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PAPER

ODONTOLOGY

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Statistical Evidence for the Similarity of the Human Dentition

ABSTRACT: Recent scrutiny of forensic science has focused on unreliability of expert witness testimony when based on statements of individuality. In bitemark analysis, assumptions regarding uniqueness of the dentition have been based on use of the product rule while ignoring correlation and nonuniformity of dental arrangement. To examine the effect of these factors, two separate sets of scanned dental models (n = 172 and n = 344) were measured and statistically tested to determine match rates. Results were compared to those of a prior study. Seven and 16 matches of the six anterior lower teeth were found in the respective data sets. Correlations and nonuniform distributions of tooth positions were observed. Simulation tests were performed to verify results. Results indicate that given experimental measurement parameters, statements of dental uniqueness with respect to bitemark analysis in an open population are unsupportable and that use of the product rule is inappropriate.

KEYWORDS: forensic science, forensic odontology, bitemarks, bitemark research statistics, dental uniqueness

It has often been stated that bitemark analysis is founded on two postulates: that the arrangement of the human anterior teeth is unique among individuals and that individual characteristics that define dental uniqueness transfer to and are recorded on the bitten substrate (1). The corollary to these premises is that the biter can be included or excluded by pattern comparison. This form of argument is known as an existential fallacy. Neither of the postulates guarantees the outcome, and if either of the postulates is untrue, then the argument is void (2).

Recent research on the second postulate suggests that distortion encountered on bitten human skin limits resolution of detail transfer. It was found in these and other studies that detail transfer may not readily occur (3–6). This forces re-examination of the claim of dental uniqueness and the measurement parameters of the dentition. Distortion from skin properties effectively reduces the resolution of measurement that can be used to compare the dentition to the bitemark. Unlike fingerprint analysis, in which details bordering on the microscopic scale are compared, a bitemark typically consists of a pattern on a larger scale that has a distortion component significant enough to include unrelated dentitions (4).

The 2009 National Academy of Science report, in its criticism of bitemark analysis, lists the concern that “the uniqueness of the human dentition has not been scientifically established” (7). This may be interpreted to indicate that efforts should be made to establish a level of uniqueness of the human dentition. However, in the critical writings of Saks, Koehler, and Cooley, the argument is made that individualization is an abstraction and that demonstration of uniqueness is unattainable (8–10). Cole’s (2) treatise entirely dismisses uniqueness as a viable descriptor.

Therefore, it would appear that the correct approach is to first establish whether dental matches can be found in an open population and to specify the measurement parameters under which the match is found.

Several recent studies that claim to support the uniqueness of the dentition based on metric traits show data that demonstrate its similarity, contrary to the claims of dental uniqueness by the authors (11–13). These studies also lacked a formal statistical approach.

An often-cited attempt to statistically confirm the unique nature of the human dentition using a large population was published in 1984 by Rawson et al. ([14]; hereafter referred to as Rawson). In this study, a strong claim was made that the large number of possible tooth locations (states) observed in their data set indicates that the “human dentition is unique beyond any reasonable doubt”. It was argued that the very large number of states seen preclude any possibility of matches to a given dentition, under their measurement protocol.

There are three primary weaknesses to this argument. First, it was not reported whether any specimens under their protocol actually matched. Second, it was assumed that specimens are equally or uniformly distributed over the possible tooth positions and that there was no bunching or gathering of individuals into common patterns of dentition. Last, the effect of correlation of dental traits was not considered (i.e., the idea that if an individual had a wide arch, then all the coordinates of the teeth positions across the arch would reflect this common property of being wide, and all possess unusually large x-coordinates of position along the width of the arch). Furthermore, the product rule was used, without incorporating any measure of correlation, to make the claim that the number of possible combinations of human tooth positions in the lower jaw alone is on the order of 6.08×10^{12} or effectively infinite.

Therefore, given the current scrutiny of impression evidence and the lack of scientific studies in this area, we address in this paper the issue of similarity of the human dentition using metric analysis and statistical methods. Rather than attempt to prove the uniqueness of the dentition, the approach taken is to establish a match rate, given definition of measurement parameters. The methods used by

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Rawson were replicated, to show that our results are not based on more sophisticated approaches to measurement, but are a feature of the data sets. Unlike Rawson, we take the additional step of examining the data for similarity. Simulation tests were also used to both validate the statistical procedures used and investigate effects because of both nonuniform (clustered) distributions and correlation.

