ORIGINAL ARTICLE

Similarity and match rates of the human dentition in three dimensions: relevance to bitemark analysis

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Abstract Uniqueness of the human dentition is a fundamental premise in bitemark analysis. Despite the importance of this key aspect of bitemark methodology, systematic studies of large populations have been limited. Furthermore, there have been no investigations of the significance of the third dimension with regard to dental uniqueness. One hundred digitally scanned mandibular models were analyzed in both 2D and three dimension (3D) using Landmark software. Additionally, 500 3D maxillary and mandibular sets were investigated for determining dental match rate. Statistical analysis was performed with geometric morphometric methods. Results show that measurements in 3D preserve more information about the dentition, reducing but not eliminating random matches in a sample population of 100 mandibular dentitions. Examination of pairs of maxillary and mandibular dentitions showed a substantial number of random matches (197 maxillary, 51 mandibular, one of both maxillary and mandibular). Conclusions indicate that a zero match rate cannot be claimed for the population studied.

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Introduction

In the 2009 National Academy of Sciences (NAS) report, the discipline of bitemark analysis was heavily criticized. Lack of fundamental research that explores the scientific basis of this technique was one of the main concerns [1, 2]. There are two core premises in this area; first that the human dentition is unique and second that the characteristics that individualize the teeth transfer to the bitten substrate [3, 4]. This study focuses on the first premise.

Critics of the concept of individualization state that this theory cannot be proven and that the idea of uniqueness is an erroneous belief [5–7]. Therefore, with regard to bitemark analysis, it would appear correct to investigate the possibility of finding a "random dental match," in other words, determining the likelihood of finding a sufficiently similar dentition such that the two cannot be distinguished within measurement resolution error.

Prior studies exploring the probability of finding matching dentitions in a given population have been conducted [8, 9]. These studies have determined that it is possible, within measurement of experimental error, to find dentitions that match in the population considered; however, these projects were performed in two dimensions (2D) only. The criticism could be made that a 2D examination is inadequate and that including the third dimension or z-axis would decrease the chances of determining a dental match.

Prior studies have also investigated three-dimensional (3D) aspects of bitemark analysis [10, 11].

In other studies, metric dimensional parameters have been used to assess variation in human dentition [12, 13]; however, this method may not be appropriate to describe dental uniqueness within the context of bitemark analysis. Describing the dimensions and angulation of individual teeth in the dentition does not help to promote an understanding of the dependant (i.e., highly correlated) relationships of teeth and the comparative shape of the dental arch as a whole [8].

If metric measurements are insufficient as descriptors, it may be more pertinent to consider the arrangement of teeth in the arch and their relative alignment through shape change analysis.

One well-established means used to describe and compare biological forms is geometric morphometric analysis (GM) [14–18]. GM methods allow for a quantitative analysis of shape by capturing the geometry of morphological structures of interest and preserving this information through statistical analysis.

Shape information can be visualized by plotting landmark positions by a Procrustes superimposition process that will give a value in Procrustes distance. Procrustes distance is a measure of the closeness in shape of Procrustes superimposed specimens and is recognized as a general-purpose measure of specimen similarity in the GM framework. The use of this type of shape change analysis software allows for a multivariate statistical approach to explore the concept of dental uniqueness.

Advances in 3D digital imaging have facilitated the use of landmark placement as coordinates. The software allows placement of landmark points, curves, and surfaces in three dimensions that are used to delineate dental features including intercanine widths, mesial–distal lengths, rotations, as well as tooth height variation.

Our goals were first to determine how important the third dimension was in determining a match rate for the human dentition, comparing 2D and 3D measurements in the same dataset. Secondly, to determine the match rate in a population of maxillary and mandibular sets of 3D digitally scanned models.

