropometric and quantitative genetic analyses strengthens this assertion.

Of the two basic approaches to the analysis of metric data in studies of population structure outlined by Relethford and Lees (1982), model-bound and model-free, the latter approach remains the one most frequently adopted in studies of physical anthropology and skeletal biology. Multivariate statistical methods, such as measures of biological distances and discriminant functions, have frequently been used in anthropology as exploratory tools for summarizing data on patterns of variability and overall similarities among groups (often accompanied by comparisons with other types of data) and for reconstructing the evolutionary histories of these groups, regardless of cause. Model-bound approaches, although methodologically appealing because they incorporate measures of population similarity directly into models of population structure to estimate one or more parameters (e.g., admixture, genetic drift, gene flow, or effective population size) like the methods used to analyze living populations, have been used less frequently in metric studies of past populations.
The approach used in the example in this chapter is model free. Mahalanobis’s generalized distance and discriminant function analysis are used to investigate patterns of craniometric variation, which, in turn, are used to reconstruct the evolutionary histories and possible origins of the groups, regardless of cause.

**AN APPLICATION**

The example of an application of some methods discussed in this chapter focuses on the population history and biological relatedness among recent and near recent peoples who occupy eastern Asia and the Pacific. Two multivariate statistical procedures, stepwise discriminant function analysis and Mahalanobis’s generalized distance, are applied to 27 cranial measurements recorded in a total of 2805 male crania representing 63 cranial series representing modern and near-modern inhabitants of Oceania, Australia, Southeast Asia, and East Asia. The data derive from earlier studies (e.g., Pietrusewsky, 1990a, 1994, 2004, 2005).

**Preparation of Data**

**Variable Selection.** Although the need in craniometric analysis to improvise new measurements continues (see, e.g., Howells, 1973), many measurements currently used by skeletal biologists can be traced to early international conventions (e.g., Frankfort Agreement of 1882) and attempts to standardize the technique to ensure the comparability of measurements (e.g., Broca, 1875; Martin and Saller, 1957; Vallois, 1965). These traditional measurements require detailed definitions, including landmark definitions and instrumentation (e.g., spreading, sliding, or coordinate calipers), which is information that is available in several recent publications (Bräuer, 1988; Buikstra and Ubelaker, 1994; Moore-Jansen et al., 1994). Although there are exceptions (e.g., Van Vark and Pasveer, 1994:233), for most multivariate analyses, it is generally preferable to begin with as many variables as possible from which subsets of variables may be selected. Which measurements are ultimately selected for analysis depends on the research questions that are being addressed. The 27 standard cranial measurements included in this application are defined in Table 16.2 later on in this chapter. The number of measurements represents the greatest number of variables comparable with all the series.

**Errors.** The reliability (i.e., the extent to which a metric variable is reproducible over time) of metric data hinges on precision (freedom from measurement error at the individual level) as well as on the dependability of the variable or its freedom from short-term random influences (Marks et al., 1989). The latter, which are generally beyond the control of the individual observer, probably are of minor concern compared with error introduced at the observer level. The recognition of climatic influences on cranial measurements (Utermhole et al., 1983), however, would seem to argue for proper storage of specimens.

Certainly, the precision of measurements can be enhanced greatly with the standardization of the technique and with calibration of the measuring equipment. Other sources of possible error (and imprecision) may be attributed to reading, recording, and/or data entry errors. If more than a single observer is involved, the possible sources of error may be compounded greatly. In the case of a single observer, the approach is to focus on intraobserver, or within-observer, reliability and replication. For intraobserver error, access to the original material offers the best solution. Interobserver (more than one observer) error is more of a concern in reliability studies. A variety of statistical techniques (from basic descriptive statistics to the analysis of variance and correlation coefficients, and so on) are available for assessing the degree of error (Utermhole and Zegura, 1982). Although the potential for interobserver error would seem to argue against the combining of data from different observers, a recent study (Willis, 1999) that uses data recorded by several independent researchers
spanning a considerable period of time concluded that interobserver error, at least among those measurements found to be common, was not a major concern. This finding should be of some comfort to future researchers contemplating metric analyses but who are otherwise denied access to the original skeletal remains.

**Missing Data.** Most multivariate procedures require complete sets of data, which often means that missing measurements, a frequent occurrence in studies involving archaeological human remains, must be supplied by estimation. A common solution to this problem is to replace the missing observation with its regressed value (Howells, 1973; Van Vark and Pasveer, 1994). Various statistical packages such as BMDP (Dixon and Brown, 1979; Dixon, 1992) contain suitable regression analysis programs for such purposes. These procedures, however, should only be used when a few of the measurements are missing either per individual and/or per variable, which means that only complete or nearly complete specimens can be used ultimately in multivariate statistical analyses. More details on missing observations and general guidelines for dealing with them are described by Howells (1973:33–35), Van Vark (1985, 1995), Van Vark and Shaafsma 1992, Van Vark and Pasveer (1994), and Schafer (1997, 1999).

In this application, missing measurements, which were minimal, were replaced with regressed values obtained through stepwise regression analysis using the computer program, PAM, of the BMDP statistical package (Dixon and Brown, 1979).

**Removal of the Size-Based Component (Z-Scores and C-Scores).** A fairly common concern in bidistance analyses that use multivariate statistical procedures is to determine the relative contribution of size and shape in distance measures. Size is defined as the magnitude of a vector of measurements on an organism, whereas shape is a function of relative proportion normalized by size (Corruccini, 1987:289, 290). Many investigators regard shape, rather than size, as being of greater importance when the taxonomic units in question are above the deme or subspecies level and, thus, warrant the removal of the size-based component (Corruccini, 1973:743). Several researchers (e.g., Brace and Hunt, 1990; Brace et al., 1990; Brace and Tracer, 1992; Howells, 1989) have advocated the use of C-scores as a way to compensate, at least partially, for the unequal influence that size differences may exert on the patterns of variation.

However, although the use of C-scores theoretically compensates for size differences and hence their unequal influence on the patterns of variation, others (e.g., Green, 1990; Pietrusewsky, 1994, 1995) have demonstrated that removal of this size-based component has little or no effect on the interpretation of patterns of craniometric variation. Accordingly, C-score measures are not used in this application.

**Cranial Series**

The approximate locations of the 63 male cranial series used in the application, representing modern and near-modern inhabitants of the Pacific, Australia, Southeast Asia, and East Asia, are shown in Fig. 16.1. Additional information for these comparative series is given in Table 16.1.

**Results of Applying Multivariate Analysis**

**Stepwise Discriminant Function Analysis.** Stepwise discriminant function analysis was applied to 27 cranial measurements recorded in 63 male cranial series using the computer program, BMDP-7M (Dixon, 1992), which was written for the mainframe computer.

A summary of the measurements, ranked according to the F-values [tests of equality of group means using classic one-way analysis of variance] received in the final step of discriminant function analysis, is given in Table 16.2. The order of the measurements in
this table provides an indication of the discriminatory power of the original variables. In this analysis, three breadth measurements (maximum cranial breadth, biorbital breadth, and minimum cranial breadth), basion–nasion length, and nasion–alveolar length received the highest ranking.

Eigenvalues, also referred to as latent roots, represent the amount of variance accounted for by each function or canonical variate, which is here expressed as the percentage of total dispersion; the level of significance tested by Bartlett’s criterion (Rao, 1952:373) for the 27 canonical variates are presented in Table 16.3. The maximum number of canonical variates (and computed eigenvalues) is equal to the number of original variables entered into the analysis. Eigenvalues identify those variates that contribute the most to the discrimination; generally values greater than 1 are considered significant, whereas those less than 1 are insignificant. This procedure thus reduces the original number of variates while retaining as much of the information in the original variables (i.e., measurements). The values under % Dispersion indicate percentage of dispersion accounted for by each corresponding transformed, or canonical, variate. In this analysis, the first three canonical variates account for 63.7% of the total variation. All eigenvalues are significant at the 1% level, which indicates significant heterogeneity for these canonical variates, or axes.

Canonical coefficients, which represent those values by which an individual’s measurements may be multiplied to obtain its score, for 27 measurements, for the first three canonical variates are given in Table 16.4.

---

**Figure 16.1** Map showing the approximate locations of the 63 cranial series used in the application. The numbers correspond to the cranial series in Table 16.1.
<table>
<thead>
<tr>
<th>Series Map No. &amp; Name (abbrev.)</th>
<th>No. of Crania</th>
<th>Location* and Number of Crania</th>
<th>Remarks</th>
</tr>
</thead>
<tbody>
<tr>
<td><strong>Polynesia</strong></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>1. Tonga-Samoan (TOG)</td>
<td>19</td>
<td>BER-3; AMS-2; DRE-1; PAR-1 BPB-4; AIM-2; AUK-5; SIM-1</td>
<td>Fourteen specimens are from Tonga and five are from Samoa. Included in the Tongan series are three skulls from Pongaimotu excavated by McKern in 1920; two from To-At-1 &amp; To-At-2 excavated by J. Davidson in 1965; and five from To-At-36 excavated by D. Spennemann in 1985–1986. The remaining specimens are from museums in Berlin, Paris, and Sydney.</td>
</tr>
<tr>
<td>2. Rapa Nui (RAP)</td>
<td>50</td>
<td>BER-5; DRE-9; PAR-36</td>
<td>Pinart collected most crania in Paris in 1887 at Vaihu and La Perouse Bay, Rapa Nui (Easter Island).</td>
</tr>
<tr>
<td>3. Hawaii (HAW)</td>
<td>60</td>
<td>BPB-20; HON-20; SIM-20</td>
<td>An equal number of specimens have been randomly chosen from three different skeletal series: Mokapu (Oahu), Honokahua (Maui), and Kauai. All specimens are presumed to be prehistoric.</td>
</tr>
<tr>
<td>4. Marquesas (MRQ)</td>
<td>63</td>
<td>PAR-49; LEP-1; BLU-1; BPB-12</td>
<td>Crania are from four islands, Fatu Hiva, Tahuata, Nuku Hiva and Hiva Oa.</td>
</tr>
<tr>
<td>5. New Zealand (NZ)</td>
<td>50</td>
<td>BRE-3; PAR-21; SAM-1; AIM-13; GOT-1; ZUR-5; DRE-6</td>
<td>A representative sample of New Zealand Maori crania from the North and South Islands of New Zealand.</td>
</tr>
<tr>
<td>6. Chatham Is. (CHT)</td>
<td>45</td>
<td>DUN-8; OTM-2 WEL-4; CAN-10 AIM-3; DRE-5 AMS-2; DAS-3 GOT-4; PAR-4</td>
<td>Moriori crania from the Chatham Islands, New Zealand.</td>
</tr>
<tr>
<td>7. Society Is. (SOC)</td>
<td>44</td>
<td>PAR-33; BPB-11</td>
<td>Crania are from the island of Tahiti, Society Islands.</td>
</tr>
<tr>
<td>8. Tuamotu Arch. (TUA)</td>
<td>18</td>
<td>PAR-18</td>
<td>Most specimens are from Makatea in the Tuamotu Archipelago.</td>
</tr>
<tr>
<td>9. Gambier Is. (GAM)</td>
<td>7</td>
<td>PAR-7</td>
<td>Dumontier collected most of these crania from an abandoned cemetery on Magareva Islands, Gambier Islands, French Polynesia, circa 1874.</td>
</tr>
<tr>
<td><strong>Island Melanesia</strong></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>10. Fiji (FIJ)</td>
<td>42</td>
<td>BER-1; SAM-3; QMB-1; DRE-4 FRE-3; CHA-1; BPB-11; PAR-7 AMS-3; DUN-6; SIM-2</td>
<td>Crania are from all major islands, including the Lau Group in the Fiji Islands.</td>
</tr>
<tr>
<td>11. Vanuatu (VAN)</td>
<td>47</td>
<td>BAS-47</td>
<td>F. Speiser collected most specimens in 1912 from Malo, Pentecost and Espiru Santo Islands, Vanuatu.</td>
</tr>
</tbody>
</table>

(Continued)
### TABLE 16.1  Continued

<table>
<thead>
<tr>
<th>Series Map No. &amp; Name (abbrev.)</th>
<th>No. of Crania</th>
<th>Location(^a) and Number of Crania</th>
<th>Remarks</th>
</tr>
</thead>
<tbody>
<tr>
<td>12. Loyalty Is. (LOY)</td>
<td>50</td>
<td>BAS-43; PAR-7</td>
<td>Crania are from Mare, Lifou, and Ouvéa Island Groups, Loyalty Islands.</td>
</tr>
<tr>
<td>13. New Caledonia (NCL)</td>
<td>50</td>
<td>BAS-34; PAR-16</td>
<td>Crania are from several coastal and inland locations on New Caledonia. Most of these specimens were collected in the late nineteenth century.</td>
</tr>
<tr>
<td>14. Santa Cruz Is. (SCR)</td>
<td>46</td>
<td>SAM-4; AMS-2; BAS-40</td>
<td>Felix Speiser collected the crania located in Basel in 1912 (Speiser, 1928).</td>
</tr>
<tr>
<td>15. Solomon Is. (SOL)</td>
<td>49</td>
<td>DRE-4; BER-1; NMV-1; QMB-3; AMS-16; DAS-10; BAS-14; GOT-1</td>
<td>Crania are from Buka Island (1), New Georgia (5), Guadalcanal (9), San Cristobal Island (7), and other locations in the Solomon Islands.</td>
</tr>
<tr>
<td>16. New Britain (NBR)</td>
<td>50</td>
<td>CHA-20; DRE-30</td>
<td>The specimens from New Britain in Dresden were collected by A. Baessler in 1900, and those in Berlin were collected by R. Parkinson in 1911. These specimens were collected from trading posts near Rabul in the Gazelle Peninsula and most likely represent Tolai crania (see Pietrusewsky, 1990b:236–237; Howells, 1973:24–25).</td>
</tr>
<tr>
<td>17. New Ireland (NIR)</td>
<td>53</td>
<td>AMS-4; BER-2; BLU-6; DRE-18; GOT-15; QMB-1; SAM-6; TUB-1</td>
<td>Pöhl collected most of the crania in Dresden in 1887–1888 from the northern end of the island; the specimens in Göttingen were collected during the Süddeutsche Expedition in 1908.</td>
</tr>
<tr>
<td>18. Admiralty Is. (ADR)</td>
<td>50</td>
<td>DRE-20; GOT-9; CHA-6; TUB-15;</td>
<td>Specimens from Hermit, Kaniet, and Manus Islands, Admiralty Islands.</td>
</tr>
</tbody>
</table>