Methods and Materials

Two data sets of the human mandible were randomly collected. Human Subject Institutional Review Board exemption was approved for each set. One set consisted of three-dimensional (3D)-laser-scanned models. In this case, the models had been taken for the purpose of construction of occlusal appliances (mouth guards). The second set combined scanned dental models collected from the patient pool at the University at Buffalo Dental School clinic and from patient pools of two private practitioners. No other information was known about the data sets, including sex. The rationale for keeping the data sets separate was to reveal whether any data or programming flaws existed in the analysis.

Given access to these data sets, it was possible to repeat the study conducted by Rawson. Unlike Rawson's approach in which tooth positions were measured from a bitemark, our study measurements were taken from casts of the teeth themselves. The spatial resolution of the 3D-laser-scanned models was nominally 10 microns (hereafter referred to as Set 1). In the 2D data set (Set 2), casts were placed on a flatbed scanner, and a digital image was obtained with a spatial resolution of 85 microns (300 dpi). One hundred seventy-two specimens were measured in Set 1 and 344 specimens measured in Set 2 using landmark methods. In these data sets, we focused only on the lower jaw.

Landmark points were first measured on our specimens, from which the same information utilized by Rawson could be extracted. The center position of each tooth and the angle the tooth made in a horizontal plane was calculated. The 2D or 3D nature of the source was immaterial as the information extracted was independent of the third dimension. The arches were oriented such that the distal of the canines touched a baseline and a perpendicular line was drawn from the baseline to the mesial of the right central incisor. This resulted in a set of three measurements per tooth, x- and y-coordinates measured with a resolution of ±1 mm and angles measured to ±5 degrees, as per Rawson.

Rawson calculated from 384 dentitions the range of possible values of each measurement for each tooth, and then the total possible number of distinct values (or states) of these measurements, using a simple product rule, multiplying the number of states appearing to determine a total number of possible states.

It was then argued that the number of possible states is simply the product of the states of the individual teeth, and that the probability of a given dentition matching any other dentition is then one over the number of possible states or measurement values. We repeated this analysis using our data sets, to see if the number of possible states in our data sets matched that reported by Rawson.

In addition, we also compared all the teeth within each data set to determine if there were any matches in the dentition, using the criteria defined by Rawson. A match is defined as conditions such that the x- and y-coordinates within ±1 mm and an angular value within ±5 degrees, so that the two specimens did not differ in any variable within the experimental accuracy of the system. We also tested the predictions of the method by looking for the number of matches of a single specific tooth at a time, and for matches of two specific teeth at a time, then three at a time and so forth.

We did not expect to see a match of an entire dentition, but we did expect to see matches of individual teeth or pairs or trios of teeth at a time. The incidence of such matching single, double, or triple teeth groupings allows us to determine if the statistical model of the probability of matches as presented in Rawson reasonably describes our results. While our data sets had only 172 and 344 specimens, respectively, we made $n(n-1)/2$ different comparisons with n specimens, which is 14,706 and 58,996 comparisons, respectively, yielding some level of statistical power. Rather than merging our two data sets into a single larger set, we chose to work with them independently, to produce two distinct replicates of Rawson's study for the rationale stated earlier.

Simulation-based Tests

Two different simulation-based tests were run for dual purposes. The first was to determine if there were errors in the software used in the analysis that might have produced the observed results. By simulating data sets with known properties, we can determine if the results produced by the software are consistent with the known properties of the data set. Second, by forming different types of simulations, we can determine the extent of the influence of several factors that produced the deviations of the observed number of matches from the number of matches appearing in the simulations or the number of matches predicted by the Rawson model.

The first simulation used was a permutation test (15). In this procedure, a simulated data set was created using the original tooth measurements but randomly assigning measurements to specimens using a random number generator. The x, y, and angle measurements were permuted independently. This process is akin to mixing and matching teeth specimens from individual specimens to create new possible specimens. This procedure preserves the distributions of individual measurements, so that histograms of the individual measurements (x, y position or angle values) are identical to the histograms seen in the original data. However, the permutation test as used here destroys all the correlation between measurements that was present in the original data. So the permutation test allows us to see how important correlation was in producing the matches seen in the original data.

As an illustration of this process, imagine we extract all the teeth in the study and replace them in the correct (but flexible) sockets in different mandibles while retaining the distribution of positions. For example, if there are 75 left canines in the center of the mean x-position, they will be replaced in that x-position but in different mandibles. This removes the effect of correlation in which those 75 would have had right canines also close to the mean in their original mandibles, but because of swapping, they now do not. Then you observe how many matches are made (repeating the swap 1000 times), and because you have removed correlation, the only remaining reason why you might have matches is the nonuniform distribution, meaning that most people have teeth in similar positions.

