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## **Multivariate Discrimination, Tooth Measurements and Early Hominid Taxonomy**

It is argued that the value of the various multivariate approaches in dealing with functional, taxonomic, and phylogenetic problems can only be determined empirically. A review of three studies dealing with multivariate analyses of the early hominid dentition suggests that at best, the multivariate statistics used are inappropriate and the results contradictory.

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There have been several recent attempts to use the early hominid dentition to determine phylogenetic relationships through sophisticated multivariate statistical analysis (Brace, Malher & Rosen, 1972; Read, 1975; Robinson & Streudel, 1973). It is my belief that these techniques constitute more than an overkill. I contend that they are inappropriate; a position not weakened by the fact that the conclusions of these papers contradict each other.

The strength of a multivariate approach is that it allows one to consider numerous factors at the same time. Many authors feel that to consider multiple variables together is to adhere to LeGros Clark's "total morphological pattern." If everything is measured, the totality of the organism must be considered (e.g. Sneath & Sokal, 1973). Others, however, suggest that the approach may more closely adhere to Finagle's third law: "plot your results, and then analyze your data." The variety of possible approaches and the availability of computers with large program libraries has led to a real tendency to use the procedure that gives the desired results. The results of a multivariate approach follow completely from the assumptions, and cannot be used to test them. In addition, the data can only be treated in an additive manner, which may or may not correspond to the biological reality underlying the association and variation of the characteristics measured.

For instance, the discriminant function allows sorting between known groups on the basis of an additive function derived from the various measurements (Kowalski, 1972). The basic underlying assumption is that we *know* both the number and the exact composition of the groups to be partitioned (Anderson, 1951). Even if the other assumption required for the proper use of the technique can be met (e.g. equivalence of covariance matrices), there is good evidence that assigning an individual to the sample whose mean is nearer in discriminate space is not necessarily the best rule (Robbins, 1961). Interpreting the results of discrimination raises equally important questions. For instance, what are the effects of size and shape variables? If size and shape can be successfully partitioned, discrimination may occur between essentially identical samples, in a biological sense, differing only allometrically. On the other hand, if size and shape are not partitioned, discrimination may not occur when significant differences exist (Blackith, 1965). One thing that should be obvious is that the ability to calculate a function that successfully discriminates groups neither adds to nor subtracts from the biological "reality" of the groups—this is an *assumption* made before the function is calculated.

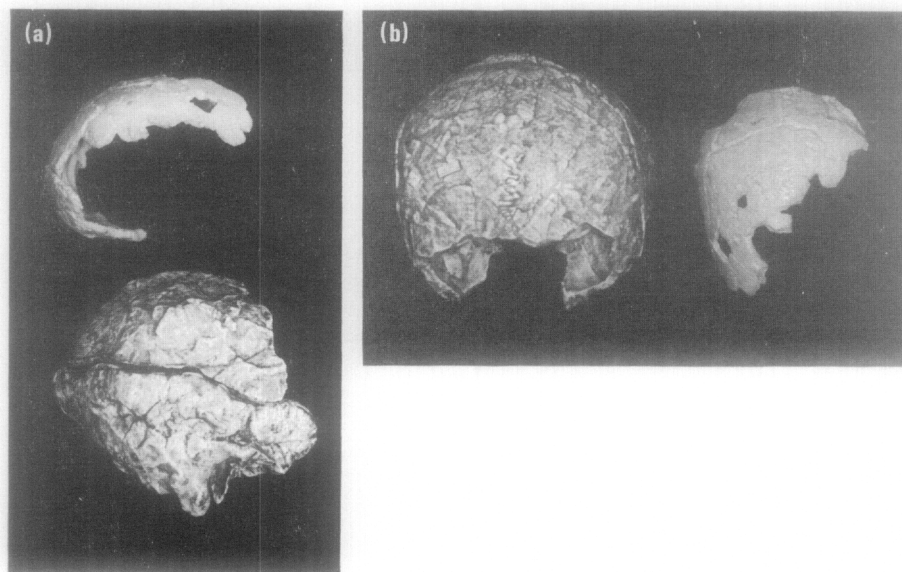
Probably the greatest single problem in discrimination analyses is the interpretation of the results. Given enough measurements, it is likely that *any* two biological groups can be successfully discriminated, regardless of how they are initially partitioned. This is a necessary consequence of the fact that every individual is different. Because of the complexity of the procedure, there seems to be no *a priori* criterion that can be used to determine whether the results "have significant value as easily understood summaries of the structure underlying the multiresponse data" (Gnanadesikan, 1970). One certain conclusion, however, is that the relative positions in a discriminant space are not necessarily measures of either functional or taxonomic relationships. In the end, what a function actually discriminates can only be determined by how the results are interpreted. It simply does not follow that the results of a discriminant analysis (or for that matter a cluster, principal components, or factor analysis) which is based on so-called functional measurements will necessarily result in functional groupings. As one of many possible examples, consider the recent attempts of McHenry & Corruccini (1975) to deal with the known australopithecine innominates and innominate fragments with a canonical analysis. The authors claim to have used "functional" measurements, and seem to therefore simply assume that the separation they show between *Homo* and the australopithecine sample on the second principal axis (accounting for 21.5% of the variation) demonstrates differences that "call for functional interpretations." Ignoring for the moment problems raised by the fact that of the five innominates used two are juvenile, the third is sub-adult, and the fourth is in unbelievably poor condition, the authors appear unaware of Lovejoy's (1974) elegant demonstration that these very differences are unrelated to the functions of the innominate in gait, and rather are the direct result of the narrower birth canal in australopithecine females, and the consequently greater lateral projection (i.e. flare) of the iliac blade.