**New Guinea**

| 19. Sepik R. (SEP)              | 50            | DRE-33; GOT-10; TUB-7                | Otto Schlaginhaufen collected the specimens in Dresden in 1909 from various locations along the Sepik River, Papua New Guinea. |
| 20. Biak Island (BIK)           | 48            | DRE-48                               | Most (45) of the specimens were collected by A.B. Meyer in 1873 on Biak Island (Mysore), Geelvink Bay, Irian Jaya. |
| 21. Fly R. (FLY)                | 42            | DRE-35; QMB-7                        | Most of the skulls in Dresden were collected by Webster in 1902 along the Fly R. of Papua New Guinea. Many of the crania are decorated and have engraved frontal bones (see Pietrusewsky, 1990b:235–236 for further details). |

(Continued)
<table>
<thead>
<tr>
<th>Series Map No. &amp; Name (abbrev.)</th>
<th>No. of Crania</th>
<th>Location a and Number of Crania</th>
<th>Remarks</th>
</tr>
</thead>
<tbody>
<tr>
<td>22. Purari Delta (PUR)</td>
<td>50</td>
<td>DRE-50</td>
<td>Decorated (engraved) skulls obtained by Messrs. Gerard and Webster between 1900 and 1902 are from along the Purari River and Purari Delta regions, Papua New Guinea.</td>
</tr>
<tr>
<td>23. D’Entrecasteaux Is. (DTX)</td>
<td>26</td>
<td>FRE-21; DRE-4; QMB-1</td>
<td>Crania are from Fergusson (16) and Normanby (10) Islands of the D’Entrecasteaux Islands.</td>
</tr>
<tr>
<td>24. Dawson Strait Is. (DAW)</td>
<td>48</td>
<td>ROM-48</td>
<td>Crania are from the islands of the Dawson Straits (between Normanby and Fergusson Islands of the D’Entrecasteaux Islands), which were collected by L. Loria on a voyage to Papua New Guinea between 1889 and 1890.</td>
</tr>
<tr>
<td>Australia/Tasmania</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>25. Murray R. (MRB)</td>
<td>50</td>
<td>AIA-39; DAM-11</td>
<td>Australian Aboriginal crania were collected by G.M. Black along the Murray River (Chowilla to Coobool) in New South Wales between 1929 and 1950.</td>
</tr>
<tr>
<td>26. New South Wales (NSW)</td>
<td>62</td>
<td>AMS-21; DAS-41</td>
<td>Australian Aboriginal crania from the coastal locations in New South Wales.</td>
</tr>
<tr>
<td>27. Queensland (QLD)</td>
<td>54</td>
<td>AMS-21; DAS-3; QMB-30</td>
<td>Australian Aboriginal crania from the southeastern and middle-eastern regions of Queensland.</td>
</tr>
<tr>
<td>28. Northern Territory (NT)</td>
<td>50</td>
<td>AIA-4; AMS-3; MMS-1; NMV-38; QMB-1; SAM-3</td>
<td>Australian Aboriginal crania from Port Darwin (39) and Arnhemland (36) in the Northern Territory, Australia.</td>
</tr>
<tr>
<td>30. Western Australia (WA)</td>
<td>47</td>
<td>WAM-47</td>
<td>Australian Aboriginal crania from the central (20), eastern (4), northern (14), and southern (9) regions of Western Australia.</td>
</tr>
<tr>
<td>31. Tasmania (TAS)</td>
<td>26</td>
<td>THM-22; CHA-1; SAM-2; NMV-1</td>
<td>The crania represent Tasmanian Aborigines.</td>
</tr>
</tbody>
</table>

(Continued)
<table>
<thead>
<tr>
<th>Series Map No. &amp; Name (abbrev.)</th>
<th>No. of Crania</th>
<th>Location* and Number of Crania</th>
<th>Remarks</th>
</tr>
</thead>
<tbody>
<tr>
<td>Micronesia</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>32. Guam (GUA)</td>
<td>46</td>
<td>BPB-42; PAR-4</td>
<td>Pre-Spanish Chamorro crania associated with <em>latte</em> structures collected in the 1920s by Hans Hornbostel along Tumon Beach, Tumon Bay, Guam. The crania are from Kosrae Island (1), Pohnpei (16), and Chuuk (7) Islands of the central and eastern Caroline Islands, Federated States of Micronesia.</td>
</tr>
<tr>
<td>33. Caroline Is. (CAR)</td>
<td>24</td>
<td>TRO-7; DRE-9; PAR-4; GOT-3; AMS-1</td>
<td></td>
</tr>
<tr>
<td>34. Marshall/Kiribati Is. (MSK)</td>
<td>13</td>
<td>PAR-6; GOT-3; FRE-3; BER-1</td>
<td>Crania are from the Marshall (7) and Kiribati (6) Islands of eastern Micronesia.</td>
</tr>
<tr>
<td>Island Southeast Asia</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>35. Sumatra (SUM)</td>
<td>39</td>
<td>BER-1; BRE-1; DRE-5; LEP-4; PAR-3; ZUR-25</td>
<td>The specimens in Zurich are designated &quot;Battak.&quot; Specific locations within the island of Sumatra are not known. Crania were collected from several different localities in Java. A great many of the specimens are indicated as representing Dayak tribes; some have elaborate decorations. An exact location is known for many of these specimens.</td>
</tr>
<tr>
<td>36. Java (JAV)</td>
<td>50</td>
<td>BER-1; BLU-8; CHA-9; DRE-1; LEP-24; PAR-7</td>
<td></td>
</tr>
<tr>
<td>37. Borneo (BOR)</td>
<td>34</td>
<td>BER-2; BRE-2; DRE-6; FRE-4; LEP-8; PAR-12</td>
<td></td>
</tr>
<tr>
<td>38. Sulawesi (SLW)</td>
<td>41</td>
<td>BAS-7; BER-10; DRE-4; FRE-7; LEP-5; PAR-8</td>
<td></td>
</tr>
<tr>
<td>39. Lesser Sunda Is. (LSN)</td>
<td>61</td>
<td>BAS-5; BER-6; BLU-2; CHA-1; DRE-17; LEP-1; PAR-6; ZUR-7</td>
<td>Crania from Bali (13), Flores (9), Sumba (1), Lombok (2), Alor (2), Timor (11), Wetar (2), Leti (4), Barbar (1), Tamimbar (13), Kai (2), and Aru (1) Islands of the Lesser Sunda Islands. Crania from the Seram (48) and Buru (17) Islands in the Southern Molucca Islands. The specimens in Paris were collected by Montano-Rey circa 1900. Most specimens are from Luzon Island.</td>
</tr>
<tr>
<td>40. S. Molucca Is. (SML)</td>
<td>65</td>
<td>FRE-47; DRE-17</td>
<td></td>
</tr>
<tr>
<td>41. Sulu (SUL)</td>
<td>38</td>
<td>LEP-1; PAR-37</td>
<td></td>
</tr>
<tr>
<td>42. Philippines (PHL)</td>
<td>28</td>
<td>BER-9; DRE-19</td>
<td></td>
</tr>
<tr>
<td>Mainland Southeast Asia</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>43. Viet Nam (VTN)</td>
<td>49</td>
<td>HCM-49</td>
<td>Specimens are from Hanoi (Van Dien Cemetery) and Ho Chi Minh City. Victims of the 1978 Khmer Rouge massacre in Bachuc Village in western Angiang Province, Viet Nam.</td>
</tr>
<tr>
<td>44. Bachuc Village (BAC)</td>
<td>51</td>
<td>BAC-51</td>
<td></td>
</tr>
</tbody>
</table>

(Continued)
<table>
<thead>
<tr>
<th>Series Map No. &amp; Name (abbrev.)</th>
<th>No. of Crania</th>
<th>Location and Number of Crania</th>
<th>Remarks</th>
</tr>
</thead>
<tbody>
<tr>
<td>45. Cambodia &amp; Laos (CML)</td>
<td>40</td>
<td>PAR-40</td>
<td>A combined sample of crania from various locations in Cambodia and Laos collected between 1877 and 1920.</td>
</tr>
<tr>
<td>46. Thailand (THI)</td>
<td>50</td>
<td>SIR-50</td>
<td>Most specimens represent dissecting room cases from Bangkok.</td>
</tr>
<tr>
<td>47. Burma (BUR)</td>
<td>16</td>
<td>ZUR-16</td>
<td>The crania in Zurich are from a series (Cat. Nos. 93-125) of skulls collected in Mandalay, Myanmar (Burma), described in a catalogue dated circa 1900.</td>
</tr>
<tr>
<td><strong>East Asia: Japan/Ryukyu Is.</strong></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>48. Kanto (KAN)</td>
<td>50</td>
<td>CHB-50</td>
<td>A dissecting room population of modern Japanese from the Kanto District of eastern Honshu. Most individuals were born during the Meiji period (1868–1911) and died well before 1940.</td>
</tr>
<tr>
<td>49. Tohoku (TOH)</td>
<td>53</td>
<td>SEN-53</td>
<td>Dissecting room specimens of modern Japanese from the Tohoku District in northern Honshu Island.</td>
</tr>
<tr>
<td>50. Kyushu (KYU)</td>
<td>51</td>
<td>KYU-51</td>
<td>Modern Japanese that derive mostly from Fukuoka Prefecture in Kyushu Island. Other specimens are from Yamaguchi, Saga, Nagasaki, and adjoining prefectures.</td>
</tr>
<tr>
<td>51. Ainu (AIN)</td>
<td>50</td>
<td>SAP-18; TKM-5; TKO-27</td>
<td>Yoshikiyo Koganei collected these skeletons in 1888–1889 from abandoned Ainu cemeteries in Hokkaido (Koganei, 1893–1894).</td>
</tr>
<tr>
<td>52. Ryukyu Is. (RYU)</td>
<td>64</td>
<td>KYO-18; KAN-21; RYU-8; KYU-5; TKO-8</td>
<td>Eighteen crania are from Tokunoshima Island, one of the Amami Islands located north of the Okinawa Group in the central Ryukyu Islands; 21 specimens are from two different locations on Kume Island, an island located west of Okinawa Island: Yattechi (17) and Hiyajo (4); and 24 specimens are from five separate islands in the Sakishima Group of the southern Ryukyu Islands: Hateruma (2); Miyako (4); Iriomote (2); Ishigaki (1), and Yonaguni Islands (12).</td>
</tr>
</tbody>
</table>

(Continued)
<table>
<thead>
<tr>
<th>Series Map No. &amp; Name (abbrev.)</th>
<th>No. of Crania</th>
<th>Location and Number of Crania</th>
<th>Remarks</th>
</tr>
</thead>
<tbody>
<tr>
<td>China/E. &amp; N.E. Asia</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>53. Shanghai (SHA)</td>
<td>50</td>
<td>SHA-50</td>
<td>The specimens are mostly from post-Qing cemeteries in Shanghai.</td>
</tr>
<tr>
<td>54. Hangzhou (HAN)</td>
<td>50</td>
<td>SHA-50</td>
<td>Ancient skeletal remains exhumed in the modern city of Hangzhou, Zhejiang Province, in eastern China.</td>
</tr>
<tr>
<td>55. Nanjing (NAJ)</td>
<td>49</td>
<td>SHA-49</td>
<td>Ancient remains exhumed from the modern city of Nanjing, Jiangsu Province, in eastern China.</td>
</tr>
<tr>
<td>56. Chengdu (CHD)</td>
<td>53</td>
<td>SHA-10; CHE-43</td>
<td>Most of these specimens date to the Ch’en Dynasty (1796–1908 A.D.) and are from Chengdu, Sichuan Province, in western China. Ten crania are from Leshan, Lizhong County, Sichuan Province.</td>
</tr>
<tr>
<td>57. Hong Kong (HK)</td>
<td>50</td>
<td>HKU-50</td>
<td>Specimens represent individuals who died in Hong Kong between 1978 and 1979.</td>
</tr>
<tr>
<td>58. Taiwan (TAI)</td>
<td>47</td>
<td>TPE-47</td>
<td>Modern Chinese living in Taiwan who trace their immediate origins to the Fujian and Guangdong provinces on the mainland of China.</td>
</tr>
<tr>
<td>59. Hainan Island (HAI)</td>
<td>47</td>
<td>TPE-47</td>
<td>Chinese immigrants originally from the Canton region of China who began arriving around 200 B.C. (Howells, 1989:108). This material was excavated by T. Kanaseki in Haikou City on Hainan Island.</td>
</tr>
<tr>
<td>60. Manchuria (MAN)</td>
<td>50</td>
<td>TKO-50</td>
<td>Many specimens are from northeastern China or the region formerly referred to as “Manchuria,” which today includes the Heilongjiang and Jilin provinces and adjacent northern Korea. A great many of these specimens are identified as soldiers or cavalrymen who died in battle in the late nineteenth century.</td>
</tr>
<tr>
<td>61. Korea (KOR)</td>
<td>32</td>
<td>KYO-7; SEN-3, TKM-2; TKO-20</td>
<td>Specific locations in Korea are known for most of these specimens.</td>
</tr>
<tr>
<td>62. Mongolia (MOG)</td>
<td>50</td>
<td>SIM-50</td>
<td>The skulls are identified as coming from Ulaanbaatar (Urga), Mongolia, and were purchased by A. Hrdlička in 1912.</td>
</tr>
</tbody>
</table>

(Continued)
<table>
<thead>
<tr>
<th>Series Map No. &amp; Number (abbrev.)</th>
<th>No. of Crania</th>
<th>Location* and Number of Crania</th>
<th>Remarks</th>
</tr>
</thead>
<tbody>
<tr>
<td>63. Atayal (ATY)</td>
<td>36</td>
<td>TPE-28; TKM-7; TKO-1</td>
<td>The specimens that are located in Taipei represent slain victims of Atayal, the second largest surviving Aboriginal tribe in Taiwan. The incident took place in 1932. T. Kanaseki collected the specimens in the same year (Howells, 1989:109).</td>
</tr>
</tbody>
</table>