The second simulation used was a Monte Carlo simulation that assumed uniform distributions of all measurements over the observed measurement ranges, which is the assumption made implicitly in Rawson's model (16). To generate such a simulation, the range of possible tooth positions was calculated from the empirical observations in Rawson's and the current data sets (see Tables 1–3). Then simulated specimens were assigned measurements randomly distributed over the observed range with no correlation between measurements. This approach produced simulated data matching Rawson's assumptions of uniform distributions with no correlations. As in the permutation test, the simulation was repeated 1000 times.

TABLE 1—*Number of states for each tooth in the lower dentition, as per Rawson's table 3. Shown is the number of states found for the* x and y *positions and tooth angle, as well as the total states for each tooth under the product rule.*

Tooth Number	*x*	*y*	Angle	Total Positions
22	4.3	2.9	8.6	107.2
23	4	5.1	10	204.0
24	2.5	5.1	9.1	116.0
25	3.1	5.5	9.0	153.5
26	4.0	4.0	9.4	150.4
27	4.1	2.5	10.1	103.5

TABLE 2—*Number of states found in the current study using 172 measurements of the lower dentition (Set 1).*

Tooth Number	*x*	*y*	Angle	Total Positions
22	6.0	2.0	12.7	154.6
23	4.3	5.3	15.1	343.8
24	1.2	6.7	13.6	107.3
25	3.6	6.0	9.8	212.1
26	5.8	7.0	9.7	391.7
27	10.4	2.2	12.8	297.3

TABLE 3—*Number of states found in the current study using 344 measurements of the lower dentition (Set 2).*

Tooth Number	*x*	*y*	Angle	Total Positions
22	7.8	2.5	14.9	291.9
23	5.8	9.9	15.6	903.1
24	1.9	9.6	13.4	246.3
25	6.1	8.3	21.4	1083.3
26	9.1	9.0	19.7	1616.1
27	9.0	4.3	24.3	937.6

Continuing the extraction analogy, in the Monte Carlo simulation, all teeth are extracted but position information is discarded, and the teeth are replaced in a manner that fills all the possible space that a tooth could be in a uniform distribution. This removed both correlation and nonuniform distribution. Now no matches are observed after 1000 random repeats, as predicted by the use of Rawson's methods.

So our two tests, permutation and Monte Carlo, are implementing mathematically interesting ideas about features of the data set, that allow us to see the disturbing effects that arise when we neglect to incorporate correlation and uniform distributions into our models of biologic systems.

Results

Table 1 lists the data from Rawson (table 3) and shows the number of states of each variable for each tooth in the lower mandible, while Tables 2 and 3 show the number of states found in the current study.

Sixteen six-tooth dentition matches appeared in the 58,996 possible comparisons in Set 2, indicating that these specimens had *x*- and *y*-coordinates of the midpoints that were within 1 mm of each other and all angles were within 5 degrees. Set 1 displayed seven distinct six-tooth matches. The results of looking at the number of matches of between 1 to 6 teeth at a time are shown in Table 4. In contrast to these observed results, the independent uniform distributions implied in Rawson's method were used to calculate the number of expected matches for each grouping of teeth given the sample size. This calculation was made using both Rawson's original state calculations and our state calculations, illustrating the difficulties posed by the use of the product rule as applied to this type of data.

TABLE 4—*Predicted numbers of matches between groupings of 1 to 6 teeth at a time, using Set 2. The expected columns are the expected numbers of matches using Rawson's product rule, given a total of 58,996, using an assumption of a uniform distribution of teeth over states. The number of states used was taken from both Rawson's table 5 and the larger number of states seen in our data set. The actual column indicates the number of matches (±1 mm or ±5 degrees) per tooth actually observed in this data set.*

	58,996		
n total	Expected Under Rawson	Expected under Current Data	Actual
Tooth 22 only	550.1	202.1	8900
Tooth 22+23	2.7	0.22	1196
22–24	0.02	0.00091	241
22–25	0.00015	8.4E-07	99
22–26	1.0E-06	5.2E-10	32
22–27	9.7E-09	5.5E-13	16