Similarly, a discrimination which results in obvious functional groupings may not incorporate functional measurements. For instance, a discriminant function based on dental measurements may separate a hominid and pongid into clearly different locomotor categories: biped and quadruped. Yet, the dentition has no direct relation to locomotion.

If the usefulness of discriminant function analysis can only be judged by how the results are interpreted, the recent attempts to use early hominid dental measurements to determine phylogenetic relationships provide little to detract from Kempthorne's (1966) observation: "I have yet to see any convincing examples of experimental data in which the standard techniques of multivariate analysis have led to scientific insight."

Brace, Mahler & Rosen (1973), for instance, use a discriminant function to conclude that Olduvai hominid 13 is a "Pithecanthropine" on the basis of its mandibular dentition. This confirms the similarity of the Olduvai 13 mandible with some of the Sangiran mandibles, and the near identity of the Sangiran and OH 13 palates demonstrated by Tobias & von Koenigswald (1964). However, it ignores the extremely small cranium associated with the OH 13 jaws, in comparison with the much larger *Homo erectus* crania associated with dentitions of the same size (Plate 1). Perhaps the authors cannot be faulted since they did not use cranial measurements in their analysis. However, what they have shown has nothing to do with the taxonomy of australopithecines, *Homo erectus*, or the contended specimens. Instead, they have shown that a discriminant function cannot completely separate these taxa on the basis of the dentition alone. Indeed, the association of "essentially erectus" dentitions with obviously australopithecine crania has been

Plate 1. A comparison of casts of part of the Olduvai Hominid 13 cranium with Sangiran 4. There is no question that the dentitions of these specimens are extremely similar. Yet, there is a considerable difference in the size and robustness of the crania. The comparison is particularly useful since virtually the same portions of the crania are preserved. In both cases, the most anterior projection of the parietals just reaches the coronal suture. In (a) OH 13 is above and in (b) to the right.



confirmed with further discoveries at both Olduvai gorge (Leakey, Clarke & Leakey, 1971) and East Rudolf (Leakey, 1974); OH 24 and ER 1813.

That calculation of a Mahalanobis  $D^2$  on tooth dimensions places the Olduvai specimen in *Homo erectus* with "resounding certainty" (p. 63) when comparisons are made with gracile australopithecine, robust australopithecine, and erectus clusters, only serves to call the use of the  $D^2$  statistic for this purpose into question (see also Read, 1975).  $D^2$  is a metric clustering technique, again relating numerous measurements additively. What makes it particularly suspect when used for hominid taxonomy is the fact that if there were a large and continuous fossil record (e.g. for instance 10 specimens per each 100,000 year interval) there is reason to believe that there would be no clusters at all throughout the course of Pleistocene human evolution. The fact is that even when clusterings seem obvious, there is reason to believe that "no single discriminator or single distance measure can tell the whole story" (Dempster, 1969: 219).