* AIM, Auckland Institute and Museum, Auckland, New Zealand; AIA, Australian Institute of Anatomy, Canberra, Australia; AMS, The Australian Museum, Sydney, Australia; AUK, University of Auckland, Auckland, New Zealand; BAC, Bachue Village, Angiang Province, Viet Nam; BAS, Naturhistorisches Museum, Basel, Switzerland; BER, Museum für Naturkunde, Berlin, Germany; BLU, Anatomisches Institut, Universität Göttingen, Göttingen, Germany; BPB, B. P. Bishop Museum, Honolulu, U.S.A.; BRE, Über-see Museum, Bremen, Germany; CAN, Canterbury Museum, Christchurch, New Zealand; CHA, Anatomisches Institut der Chirurgie, Humboldt Universität, Berlin, Germany; CHB, Chiba University School of Medicine, Chiba, Japan; CHE, Dept. of Anatomy, Chengdu College of Traditional Chinese Medicine, Chengdu, China; DAM, Dept. of Anatomy, University of Melbourne, Melbourne, Australia; DAS, Dept. of Anatomy, University of Sydney, Sydney, Australia; DUN, Dept. of Anatomy, University of Otago, Dunedin, New Zealand; DRE, Museum für Völkerkunde, Dresden, Germany; FMN, Field Museum of Natural History, Chicago, U.S.A.; FRE, Institut für Humangenetik und Anthropologie, Universität Freiburg, Freiburg im Breisgau, Germany; GOT, Institut für Anthropologie, Universität Göttingen, Göttingen, Germany; HCM, Faculty of Medicine, Ho Chi Minh City, Viet Nam; HON, Honokahua, Maui, Hawaii, U.S.A.; HKU, University of Hong Kong, Hong Kong; KAN, Kanegusuku Storage Room, Board of Education Cultural Division, Kanegusuku, Okinawa, Japan; KYO, Physical Anthropology Laboratory, Faculty of Science, Kyoto University, Kyoto, Japan; KYU, Dept. of Anatomy, Faculty of Medicine, Kyushu University, Fukuoka, Japan; LEP, Anatomisches Institut, Karl Marx Universität, Leipzig, Germany; MMS, Macleay Museum, University of Sydney, Sydney, Australia; NMV, National Museum of Victoria, Melbourne, Australia; NTU, Dept. of Anatomy, National Taiwan University, Taipei, Taiwan; OT, Otago Museum and Art Gallery, Otago, New Zealand; PAR, Musée de l’Homme, Paris, France; QMB, Queensland Museum, Brisbane, Australia; ROM, Instituto di Antropologia, University of Rome, Rome, Italy; RYU, University of the Ryukyus, Naha, Okinawa Is., Japan; SAM, South Australian Museum, Adelaide, Australia; SAP, Dept. of Anatomy, Sapporo Medical College, Sapporo, Japan; SEN, Dept. of Anatomy, School of Medicine, Tohoku University, Sendai, Japan; SHA, Institute of Anthropology, College of Life Sciences, Fudan University, Shanghai, China; SIM, National Museum of Natural History, Smithsonian Institution, Washington, D.C., U.S.A.; SIR, Dept. of Anatomy, Siriraj Hospital, Bangkok, Thailand; THM, Tasmanian Museum and Art Gallery, Hobart, Australia; TKM, Medical Museum, University Museum, University of Tokyo, Tokyo, Japan; TKO, University Museum, University of Tokyo, Tokyo, Japan; TPE, Academia Sinica, Nankang, Taipei, Taiwan; TUB, Institut für Anthropologie u. Humangenetik, Universität Tübingen, Tübingen, Germany; WAM, Western Australian Museum, Perth, Australia; WEL, National Museum of New Zealand, Wellington, New Zealand; ZUR, Anthropologisches Institut, Universität Zürich, Zürich, Germany.

Biorbital breadth, nasion–alveolar height, nasal height, basion–prosthion length, and naso–occipital length (those variables with the highest coefficients regardless of sign) are the most important variables in producing group separation in the first canonical variate. This first variate may, therefore, be defined as a biorbital breadth, facial and nasal height, and cranial base and vault length discriminator. Minimum cranial breadth, orbital height, alveolar breadth, nasal height, and nasal breadth are most responsible for group separation produced in the second canonical variate. Maximum cranial length, orbital breadth, nasal height, and bizugal breadth are primarily responsible for the discrimination produced in the third canonical variate. Often, such procedures are used as a means of selecting specific variables for additional multivariate analyses.

Table 16.5 contains the overall group classification results based on posterior probabilities, regular and jackknifed, for this analysis. A mathematical explanation of posterior probability is given in Van Vark and Schaafsma.
Table 16.2 Summary Ranking of Cranial Measurements According to F-values Received in the Final Step of Discriminant Function Analysis (63 male groups, 27 measurements)

<table>
<thead>
<tr>
<th>Step No.</th>
<th>Measurementa,b</th>
<th>F-Value</th>
<th>d.f.B/d.f.Wc</th>
<th>p0</th>
</tr>
</thead>
<tbody>
<tr>
<td>1</td>
<td>Maximum cranial breadth (M-8)</td>
<td>47.6</td>
<td>62/2742</td>
<td>*</td>
</tr>
<tr>
<td>2</td>
<td>Biorbital breadth (H-EKB)</td>
<td>20.7</td>
<td>62/2741</td>
<td>*</td>
</tr>
<tr>
<td>3</td>
<td>Minimum cranial breadth (M-14)</td>
<td>26.2</td>
<td>62/2740</td>
<td>*</td>
</tr>
<tr>
<td>4</td>
<td>Basion–nasion length (M-5)</td>
<td>17.6</td>
<td>62/2739</td>
<td>*</td>
</tr>
<tr>
<td>5</td>
<td>Nasion–alveolare (M-48)</td>
<td>14.4</td>
<td>62/2738</td>
<td>*</td>
</tr>
<tr>
<td>6</td>
<td>Maximum cranial length (M-1)</td>
<td>12.1</td>
<td>62/2737</td>
<td>*</td>
</tr>
<tr>
<td>7</td>
<td>Basion–bregma height (M-17)</td>
<td>12.5</td>
<td>62/2736</td>
<td>*</td>
</tr>
<tr>
<td>8</td>
<td>Biauricular breadth (M-11b)</td>
<td>12.0</td>
<td>62/2735</td>
<td>*</td>
</tr>
<tr>
<td>9</td>
<td>Basion–prostion (M-40)</td>
<td>10.9</td>
<td>62/2734</td>
<td>*</td>
</tr>
<tr>
<td>10</td>
<td>Nasal height (H-NLH)</td>
<td>10.4</td>
<td>62/2733</td>
<td>*</td>
</tr>
<tr>
<td>11</td>
<td>Nasion–occipital length (M-1d)</td>
<td>8.3</td>
<td>62/2732</td>
<td>*</td>
</tr>
<tr>
<td>12</td>
<td>Nasal breadth (M-54)</td>
<td>8.1</td>
<td>62/2730</td>
<td>*</td>
</tr>
<tr>
<td>13</td>
<td>Bijdugal breadth [M-45(1)]</td>
<td>8.0</td>
<td>62/2731</td>
<td>*</td>
</tr>
<tr>
<td>14</td>
<td>Bifrontal breadth (M-43)</td>
<td>7.3</td>
<td>62/2729</td>
<td>*</td>
</tr>
<tr>
<td>15</td>
<td>Alveolar breadth (M-61)</td>
<td>7.1</td>
<td>62/2728</td>
<td>*</td>
</tr>
<tr>
<td>16</td>
<td>Mastoid height (H-MDL)</td>
<td>6.9</td>
<td>62/2727</td>
<td>*</td>
</tr>
<tr>
<td>17</td>
<td>Cheek height (H-WMH)</td>
<td>6.6</td>
<td>62/2726</td>
<td>*</td>
</tr>
<tr>
<td>18</td>
<td>Nasion–bregma chord (M-29)</td>
<td>5.7</td>
<td>62/2725</td>
<td>*</td>
</tr>
<tr>
<td>19</td>
<td>Orbital height, left (M-52)</td>
<td>5.3</td>
<td>62/2724</td>
<td>*</td>
</tr>
<tr>
<td>20</td>
<td>Bimaxillary breadth (M-46)</td>
<td>4.9</td>
<td>62/2723</td>
<td>*</td>
</tr>
<tr>
<td>21</td>
<td>Orbital breadth, left (M-51a)</td>
<td>4.7</td>
<td>62/2720</td>
<td>*</td>
</tr>
<tr>
<td>22</td>
<td>Bistephanic breadth (H-STB)</td>
<td>4.7</td>
<td>62/2722</td>
<td>*</td>
</tr>
<tr>
<td>23</td>
<td>Maximum frontal breadth (M-10)</td>
<td>5.5</td>
<td>62/2721</td>
<td>*</td>
</tr>
<tr>
<td>24</td>
<td>Minimum frontal breadth (M-9)</td>
<td>4.1</td>
<td>62/2719</td>
<td>*</td>
</tr>
<tr>
<td>25</td>
<td>Mastoid width (H-MDB)</td>
<td>3.8</td>
<td>62/2718</td>
<td>*</td>
</tr>
<tr>
<td>26</td>
<td>Bregma–lambda chord (M-30)</td>
<td>3.5</td>
<td>62/2717</td>
<td>*</td>
</tr>
<tr>
<td>27</td>
<td>Biasterionic breadth (M-12)</td>
<td>3.3</td>
<td>62/2716</td>
<td>*</td>
</tr>
</tbody>
</table>

aM = Martin and Saller (1957) [the numbers after M refer to the original numbered measurements in this standard].
bH = Howells (1973) [the letters after H refer to the designations used by Howells].
cd.f.B/d.f.W = degrees of freedom between/degrees of freedom within.
dp ≤ .01; n.s. = not significant.

(1992:244–255). Jackknifed classification is a common cross-validation procedure used in multiple discriminant analysis, where cases are classified without using misclassified individuals in computing the classification function.

Mongolia, Swanport (Australia), Chatham Islands (New Zealand), Rapa Nui (Easter Island), Guam, Dawson Strait, Ainu, Tasmania, and Western Australia are among the series having the best jackknifed classification results (i.e., more than 57% of the cases are assigned correctly to each of these original groups). Groups with the poorest jackknifed classification results (less than 20% of the cases correctly classified to their original group) include the Solomon Islands, Lesser Sunda Island, New Ireland, Hangzhou, Sulawesi, Hainan Island, Nanjing, Borneo, Sumatra, Shanghai, and Fiji series; eight of the series with poor classification results represent Chinese and Southeast Asian island cranial series.

Inspection of some jackknifed classification results obtained from stepwise discriminant function analysis showing the cases classified at the end of the stepping process are shown in Table 16.6. These results reveal that only 3 of
<table>
<thead>
<tr>
<th>Canonical Variate</th>
<th>Eigenvalue</th>
<th>% Dispersion</th>
<th>Cumulative % Dispersion</th>
<th>d.f.(^a)</th>
<th>(p)(^b)</th>
</tr>
</thead>
<tbody>
<tr>
<td>1</td>
<td>3.43542</td>
<td>41.7</td>
<td>41.7</td>
<td>88</td>
<td>*</td>
</tr>
<tr>
<td>2</td>
<td>1.13325</td>
<td>13.7</td>
<td>55.4</td>
<td>86</td>
<td>*</td>
</tr>
<tr>
<td>3</td>
<td>0.68543</td>
<td>8.3</td>
<td>63.7</td>
<td>84</td>
<td>*</td>
</tr>
<tr>
<td>4</td>
<td>0.56173</td>
<td>6.8</td>
<td>70.5</td>
<td>82</td>
<td>*</td>
</tr>
<tr>
<td>5</td>
<td>0.37941</td>
<td>4.6</td>
<td>75.1</td>
<td>80</td>
<td>*</td>
</tr>
<tr>
<td>6</td>
<td>0.28659</td>
<td>3.5</td>
<td>78.6</td>
<td>78</td>
<td>*</td>
</tr>
<tr>
<td>7</td>
<td>0.24680</td>
<td>3.0</td>
<td>81.6</td>
<td>76</td>
<td>*</td>
</tr>
<tr>
<td>8</td>
<td>0.20748</td>
<td>2.5</td>
<td>84.1</td>
<td>74</td>
<td>*</td>
</tr>
<tr>
<td>9</td>
<td>0.17662</td>
<td>2.2</td>
<td>86.3</td>
<td>72</td>
<td>*</td>
</tr>
<tr>
<td>10</td>
<td>0.14432</td>
<td>1.7</td>
<td>88.0</td>
<td>70</td>
<td>*</td>
</tr>
<tr>
<td>11</td>
<td>0.13498</td>
<td>1.6</td>
<td>89.6</td>
<td>68</td>
<td>*</td>
</tr>
<tr>
<td>12</td>
<td>0.12389</td>
<td>1.5</td>
<td>91.1</td>
<td>66</td>
<td>*</td>
</tr>
<tr>
<td>13</td>
<td>0.11808</td>
<td>1.5</td>
<td>92.6</td>
<td>64</td>
<td>*</td>
</tr>
<tr>
<td>14</td>
<td>0.09761</td>
<td>1.2</td>
<td>93.8</td>
<td>62</td>
<td>*</td>
</tr>
<tr>
<td>15</td>
<td>0.08235</td>
<td>1.0</td>
<td>94.8</td>
<td>60</td>
<td>*</td>
</tr>
<tr>
<td>16</td>
<td>0.07295</td>
<td>0.8</td>
<td>95.6</td>
<td>58</td>
<td>*</td>
</tr>
<tr>
<td>17</td>
<td>0.06267</td>
<td>0.8</td>
<td>96.4</td>
<td>56</td>
<td>*</td>
</tr>
<tr>
<td>18</td>
<td>0.06016</td>
<td>0.7</td>
<td>97.1</td>
<td>54</td>
<td>*</td>
</tr>
<tr>
<td>19</td>
<td>0.04573</td>
<td>0.6</td>
<td>97.7</td>
<td>52</td>
<td>*</td>
</tr>
<tr>
<td>20</td>
<td>0.03864</td>
<td>0.5</td>
<td>98.2</td>
<td>50</td>
<td>*</td>
</tr>
<tr>
<td>21</td>
<td>0.03053</td>
<td>0.3</td>
<td>98.5</td>
<td>48</td>
<td>*</td>
</tr>
<tr>
<td>22</td>
<td>0.02999</td>
<td>0.4</td>
<td>98.9</td>
<td>46</td>
<td>*</td>
</tr>
<tr>
<td>23</td>
<td>0.02392</td>
<td>0.3</td>
<td>99.2</td>
<td>44</td>
<td>*</td>
</tr>
<tr>
<td>24</td>
<td>0.02213</td>
<td>0.3</td>
<td>99.5</td>
<td>42</td>
<td>*</td>
</tr>
<tr>
<td>25</td>
<td>0.01979</td>
<td>0.2</td>
<td>99.7</td>
<td>40</td>
<td>*</td>
</tr>
<tr>
<td>26</td>
<td>0.01491</td>
<td>0.2</td>
<td>99.9</td>
<td>38</td>
<td>*</td>
</tr>
<tr>
<td>27</td>
<td>0.01041</td>
<td>0.1</td>
<td>100.0</td>
<td>36</td>
<td>*</td>
</tr>
</tbody>
</table>

\(d.f. = \text{degrees of freedom} = (p + q - 2), (p + q - 4).\)

\(p \leq 0.01\) when eigenvalues are tested for significance according to criterion \(N - \frac{1}{2} (p + q) \log_e (\lambda + 1)\), where \(N = \text{total number of crania, } p = \text{number of variables, } q = \text{number of groups, and } \lambda = \text{eigenvalue, all of which are distributed approximately as chi-square (Rao, 1952:373).}\)

The 49 crania originally assigned to the Solomon Islands are reassigned to the Solomon Islands series; the remaining specimens originally assigned to this cranial series are "misclassified" to cranial series from the islands of Melanesia and the Caroline Islands. The New Ireland, Solomon Islands, Sumatra, and Southern Moluccas series each have reclassifications to 25 or more groups in this analysis!