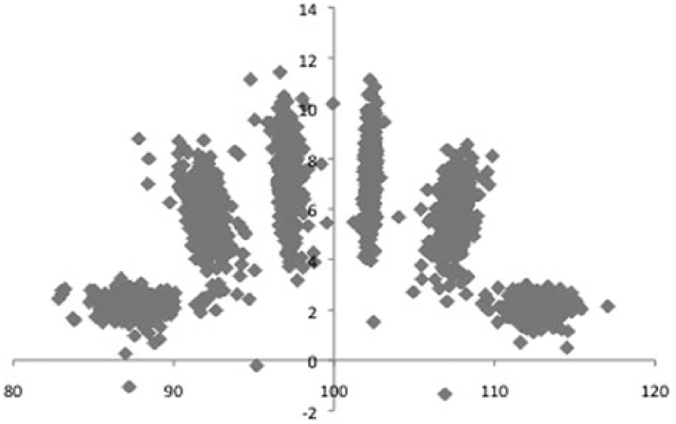

FIG. 1—*This plot replicates figure 5 in Rawson, produced using our data set, Set 2, lower dentition, 344 dental arches shown. The clusters of points represent the midpoints of the six anterior teeth. The clustering of the data points is notable and indicates strong nonuniform distribution and correlation between relative tooth positions. Axes are in mm.*

The question might then be asked, why are there so many more matches than expected, given the number of states in the data? The explanation lies in the fact that the specimens are not uniformly distributed over the states, or in other words, the occupation of the states is not uniform. Consider the *x*-coordinate values of tooth 22 in Set 2, Fig. 1. The *x*-coordinates range over 6 mm, so given our measurement resolution of ±1 mm, we have roughly six states in this variable. We might expect the chance that two randomly picked specimens would match on this measure are 1 in 6, and that of our 58,996 possible pair wise comparisons, 9832 of these should be a match. But when we actually do the counting of our data set, we find 30,431 matches or a rate of over 50% matches (Table 5)!

This can be explained by examination of a histogram of our data split for this particular measurement, Fig. 2, in which we find that the distribution is far from uniform. In this histogram, if the distribution were uniform, each bar would have the same height. However, it is closer to a normal distribution with a mean of 112.5 and standard deviation close to 1. So if we have a tooth with an *x*-position close to the mean and if we believe the normal distribution is correct, then roughly 66% of all specimens will be within ±1 mm

TABLE 5—*Matches for groupings of 1 to 6 teeth, using the 172 specimens in Set 1. Columns calculated as per Table 4.*

	14,706		
n total	Expected Under Rawson	Expected under Current Data	Actual
22	137.1	95.1	2453
22–23	0.67	0.47	482
22–24	0.0058	0.0040	147
22–25	3.8E-05	2.6E-05	51
22–26	2.5E-07	1.7E-07	15
22–27	2.4E-09	1.7E-09	7

of the specimen. Obviously, not all randomly drawn specimens will be near the mean, but most of them are close, and thus have a number of other specimens within ±1 mm. The same nonuniform distribution can be seen in Rawson's figure 6. The fact that the match rates are much higher than expected in a single tooth indicates that correlation between the teeth is not the sole source of the matches.

Correlation Structure

When we compute the probability that two independent events both occur, we can use the familiar product rule. So if event A occurs with odds 1/6 and B occurs with odds 1/10, the chance that A and B both occur is 1/6*1/10 = 1/60, the familiar product rule.

But most biologic systems have correlations, which mean that the events or variables are not independent. Suppose we report an account of a mugging by a tall robber, tall enough (say 6′4″) that the chances of a random man being that tall are 1/100. Now suppose we also know our mugger weighed over 300 pounds, and that only one man in 100 weighs that much (these values are examples only, the probabilities of heights and weights quoted are not accurate). Are the odds that a random man is that tall and than heavy then 1/100* 1/100 = 1/10,000? No, probably not, because men over 6′4″ are all pretty heavy individuals, as human weight and height are correlated.

If we examine the *x*-positions of teeth 22 and 23 in our Set 2, we find they have a correlation of 0.75, which is relatively high, meaning that the value of the *x*-position of one of them is highly predictive of the other. We can examine this using a biplot as shown in Fig. 3*a*. It is clear from this plot that if two specimens are similar in the *x*-location of tooth 22, then the *x*-position of tooth 23 is also probably similar as well. Figure 3*b* shows the same data after permutation, with correlation removed. The data is still clustered but no longer has the diagonal correlation. The horizontal spread of the points is simply an indication that the canine has a larger spread of possible positions in the *x*-axis (arch width).

