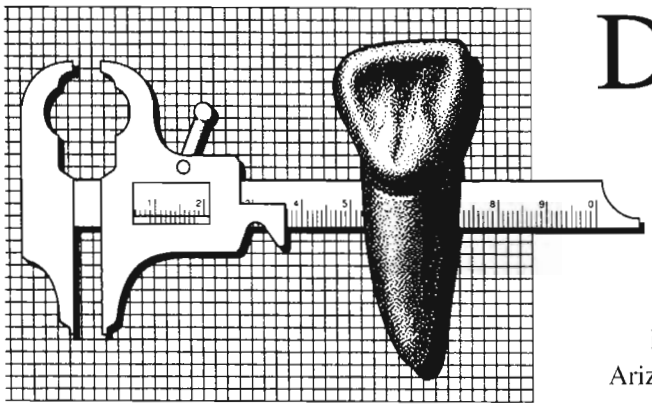

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A Strategy for Comparing Odontometrics Among Groups

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Several anthropologists and human biologists have written of their disenchantment with tooth dimensions as discriminators among human groups. While the dentition consists of numerous logical variables, such as mesiodistal and buccolingual crown diameters of the 32 permanent teeth providing a measurement battery of 64 variables, all of the variables tend to behave much the same analytically because of the strong positive collinearity among them (Moorrees and Reed, 1964; Henderson, 1975; Yuen et al., 1996).

Teeth comprise meristic series, as do phalanges of the hand and foot and vertebrae of the spinal column (Huxley and de Beer, 1934). Elements within a series have a common origin embryologically, and, although they display clinal variation in size, shape, and variability, they are developmentally and functionally integrated so that, statistically, there are far fewer orthogonal vectors of variation than suggested by the many dental or bony elements. This is quite different than when an equal-size battery of craniometrics, anthropometrics, or osteometrics are analyzed because there are more statistically independent constellations of variables in these latter situations. This probably is why Falk and Corruccini (1982) found craniometrics to be more powerful discriminators than an equal number of tooth dimensions.

On a worldwide basis, tooth size of contemporary humans is distributed unimodally, but it is positively skewed because of megadont Australians (Fig. 1). In contrast, there evidently are no "microdont" peoples. A logical question is: Given the continuum in tooth size across the species, with no apparent racial divisions, what can be done analytically to distinguish among human groups? Size per se is uninformative. Put a different way, researchers have, at least since the ground-breaking efforts of Muhlreiter (1874), expended great effort collecting and publishing tooth size data, but to what end?

This paper outlines an analytical approach that removes much of the influence of size from tooth dimensions and also accounts for the considerable statistical redundancy of tooth size within and among morphogenetic fields. This approach first was first discussed at the Physical Anthropology Meetings (Harris and Rathbun, 1988; Harris, 1989), and we used it to contrast tooth size patterns of American blacks and whites (Harris and Rathbun, 1989). It also was applied to a worldwide collation of samples to show that relative tooth size differs among geographic races (Harris and Rathbun, 1991). I tended to skirt the methodological issues in these papers because they seemed straightforward (cf. Sneath and Sokal, 1973). Recent inquiries suggest that it would be useful to focus more narrowly on the method.

MULTIPLE COLLINEARITY

Correlation coefficients are positive and fairly large between crown dimensions of all 32 permanent teeth (Moorrees and Reed, 1964; Garn et al., 1965). Statistically, this means the informational content is diminished relative to uncorrelated traits because more or less of the variation among tooth

dimensions is redundant. Correlations tend to be higher within morphogenetic fields (Harris and Bailit, 1988), but all combinations of teeth exhibit significant variable redundancy.

Principal components analysis (PCA) is a multivariate statistical method of extracting a few compound variables that retain most of the shared variation. PCA is a special case of factor analysis (e.g., Harmon, 1967; Gorsuch, 1983), the technical constraint being that the communalities in the correlation matrix are set to one so the resulting vectors are statistically independent (orthogonal) of one another. On the other hand, there is a great conceptual difference between PCA and factor analysis. PCA makes no assumption about any latent model of causation; it is foremost a data reduction procedure. Factor analysis assumes that the covariance structure among the measured variables results from underlying factors that exert causal influence on these observed variables.