Methods and materials

All necessary Human Subject Institutional Review Board protocols were completed for this project and an exemption was granted. Five hundred maxillary and mandibular sets (1,000 total) of 3D laser-scanned digital dental model images of patient dentitions were obtained from a dental laboratory. All patient identifying information was stripped from the file. The 3D datasets were collected for use in fabrication of occlusal guards (night guards) from private practice dentists from across the United States. Thus, the data represented a sample of convenience from a cross section of patients of unknown provenience. The alignment patterns ranged from relatively straight to severely mal-aligned.

2D/3D comparison methodology

One hundred of the mandibular 3D laser scans were randomly selected for use in the comparison of 3D measurements to 2D measurements. The criterion for inclusion was a full complement of anterior teeth (canine to canine). In actual bitemark casework, it is typically the six anterior teeth that impress the skin [3]. Therefore, this study used these teeth for analysis.

The models were oriented in a fixed occlusal view position and landmark placement was performed using a Landmark freeware [19]. The landmarks were placed on the mesial to the distal end points of each incisal edge and also the midpoint of each canine. This resulted in a total of 14 landmarks in 3D (hereafter referred to as 3D-14). The z-axis information for each point was discarded, forming now, a

Fig. 1 a Landmark placement of the incisal edges of the 3D model digital scans. It is uncertain if the landmark on the lateral incisor is correctly placed (*arrow*). **b** Using the rotational capabilities of the program, it can be seen that the landmark was placed too far to the facial of the incisal edge (*arrow*). This is easily correctable with the program
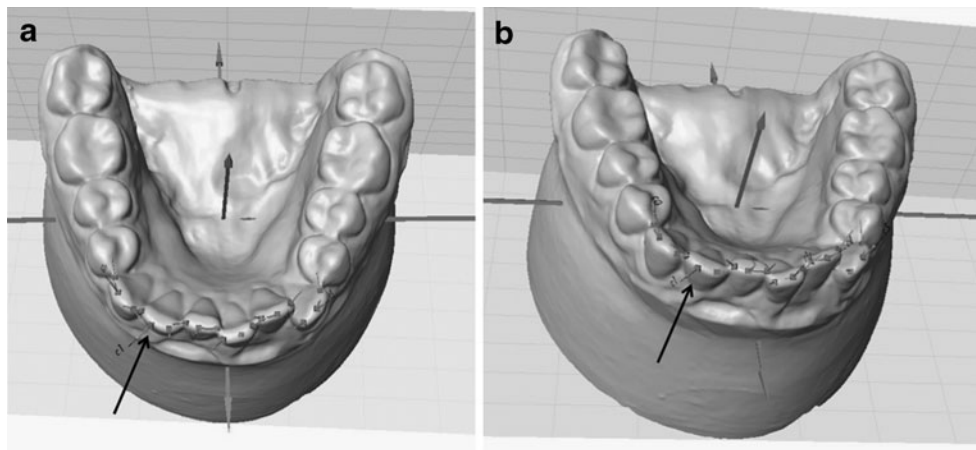
Results: Mandibular
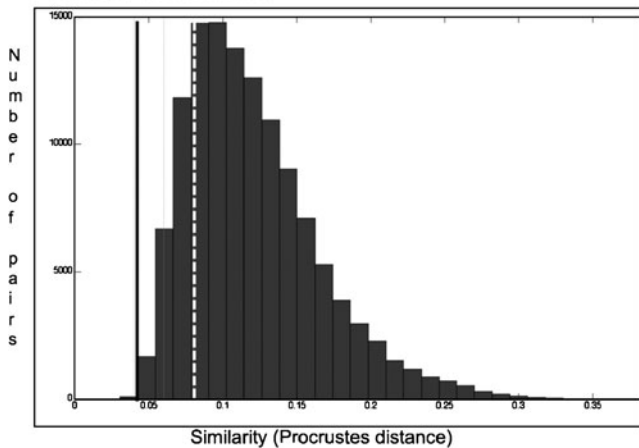
Out of 497 individuals, 51 had matches
123,256: N(N-1)/2) pairwise comparisons

Fig. 2 The histogram shows the distribution of the Procrustes distance for the mandibular dataset. The vertical axis is the number of pairwise comparisons. The specimens at the left are very similar and to the right they become increasingly dissimilar. Clustering or non-uniform distribution is clearly evident and the clustering is around an intermediate value. The *solid dark line* is at a Procrustes distance of 0.04, our error measurement threshold. The *dashed white line* shows 100% degradation of resolution (.08)

2D dataset with 14 landmarks (hereafter referred to as 2D-14). These data were compared to the same 100 dentitions analyzed in 3D using the ability to rotate the image.