FIG. 2—*A histogram of distribution of the* x*-position of tooth 22 in Set 2,* x*-axis in mm,* y*-axis number of teeth. Over the roughly 6 mm of observed tooth position, most are clustered around the center. This is a nonuniform distribution. Had the tooth positions been evenly distributed, each histogram bar would have the same height.*

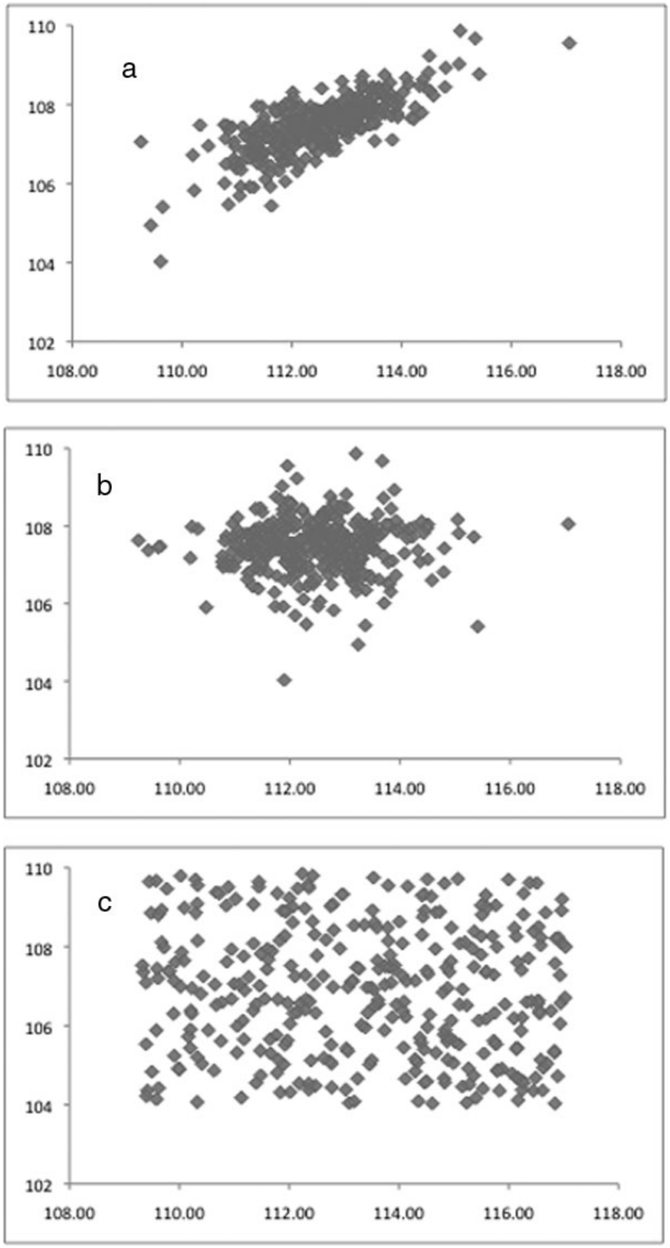

FIG. 3—*The upper plot (a) shows the* x*-positions of teeth 22 and 23 plotted against each other. These coordinates have a correlation of 0.75, so there is a general diagonal pattern to this data. The middle plot (b) is a permuted version of the same data on the same axes, which still shows clustering of the data in the center of the plot, no longer having a general diagonal pattern. The correlation has been removed. The horizontal elongation is because the canine (tooth 22) has a greater range of positions in the* x*-axis (narrow vs. wide arch). The final plot (c) shows a Monte Carlo simulation of the same data, using a uniform, noncorrelated model, as implied by Rawson's calculations. Notice the lack of both clustering of the data points and any diagonal structure in the last plot, which clearly reduce the number of overlapping points in the plot.*

Figure 3*c* shows the data after a Monte Carlo simulation. The data are now distributed in a uniform manner over the available space, and the number of overlapping points is clearly reduced.

Simulation-based Test Results

The permutation test allowed us to see how important correlation was in producing the matches seen in the original data. When we performed 1000 such permutation simulations based on Set 2, we could see that in 66 simulations of the 1000 total performed, there was one matched pair of lower dentitions, and in five simulations there were two such matches. In the same number of simulations using Set 1, there were 52 instances of a single-matched pair and in four cases there were two matches.

Using the Monte Carlo simulation that assumed uniform distributions, one thousand simulations of both Sets 1 and 2 were performed and no matches were found.