The misclassifications of the Polynesian series are generally among other Polynesian groups, although a few are misclassified to an Southeast Asian (e.g., Southern Moluccas, Lesser Sunda Islands, or Java) island series, Fiji, or one of the cranial series from the islands of Melanesia. Five of the New Zealand Maori crania are assigned to Southern Moluccas, and seven others are reassigned to Loyalty, Solomon, or New Ireland.

Most of the misclassifications between the New Guinea and the Melanesian series are to a series from the same geographical region. As expected, most of the misclassifications among the Australian/Tasmanian series are to these and to some of the Melanesian series. Misclassifications for the cases originally
<table>
<thead>
<tr>
<th>Metric</th>
<th>Canonical Variate 1</th>
<th>Canonical Variate 2</th>
<th>Canonical Variate 3</th>
</tr>
</thead>
<tbody>
<tr>
<td>Maximum cranial length (M-1)</td>
<td>0.08825</td>
<td>-0.08027</td>
<td>-0.15823</td>
</tr>
<tr>
<td>Orbital breadth, left (M-51a)</td>
<td>0.09176</td>
<td>0.03942</td>
<td>-0.12983</td>
</tr>
<tr>
<td>Nasal height (H-NLH)</td>
<td>0.10629</td>
<td>0.10212</td>
<td>0.09897</td>
</tr>
<tr>
<td>Biaural breadth (M-451)</td>
<td>-0.02228</td>
<td>0.09763</td>
<td>-0.09039</td>
</tr>
<tr>
<td>Basion-bregma height (M-17)</td>
<td>-0.02201</td>
<td>0.04550</td>
<td>0.08050</td>
</tr>
<tr>
<td>Biaural breadth (M-11b)</td>
<td>-0.01973</td>
<td>0.06519</td>
<td>-0.07778</td>
</tr>
<tr>
<td>Nasion-alveolate (M-48)</td>
<td>-0.12798</td>
<td>-0.08643</td>
<td>-0.06925</td>
</tr>
<tr>
<td>Nasion-occipital length (M-1d)</td>
<td>-0.09897</td>
<td>0.08086</td>
<td>0.06442</td>
</tr>
<tr>
<td>Mastoid width (H-MDB)</td>
<td>-0.03215</td>
<td>0.02777</td>
<td>0.06404</td>
</tr>
<tr>
<td>Bistephanic breadth (H-STB)</td>
<td>-0.03680</td>
<td>0.05350</td>
<td>0.06035</td>
</tr>
<tr>
<td>Orbital height, left (M-52)</td>
<td>-0.03903</td>
<td>0.11651</td>
<td>-0.05403</td>
</tr>
<tr>
<td>Bifrontal breadth (M-43)</td>
<td>-0.03779</td>
<td>-0.08027</td>
<td>0.05216</td>
</tr>
<tr>
<td>Bimaxillary breadth (M-46)</td>
<td>-0.06497</td>
<td>-0.00025</td>
<td>0.04754</td>
</tr>
<tr>
<td>Minimum frontal breadth (M-9)</td>
<td>0.05735</td>
<td>-0.01817</td>
<td>-0.04493</td>
</tr>
<tr>
<td>Biorbital breadth (H-EBK)</td>
<td>0.14151</td>
<td>-0.02456</td>
<td>0.04411</td>
</tr>
<tr>
<td>Maximum frontal breadth (M-10)</td>
<td>-0.01108</td>
<td>-0.06485</td>
<td>-0.03890</td>
</tr>
<tr>
<td>Basion-nasion length (M-5)</td>
<td>-0.04514</td>
<td>0.03642</td>
<td>-0.03873</td>
</tr>
<tr>
<td>Bregma-lambda chord (M-30)</td>
<td>0.01679</td>
<td>-0.01977</td>
<td>0.02805</td>
</tr>
<tr>
<td>Basion-prosthion (M-40)</td>
<td>0.10021</td>
<td>0.05748</td>
<td>0.02460</td>
</tr>
<tr>
<td>Nasal breadth (M-54)</td>
<td>-0.01999</td>
<td>-0.09942</td>
<td>-0.02160</td>
</tr>
<tr>
<td>Maximum cranial breadth (M-8)</td>
<td>-0.05423</td>
<td>-0.00605</td>
<td>-0.01649</td>
</tr>
<tr>
<td>Biasterionic breadth (M-12)</td>
<td>0.01295</td>
<td>-0.03754</td>
<td>-0.01514</td>
</tr>
<tr>
<td>Mastoid height (H-MDL)</td>
<td>0.04276</td>
<td>0.07088</td>
<td>0.01043</td>
</tr>
<tr>
<td>Minimum cranial breadth (M-14)</td>
<td>-0.09832</td>
<td>-0.12304</td>
<td>0.00823</td>
</tr>
<tr>
<td>Nasion-bregma chord (M-29)</td>
<td>0.05184</td>
<td>0.03643</td>
<td>-0.00731</td>
</tr>
<tr>
<td>Alveolar breadth (M-61)</td>
<td>0.06024</td>
<td>-0.10264</td>
<td>0.00553</td>
</tr>
<tr>
<td>Cheek height (H-WMH)</td>
<td>-0.07379</td>
<td>0.09241</td>
<td>0.00249</td>
</tr>
</tbody>
</table>

Most importantly, these classification results serve to highlight those regions (e.g., Solomon Islands, Lesser Sunda Islands, Southern Moluccas, Vietnam, Taiwan, and Hainan Island) that exhibit the greatest heterogeneity and possibly where contact with other regions was the most intense and/or sustained.

A plot showing the 63 group means on the first two canonical variates results in three separate clusters shown in Fig. 16.2. Cranial series from Australia, New Guinea, and geographical Melanesia are contained in one of these general clusters, with little overlap between the Australian and the Melanesian series. The Polynesian cranial series and those from Guam and the Marshall-Kiribati Islands form a second isolated constellation in this diagram.
### TABLE 16.5

<table>
<thead>
<tr>
<th>Group</th>
<th>Regular Results</th>
<th>Jackknifed Results</th>
</tr>
</thead>
<tbody>
<tr>
<td>MOG</td>
<td>82.0</td>
<td>MOG</td>
</tr>
<tr>
<td>SAS</td>
<td>80.6</td>
<td>SAS</td>
</tr>
<tr>
<td>RAP</td>
<td>76.0</td>
<td>CHT</td>
</tr>
<tr>
<td>CHT</td>
<td>75.6</td>
<td>RAP</td>
</tr>
<tr>
<td>TAS</td>
<td>73.1</td>
<td>GUA</td>
</tr>
<tr>
<td>TUA</td>
<td>72.2</td>
<td>DAW</td>
</tr>
<tr>
<td>AIN</td>
<td>72.0</td>
<td>AIN</td>
</tr>
<tr>
<td>GUA</td>
<td>69.6</td>
<td>TAS</td>
</tr>
<tr>
<td>DAW</td>
<td>68.8</td>
<td>WA</td>
</tr>
<tr>
<td>WA</td>
<td>63.8</td>
<td>TAI</td>
</tr>
<tr>
<td>TAI</td>
<td>63.8</td>
<td>BUR</td>
</tr>
<tr>
<td>BUR</td>
<td>62.5</td>
<td>PUR</td>
</tr>
<tr>
<td>PUR</td>
<td>60.0</td>
<td>TAI</td>
</tr>
<tr>
<td>TOG</td>
<td>57.9</td>
<td>CHD</td>
</tr>
<tr>
<td>DTX</td>
<td>57.7</td>
<td>ADR</td>
</tr>
<tr>
<td>GAM</td>
<td>57.1</td>
<td>HK</td>
</tr>
<tr>
<td>CHD</td>
<td>56.6</td>
<td>CML</td>
</tr>
<tr>
<td>SCR</td>
<td>56.5</td>
<td>SCR</td>
</tr>
<tr>
<td>NCL</td>
<td>56.0</td>
<td>ATY</td>
</tr>
<tr>
<td>ADR</td>
<td>56.0</td>
<td>BAC</td>
</tr>
<tr>
<td>ATY</td>
<td>55.6</td>
<td>NCL</td>
</tr>
<tr>
<td>HAW</td>
<td>55.0</td>
<td>MRB</td>
</tr>
<tr>
<td>CML</td>
<td>55.0</td>
<td>RYU</td>
</tr>
<tr>
<td>LOY</td>
<td>54.0</td>
<td>NZ</td>
</tr>
<tr>
<td>BAC</td>
<td>52.9</td>
<td>TOG</td>
</tr>
<tr>
<td>MRB</td>
<td>52.0</td>
<td>MAN</td>
</tr>
<tr>
<td>HK</td>
<td>52.0</td>
<td>TOH</td>
</tr>
<tr>
<td>TOH</td>
<td>50.9</td>
<td>DTX</td>
</tr>
<tr>
<td>MAN</td>
<td>50.0</td>
<td>KAN</td>
</tr>
<tr>
<td>SUL</td>
<td>47.4</td>
<td>KYU</td>
</tr>
<tr>
<td>MSK</td>
<td>46.2</td>
<td>FLY</td>
</tr>
<tr>
<td>RYU</td>
<td>45.0</td>
<td>NSW</td>
</tr>
<tr>
<td>KOR</td>
<td>43.8</td>
<td>NT</td>
</tr>
<tr>
<td>NZ</td>
<td>40.0</td>
<td>THI</td>
</tr>
<tr>
<td>THI</td>
<td>40.0</td>
<td>GAM</td>
</tr>
<tr>
<td>PHL</td>
<td>39.3</td>
<td>NBR</td>
</tr>
<tr>
<td>KYU</td>
<td>39.2</td>
<td>SOC</td>
</tr>
<tr>
<td>QLD</td>
<td>38.9</td>
<td>VTN</td>
</tr>
<tr>
<td>NSW</td>
<td>38.7</td>
<td>SUL</td>
</tr>
<tr>
<td>FLY</td>
<td>38.1</td>
<td>BUR</td>
</tr>
<tr>
<td>NBR</td>
<td>38.0</td>
<td>KOR</td>
</tr>
<tr>
<td>NT</td>
<td>38.0</td>
<td>QLD</td>
</tr>
<tr>
<td>CAR</td>
<td>37.5</td>
<td>LOY</td>
</tr>
</tbody>
</table>

### TABLE 16.5 Continued

<table>
<thead>
<tr>
<th>Group</th>
<th>Regular Results</th>
<th>Jackknifed Results</th>
</tr>
</thead>
<tbody>
<tr>
<td>VTN</td>
<td>36.7</td>
<td>SEP</td>
</tr>
<tr>
<td>VAN</td>
<td>36.2</td>
<td>VAN</td>
</tr>
<tr>
<td>KAN</td>
<td>36.0</td>
<td>MSK</td>
</tr>
<tr>
<td>SHA</td>
<td>36.0</td>
<td>SML</td>
</tr>
<tr>
<td>MRQ</td>
<td>34.9</td>
<td>BIK</td>
</tr>
<tr>
<td>SEP</td>
<td>34.0</td>
<td>MRQ</td>
</tr>
<tr>
<td>FIJ</td>
<td>33.3</td>
<td>JAV</td>
</tr>
<tr>
<td>BIK</td>
<td>33.3</td>
<td>PHL</td>
</tr>
<tr>
<td>BOR</td>
<td>32.4</td>
<td>CAR</td>
</tr>
<tr>
<td>HAI</td>
<td>31.9</td>
<td>FIJ</td>
</tr>
<tr>
<td>JAV</td>
<td>30.0</td>
<td>SHA</td>
</tr>
<tr>
<td>SML</td>
<td>29.2</td>
<td>SUM</td>
</tr>
<tr>
<td>SOC</td>
<td>27.3</td>
<td>BOR</td>
</tr>
<tr>
<td>SUM</td>
<td>25.6</td>
<td>NAJ</td>
</tr>
<tr>
<td>HAN</td>
<td>24.0</td>
<td>HAI</td>
</tr>
<tr>
<td>NAJ</td>
<td>22.4</td>
<td>SLW</td>
</tr>
<tr>
<td>NIR</td>
<td>20.8</td>
<td>HAN</td>
</tr>
<tr>
<td>SOL</td>
<td>20.4</td>
<td>NIR</td>
</tr>
<tr>
<td>SLW</td>
<td>19.5</td>
<td>LSN</td>
</tr>
<tr>
<td>LSN</td>
<td>13.1</td>
<td>SOL</td>
</tr>
</tbody>
</table>

The remaining groups, representing cranial series from eastern and northern Asia and mainland and island Southeast Asia, form a relatively compact third grouping. The cranial series representing the Southern Moluccas and Caroline Islands are peripheral members of the greater Melanesian–Australian grouping.