For the 3D analysis, landmarks were again placed on the 100 3D models, this time using the rotational capabilities of the software to ensure that the true incisal edges were delineated (Fig. 1a, b). Instead of two data points that described each tooth, a curve consisting of 10 data points was placed on the incisal edges to capture the 3D data. This resulted in 60 points per arch describing mesial to distal width, angulation, incisal edge shape of each tooth (for example, the height of the canine cusp tip), and relative tooth position in the arch in

3D (hereafter referred to as 3D-60). The 3D-60 set, thus differs from the 3D-14 set in that is has more measured points (60 vs. 14) and in that the landmark placements in 3D-60 were made using the ability of the software to rotate the specimen in 3D as the landmarks were placed.

The error rate was also determined for the 2D and 3D data sets using the root mean square (RMS) variation around the mean shape obtained in repeated measurements of a single specimen. Variation of the dentitions was measured as the mean summed squared Procrustes distance about the mean shape in the data set (i.e., the population mean or the mean specimen shape if using repeated measures). The square root of this variance measure is the RMS scatter about the mean, which is somewhat similar in nature to a standard deviation, although done in a multivariate sense using Procrustes distance, rather than in the more familiar univariate sense [9].

However, when working with different numbers of landmarks or from landmarks in 2D to 3D, there is a shift from one high dimensional statistical space to another. This is equivalent to going from length to area to volume. These are very different types of measurements and it is difficult to directly compare variances. To remove this difficulty, the ratios of variances was calculated, specifically the ratio of the repeated measures variance to the population variance, as a way of comparing variances from one set of measurements to another. This ratio established more reasonable grounds for comparison than the variances themselves.

3D match rate methodology

The population of 500 hundred maxillary and 500 mandibular model 3D sets was used for this portion. Four maxillary models and three mandibular models were dropped from the study. Thus, the final number was 496

Fig. 3 Illustration of the two most similar mandibular dentitions. The match is at a Procrustes distance of 0.0338

.0338
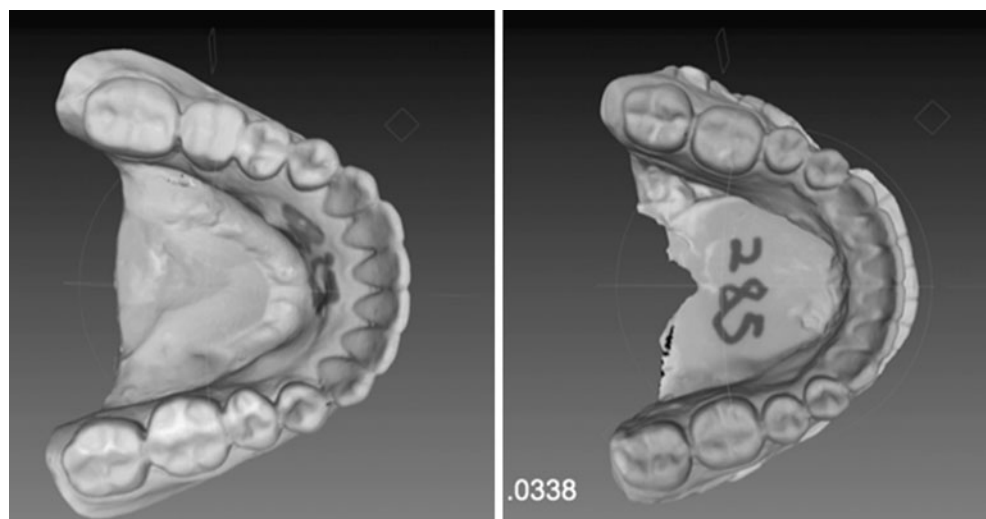
maxillary and 497 mandibular models. One mandibular model did not have a corresponding counterpart.