There has been confusion about the correlation matrix submitted to PCA. The conventional method used in numerical taxonomy is to submit the ontogenetic, inter-individual matrix measured on a sample of a biological population. PCA result of this kind are available in Potter et al. (1968), Henderson (1975), Townsend (1976), and Harris and Bailit (1988), among others. Within limits of sampling fluctuation and minor differences in method, these PCA from diverse human samples are

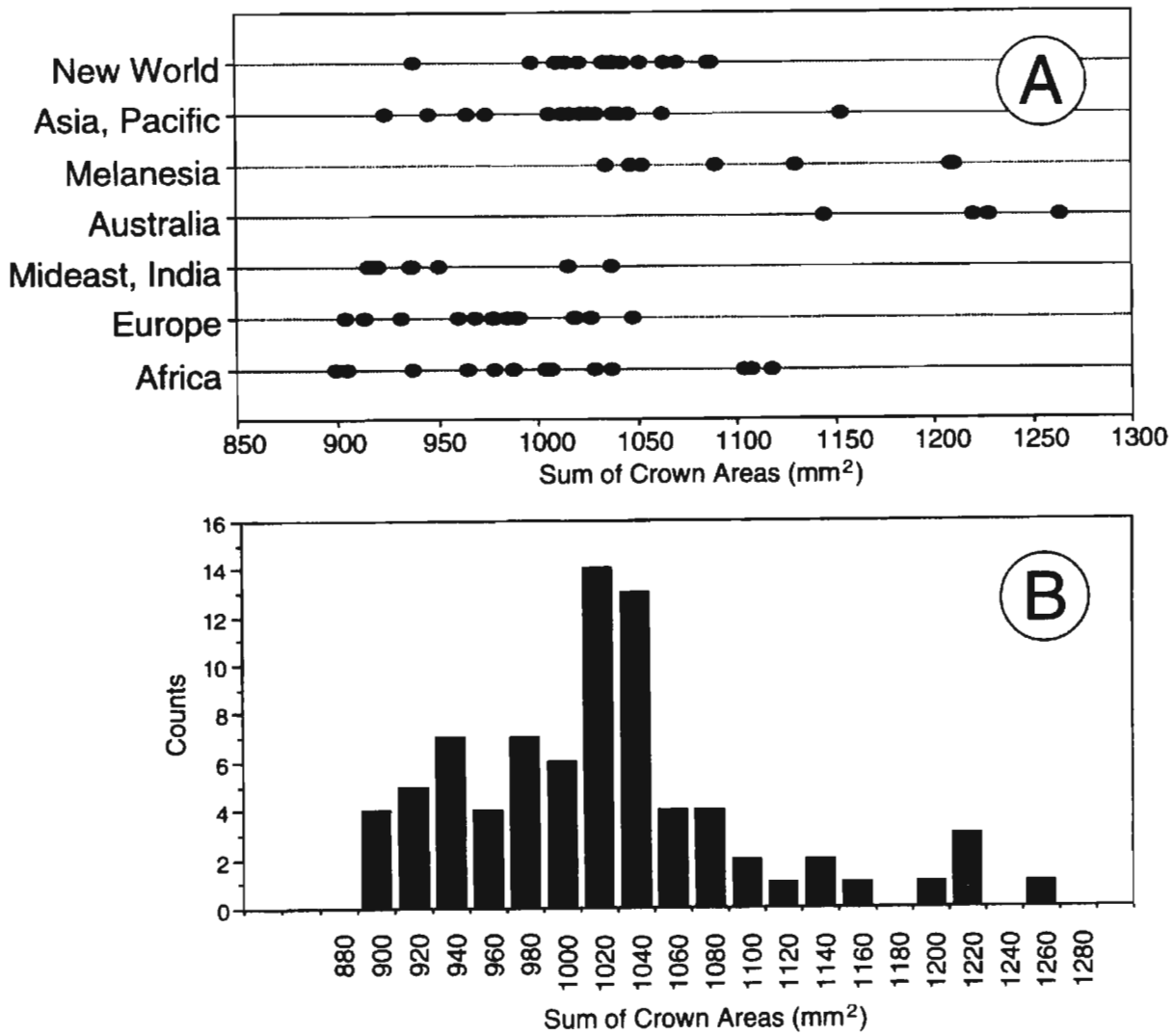

Fig. 1. Two displays of the worldwide distribution of summed crown areas for contemporary human groups (k = 79 groups). Summed area omits third molars, since data are unreported for many groups. Note the positive skewness of the histogram.

remarkably similar. Critics have claimed that the reference sample biases the result, but there is no quantitative data that the number or nature of the components differs among contemporary groups. It seems of more importance to minimize sampling fluctuation by using a large sample, such as that described by Harris and Bailit (1988).

There is, importantly, a quite different correlation matrix that can be submitted to PCA, namely a matrix generated among groups, which I term a microphylogenetic matrix. For example, a matrix of pairwise comparisons could be generated from the 78 samples used by Harris and Rathbun (1991), where the worldwide samples rather than the individuals within a sample are the observational units. There is no reason *de facto* to prefer the ontogenetic or the phyogenetic matrix, but they certainly are not the same and they have quite different interpretations. Consequently, ordination on the two matrices yields quite distinct outcomes. This makes it imperative to understand the differences. I have addressed this briefly (Harris, 1996), and a fuller interpretation is forthcoming (Harris, n.d.).

