PAPER

ODONTOLOGY

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A Framework for Estimating Probability of a Match in Forensic Bite Mark Identification*,[†]

ABSTRACT: In forensic dentistry, a human expert typically does the comparison and identification based on bite marks. Unlike DNA analysis, however, there is no quantitative basis with which to assign a probability for this given match. This paper proposes a framework for empirically estimating the probability of such a bite mark match and reports on initial experimental results. The methodology involved collection of dental population data (3D dental casts and bite mark images), image analysis for quantitatively measuring the degree of match (based on chamfer distance), and performing a logistic regression analysis using the collected population data to estimate the probability of match from the calculated degree of match. The model correctly predicted 35 of the 42 matches and 585 of the 588 mismatches. The method also has potential for use in other forensic applications in which the assignment of quantitative probabilities is important.

KEYWORDS: forensic science, bite mark, three-dimensional dental model, probability of match, chamfer distance, logistic regression

Forensic dentistry generally addresses the problem of identifying individuals based on the properties of teeth. By looking at the location, orientation, presence/absence, and dental work, people can be matched to dental records or bite mark impressions for identification.

One application of forensic dentistry, and the subject of this paper, is identifying individuals based on bite mark impressions, particularly matching bite marks left on victims to the perpetrator or matching bite marks left on criminals to the victim in instances of violent crime. It is legally relevant to match the bite mark with high confidence to the person who left it. It is also important to be able to assign a quantitative measure of the quality of the match based on objective measures. "Bite mark evidence has been almost universally accepted in the courts, but the fundamental validity and scientific basis for its use is frequently challenged (p. 1385) (1)."

This paper focuses on the calculation of a probability of a given match being the correct one based on a goodness-of-fit measure computed geometrically and a statistical analysis of a population of three-dimensional (3D) dental casts and bite mark images generated from them. The method to compute a goodness-of-fit measure using image processing and geometric methods has been presented elsewhere (2). This paper builds upon the goodness-of-fit measure presented there and proposes a framework for developing the estimation of the probability measure from these results. The system is envisioned to be used in conjunction with a forensic odontologist who would be doing the actual analysis and the judgment of match. The proposed framework would then assign a quantitative probability measure for the candidate match produced by the forensic odontologist. In the matching experiments reported in this paper, the maxillary and mandibular anterior teeth (upper and lower, central and lateral incisors and canines) were used.

Related Work

There are two main applications of forensic dentistry: (i) identifying deceased individuals by matching antemortem and postmortem dental records and (ii) identifying criminals based on bite marks (1,3). For the first type of application, typically 2D images, such as dental radiographs and the actual teeth or their 2D images, have been used. In many situations, the identification is made manually on 2D image data by experts using software tools, such as Adobe Photoshop, to obtain the best alignment (4). Chen and Jain developed a semi-automated approach for the comparison (5,6). This method uses image registration methods applied to extracted tooth contours in potential radiographs to determine whether there is a match.

In this paper, we focus on the second application, namely the identification based on bite mark impression left behind in a crime scene. Identification based on bite mark impression is made based on the shapes and arrangements of the bite mark impressions left behind and the degree of match to the teeth of the human who might have left these impressions. The bite mark impressions can be of varying qualities, and the matching of 3D teeth information

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to the 2D bite mark impressions can be difficult. Sweet (3) explores methods for identifying criminals based on bite marks. This is performed by comparing unique attributes and patterns in the suspect's teeth with similar characteristics in the injury. Naru and Dykes (7,8) utilize image enhancement and image processing tools with overlays to obtain a degree of match between images of bite mark injury and suspect dentition. McNamee et al. (9) conducted a comparative reliability study of captured bite mark overlays and showed little variation between the positions of tooth edges captured by different examiners.

More recent work involves using 3D digitized models of teeth, typically obtained using dental casts of the human subjects (10). Planar cross-sections from 3D digital models are identified manually to be matched against bite mark impressions. Others have used similar approaches to varying extents of automation (11). Previously, we have attempted to use 3D geometric models of candidate teeth to match 2D bite mark images in a partially automated way using image processing methods (2).

Matching of 3D teeth models to 3D bite marks has also been studied (12). However, obtaining 3D bite mark data in real situations is not easy; therefore, the usefulness of such techniques is not clear. Techniques other than 2D or 3D data alignment have also been tried (13).