The plot of the 63 group means on the first three canonical variates, which is separated into two diagrams for easier viewing, is presented in Figs. 16.3 and 16.4. The Atayal series is included in both representations to provide continuity in viewing these plots. The Polynesian and two Micronesian cranial series are well separated from the Australian and Melanesian samples in Fig. 16.3. The Admiralty Island, Marshall-Kiribati, and Caroline cranial series occupy intermediate positions between these two major groupings. The island and mainland Southeast Asian cranial series form a relatively distinct association in Fig. 16.4. The Chinese, Japanese,
<table>
<thead>
<tr>
<th>Tonga-Samoa (19)</th>
<th>Rapa Nui (50)</th>
<th>Hawaii (60)</th>
<th>Marquesas (63)</th>
<th>New Zealand (50)</th>
<th>Chatham Is. (45)</th>
<th>Society Is. (44)</th>
<th>Tuamotu Arch. (18)</th>
</tr>
</thead>
<tbody>
<tr>
<td>TOG 7</td>
<td>RAP 35</td>
<td>HAW 30</td>
<td>MRQ 14</td>
<td>NZ 19</td>
<td>CHT 32</td>
<td>SOC 12</td>
<td>TUA 9</td>
</tr>
<tr>
<td>HAW 3</td>
<td>GAM 6</td>
<td>TOG 3</td>
<td>TUA 9</td>
<td>SML 5</td>
<td>NZ 2</td>
<td>TUA 11</td>
<td>SOC 3</td>
</tr>
<tr>
<td>FIJ 2</td>
<td>HAW 2</td>
<td>RAP 3</td>
<td>SOC 6</td>
<td>MRQ 3</td>
<td>GUA 2</td>
<td>HAW 5</td>
<td>RAP 1</td>
</tr>
<tr>
<td>GAM 1</td>
<td>SOC 1</td>
<td>CHT 3</td>
<td>FIJ 5</td>
<td>TUA 3</td>
<td>HAW 1</td>
<td>CAR 3</td>
<td>NZ 1</td>
</tr>
<tr>
<td>GUA 1</td>
<td>TUA 1</td>
<td>SOC 3</td>
<td>NZ 4</td>
<td>LOY 3</td>
<td>SOC 1</td>
<td>MRQ 2</td>
<td>GAM 1</td>
</tr>
<tr>
<td>JAV 1</td>
<td>FIJ 1</td>
<td>GUA 3</td>
<td>HAW 3</td>
<td>CHT 2</td>
<td>GAM 1</td>
<td>CHT 2</td>
<td>CAR 1</td>
</tr>
<tr>
<td>CML 1</td>
<td>LOY 1</td>
<td>MRQ 2</td>
<td>RAP 2</td>
<td>SOL 2</td>
<td>FIJ 1</td>
<td>FIJ 2</td>
<td>SML 1</td>
</tr>
<tr>
<td>KAN 1</td>
<td>NIR 1</td>
<td>GAM 2</td>
<td>GAM 2</td>
<td>NIR 2</td>
<td>SEP 1</td>
<td>KYU 2</td>
<td>SUL 1</td>
</tr>
<tr>
<td>RYU 1</td>
<td>DAW 1</td>
<td>KAN 2</td>
<td>LSN 2</td>
<td>RAP 1</td>
<td>JAV 1</td>
<td>TOG 1</td>
<td></td>
</tr>
<tr>
<td>TAI 1</td>
<td>MSK 1</td>
<td>ADR 1</td>
<td>AIN 2</td>
<td>HAW 1</td>
<td>AIN 1</td>
<td>RAP 1</td>
<td></td>
</tr>
</tbody>
</table>

<table>
<thead>
<tr>
<th>Gambier Is. (7)</th>
<th>Fiji (42)</th>
<th>Vanuatu (47)</th>
<th>Loyalty Is. (50)</th>
<th>New Caledonia (50)</th>
<th>Santa Cruz Is. (46)</th>
<th>Solomon Is. (49)</th>
<th>New Britain (50)</th>
</tr>
</thead>
<tbody>
<tr>
<td>RAP 2</td>
<td>FIJ 7</td>
<td>VAN 11</td>
<td>LOY 12</td>
<td>NCL 20</td>
<td>SCR 20</td>
<td>NBR 6</td>
<td>NBR 14</td>
</tr>
<tr>
<td>GAM 2</td>
<td>LOY 7</td>
<td>NBR 7</td>
<td>NCL 12</td>
<td>LOY 9</td>
<td>VAN 5</td>
<td>NBR 5</td>
<td>VAN 10</td>
</tr>
<tr>
<td>TUA 1</td>
<td>CHT 3</td>
<td>BIK 5</td>
<td>SCR 4</td>
<td>NIR 3</td>
<td>NT 4</td>
<td>SEP 4</td>
<td>NT 5</td>
</tr>
<tr>
<td>FIJ 1</td>
<td>TOG 2</td>
<td>NSW 3</td>
<td>FIJ 3</td>
<td>NT 3</td>
<td>LOY 3</td>
<td>FIJ 3</td>
<td>NIR 3</td>
</tr>
<tr>
<td>GUA 1</td>
<td>NBR 2</td>
<td>TAS 3</td>
<td>QLD 3</td>
<td>VAN 2</td>
<td>NBR 3</td>
<td>LOY 3</td>
<td>SOL 2</td>
</tr>
<tr>
<td>FLY 2</td>
<td>LOY 2</td>
<td>SOL 2</td>
<td>NBR 2</td>
<td>SEP 3</td>
<td>NCL 3</td>
<td>SEP 2</td>
<td></td>
</tr>
<tr>
<td>DAW 2</td>
<td>NCL 2</td>
<td>NIR 2</td>
<td>SEP 2</td>
<td>PUR 2</td>
<td>SOL 3</td>
<td>FLY 2</td>
<td></td>
</tr>
<tr>
<td>SUL 2</td>
<td>NIR 2</td>
<td>BIK 2</td>
<td>TOG 1</td>
<td>DTX 2</td>
<td>SCR 2</td>
<td>PUR 2</td>
<td></td>
</tr>
<tr>
<td>SOC 1</td>
<td>FLY 2</td>
<td>CAR 2</td>
<td>RAP 1</td>
<td>CAR 2</td>
<td>DTX 2</td>
<td>TOG 1</td>
<td></td>
</tr>
<tr>
<td>TUA 1</td>
<td>DAW 2</td>
<td>RAP 1</td>
<td>HAW 1</td>
<td>NCL 1</td>
<td>CAR 2</td>
<td></td>
<td></td>
</tr>
<tr>
<td>-----------------</td>
<td>-------------------</td>
<td>--------------</td>
<td>---------------</td>
<td>------------</td>
<td>------------------</td>
<td>------------------------</td>
<td>------------------</td>
</tr>
<tr>
<td>NBR 6</td>
<td>ADR 23</td>
<td>SEP 12</td>
<td>BIK 11</td>
<td>FLY 13</td>
<td>PUR 26</td>
<td>DTX 9</td>
<td>DAW 29</td>
</tr>
<tr>
<td>NIR 5</td>
<td>SEP 4</td>
<td>BIK 5</td>
<td>FIJ 5</td>
<td>PUR 9</td>
<td>FLY 10</td>
<td>DAW 3</td>
<td>DTX 5</td>
</tr>
<tr>
<td>BIK 5</td>
<td>BIK 4</td>
<td>SEP 5</td>
<td>DTX 3</td>
<td>SCR 2</td>
<td>SCR 2</td>
<td>ATY 2</td>
<td></td>
</tr>
<tr>
<td>ADR 4</td>
<td>SML 3</td>
<td>VAN 4</td>
<td>VAN 2</td>
<td>SOL 2</td>
<td>SOL 2</td>
<td>WA 2</td>
<td></td>
</tr>
<tr>
<td>LOY 3</td>
<td>BOR 2</td>
<td>MSK 4</td>
<td>NBR 3</td>
<td>SCR 2</td>
<td>FIJ 1</td>
<td>ADR 1</td>
<td>SML 2</td>
</tr>
<tr>
<td>NCL 3</td>
<td>RAP 1</td>
<td>DTX 3</td>
<td>PUR 3</td>
<td>WA 2</td>
<td>NCL 1</td>
<td>SEP 1</td>
<td>NBR 1</td>
</tr>
<tr>
<td>SEP 3</td>
<td>MRQ 1</td>
<td>CAR 3</td>
<td>NBR 2</td>
<td>JAV 2</td>
<td>BIK 1</td>
<td>SEP 1</td>
<td></td>
</tr>
<tr>
<td>FLY 2</td>
<td>SOC 1</td>
<td>SUL 3</td>
<td>FLY 2</td>
<td>FIJ 1</td>
<td>NIR 1</td>
<td>FLY 1</td>
<td>BIK 1</td>
</tr>
<tr>
<td>CAR 2</td>
<td>FIJ 1</td>
<td>SOL 2</td>
<td>DTX 2</td>
<td>SOL 1</td>
<td>ADR 1</td>
<td>NT 1</td>
<td>FLY 1</td>
</tr>
<tr>
<td>SML 2</td>
<td>VAN 1</td>
<td>ADR 2</td>
<td>RAP 1</td>
<td>SEP 1</td>
<td>BIK 1</td>
<td>TAS 1</td>
<td>QLD 1</td>
</tr>
</tbody>
</table>

<table>
<thead>
<tr>
<th></th>
<th></th>
<th></th>
<th></th>
<th></th>
<th></th>
<th></th>
<th></th>
</tr>
</thead>
<tbody>
<tr>
<td>MRB 20</td>
<td>NSW 19</td>
<td>QLD 13</td>
<td>NT 15</td>
<td>SAS 27</td>
<td>WA 27</td>
<td>TAS 15</td>
<td>GUA 28</td>
</tr>
<tr>
<td>WA 9</td>
<td>QLD 14</td>
<td>NSW 10</td>
<td>MRB 7</td>
<td>QLD 3</td>
<td>TAS 4</td>
<td>NSW 2</td>
<td>HAW 4</td>
</tr>
<tr>
<td>NSW 5</td>
<td>NT 8</td>
<td>MRB 8</td>
<td>WA 6</td>
<td>MRB 2</td>
<td>NT 3</td>
<td>NZ 1</td>
<td>TOG 3</td>
</tr>
<tr>
<td>QLD 4</td>
<td>SAS 5</td>
<td>NT 7</td>
<td>NSW 5</td>
<td>VAN 1</td>
<td>NSW 2</td>
<td>VAN 1</td>
<td>MRQ 3</td>
</tr>
<tr>
<td>NT 4</td>
<td>MRB 3</td>
<td>WA 5</td>
<td>QLD 4</td>
<td>NBR 1</td>
<td>SAS 2</td>
<td>ADR 1</td>
<td>CML 2</td>
</tr>
<tr>
<td>VAN 2</td>
<td>SCR 2</td>
<td>VAN 2</td>
<td>SCR 3</td>
<td>NSW 1</td>
<td>VAN 1</td>
<td>SEP 1</td>
<td>NZ 1</td>
</tr>
<tr>
<td>LOY 1</td>
<td>BIK 2</td>
<td>SOL 2</td>
<td>FIJ 2</td>
<td>AIN 1</td>
<td>LOY 1</td>
<td>MRB 1</td>
<td>NIR 1</td>
</tr>
<tr>
<td>NCL 1</td>
<td>WA 2</td>
<td>LOY 1</td>
<td>SOL 2</td>
<td>SOL 1</td>
<td>WA 1</td>
<td>SUM 1</td>
<td></td>
</tr>
<tr>
<td>SEP 1</td>
<td>NZ 1</td>
<td>NBR 1</td>
<td>VAN 1</td>
<td>NBR 1</td>
<td>BOR 1</td>
<td>JAV 1</td>
<td></td>
</tr>
<tr>
<td>PUR 1</td>
<td>LOY 1</td>
<td>FLY 1</td>
<td>NCL 1</td>
<td>DAW 1</td>
<td>KAN 1</td>
<td>SUL 1</td>
<td></td>
</tr>
</tbody>
</table>

(Continued)
<table>
<thead>
<tr>
<th></th>
<th></th>
<th></th>
<th></th>
<th></th>
<th></th>
<th></th>
<th></th>
</tr>
</thead>
<tbody>
<tr>
<td>(24)</td>
<td>(13)</td>
<td>(39)</td>
<td>(50)</td>
<td>(34)</td>
<td>(41)</td>
<td>(61)</td>
<td>(65)</td>
</tr>
<tr>
<td>CAR 5</td>
<td>MSK 3</td>
<td>SUM 6</td>
<td>JAV 11</td>
<td>BOR 5</td>
<td>CML 7</td>
<td>BOR 6</td>
<td>SML 15</td>
</tr>
<tr>
<td>NBR 4</td>
<td>NZ 2</td>
<td>BOR 3</td>
<td>CML 6</td>
<td>SLW 4</td>
<td>SLW 5</td>
<td>LSN 5</td>
<td>MRQ 6</td>
</tr>
<tr>
<td>RAP 1</td>
<td>NIR 2</td>
<td>JAV 2</td>
<td>SLW 4</td>
<td>LSN 3</td>
<td>BOR 3</td>
<td>NZ 4</td>
<td>NIR 3</td>
</tr>
<tr>
<td>HAW 1</td>
<td>MRQ 1</td>
<td>SUL 2</td>
<td>LSN 3</td>
<td>JAV 2</td>
<td>LSN 3</td>
<td>JAV 3</td>
<td>SEP 4</td>
</tr>
<tr>
<td>MRQ 1</td>
<td>SOC 1</td>
<td>BUR 2</td>
<td>SUL 3</td>
<td>SUL 2</td>
<td>THI 3</td>
<td>SLW 3</td>
<td>SEP 4</td>
</tr>
<tr>
<td>SOC 1</td>
<td>TUA 1</td>
<td>TOH 2</td>
<td>BAC 3</td>
<td>HAW 1</td>
<td>TOG 2</td>
<td>PHL 3</td>
<td>DAW 3</td>
</tr>
<tr>
<td>FIJ 1</td>
<td>ADR 1</td>
<td>SHA 2</td>
<td>THI 3</td>
<td>NCL 1</td>
<td>NIR 2</td>
<td>CML 3</td>
<td>HAW 2</td>
</tr>
<tr>
<td>VAN 1</td>
<td>BIK 1</td>
<td>RAP 1</td>
<td>TOG 1</td>
<td>SOL 1</td>
<td>JAV 2</td>
<td>TOG 2</td>
<td>LOY 2</td>
</tr>
<tr>
<td>NCL 1</td>
<td>CAR 1</td>
<td>MRQ 1</td>
<td>NZ 1</td>
<td>ADR 1</td>
<td>SOL 2</td>
<td>NBR 2</td>
<td>ADR 2</td>
</tr>
<tr>
<td>SCR 1</td>
<td>FIJ 1</td>
<td>SOC 1</td>
<td>BIK 1</td>
<td>VTN 2</td>
<td>NBR 2</td>
<td></td>
<td></td>
</tr>
</tbody>
</table>