The reason to condense the raw odontometric data to principal components is three-fold. Foremost, PCA combines strongly intercorrelated variables into fewer compound variables, so there is data reduction—most of the shared variance can be redefined along the axes of major information in the data structure. Secondly, the principal components disclose the statistical and—presumably—the developmental fields controlling tooth size. This greatly aids interpretation. Teeth do not develop independently; their size and shape are determined by their position in the arches, so it makes little biological sense to analyze data univariately (Harzer, 1987). Thirdly, the principal components are statistically independent of one another, which also simplifies interpretation as well as subsequent statistical testing.

In passing, there are several schools of thought about the number of principal components to extract. If no criterion is used, there are as many components as variables in the data, but the first few almost invariably account for most of the shared variance. It has been popular to retain those components with eigenvalues of at least one. This stems from Guttman (1954) and Kaiser's work (1960). Since the variables are normalized to a mean of zero and unit variance, each contributes one unit of variance to the total variance in the data set. When a component has an eigenvalue above 1.0, it is accounting for more variance than in one variable. Since a goal of PCA is to reduce the measurement battery to a small number of components, components containing less information than one variable are trivial and discarded. This eigenvalue-one criterion is, however, inflexible and can lead to mistakes. It is not truly a mathematical criterion, but an approximate gauge.

A flexible and practical approach is the scree test (Cattell, 1966), which is a plot of the eigenvalues in the decreasing order they are extracted. A scree plot generally is an option on mainframe programs, and the visual technique is to look for a break, an inflection point, between big and small

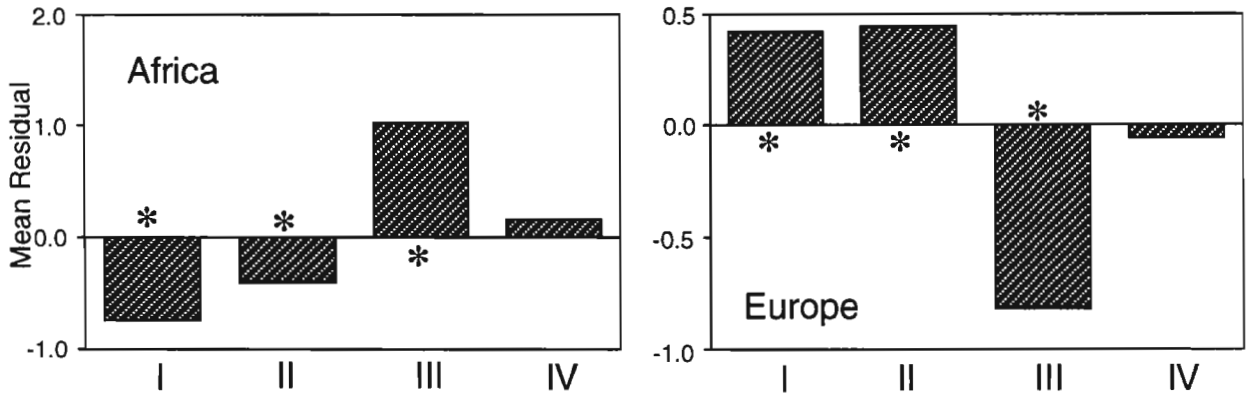

Fig. 2. Plots of the mean residual scores for four principal components averaged for 13 sub-Saharan African samples and 15 European and derived groups. Asterisks flag those residuals significantly different from zero. Africans and Europeans have mirror patterns of tooth size apportionment.

eigenvalues. Components before the break are assumed to be meaningful and are retained; the small ones are discarded, producing a truncated solution. The scree plot works best in conjunction with the eigenvalue-one criterion as an empirical gauge of the number of components to retain.

Unrotated principal components can be difficult to interpret, so the factor loadings typically are rotated to a simpler final solution. Computer programs afford several rotation options, but varimax rotation (Kaiser, 1958) is used most commonly with PCA. It is an orthogonal rotation, so components remain uncorrelated. Varimax rotation maximizes variance within a component, which means that variables' loadings are "pushed" towards 0 or 1, thereby reducing the number of variables with hard-to-interpret intermediate loadings. Rotation to a simpler solution occurs with no loss of information. Indeed, rotation is optional depending on interpretability of the initial solution.

COMPONENT SCORES

PCA does not eliminate the effects of size. Once PCA has been performed and it is decided how many components will be retained, the final solution can be used to generate principal component scores (confusingly termed factor scores) for each group. This is accomplished as an output option in most statistical packages. In brief, each variable is standardized across all samples using the conventional z-transformation. Then, for each component, the products of the variable weighting coefficient for the component and the group's z score are summed. This calculation also distinguishes PCA from factor analysis, because factor scores are summed column-wise down the weightings for a component, whereas factor analysis assumes that observed variables are linear combinations of underlying factors, so scores are summed row-wise across components (Gorsuch, 1983). Since standardization is performed across groups, those with large tooth dimensions will have large z scores and, in turn, large factor scores, and vice versa for groups with small teeth. This means that size effects are carried along to the factor scores.