Another similar example is provided by Read (1975). Here, solutions to a number of different questions are attempted using a variety of multivariate techniques. First, a correlation analysis was used to determine whether there is an allometric relation between length and breadth measurements in the teeth of various *Homo sapiens* populations. Read concludes that there is no allometric relation, which is surely no surprise since the derivation of the allometric equation (Huxley, 1932) precedes from the assumption that the rate of growth in two structures (related by the allometric equation  $Y = aX^k$ ) is proportional to the amount of tissue already present:

$$\begin{aligned}\Delta X &= C_1 X \\ \Delta Y &= C_2 Y \\ \frac{\Delta x}{\Delta y} &= \frac{dx}{dy} = k \frac{x}{y}.\end{aligned}$$

This is an unrealistic model for the growth of tooth length and breadth. Projection of the principal axis is then used to "predict" the ancestral condition, apparently under the assumption that because the teeth of fossil hominids are larger, they represent "blown up" versions of modern teeth. Finally, a test for "outliers" was applied to the fossil hominid teeth using the major axis projection as its base. It was concluded that the only outliers are members of what Read calls the "*A. boisei*" lineage. A Mahalanobis  $D^2$  is used to "confirm" the distinctiveness of the boisei teeth, as well as to "confirm" the distinctiveness of the Swartkrans and Sterkfontein samples from each other (a conclusion contradicting the  $D^2$  calculated by Brace, Mahler & Rosen which "confirms" the similarity of these site-samples to each other), and a discriminant analysis "confirms" the "confirmation" by showing that it can successfully distinguish groups that are assumed to be separate (another unsurprising conclusion since this is what the function is designed to do).

In the end, Read concludes that the *boisei* sample represents a separate lineage. It is worthwhile to stop and consider what this means both mathematically and biologically. The East African australopithecine sample is known to be more variable than the South African sample. This is likely because the sample represents far more variation in both space and time. There is a notable contrast between the East African sample, spanning at least 1000 miles and a time period of millions of years, and the South African site of Swartkrans which provides the largest single component of the South African sample but represents a single locality and a timespan which may be no more than 20,000

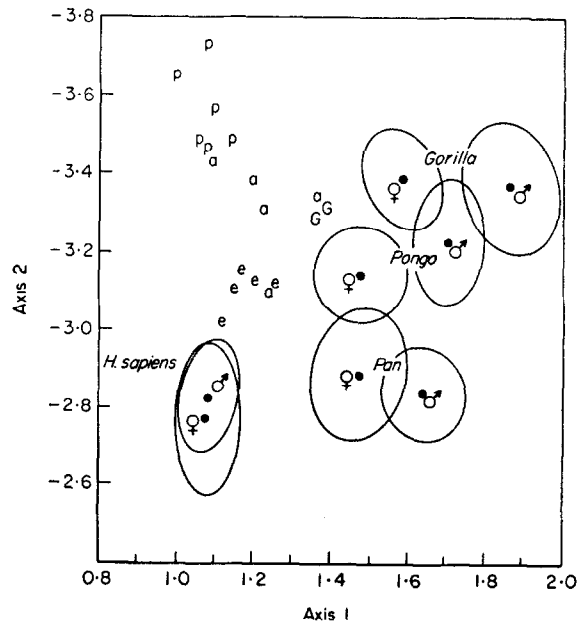
years (Brain, 1970). In South Africa the taxonomy is site-specific (e.g. Sterkfontein is "*A. africanus*," Swartkrans, *A. robustus*," and so on). However, as the East African specimens were discovered, taxonomic designations were specimen-specific. The underlying compositions of the resulting taxa, in other words, are completely different. The "*A. boisei*" taxon consists of specimens with the largest postcanine teeth. The sole criterion for placement in the taxon was the size of the posterior teeth, and I question whether 21 journal pages and an unknown but large amount of computer time has, in this instance, accomplished anything but a verification of the fact that the East African workers were successfully able to distinguish large from small postcanine teeth.

What happens when there is "good discrimination?" Robinson & Steudel (1973) calculate four discriminant functions which clearly separate *Homo sapiens* from the three great ape species and all of these from the fossil hominids. The authors give one of the mandibular and one of the maxillary functions. Centroids are presented for the living taxa representing the 95% interval, but the three fossil hominid taxa discussed are only represented as single points ("*Paranthropus*," "*H. africanus*," "*H. erectus*").

The maxillary function presented as the authors' Figure 4 and explicitly defined in their Table 3 is useful to consider in some detail for this discussion. The function is based on measurements of  $C^1-M^1$ . Discrimination was attempted using a  $\log_e$  transform on the length and breadth measurements. The authors' results are presented in Figure 1, along with scores for the individual members of the taxa discussed which I have calculated.