<table>
<thead>
<tr>
<th>Sulu (38)</th>
<th>Philippines (28)</th>
<th>Viet Nam (49)</th>
<th>Bachuc Village (51)</th>
<th>Cambodia &amp; Laos (40)</th>
<th>Thailand (50)</th>
<th>Burma (16)</th>
<th>Kanto (50)</th>
</tr>
</thead>
<tbody>
<tr>
<td>SUL 10</td>
<td>PHL 6</td>
<td>VTN 13</td>
<td>BAC 21</td>
<td>CML 18</td>
<td>THI 15</td>
<td>BUR 4</td>
<td>KAN 16</td>
</tr>
<tr>
<td>CML 7</td>
<td>VTN 5</td>
<td>PHL 6</td>
<td>CML 4</td>
<td>SUL 5</td>
<td>BAC 6</td>
<td>CML 3</td>
<td>KYU 5</td>
</tr>
<tr>
<td>JAV 3</td>
<td>SLW 2</td>
<td>ATY 4</td>
<td>THI 4</td>
<td>SOL 2</td>
<td>KAN 5</td>
<td>TOH 2</td>
<td>ATY 3</td>
</tr>
<tr>
<td>BOR 3</td>
<td>BAC 2</td>
<td>RYU 4</td>
<td>HAI 3</td>
<td>MSK 2</td>
<td>CML 3</td>
<td>ADR 1</td>
<td>HK 3</td>
</tr>
<tr>
<td>SLW 3</td>
<td>TOG 1</td>
<td>HK 3</td>
<td>VTN 2</td>
<td>SLW 2</td>
<td>SUM 1</td>
<td>LSN 2</td>
<td></td>
</tr>
<tr>
<td>TOG 1</td>
<td>ADR 1</td>
<td>BAC 2</td>
<td>BUR 2</td>
<td>HAW 1</td>
<td>PHL 2</td>
<td>SLW 1</td>
<td>THI 2</td>
</tr>
<tr>
<td>HAW 1</td>
<td>ATY 1</td>
<td>THI 2</td>
<td>HK 2</td>
<td>SEP 1</td>
<td>VTN 2</td>
<td>LSN 1</td>
<td>TOH 2</td>
</tr>
<tr>
<td>TUA 1</td>
<td>SUM 1</td>
<td>SHA 2</td>
<td>TAI 2</td>
<td>SUM 1</td>
<td>HK 2</td>
<td>SUL 1</td>
<td>SHA 2</td>
</tr>
<tr>
<td>NIR 1</td>
<td>JAV 1</td>
<td>TOG 1</td>
<td>KOR 2</td>
<td>BOR 1</td>
<td>HAI 2</td>
<td>HAN 1</td>
<td>HAN 2</td>
</tr>
<tr>
<td>ADR 1</td>
<td>BOR 1</td>
<td>SOL 1</td>
<td>HAW 1</td>
<td>LSN 1</td>
<td>KOR 2</td>
<td>MAN 1</td>
<td>MAN 2</td>
</tr>
<tr>
<td>Tohoku (53)</td>
<td>Kyushu (51)</td>
<td>Ainu (50)</td>
<td>Ryukyu Is. (64)</td>
<td>Shanghai (50)</td>
<td>Hangzhou (50)</td>
<td>Nanjing (49)</td>
<td>Chengdu (53)</td>
</tr>
<tr>
<td>------------</td>
<td>-------------</td>
<td>----------</td>
<td>-----------------</td>
<td>---------------</td>
<td>---------------</td>
<td>--------------</td>
<td>--------------</td>
</tr>
<tr>
<td>TOH</td>
<td>KYU</td>
<td>AIN</td>
<td>RYU</td>
<td>SHA</td>
<td>SHA</td>
<td>NAJ</td>
<td>CHD</td>
</tr>
<tr>
<td>19</td>
<td>16</td>
<td>29</td>
<td>23</td>
<td>12</td>
<td>12</td>
<td>7</td>
<td>26</td>
</tr>
<tr>
<td>KYU</td>
<td>KAN</td>
<td>KAN</td>
<td>AIN</td>
<td>HAN</td>
<td>HAN</td>
<td>MAN</td>
<td>NAJ</td>
</tr>
<tr>
<td>6</td>
<td>8</td>
<td>5</td>
<td>5</td>
<td>8</td>
<td>6</td>
<td>7</td>
<td>4</td>
</tr>
<tr>
<td>AIN</td>
<td>TOH</td>
<td>TOH</td>
<td>VTN</td>
<td>NAJ</td>
<td>NAJ</td>
<td>SHA</td>
<td>MOG</td>
</tr>
<tr>
<td>4</td>
<td>4</td>
<td>3</td>
<td>4</td>
<td>7</td>
<td>6</td>
<td>5</td>
<td>4</td>
</tr>
<tr>
<td>KOR</td>
<td>KOR</td>
<td>KYU</td>
<td>TOH</td>
<td>THI</td>
<td>CHD</td>
<td>HAN</td>
<td>VTN</td>
</tr>
<tr>
<td>4</td>
<td>4</td>
<td>3</td>
<td>3</td>
<td>4</td>
<td>5</td>
<td>5</td>
<td>3</td>
</tr>
<tr>
<td>ATI</td>
<td>RYU</td>
<td>RYU</td>
<td>TAI</td>
<td>KAN</td>
<td>HK</td>
<td>CHD</td>
<td>HK</td>
</tr>
<tr>
<td>3</td>
<td>3</td>
<td>2</td>
<td>3</td>
<td>4</td>
<td>5</td>
<td>5</td>
<td>3</td>
</tr>
<tr>
<td>MAN</td>
<td>HK</td>
<td>RAP</td>
<td>TOG</td>
<td>CHD</td>
<td>MOG</td>
<td>HK</td>
<td>SHA</td>
</tr>
<tr>
<td>3</td>
<td>3</td>
<td>1</td>
<td>2</td>
<td>4</td>
<td>4</td>
<td>3</td>
<td>2</td>
</tr>
<tr>
<td>LSN</td>
<td>ATI</td>
<td>HAW</td>
<td>ATY</td>
<td>HK</td>
<td>SUM</td>
<td>SUM</td>
<td>HAN</td>
</tr>
<tr>
<td>2</td>
<td>2</td>
<td>1</td>
<td>2</td>
<td>4</td>
<td>2</td>
<td>2</td>
<td>2</td>
</tr>
<tr>
<td>KAN</td>
<td>TAI</td>
<td>CHT</td>
<td>MSK</td>
<td>MAN</td>
<td>LSN</td>
<td>RYU</td>
<td>CHT</td>
</tr>
<tr>
<td>2</td>
<td>2</td>
<td>1</td>
<td>2</td>
<td>2</td>
<td>2</td>
<td>2</td>
<td>1</td>
</tr>
<tr>
<td>TAI</td>
<td>HAI</td>
<td>FIJ</td>
<td>KYU</td>
<td>MOG</td>
<td>MAN</td>
<td>KOR</td>
<td>LSN</td>
</tr>
<tr>
<td>2</td>
<td>2</td>
<td>1</td>
<td>2</td>
<td>2</td>
<td>2</td>
<td>2</td>
<td>1</td>
</tr>
<tr>
<td>CHT</td>
<td>MAN</td>
<td>CAR</td>
<td>HAI</td>
<td>TOG</td>
<td>ADR</td>
<td>SEP</td>
<td>BUR</td>
</tr>
<tr>
<td>1</td>
<td>2</td>
<td>1</td>
<td>2</td>
<td>1</td>
<td>1</td>
<td>1</td>
<td>1</td>
</tr>
</tbody>
</table>

<table>
<thead>
<tr>
<th>Hong Kong (50)</th>
<th>Taiwan (47)</th>
<th>Hainan Is. (47)</th>
<th>Manchuria (50)</th>
<th>Korea (32)</th>
<th>Mongolia (50)</th>
<th>Atayal (36)</th>
</tr>
</thead>
<tbody>
<tr>
<td>HK</td>
<td>TAI</td>
<td>HAI</td>
<td>MAN</td>
<td>KOR</td>
<td>MOG</td>
<td>ATY</td>
</tr>
<tr>
<td>23</td>
<td>24</td>
<td>6</td>
<td>18</td>
<td>8</td>
<td>40</td>
<td>15</td>
</tr>
<tr>
<td>HAN</td>
<td>TOH</td>
<td>KOR</td>
<td>RYU</td>
<td>HAI</td>
<td>SHA</td>
<td>DAW</td>
</tr>
<tr>
<td>5</td>
<td>4</td>
<td>6</td>
<td>4</td>
<td>5</td>
<td>2</td>
<td>4</td>
</tr>
<tr>
<td>MAN</td>
<td>HAI</td>
<td>BUR</td>
<td>CHD</td>
<td>TOH</td>
<td>CHD</td>
<td>KAN</td>
</tr>
<tr>
<td>4</td>
<td>3</td>
<td>4</td>
<td>4</td>
<td>3</td>
<td>2</td>
<td>3</td>
</tr>
<tr>
<td>KYU</td>
<td>KOR</td>
<td>RYU</td>
<td>HK</td>
<td>KOR</td>
<td>THI</td>
<td>AIN</td>
</tr>
<tr>
<td>3</td>
<td>3</td>
<td>4</td>
<td>3</td>
<td>3</td>
<td>1</td>
<td>2</td>
</tr>
<tr>
<td>THI</td>
<td>BAC</td>
<td>TAI</td>
<td>KOR</td>
<td>HAW</td>
<td>THI</td>
<td>AIN</td>
</tr>
<tr>
<td>2</td>
<td>2</td>
<td>4</td>
<td>3</td>
<td>2</td>
<td>1</td>
<td>2</td>
</tr>
<tr>
<td>TAI</td>
<td>LSN</td>
<td>THI</td>
<td>ATY</td>
<td>NAJ</td>
<td>TOH</td>
<td>KOR</td>
</tr>
<tr>
<td>2</td>
<td>1</td>
<td>3</td>
<td>2</td>
<td>2</td>
<td>1</td>
<td>2</td>
</tr>
<tr>
<td>TOG</td>
<td>SML</td>
<td>GUA</td>
<td>KAN</td>
<td>ATO</td>
<td>RYU</td>
<td>ADR</td>
</tr>
<tr>
<td>1</td>
<td>1</td>
<td>2</td>
<td>2</td>
<td>1</td>
<td>1</td>
<td>1</td>
</tr>
<tr>
<td>CHT</td>
<td>PHL</td>
<td>PHL</td>
<td>TOH</td>
<td>SUM</td>
<td>HAN</td>
<td>SEP</td>
</tr>
<tr>
<td>1</td>
<td>1</td>
<td>2</td>
<td>2</td>
<td>1</td>
<td>1</td>
<td>1</td>
</tr>
<tr>
<td>ADR</td>
<td>VTN</td>
<td>CHD</td>
<td>KYU</td>
<td>BOR</td>
<td>HAI</td>
<td>PHL</td>
</tr>
<tr>
<td>1</td>
<td>1</td>
<td>2</td>
<td>2</td>
<td>1</td>
<td>1</td>
<td>1</td>
</tr>
<tr>
<td>ATY</td>
<td>CML</td>
<td>HK</td>
<td>SHA</td>
<td>PHL</td>
<td>TOH</td>
<td></td>
</tr>
<tr>
<td>1</td>
<td>1</td>
<td>2</td>
<td>2</td>
<td>1</td>
<td>1</td>
<td>1</td>
</tr>
</tbody>
</table>

See Table 16.1 for explanation of abbreviations.
Figure 16.2 A plot of 63 group means on the first two canonical variates that results from the application of stepwise discriminant function analysis to 27 cranial measurements.

Manchurian, and Korean cranial series, including the Ainu, form another separate grouping. The cranial series from Mongolia is the most isolated series in this representation.

To examine differences between individual groups more closely requires another multivariate procedure, namely Mahalanobis's generalized distance.

Figure 16.3 A plot of 35 of the 63 groups on the first three canonical variates that results from the application of stepwise discriminant function analysis to 27 cranial measurements.
**Mahalanobis’s Generalized Distance-D^2.** Some of the results of applying Mahalanobis’s generalized distances to the same measurements analyzed by stepwise discriminant function analysis are given in Table 16.7. The results given in this table list the ten smallest distances for each of the 63 groups, which are groups that are most similar to each of these groups.

Although the cranial series from Polynesia and Micronesia are generally closest to other Polynesian/Micronesian series, several island Southeast Asian series (e.g., Java, Borneo, Sulawesi, Sulu, Lesser Sunda Islands, and Southern Moluccas) rank among the smallest distances for Tonga-Samoa, Hawaii, Marquesas New Zealand, Chatham Islands, and Tuamotu. The cranial series from the Southern Moluccas, followed by Marquesas, Marshall-Kiribati, Solomon Islands, Caroline Islands, New Ireland, and Biak Island, are among the groups closest to the New Zealand Maori series. A few island Melanesian cranial series (e.g., Fiji, Loyalty, and New Caledonia) are among the smallest distances to the Polynesian series. Among the distances closest to the Caroline Islands and Marshall/Kiribati Islands series are those associated with these two series, New Zealand, Marquesas, several Melanesian series, and the Southern Moluccas series.

Inspection of the smallest distances for the island Melanesian (e.g., Fiji, Vanuatu, Loyalty, or New Caledonia) and New Guinea series (e.g., Sepik, Fly River, or Purari Delta) reveals that most of these are associated with cranial series from the same geographical region as well as the Caroline, Marshall-Kiribati, and Southern Moluccas series. Without exception the distances closest to the Australian series are other Australian/Tasmanian and Melanesian (e.g., New Britain, Vanuatu, or Santa Cruz) series.

Interestingly, one series from geographical Melanesia, Admiralty Island, is found to be closest to the Southern Moluccas series and several other island Southeast Asian series, including Borneo, Sulu, and the Lesser Sunda Islands.