To our knowledge, there has not been an attempt to assign a probability based on a population of dental casts of the degree of match of the bite marks to the teeth. In our view, this is a separate issue from the techniques to find the best match (automated or manually) to which this probability is assigned.

Methods and Materials

Framework for Estimating Probability of Match

The approach to estimate the probability of match for a 3D dental model to a 2D bite mark image described in this paper relies on a set of anonymous 3D dental casts, a goodness-of-fit measure previously developed (2) to assess the alignment of two 2D contours, and a statistical estimation to assign probabilities for a given match.

The general steps for the process were as follows:

- Create a 3D digitization of the set of dental casts (we used 15 dental casts in this study).
- Generate a set of bite mark images using these dental casts.
- Generate 2–3 bite mark images from each dental cast.
- For each bite mark image, generate further degraded images with different degrees of blur using Adobe Photoshop software.
- Extract 2D contours from the digitized 3D models of the dental casts.
- Extract 2D contours from the digitized bite mark images. These bite mark contours were extracted manually.
- Compare each bite mark image contour to each contour from the dental model by finding the ideal alignment and calculating goodness of fit.
- Select the one with maximum goodness-of-fit value as the match.
- Use this collection of goodness-of-fit values to fit a logistic regression model and estimate the parameters of the logistic regression model.
- When a new bite mark to 3D model match is identified, compute its goodness of fit using the aforementioned steps and use this goodness of fit in the estimated logistic regression model to compute the probability of a match.

In the following sections, we will describe the details of these steps and the experimental results. The image processing algorithms

used for obtaining the best alignment and the goodness of fit used in this paper are described elsewhere (2). The rest of the process that utilized the goodness-of-fit measure to estimate the probability of match is described later.

Data Collection

To test our method, there were two sets of data collected. One was the collection of 3D models of teeth, and the second was the collection of images of bite mark impressions made by these teeth.

The Indiana Forensic Institute in Indianapolis obtained 15 anonymous dental casts, from the Indiana University School of Dentistry, which were used to test our methods. The dental casts were 3D models of volunteers' upper and lower jaws and teeth. The setup for scanning the dental casts is shown in Fig. 1. Each dental cast was scanned from a distance of 50 cm to produce a complete 3D digitized model. The dental cast was placed on a turntable and scanned with a laser scanner in 30° increments. A final scan was made from the top. Each scan generated a partial 3D model (often called a 2 1/2 D model in computer vision literature). The scanner was a Minolta VIVID 910 non-contact 3-D digitizer (Konica Minolta Sensing, Inc., Osaka, Japan). The scanner worked in parallel with the Konica Minolta Polygon Editing Tool that was used to stitch together each 2 1/2 D scan to create a single complete 3D model of the dental cast. Figure 2 shows a typical digitized dental model.

The bite mark images were generated using the dental casts. To generate bite marks, the tips of the teeth in the 3D casts were coated with lipstick, and the models were pressed upon a soft, foam cushion with 5 lbs of force. The foam cushion was the torso of a child's doll, *c.* 7.5 cm in diameter (Fig. 3). Three bite mark simulations per model were performed. The resulting bite marks were then photographed as a 2D digital color image. A ruler was placed on the doll when taking the bite mark images to record the true scale of the bite marks. Figure 4 shows a sample bite mark image generated by this process.

Contour Matching Algorithm and Computing the Goodness of Fit

The 2D contours from the 3D model and the 2D bite mark image were extracted. The image processing and geometric algorithms for doing this were described (2). The algorithms for