According to the authors, axis 1 (the horizontal axis) accounts for 60.5% of the discrimination. They suggest that it is the hominoid families that are separated along this axis "primarily as a result of high values for the mesiodistal length of canines and third premolars" (p. 519). The axis is a measure of anterior tooth size, although not necessarily *relative* anterior tooth size as the authors state since the axis shows *Pan* with the

Figure 1. Graphic representation of the fourth discriminant function presented by Robinson & Steudel. The figure is a reproduction of their Figure 4, with the singular points given for "*Paranthropus*" *H. africanus*, and *H. erectus* removed and replaced with the positions of each known specimen. "p" represents "*Paranthropus*," "a" represents Lower Pleistocene hominids attributed to *Homo* (e.g. *Homo africanus*, *Homo habilis*, etc.), and "e" represents *H. erectus*. The two points labeled "G" represent four female gorilla specimens that fall within the australopithecine range. The gorilla data is from Mahler (1973).



smallest values for the pongids and *Gorilla* with the largest whereas in actuality *Pan* has the largest canine area relative to the posterior areas and *Gorilla* has the smallest (sexes considered separately).

Axis 2 (the vertical axis), accounting for 34% of the discrimination, is largely a measure of posterior tooth size. The authors feel that this axis separates species within the families, and that a progression from "*Paranthropus*" to *H. sapiens* is suggested by the relative positions (contradicting Read, 1975). In fact, relative position is considered a measure of closeness of relationship, and it is suggested that the closer position of "*H. africanus*" to "*H. erectus*," when compared with the distance of the former to "*Paranthropus*," has phylogenetic significance.

What sense does this make? Examination of Figure 1 shows that the Lower Pleistocene sample assigned to "*Homo*" is uniformly closer to the pongids than any other hominid grouping. One hominid specimen actually falls on the border of the *Pan* and *Pongo* female centroids on axis 1. In addition, when a large number of gorillas were plotted using this function, four were found that fell into the australopithecine range (specifically within the range of the smaller australopithecines). Since the hominids are assumed to have a pongid ancestry, characterized by Dryopithecines with large conical canines compared with the postcanine teeth, one might conclude that the "*Homo*" sample represents the ancestral condition, rather than the "*Paranthropus*" sample suggested by the authors.

If the phylogenetic arguments used for the hominids were applied to the pongids, one might conclude that *Gorilla* represents the ancestral condition, and that *Pongo* is more closely related to *Gorilla* than *Gorilla* is related to *Pan*. These are rather unlikely conclusions.

What is much more likely is that the various discriminant scores represent what the discriminant function calculates: a maximized sorting based on the dental measurements used. It is surely no surprise that a discriminant can sort specimens with a larger postcanine dentition from specimens with a smaller one. The function sets up four groups, representing the possible combinations of a larger and smaller anterior dentition, and a larger and smaller posterior dentition.

If there is any further information here at all, it is in the unique resemblance of the two Lower Pleistocene hominid groups to each other, in contrast with later hominid groups. The two hominid groups from the Lower Pleistocene seem to represent a continuous distribution on this plot, split in the middle into "*Homo*" and "*Paranthropus*". In both groups there is a negative relation between the axis 1 score and the axis 2 score, representing, after a fashion, anterior and posterior tooth size. To quantify this, a regression of the axis 2 onto the axis 1 scores for the individuals was attempted (treating axis 2 as a positive number). The "*Paranthropus*" slope was calculated to be  $-0.1998$ , and the Lower Pleistocene "*Homo*" slope  $-0.1453$ . These are virtually identical to each other, and contrast with the *erectus* slope of  $+0.5353$ .

In sum, Robinson & Steudel have actually shown that while discrimination between hominid and pongid taxa is possible, it is far from unambiguous. Of greater importance, however, this example demonstrates that positions in discriminant space relate no necessary taxonomic information for either the placement of specimens within groups, the biological reality of the groups themselves, or the phylogenetic relations between the groups discriminated.

I believe that the important questions which must be asked about the recent onslaught of multivariate techniques used in solution of taxonomic, phylogenetic, and functional

questions are whether these techniques are appropriate for the types of *taxonomic* and *functional* questions asked and whether they can reveal any unique scientific insights. General discussions of this problem (i.e. Kowalski, 1972) conclude that in the end these questions must be answered empirically. Only the demonstration of new insights can show that new insights are obtainable. From this short review of three publications concerning problems within a single area of early hominid evolution, it is difficult to reach anything but a negative conclusion.

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