REGRESSION ON SIZE

One wants to eliminate size effects, especially in dental metrics because size effects are large and they obscure shape differences. Analysis of odontometrics traditionally has been unproductive because the overwhelming effect of size produces an uninformative, one-dimensional result. There are several ways to reduce size effects (e.g., Corruccini, 1987; Darroch and Mosimann, 1985). One strategy that cannot be advocated is to discard the first principal component. It has been argued that PC 1 generally is "overall size" in biological contexts, because all the correlations of the variables on PC 1 are positive and subequal in strength. The first component generally is controlled by size, but much shape information may also reside there as well.

An alternative is to remove the effects of size using multiple linear regression (e.g., Draper and Smith, 1966; Kleinbaum and Kupper, 1978). The least squares best-fit equation is calculated for each PC score across all of the groups under analysis, and the residuals (observed-minus-expected values) are computed and saved for further analysis. Calculation and use of residuals is fundamental to regression analysis; Freund and Littell (1991) offer a useful text in this regard.

The question is what variable is a practical measure of overall size. There are several choices, but, empirically, Brace's (1980) summary measure of occlusal area, termed TS, accounts for considerable variance in the dependent PC scores. TS is the sum across the 14 tooth types of the sample's ΣMDxBL crown diameters (third molars are excluded simply because they seldom are reported in the literature). Actually, I advocate using three predictors of overall tooth size in a multiple linear equation, namely, TS, which is Σ(MDxBL), and ΣMD, and ΣBL. These three collectively are more effective than TS alone because some principal components are more aligned with length or width than area.

ANALYSIS OF RESIDUALS

A residual is the amount a group's PC score is above or below the amount predicted from size of the dentition. If underestimated, so the residual is negative, the group has a disproportionately small

score; tooth dimensions heavily weighted on that component are not as large as expected given the group's overall tooth size. Consequently, less tooth substance has been "apportioned" to dimensions reflected by that component. Inspection of residuals for the group's other components may (but need not necessarily) show where greater than predicted amounts of tooth substance have been apportioned. I originally purloined the word apportionment from Lewontin (1972) who used it in quite a different context, but its uptake by other dental researchers suggests it carries the appropriate connotation.

Figure 2 is a brief example taken from a larger, unpublished analysis. Residuals averaged for 13 samples of sub-Saharan African blacks and for 15 European and derived white groups are graphed. Other geographic groupings are omitted here. The four principal components are (1) mesiodistal widths of the anterior teeth (I1, I2, C) in the two arches, (2) an MD versus BL contrast that extends throughout the dentition, (3) MD and BL size of the premolars, and (4) MD and BL size of the molars. Fig. 2 shows that Africans—relative to their overall tooth size have disproportionately small anterior MD widths; their BL dimensions (PC 2) are smaller than expected; and their premolars (PC 3) are significantly larger than predicted. Of the several geographic groups compared, it is interesting that the European samples possess tooth size apportionments just about opposite those of Africans: Europeans are characterized by relatively large anterior teeth, large buccolingual crown diameters, and small premolars. Africans and Europeans have experienced opposite approaches to the apportionment of tooth size across the morphogenetic fields. In passing, neither group departed from expectation for molar size (PC 4). It seems that Amerindians are the only geographic group to do so; they have disproportionately large molars (Harris, n.d.).

OTHER APPLICATIONS

This method has been used to assess broad differences among human groups at the level Garn (1965) termed geographic races (Harris and Rathbun, 1991; Harris, n.d.). Others (Hemphill, 1991; Lukacs and Hemphill, 1993) have applied the method within a culture area. It also should be insightful to apply the method to temporally sequenced samples (e.g., Hinton et al., 1980), since it is unlikely that change in size of the dentition would be isometric across all morphogenetic fields.

The nature of sexual dimorphism also can be explored with this method. Sexual dimorphism has been defined as a difference in size (e.g., (M-F)/F) on a tooth-by-tooth basis (e.g., Garn et al., 1967b), but the apportionment of tooth size provides a different perspective. First, the method combines individual dimensions based on their statistical and, presumably, genetic relationships, so one is dealing with compound variables incorporating metric information across several teeth. This should be more truly reflective of the underlying control mechanisms governing tooth size than repeated univariate comparisons (Potter, 1972). Secondly, dimorphism would be defined as a difference in the apportionment of size across teeth, so there is a multivariable comparison of relative size (shape) between the sexes. This would complement research that found univariate sex differences in crown shape (Garn et al., 1967a; Rosenzweig, 1970).There is no restriction to using this method with humans; it should prove as insightful when applied to other species.

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