In evaluating the results of these simulations, we find that the Monte Carlo simulations produce exactly the expected results. This simulation mimics the assumptions of Rawson's model, and as expected, produced no matching lower dentitions. We take this as an indication that our software is performing as expected, and that using both assumptions of Rawson's model, there are indeed no matches. The permutation tests did show evidence of some matches, although never as many (16 matches in Set 2, seven in Set 1) as in the original data. From this, we conclude that the correlation structure in the original data set was a major factor in producing the observed matches, as we never saw this many matches over 1000 simulations per set without the correlation. The complete lack of matches in the Monte Carlo simulation also indicates the problem with assuming uniform distributions. We do not currently have a clear method of determining which feature (correlations or nonuniform distributions) is really the dominant factor.

Discussion

The assumption that the human dentition is unique has been examined from a metric statistical approach using a data set of reasonable size, replicating prior methodology but with consideration of correlation and uniformity of distribution of dental characteristics previously ignored. Rather than attempting to prove uniqueness, this paper simply reports analysis of dental characteristics in two open populations. The number of possible states is indeed vast, but human teeth occupy relatively few of them, so that matches are far more common than is implied by the number of states.

From a practical forensic perspective, empirical studies have shown distortion in skin on a scale of several millimeters with sometimes dramatic angular changes (4,6). The results in this study represent the minimum match rate using measurements from dental models with a resolution of ±1 mm and ±5 degrees. If distortion because of impression in the skin is considered, worsening measurement resolution, the match rate will increase, with the added possibility of inclusion of false positives. Our results show that given our measurement parameters, statements concerning dental uniqueness with respect to bitemark analysis in an open population are unsupportable.

Simulation tests were performed in this study as internal controls, and results indicated that correlation and nonuniform distributions of dental features significantly contribute to the frequency of match.

It is rational to conceive that the human dental arch shape would fit within a finite boundary as determined by our species. It is also rational to anticipate that the number of matches will increase as the database size is enlarged. That conclusion is borne out by this empirical study. This important concept can be stated simply. Had we combined our two data sets, there would have been many more pairwise comparisons and thus more possibilities for a match. The number of matches increases geometrically with database size as the number of possible comparisons of n specimens increases with the square of n as the number of possible comparisons is $n(n-1)/2$. In a closed population when comparing a small number of dentitions, the likelihood of a match is low, but still possible. The implication of this study is that given a large enough population the next dentition compared to the database will be highly likely to match an existing sample.

It may also be anticipated that in an open population more common dental alignments may match more frequently than rare malalignment patterns. This article does not address this. More robust geometric shape analysis methods would be needed to study this issue. The socioeconomic status of the populations in this study is unknown as is the dental reason for an individual's presence in the data set. Further studies could include demographic or dental treatment information to investigate the effect of these variables. These factors do not affect the conclusions reported here, as the goal was simply to compare a large number of dentitions as a preliminary approach to estimating dental match rate.

Studies using the types of statistical approaches common in medicine or elsewhere in the biologic sciences are extremely rare in the bitemark literature (1). Confidence in the notion of dental uniqueness in bitemark analysis has been based on anecdotal knowledge, the use of inappropriate statistics, and precedence of admission in the courtroom. In contrast, other areas, such as DNA comparison, have evolved out of scientific research, with an extensive statistical framework accompanying the biochemistry of the genome. This tight linkage of statistical methods to pattern information (expressed as DNA sequences) has resulted in an extremely robust forensic tool.

Isolation of forensic experts from the statistical community can result in the failure to communicate about the implications of both statistics and biologic structure. Research is needed about sameness versus difference, measurement resolution and error in the context of forensics, and in the context of biologic structures (2). Critically important is the concept that forensic dental experts should not only know how to perform a procedure but also recognize the limitations of the procedure. This is vital to ensure that forensic odontologists deliver the best possible service to the criminal justice system. Therefore, it is imperative that the individuality of the human dentition is realistically depicted.

The individuality fallacy, as described by Saks and Koehler, suggests that uniqueness cannot be demonstrated (8). Even if it was possible to adequately conclude that uniqueness could be determined, uniqueness does not imply that mistakes in identification could not be made between similar individuals. The debate spurred by the legal community and the National Academy of Sciences report concerning individualization and uniqueness will no doubt require a tightening of scientific rigor in the fields of forensics. However, existing expertise and knowledge can readily be applied. In Saks and Koehler' words, "forensic identification scientists can help themselves…by forswearing exaggerated, definitive conclusions in favor of humbler, scientifically justifiable and probabilistic conclusions" (8). This article attempts to provide the basis for this in bitemark analysis.

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