Most of the cranial series closest to the island and mainland Southeast Asian series are generally from Southeast Asia. Somewhat surprisingly, the cranial series closest to one of the island Southeast Asian series, the
<table>
<thead>
<tr>
<th>Tonga-Samoan</th>
<th>Rapa Nui</th>
<th>Hawaii</th>
<th>Marquesas Islands</th>
<th>New Zealand</th>
<th>Chatham Islands</th>
</tr>
</thead>
<tbody>
<tr>
<td>HAW</td>
<td>6.643</td>
<td>GAM</td>
<td>5.439&lt;sup&gt;b&lt;/sup&gt;</td>
<td>TOG</td>
<td>6.643</td>
</tr>
<tr>
<td>SLW</td>
<td>8.290&lt;sup&gt;a&lt;/sup&gt;</td>
<td>MRQ</td>
<td>8.811</td>
<td>SUL</td>
<td>7.953</td>
</tr>
<tr>
<td>CML</td>
<td>8.557&lt;sup&gt;a&lt;/sup&gt;</td>
<td>CAR</td>
<td>10.236</td>
<td>JAV</td>
<td>8.143</td>
</tr>
<tr>
<td>SUL</td>
<td>8.704&lt;sup&gt;a&lt;/sup&gt;</td>
<td>HAW</td>
<td>10.712</td>
<td>NZ</td>
<td>8.371</td>
</tr>
<tr>
<td>LSN</td>
<td>8.805</td>
<td>MSK</td>
<td>11.045</td>
<td>GUA</td>
<td>8.898</td>
</tr>
<tr>
<td>THI</td>
<td>10.403</td>
<td>LOY</td>
<td>12.033</td>
<td>CHT</td>
<td>9.633</td>
</tr>
</tbody>
</table>

<table>
<thead>
<tr>
<th>Society Islands</th>
<th>Tuamotu Islands</th>
<th>Gambier Islands</th>
<th>Fiji</th>
<th>Vanuatu</th>
<th>Loyalty Islands</th>
</tr>
</thead>
<tbody>
<tr>
<td>MRQ</td>
<td>3.583</td>
<td>SOC</td>
<td>4.690&lt;sup&gt;b&lt;/sup&gt;</td>
<td>RAP</td>
<td>5.439&lt;sup&gt;b&lt;/sup&gt;</td>
</tr>
<tr>
<td>TUA</td>
<td>4.690&lt;sup&gt;b&lt;/sup&gt;</td>
<td>MRQ</td>
<td>7.167</td>
<td>MRQ</td>
<td>5.819&lt;sup&gt;b&lt;/sup&gt;</td>
</tr>
<tr>
<td>MSK</td>
<td>7.364&lt;sup&gt;b&lt;/sup&gt;</td>
<td>MSK</td>
<td>10.102</td>
<td>NZ</td>
<td>7.462&lt;sup&gt;b&lt;/sup&gt;</td>
</tr>
<tr>
<td>GAM</td>
<td>8.551&lt;sup&gt;b&lt;/sup&gt;</td>
<td>NZ</td>
<td>11.019</td>
<td>SOC</td>
<td>8.551&lt;sup&gt;b&lt;/sup&gt;</td>
</tr>
<tr>
<td>NZ</td>
<td>8.796</td>
<td>GAM</td>
<td>12.724&lt;sup&gt;b&lt;/sup&gt;</td>
<td>CHT</td>
<td>10.105&lt;sup&gt;b&lt;/sup&gt;</td>
</tr>
<tr>
<td>HAW</td>
<td>9.906</td>
<td>HAW</td>
<td>14.688</td>
<td>HAW</td>
<td>10.641&lt;sup&gt;b&lt;/sup&gt;</td>
</tr>
<tr>
<td>CAR</td>
<td>9.914</td>
<td>CAR</td>
<td>14.994&lt;sup&gt;b&lt;/sup&gt;</td>
<td>MSK</td>
<td>11.845&lt;sup&gt;b&lt;/sup&gt;</td>
</tr>
<tr>
<td>TOG</td>
<td>10.963</td>
<td>TOG</td>
<td>15.249&lt;sup&gt;b&lt;/sup&gt;</td>
<td>TUA</td>
<td>12.724&lt;sup&gt;b&lt;/sup&gt;</td>
</tr>
<tr>
<td>RAP</td>
<td>11.087</td>
<td>RAP</td>
<td>15.386</td>
<td>FIJ</td>
<td>13.014&lt;sup&gt;b&lt;/sup&gt;</td>
</tr>
<tr>
<td>FIJ</td>
<td>11.632</td>
<td>SML</td>
<td>15.921</td>
<td>GUA</td>
<td>13.968&lt;sup&gt;b&lt;/sup&gt;</td>
</tr>
</tbody>
</table>

<table>
<thead>
<tr>
<th>New Caledonia</th>
<th>Santa Cruz Islands</th>
<th>Solomon Islands</th>
<th>New Britain</th>
<th>New Ireland</th>
<th>Admiralty Islands</th>
</tr>
</thead>
<tbody>
<tr>
<td>LOY</td>
<td>3.313</td>
<td>NBR</td>
<td>4.747</td>
<td>NIR</td>
<td>2.389&lt;sup&gt;a&lt;/sup&gt;</td>
</tr>
<tr>
<td>NBR</td>
<td>5.982</td>
<td>NT</td>
<td>5.089&lt;sup&gt;a&lt;/sup&gt;</td>
<td>CAR</td>
<td>3.515&lt;sup&gt;b&lt;/sup&gt;</td>
</tr>
<tr>
<td>SOL</td>
<td>6.270</td>
<td>VAN</td>
<td>5.244</td>
<td>SEP</td>
<td>3.873</td>
</tr>
<tr>
<td>------</td>
<td>--------</td>
<td>-----</td>
<td>--------</td>
<td>-----</td>
<td>--------</td>
</tr>
<tr>
<td>NIR</td>
<td>6.284</td>
<td>SOL</td>
<td>5.932</td>
<td>BIK</td>
<td>4.093</td>
</tr>
<tr>
<td>VAN</td>
<td>6.652</td>
<td>NCL</td>
<td>6.716</td>
<td>NBR</td>
<td>4.170</td>
</tr>
<tr>
<td>SCR</td>
<td>6.716</td>
<td>NIR</td>
<td>6.879</td>
<td>DTX</td>
<td>4.620(^a)</td>
</tr>
<tr>
<td>MSK</td>
<td>8.044(^b)</td>
<td>PUR</td>
<td>7.613</td>
<td>FLY</td>
<td>4.874</td>
</tr>
<tr>
<td>SEP</td>
<td>8.134</td>
<td>FLY</td>
<td>7.883</td>
<td>FIJ</td>
<td>5.010</td>
</tr>
</tbody>
</table>

<table>
<thead>
<tr>
<th>Sepik R.</th>
<th>Biak Island</th>
<th>Fly R.</th>
<th>Purari Delta</th>
<th>D'Entrecasteaux Islands</th>
<th>Dawson Strait</th>
</tr>
</thead>
<tbody>
<tr>
<td>DTX</td>
<td>3.714(^b)</td>
<td>NIR</td>
<td>3.825</td>
<td>PUR</td>
<td>2.101(^b)</td>
</tr>
<tr>
<td>SOL</td>
<td>3.873</td>
<td>SML</td>
<td>3.873</td>
<td>SEP</td>
<td>4.226</td>
</tr>
<tr>
<td>NIR</td>
<td>4.011</td>
<td>SEP</td>
<td>4.015</td>
<td>SOL</td>
<td>4.874</td>
</tr>
<tr>
<td>BIK</td>
<td>4.015</td>
<td>SOL</td>
<td>4.093</td>
<td>BIK</td>
<td>5.317</td>
</tr>
<tr>
<td>CAR</td>
<td>5.297(^a)</td>
<td>FJ</td>
<td>4.232</td>
<td>DTX</td>
<td>6.129(^a)</td>
</tr>
<tr>
<td>DAW</td>
<td>5.892</td>
<td>FLY</td>
<td>5.317</td>
<td>FJ</td>
<td>6.488</td>
</tr>
<tr>
<td>SML</td>
<td>6.083</td>
<td>DAW</td>
<td>5.498</td>
<td>VAN</td>
<td>7.659</td>
</tr>
<tr>
<td>MSK</td>
<td>6.195</td>
<td>CAR</td>
<td>5.535(^a)</td>
<td>CAR</td>
<td>7.669</td>
</tr>
</tbody>
</table>

<table>
<thead>
<tr>
<th>Murray R.</th>
<th>New South Wales</th>
<th>Queensland</th>
<th>Northern Territory</th>
<th>Swanport, S.A.</th>
<th>Western Australia</th>
</tr>
</thead>
<tbody>
<tr>
<td>QLD</td>
<td>2.696(^a)</td>
<td>QLD</td>
<td>1.575(^b)</td>
<td>NSW</td>
<td>1.575(^b)</td>
</tr>
<tr>
<td>NSW</td>
<td>2.840</td>
<td>MRB</td>
<td>2.840</td>
<td>NT</td>
<td>2.560(^a)</td>
</tr>
<tr>
<td>NT</td>
<td>2.850(^a)</td>
<td>NT</td>
<td>3.238</td>
<td>MRB</td>
<td>2.696(^a)</td>
</tr>
<tr>
<td>VAN</td>
<td>6.738</td>
<td>VAN</td>
<td>5.344</td>
<td>VAN</td>
<td>5.954</td>
</tr>
<tr>
<td>WA</td>
<td>6.875</td>
<td>WA</td>
<td>5.943</td>
<td>WA</td>
<td>6.345</td>
</tr>
</tbody>
</table>

(Continued)
<table>
<thead>
<tr>
<th>Murray R.</th>
<th>New South Wales</th>
<th>Queensland</th>
<th>Northern Territory</th>
<th>Swanport, S.A.</th>
<th>Western Australia</th>
</tr>
</thead>
<tbody>
<tr>
<td>TAS</td>
<td>NBR</td>
<td>7.013</td>
<td>SAS</td>
<td>8.069</td>
<td>WA</td>
</tr>
<tr>
<td>SCR</td>
<td>BIK</td>
<td>8.679</td>
<td>FIJ</td>
<td>8.320</td>
<td>BIK</td>
</tr>
<tr>
<td>SOL</td>
<td>TAS</td>
<td>8.893</td>
<td>TAS</td>
<td>8.442</td>
<td>FLY</td>
</tr>
</tbody>
</table>

<table>
<thead>
<tr>
<th>Tasmania</th>
<th>Guam</th>
<th>Caroline Islands</th>
<th>Marshall-Kiribati Islands</th>
<th>Sumatra</th>
<th>Java</th>
</tr>
</thead>
<tbody>
<tr>
<td>QLD</td>
<td>8.442</td>
<td>HAW</td>
<td>8.898</td>
<td>SOL</td>
<td>3.515b</td>
</tr>
<tr>
<td>VAN</td>
<td>8.436</td>
<td>TOG</td>
<td>9.006</td>
<td>NIR</td>
<td>3.663b</td>
</tr>
<tr>
<td>MRB</td>
<td>8.733</td>
<td>NZ</td>
<td>9.412</td>
<td>MSK</td>
<td>4.239b</td>
</tr>
<tr>
<td>NBR</td>
<td>10.662</td>
<td>BOR</td>
<td>9.977</td>
<td>BIK</td>
<td>5.535b</td>
</tr>
<tr>
<td>WA</td>
<td>10.729</td>
<td>SUM</td>
<td>10.198</td>
<td>NZ</td>
<td>6.061</td>
</tr>
<tr>
<td>NT</td>
<td>12.085</td>
<td>SUL</td>
<td>10.286</td>
<td>FIJ</td>
<td>6.091a</td>
</tr>
<tr>
<td>SAS</td>
<td>12.822</td>
<td>MRQ</td>
<td>10.714</td>
<td>SML</td>
<td>6.448</td>
</tr>
<tr>
<td>BIK</td>
<td>14.168</td>
<td>SLW</td>
<td>11.794</td>
<td>NCL</td>
<td>7.174</td>
</tr>
<tr>
<td>SML</td>
<td>14.700</td>
<td>CML</td>
<td>11.859</td>
<td>LOY</td>
<td>7.500</td>
</tr>
</tbody>
</table>

<table>
<thead>
<tr>
<th>Borneo</th>
<th>Sulawesi</th>
<th>Lesser Sunda</th>
<th>S. Molucca Islands</th>
<th>Sulu</th>
<th>Philippines</th>
</tr>
</thead>
<tbody>
<tr>
<td>LSN</td>
<td>JAV</td>
<td>2.334b</td>
<td>BOR</td>
<td>1.810b</td>
<td>3.553</td>
</tr>
<tr>
<td>SUM</td>
<td>CML</td>
<td>2.607b</td>
<td>SUM</td>
<td>2.622a</td>
<td>3.873</td>
</tr>
<tr>
<td>SLW</td>
<td>BOR</td>
<td>2.658b</td>
<td>SLW</td>
<td>2.737b</td>
<td>4.255</td>
</tr>
<tr>
<td>SUL</td>
<td>LSN</td>
<td>2.737a</td>
<td>JAV</td>
<td>3.611</td>
<td>4.373</td>
</tr>
<tr>
<td>JAV</td>
<td>SUL</td>
<td>2.853b</td>
<td>PHL</td>
<td>3.706a</td>
<td>4.865</td>
</tr>
<tr>
<td>PHL</td>
<td>SUM</td>
<td>3.125b</td>
<td>VTN</td>
<td>4.608</td>
<td>5.328</td>
</tr>
<tr>
<td>VTN</td>
<td>PHL</td>
<td>3.426b</td>
<td>SUL</td>
<td>4.852</td>
<td>5.489</td>
</tr>
<tr>
<td>CML</td>
<td>THI</td>
<td>3.952</td>
<td>SML</td>
<td>4.865</td>
<td>5.930</td>
</tr>
<tr>
<td>SML</td>
<td>VTN</td>
<td>5.408</td>
<td>SOL</td>
<td>5.430</td>
<td>6.083</td>
</tr>
<tr>
<td>SOL</td>
<td>BAC</td>
<td>5.918</td>
<td>RYU</td>
<td>5.980</td>
<td>6.185</td>
</tr>
</tbody>
</table>