Following landmark data point extraction, statistical analysis was completed to describe the configuration of the human dentition and to determine match rates in the population studied. An RMS scatter of .04 Procrustes units was used as error threshold (0.04~95% confidence or two standard deviations) for finding match rates in the 3D population.

Results

2D/3D comparison

For the 2D-14 data, out of 4,950 possible comparisons [N(N−1)/2], there were 22 matches within error measurement threshold and nine matches in the 3D-14 data set. The same number of comparisons in the 3D-60 set resulted in one match. Simple inclusion of the third dimension reduced the match rate by over 50%, and the inclusion of 60 landmarks and the ability to rotate the specimen while placing landmarks greatly reduced the rate.

The RMS scatter for the 2D-14 data was 0.021, for the 3D-14 data, 0.0228, and the 3D-60 data, 0.020, which appear identical; however, when the RMS scatter is expressed as a percentage of the total population variance, the 2D-14 data showed 6.49%, the 3D-14 data was at 6.11%, and the 3D-60 set was at 4.7%. The change in these ratios of variance is due to the changes in dimensionality and in the number of landmarks present.

Results: Maxillary
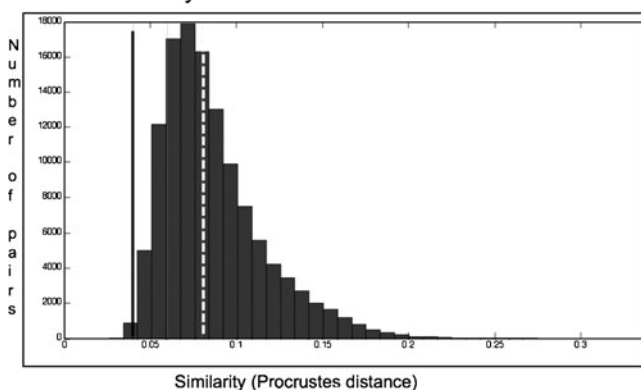
Out of 496 individuals, 197 had matches
122,760 pairwise comparisons (N(N−1)/2)

Fig. 4 Procrustes distance distribution for the maxillary dataset. Again, the *solid dark line* depicts our error measurement threshold. The *dashed white line* shows 100% degradation of resolution (0.08). Comparison of this figure to Fig. 2 shows that for maxillas, the distribution is tighter and shifted to the left, meaning that there is more similarity between maxillas

Table 1 Match distribution in the mandibular arch

Number of individuals	Number of matches
42	1
5	2
3	4
1	6

3D analysis

The RMS scatter for the 3D-60 data was 0.020 and a Procrustes distance of below 0.04 was used as the cutoff point for matches (0.04~95% confidence based on examination of all pairwise distances in repeated measures data).

Analysis of the 497 mandibular dentitions showed that out of 497 individuals, 51 had matches [123,256 to (N(N-1)/2) comparisons] with a RMS below .04. Figure 2 depicts the histogram resulting from the data. Some model dentitions had more than one match. Figure 3 shows two of the most similar matching dentitions.

Analysis of the 496 maxillary dentitions showed that out of 496 individuals, 197 had matches (122,760 comparisons (N(N-1)/2) with an RMS below 0.04. Figure 4 shows the histogram of data distribution. Some model dentitions had more than one match in the maxillary population as well. Tables 1 and 2 show match distribution for both maxillary and mandibular arches. Figure 5 illustrates two of the most similar matching maxillary dentitions.

Importantly, the more densely sampled 3D-60 set showed one match of both maxillary and mandibular dentitions between two individuals in the sample population.

