

# Shape Measurement Tools in Impression Evidence: Application To Bitemarks

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## Introduction:

Bitemark analysis was highly criticized in the 2009 NAS report for lack of scientific basis. The method assumes that the human dentition is unique and that individual detail transfers to the skin.

However, the dentition has not been proven to be unique, particularly when we consider the evidence left in a bitemark, typically the edges of the anterior dentition.

Rather than attempt to establish uniqueness we looked instead at whether matches could be found in different populations, an approach not seen in earlier work. One well established means to describe and compare biological forms is Geometric Morphometric analysis (GM). GM allows for quantitative examination of shape by capturing the geometry of structures and preserving this information through statistical analysis. This method was used to explore the concept of dental similarity with three different sample populations in 2D and 3D.

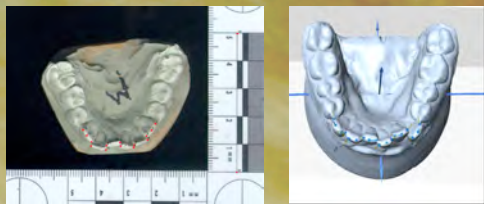


Fig 1 a and b: Example of landmark placement on both 2D (left) and 3D (right), data sets. There are 14 data points in the 2D set and 60 in the 3D. Note that there are 3 measured points on each canine in the 2D set.

## Methods:

Three separate populations were studied: 2D general population (N=410 mandibular dentitions, 2D orthodontically treated (N=110 mandibular dentitions) and a 3D general population (N=1000) of maxillary (500) and mandibular (500) sets.

Landmark points were placed on the incisal edges of the 6 anterior teeth with TPSdig freeware for the 2D sets and Landmark freeware for the 3D set. The data was analyzed statistically with IMP freeware. A Procrustes (geometric measure of similarity) distance threshold, determined by intra operator (repeated measures) error, was determined to have a Root Mean Square (RMS) value of 0.03 for the 2D set and 0.02 for the 3D. This distance thus established what it means for dentitions to *match*: they are as similar as repeated measurements of a single specimen, i.e. within twice the RMS scatter. We also used these data sets and a simpler traditional measurement protocol (Rawson et al. 1984), and obtained similar results (not shown).

## Results 2D general population:

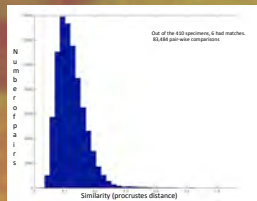


Fig 2: Histogram of distribution of Procrustes distance for the 2D general population dataset. To the left the samples are very similar and to the right they are becoming increasingly dissimilar. Most of the population is clustered towards the similar side. The dashed line depicts error measurement threshold of 0.03.

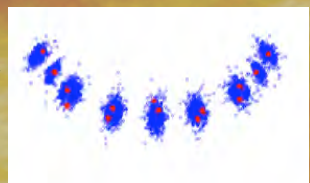


Fig 3: Scatter plot showing occupation of shape space for the 6 anterior teeth. Notice much tighter grouping than the general population. Variance 0.0084. Superimposed in red is a set of 10 repeated measurements of a single dentition, variance 0.00225. The scatter of red points shows the level of uncertainty of these measurements from images at 300 dpi.

## Results 2D orthodontically treated:

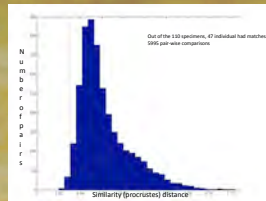


Fig 4: Histogram of Procrustes distance distribution for the 2D orthodontically treated population dataset. Note that compared to the general population, the clustering occurs at much smaller distance, meaning that this population is more similar.

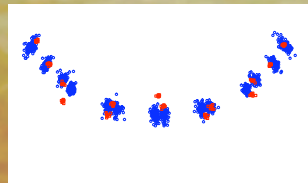


Fig 5: Scatter plot showing occupation of shape space for the 6 anterior teeth. Notice much tighter grouping than the general population. Variance 0.0022. Superimposed in red is a set of 10 repeated measurements of a single (non-orthodontically treated) dentition, variance 0.00225.

## Results 3D general population:

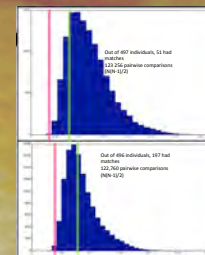


Fig 6: Histograms comparing the mandibular (top) with the maxillary dentitions in 3D. Note the increased match rate in the maxillary set. Level of orthodontic treatment is unknown, but mixed.



Fig 7: Examples of the two of most similar matching mandibular dentitions. Procrustes distance of 0.038.

## Conclusions:

- Matches were found in all three populations. The matching dentitions were all relatively straight.
- As expected, orthodontic treatment had a strong effect on dental matches.
- Future projects need to determine likelihood of a match to any particular dental mal-alignment pattern.
- For the 3D match maxillary and mandibular sets, the majority of mal-alignment can be seen in the mandibular arch.
- The effect of resolution loss due to the skin was not studied here. However there is distortion once teeth impress the tissue, reducing resolution of dental detail, and potentially increasing match rate.
- Caution should be exercised in claims of individuality of the human dentition until more research is completed.



Fig 8: Example of searching for matches to a particular dentition. The dentition in the upper left was the dentition in question.

**References:**  
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