



### F33 Patterns of Variation and Match Rates of the Anterior Biting Dentition With Regard to Size and Shape: Characteristics of a Database of 3D Scanned Dentitions

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The goal of this presentation is to describe dental shape variation and shape matches in a large population of three-dimensional (3D) dental models.

This presentation will impact the forensic science community by addressing one fundamental premise of bitemark analysis, that of “uniqueness” of the human anterior dentition.

Critics of the concept of “uniqueness” claim that individuality cannot be proven since examination of every individual that exists, and has existed, is not possible. To this end, it might best to describe “uniqueness” as “sufficiently similar” such that two objects cannot be measurably distinguished once impressed in a substrate.

To state that two objects are indistinguishable requires a definition of measurement resolution and error. In any given system, these parameters may be determined by repeated measures of an object in question. Any two (or more) objects that fall below this defined error threshold, when compared with each other, may be said to be indistinguishable.

An established means to study size variation in shape in biological systems is landmark based Geometric Morphometric analysis (GM). It is a multivariate approach and allows statistical comparison of the change in shape in large datasets. With this approach, shape information can be visualized by plotting landmark positions in Procrustes superimposition, a method of optimally matching one shape to another. This technique can be performed with or without scale and for this study both approaches were used. Procrustes distances can be used to summarize variations in populations, to express the degree of similarity of individual specimens, means of populations, or to search for matches between specimens.

Another statistical tool available in the GM framework is Principal Component Analysis (PCA). This allows for determination of which shape aspect is responsible for the most variation. Finally Partial Least Square (PLS) was utilized to observe patterns of covariation in maxillary and mandibular data.

In this study, the anterior human dentition was examined in 3D data using size-preserving Procrustes (Procrustes-SP) methods, as well as scale-independent Procrustes methods.

A collection of 1,099 distinct paired sets of 3D scanned maxillary and mandibular dentitions were obtained from a commercial dental laboratory, which produced these scans for the production of occlusal guards (night guards). Of these, 497 pairs were taken from an earlier data set (Bush, Bush, and Sheets, 2010) and 602 pairs were newly measured for this study. The individuals involved were private practice patients from dental practices across the United States. All patient identifying information was stripped from the data prior to any additional processing. This was a sample of convenience, containing a wide range of alignment patterns, from relatively straight to fairly mal-aligned. All necessary Human Subject Institutional Review Board protocols were completed for this project and exemption was granted.

Curves were placed which delineated the incisal edges of the six anterior teeth in both uppers and lowers. Each curve contained 10 landmark data points on each incisal edge. A total of 60 data points in 3D were obtained for each arch.

Following landmark data point extraction, statistical analysis was completed to describe the variation in these human biting dentitions and to determine match rates in the population studied. The statistical tools, as described above, were used in conjunction with LM methods to produce a summary of the variation present in this large data set, as an initial approach to understanding the types of variation present in the population of dentitions.

Results indicate that, measurably indistinguishable maxillary and mandibular dentitions could be found (defined as a match rate). The paired dentitions were also evaluated as a set. Two specimens (one pair) with just shape information, and four specimens (two pairs) with size and shape were found to be indistinguishable in the dataset. PCA revealed definite patterns of common mal-alignment, allowing exploration of the variation that exists in this population.

The sensitivity of match rate on measurement error was also determined by searching for matches as a function of assumed error level, indicating rapid increases in match rate as measurement error increased. The nature of the relationship of arch width and centroid size among and between the maxilla and mandible was examined. Lastly, Principle Components Analysis and Partial Least Squares revealed readily interpretable patterns of variation and covariation in the data, with both dominated by the variation in relative arch width.

It was concluded that arch width was the principal factor in variation. A number of specimens were found to be measurably indistinguishable when investigating the maxillary and mandibular arches separately. When investigated as a set, incorporating size caused an increase in the number of specimens that were indistinguishable.

**Forensic Science, Dental Uniqueness, Bitemarks**