It can be seen that many more matches were found in the maxillary dentition. Comparison of the histograms (Figs. 2, 4) illustrates this finding as the histogram is more densely populated towards the left side (similarity). The right hand tail in the histogram indicates increasing dissimilarity. It must be stressed that these maxillary and

Table 2 Match distribution in the maxillary arch

Number of individuals	Number of matches
117	1
29	2
21	3
5	4
6	5
6	6
3	7
6	8
1	9, 11, 13, 16

Fig. 5 Illustration of the two most similar matching maxillary dentitions. The match is at a Procrustes distance of 0.0339
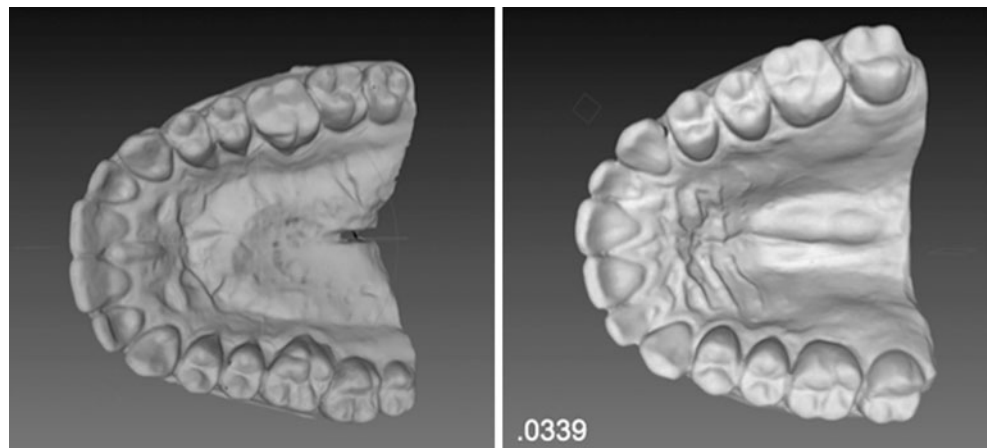
mandibular model samples are sets and not independent populations. This finding illustrates that for most people, the majority of mal-alignment of teeth may be found in the mandibular arch.

Discussion

This study suggests that with regard to the shape of the six anterior teeth of the maxilla and mandible (12 teeth total),

there is not enough variation in the alignment pattern to make statements of confidence regarding dental uniqueness. The position and angulation of the human dentition is far from individual on this scale. The authors acknowledge that in actual bitemark cases, it is possible that more than the six anterior teeth will leave an impression.

It must be stressed that this study only sought to find a match rate in a certain population of convenience, and as expected, all of the matching pairs consisted of relatively straight dental alignments (Fig. 6). Investigation of the