b: Indicates the distance in kilometers.
<table>
<thead>
<tr>
<th>Viet Nam</th>
<th>Bachuc Village</th>
<th>Cambodia &amp; Laos</th>
<th>Thailand</th>
<th>Burma</th>
<th>Kanto</th>
</tr>
</thead>
<tbody>
<tr>
<td>PHL</td>
<td>2.353&lt;sup&gt;b&lt;/sup&gt;</td>
<td>THI 3.169</td>
<td>SLW 2.607&lt;sup&gt;b&lt;/sup&gt;</td>
<td>BAC 3.169</td>
<td>SUL 6.202&lt;sup&gt;b&lt;/sup&gt;</td>
</tr>
<tr>
<td>RYU</td>
<td>4.247</td>
<td>HAI 3.780</td>
<td>SUL 2.742&lt;sup&gt;b&lt;/sup&gt;</td>
<td>SLW 3.952</td>
<td>SUM 6.442&lt;sup&gt;b&lt;/sup&gt;</td>
</tr>
<tr>
<td>THI</td>
<td>4.296</td>
<td>VTN 5.139</td>
<td>JAV 3.498&lt;sup&gt;a&lt;/sup&gt;</td>
<td>VTN 4.296</td>
<td>CML 7.013&lt;sup&gt;a&lt;/sup&gt;</td>
</tr>
<tr>
<td>SUM</td>
<td>4.333</td>
<td>CML 5.757</td>
<td>BOR 5.168</td>
<td>JAV 4.321</td>
<td>SLW 7.216&lt;sup&gt;b&lt;/sup&gt;</td>
</tr>
<tr>
<td>LSN</td>
<td>4.608</td>
<td>SLW 5.918</td>
<td>THI 5.495</td>
<td>PHL 4.821&lt;sup&gt;a&lt;/sup&gt;</td>
<td>JAV 7.324&lt;sup&gt;a&lt;/sup&gt;</td>
</tr>
<tr>
<td>BOR</td>
<td>4.871</td>
<td>JAV 6.036</td>
<td>BAC 5.757</td>
<td>CML 5.495</td>
<td>BAC 7.464&lt;sup&gt;a&lt;/sup&gt;</td>
</tr>
<tr>
<td>KOR</td>
<td>5.090</td>
<td>PHL 6.235&lt;sup&gt;b&lt;/sup&gt;</td>
<td>PHL 5.955</td>
<td>HAI 5.558</td>
<td>THI 7.756&lt;sup&gt;a&lt;/sup&gt;</td>
</tr>
<tr>
<td>BAC</td>
<td>5.139</td>
<td>KOR 6.358</td>
<td>LSN 5.991</td>
<td>KAN 5.933</td>
<td>VTN 9.208</td>
</tr>
<tr>
<td>HAI</td>
<td>5.191</td>
<td>HK 6.910</td>
<td>SUM 6.413</td>
<td>SUM 5.936</td>
<td>BOR 9.328&lt;sup&gt;b&lt;/sup&gt;</td>
</tr>
<tr>
<td>SLW</td>
<td>5.408</td>
<td>SUL 7.213</td>
<td>BUR 7.013&lt;sup&gt;b&lt;/sup&gt;</td>
<td>KOR 6.100</td>
<td>HAI 9.586</td>
</tr>
<tr>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Tohoku</td>
<td>Kyushu</td>
<td>Ainu</td>
<td>Ryukyu Islands</td>
<td>Shanghai</td>
<td></td>
</tr>
<tr>
<td>KYU</td>
<td>2.167</td>
<td>TOH 2.167</td>
<td>KYU 5.371</td>
<td>VTN 4.247</td>
<td>HAN 0.549&lt;sup&gt;b&lt;/sup&gt;</td>
</tr>
<tr>
<td>KOR</td>
<td>3.219&lt;sup&gt;b&lt;/sup&gt;</td>
<td>KAN 2.784&lt;sup&gt;a&lt;/sup&gt;</td>
<td>TOH 6.067&lt;sup&gt;a&lt;/sup&gt;</td>
<td>KYU 4.790</td>
<td>NAJ 1.985&lt;sup&gt;b&lt;/sup&gt;</td>
</tr>
<tr>
<td>SLW</td>
<td>3.333</td>
<td>KOR 2.844&lt;sup&gt;b&lt;/sup&gt;</td>
<td>RYU 6.366</td>
<td>KOR 5.280</td>
<td>CHD 3.827</td>
</tr>
<tr>
<td>CML</td>
<td>4.659</td>
<td>RYU 4.790</td>
<td>KAN 6.402</td>
<td>HAI 5.638</td>
<td>HK 3.887</td>
</tr>
<tr>
<td>SUL</td>
<td>5.438</td>
<td>HAI 4.876</td>
<td>SUM 6.840</td>
<td>TAI 5.842</td>
<td>MAN 5.894</td>
</tr>
<tr>
<td>AIN</td>
<td>6.067</td>
<td>LSN 5.011</td>
<td>LSN 8.503</td>
<td>LSN 5.980</td>
<td>KOR 5.901</td>
</tr>
<tr>
<td>NAJ</td>
<td>6.179</td>
<td>MAN 5.198</td>
<td>VTN 9.644</td>
<td>SUM 6.303</td>
<td>SUM 6.269</td>
</tr>
</tbody>
</table>

(Continued)
<table>
<thead>
<tr>
<th>Table 16.7 Continued</th>
</tr>
</thead>
<tbody>
<tr>
<td>Hangzhou</td>
</tr>
<tr>
<td>SHA</td>
</tr>
<tr>
<td>NAJ</td>
</tr>
<tr>
<td>HK</td>
</tr>
<tr>
<td>CHD</td>
</tr>
<tr>
<td>MAN</td>
</tr>
<tr>
<td>KOR</td>
</tr>
</tbody>
</table>

<table>
<thead>
<tr>
<th>Hainan Island</th>
<th>Manchuria</th>
<th>Korea</th>
<th>Mongolia</th>
<th>Atayal</th>
</tr>
</thead>
<tbody>
<tr>
<td>KOR</td>
<td>2.415&lt;sup&gt;b&lt;/sup&gt;</td>
<td>NAJ</td>
<td>3.302</td>
<td>HAI</td>
</tr>
<tr>
<td>TAI</td>
<td>3.165&lt;sup&gt;a&lt;/sup&gt;</td>
<td>KOR</td>
<td>3.645&lt;sup&gt;a&lt;/sup&gt;</td>
<td>KYU</td>
</tr>
<tr>
<td>BAC</td>
<td>3.780</td>
<td>TOH</td>
<td>4.659</td>
<td>TOH</td>
</tr>
<tr>
<td>KYU</td>
<td>4.876</td>
<td>HAN</td>
<td>4.994</td>
<td>MAN</td>
</tr>
<tr>
<td>VTN</td>
<td>5.191</td>
<td>KYU</td>
<td>5.198</td>
<td>TAI</td>
</tr>
<tr>
<td>THI</td>
<td>5.558</td>
<td>CHD</td>
<td>5.678</td>
<td>KAN</td>
</tr>
<tr>
<td>RYU</td>
<td>5.638</td>
<td>HK</td>
<td>5.734</td>
<td>NAJ</td>
</tr>
<tr>
<td>MAN</td>
<td>5.804</td>
<td>HAI</td>
<td>5.804</td>
<td>VTN</td>
</tr>
<tr>
<td>ATY</td>
<td>6.271</td>
<td>SHA</td>
<td>5.894</td>
<td>RYU</td>
</tr>
</tbody>
</table>

<sup>a</sup>Variance ratio significant at 5% level.
<sup>b</sup>Variance ratio not significant at 5% level.
Southern Moluccas, is New Zealand, a Polynesian series. Seven of the smallest
distances to the Southern Moluccas include seven series from New Guinea and the neighboring
regions of island Melanesia, (i.e., New Ireland, Admiralty, Dawson, Admiralty Islands, and
D’Entrecestaux).

Several Southeast Asian series are among the ten smallest distances to the Japanese series.

Korea generally ranks in the top ten closest
groups to the Japanese and Chinese series.
Although not significant, Korea is closest to
the Hainan Island series. Other groups closest
to Hainan Island include Taiwan Chinese, two
Vietnamese series, Thailand, and the Ryukyu
Islands.

The groups found to be closest to the Ainu cranial series include several modern Japanese

---

Figure 16.5 Dendrogram showing the relationship of 63 groups that results from a cluster analysis (UPGMA) of
Mahalanobis’s distances using 27 cranial measurements.
followed by the Ryukyu Islanders and several island Southeast Asian series. Distances closest to the Ryukyu Islands include Vietnam, Kyushu, Korea, Hainan Island, Taiwan, Lesser Sunda Islands, and Sumatra. The series closest to the Atayal (Taiwan Aborigines) series include three Japanese series, Korea, Hainan Island, and Vietnam.

Applying the UPGMA clustering algorithm to these distances results in the dendrogram shown in Fig. 16.5. Two major divisions are evident in this diagram of relationships, the first includes all Asian (North, East and Southeast Asia) and Polynesian cranial series and the second includes all Australian, Tasmanian, New Guinea and Melanesian cranial series.

With the exception of New Zealand, the Polynesian (and one from Guam) cranial series form a distinct cluster that ultimately connects to one containing East Asian, North Asian, and Southeast Asian cranial series. The New Zealand Maori and Southern Moluccas cranial series group with three Melanesian (Fiji, Solomon Islands, and New Ireland) series, a single north coastal New Guinea series (Biak Island), and two Micronesian cranial series (Caroline Islands and Marshall-Kiribati Islands).

The cranial samples representing Southeast Asia occupy two separate clusters, representing primarily the mainland and island Southeast Asia series, respectively. The cranial series representing modern Japanese align with Taiwan and Hainan Island Chinese, Korea, and more remotely with the Ryukyu Islands and Atayal (Taiwan Aboriginal) series. The remaining series representing China and Manchuria occupy a separate branch. The Ainu and Mongolian series are the last two series to connect with this exclusively Asian division that comprises the cranial series from Northern, Eastern, and Southeast Asia.

**Discussion of Results.** The results of the multivariate cranioemetric analysis used in this application indicate the presence of two major divisions representing the inhabitants of the Pacific and neighboring regions of eastern Asia. One of these major divisions includes cranial series representing the indigenous inhabitants of Australia, Tasmania, and geographical Melanesia, whereas a second major division includes cranial series from East Asia, North Asia, Southeast Asia, and Remote Oceania. The sharpness of the distinction suggests separate origins for the indigenous inhabitants of these two regions, one that coincides with the initial peopling of Australia and Near Oceania and a second event that accounts for the earliest human colonization of Remote Oceania.

Likewise, in these results, the Polynesian cranial series occupy a separate branch of the greater East/Southeast Asian division, one that is well removed from the division that includes all the cranial series from Melanesia and Australia, which is a relationship that is more consistent with an ancestral homeland for Polynesians in Eastern and Southeast Asia rather than one within geographically adjacent Melanesia. The classification results (Table 16.6) and detailed inspection of Mahalanobis's distances (Table 16.7) also indicate connections between several of the Polynesian series and cranial series from eastern Indonesia. The Micronesian series are variable; some (e.g., Guam) show Polynesian affinities, whereas others (e.g., Caroline Islands) reveal connections with Melanesia.

These multivariate cranioemetric results share much in common with archeological, historical linguistic, and recent molecular genetic evidence (e.g., Blust, 1995; Kirch, 1997, 2000; Lum and Cann, 1998; Lum et al., 1998; Melton et al., 1995; Merriwether et al., 1999; Oppenheimer and Richards, 2001; Redd et al., 1995; Richards et al., 1998; Su et al., 2000) that favors a relatively rapid eastward migration and colonization of Remote Oceania by peoples and cultures (the so-called Lapita expansion) whose ancestors are traceable to somewhere in eastern island Southeast Asia.

In these same results, island and mainland Southeast Asian cranial series form two separate
branches well separated from the East and North Asian series, which is a distinction that implies long-term in situ development in both regions rather than displacement (see, e.g., Bellwood, 1997) to account for the current-day inhabitants of Southeast Asia, conclusions that are supported by dental (e.g., Turner, 1987, 1989, 1992) and other studies that use cranio metric data (e.g., Hanihara, 1996).

Finally, contrary to others (e.g., Brace et al., 1990), there is no support for a close biological connection between the Ainu and the Polynesian series in these results. Rather, the Ainu are members (albeit marginal) of a greater East/North Asian division and do not connect directly with any of the Polynesian series, which is a conclusion supported by other skeletal evidence (see, e.g., Hanihara, 1993, 1996).

**CONCLUSIONS**

The application of analytical methods to metric data, which has characterized physical anthropology since its inception, remains a major focus of interest in biological anthropology. Likewise, determining biological relatedness, as in the application provided in this chapter, continues to attract considerable attention in skeletal biology and physical anthropology. Multivariate statistical procedures remain the most robust procedures available for analyzing both metric and nonmetric variation. Discriminant function analysis and Mahalanobis's generalized distance constitute two of the most popular multivariate procedures for determining biological relatedness and for classification of unknown specimens using metric variables. Various clustering procedures and other methods of ordination provide an important means of visualizing multivariate results.

The general reluctance among anthropologists and skeletal biologists to use multivariate statistical procedures, stems, in part, from the complex, often daunting, mathematical theory that underlies these methods. Refinements of the methodological and theoretical concerns, which have often resulted in mathematical adjustments or "corrections" to the existing procedures, have done little to advance the easy acceptance and use of these methods. However, given that many of these methods are now readily available in statistical packages designed for personal computers lessens the need for users to be highly skilled or trained in mathematics and/or statistics.

Coinciding with anthropologists' earliest applications of multivariate statistical procedures to metric data, the principal concern has been determining past relationships and classification or allocation of individual (usually fossil) specimens. More recently, the controversy surrounding the discovery of the Kennewick skeleton (Chatters, 2001) and determining ancestral–descendant relationships of skeletal remains of indigenous peoples has attracted considerable attention. This trend, which primarily addresses biological relationships of past populations, is likely to continue well into the future. Likewise, the use of multivariate statistical procedures for classificatory purposes will most certainly continue to find applications in forensic anthropology and in cases involving repatriation claims and NAGPRA legislation. Although global appraisals of skeletal (especially cranial) variation will undoubtedly continue, studies of human skeletal remains having more restricted regional and temporal focus are likely to increase in the future.

With the recognition by bioarchaeologists of the importance of determining biological relatedness to contextualize issues pertaining to health, disease, nutrition, demography, and epidemiology in past populations, studies that apply multivariate statistical procedures to metric and nonmetric data are expected to increase in number.

Finally, given the statistical and mathematical underpinnings of the methods and the problems associated with interpreting the results
of multivariate statistical analyses, physical anthropologists and skeletal biologists, especially those highly tutored in quantitative methods, are expected to continue to refine the methodological and theoretical concerns associated with these methods. It is anticipated that these endeavors will make these methods both more accessible and relevant for analyzing and interpreting anthropological and skeletal biological data.

ACKNOWLEDGMENTS

My thanks to Billie Ikeda of the University of Hawaii Instructional Support Center for her assistance with producing the figures used in this chapter. I am grateful for the assistance of Scott Reinke and Rona Ikehara-Quebral in data analysis. As always, I am extremely grateful to Michele Toomay Douglas for her comments in preparing this chapter. My thanks to RoutledgeCurzon (London) for permission to reproduce the five illustrations in this chapter that first appeared in Pietrusewsky (2005). Permission to examine the cranial series used in the example used in this chapter has been acknowledged elsewhere (Pietrusewsky, 1994, 1995, 2004; Pietrusewsky and Chang, 2003).

REFERENCES


Burmanusga M, Leach F. 1993. Coordinate geometry of Mori or crania and comparisons with Maori. Man Cult Oceania 9:1–43.


SPSS, Inc. 1999a. SPSS Advanced Models 10.0. Chicago, Ill.: SPSS, Inc.

SPSS, Inc. 1999b. SPSS Base 10.0 Applications Guide. Chicago, Ill.: SPSS, Inc.

SPSS, Inc. 1999c. SYSTAT 9 Statistics I and II. Chicago, Ill.: SPSS, Inc.


Van Vark GN. 1976. A critical evaluation of the application of multivariate statistical methods to
the study of human populations from their skeletal remains. Homo 27:94–114.