Fig. 6 Most of the matching dentitions had a relatively straight alignment. The examples here are the most mal-aligned matching maxillary dentitions. The mal-alignment seen is slight rotation of the lateral incisor (*arrows*). Procrustes distances are given for the two dentitions (*right*) that match the one in question (*left*)
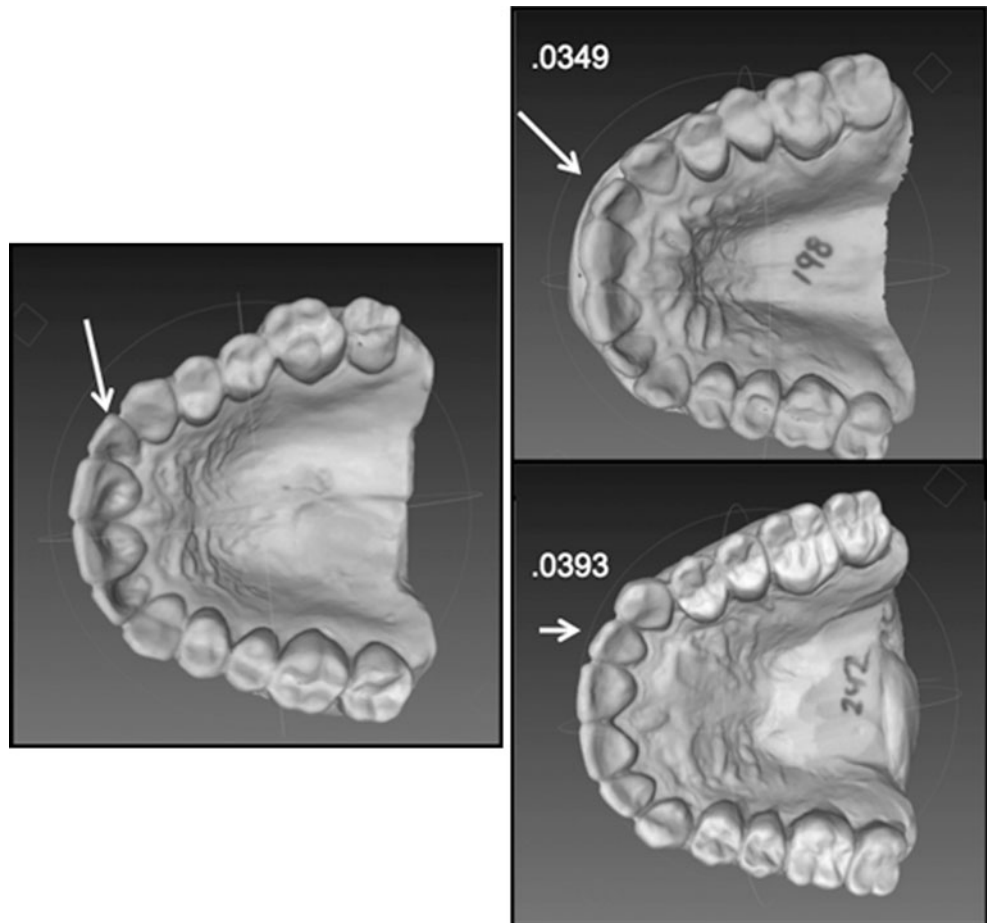
likelihood of finding a match to a particular dental alignment pattern and the frequency of occurrence of any one mal-alignment pattern are not addressed in this paper. Obviously, some configurations will occur less often than others, and there may be population-specific effects (more possible mal-alignments in geographic regions where dental care access is limited).

A previous study showed that orthodontic treatment increases the match rate as it reduces the variation significantly in the teeth [9]. It was unknown what percentage of the current population had undergone orthodontic treatment, and it was possible that the population was biased in this direction, but this was considered acceptable as representing a certain cross section of society. Given that the data was collected from patients having occlusal guards constructed, there is no guarantee this data set is free of socioeconomic bias.

The hypothesis tested in this study was that dental match rates would decrease when going from the two to three dimensions. This was found to be the case. The simple inclusion of 3D information without any other alteration of the measurement protocol reduced the match rate significantly, as seen in the comparison of the 2D-14 data to the 3D-14 data. Inclusion of more data points going to 3D-60 further reduced the match rate.

The current work explores the effect of incorporating the 3rd dimension on the dental match rate. It may be further argued that the appearance of a bitemark on the skin has a relationship to the 3D shape of the dentition. That issue is not addressed in this study.

The difference noted between mandibular and maxillary match rates noted here was a novel but not unexpected finding, lending credence to the concept of higher incidence of crowding in the lower arch. In addition, this is the first report of a match in shape of both arches between two individuals. It is imperative therefore, that a probabilistic approach is taken in order to avoid unfounded statements of certainty in the courtroom. The American Board of Forensic Odontology (ABFO) reference manual states detailed guidelines with regard to bitemark analysis [20]. The guidelines suggest that without statistical analysis, research may be less than credible [20]. This paper supports the ABFO position.

Conclusions

This study expressly focused on one of the odontological research queries of the NAS report, namely is there proof of the identification of individuals from the arrangement of their teeth? [1]. The current study suggests that there may not be a scientific basis for a *general* expression of dental uniqueness when the incisal edges of the six anterior teeth are considered, as significant match rates were determined.

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