FIG. 1—*The 3D digitization setup with the Minolta VIVID 910 non-contact 3-D digitizer (the white rectangular box on the left) and the rotating platform with the dental cast on it.*
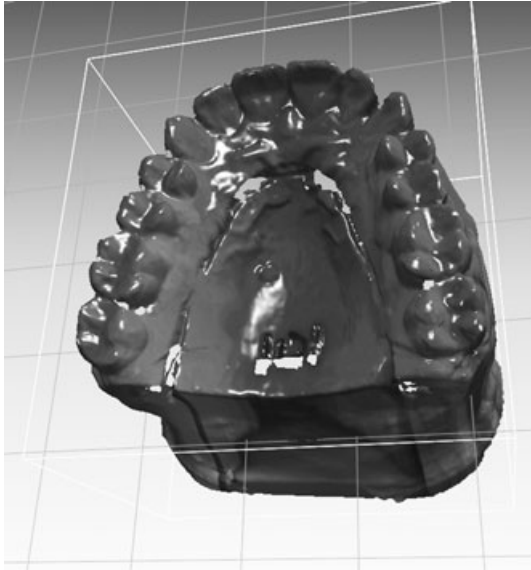
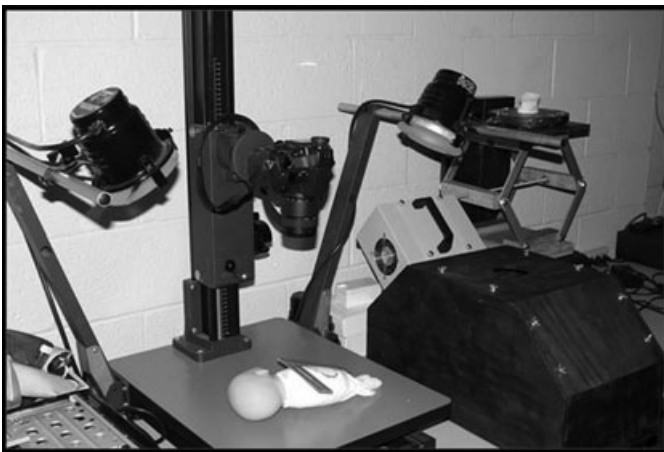FIG. 2—*An example 3D scan of the dental cast.*

FIG. 3—*The setup for generating the bite mark images using the dental cast. Lipstick-coated teeth of dental casts were used to bit into the toy doll's torso and the results imaged with a camera.*
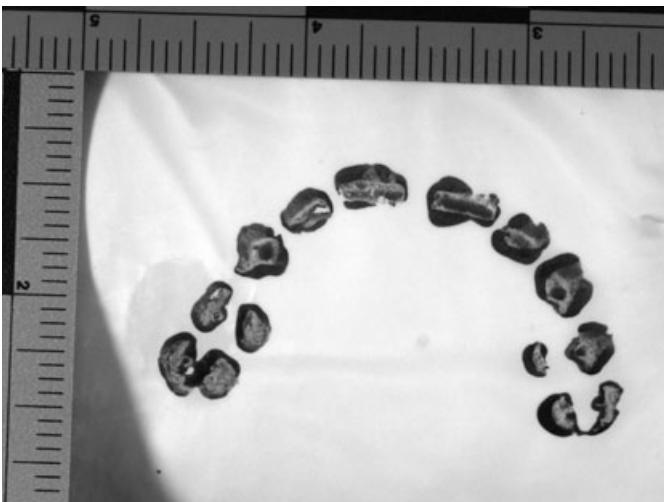

FIG. 4—*An example bite mark image generated by the setup in Fig. 3.*

matching these 2D contours were also presented in detail there. Because the probability estimation depends on the goodness-of-fit measure, a brief summary of how it was computed is given in this section before the description of the method of estimating the probabilities.

Given two 2D contours, a measure of similarity, assuming proper alignment, was desired. There were two parts to computing this measure: (i) finding the optimum alignment of the two contours and (ii) given this optimum alignment, how similar or dissimilar the two contours were in shape. The first part involved a search in the 2D plane, and the second part involved computation of some sort of a distance metric between the two 2D contours. In the fields of image processing, computer vision, and computational geometry, distance transforms, in particular chamfer distance, was developed and used to handle both the 2D search and similarity measure aspects of recognizing (thus matching) the model contour in the image. In this task, the 2D contours obtained from the 3D dental models were the model contours that were matched against the 2D contours extracted from the bite mark images.

Chamfer Distance—Once the 2D contours from the 3D model and the bite mark images were obtained as described in the previous section, the best match between the 2D bite mark image contour and each of the candidate model contours was formed. The matching between the contours was computed by finding the best 2D alignment according to the goodness-of-fit measure defined in this section. This search for the best alignment was made over the rigid 2D transformation space. The goodness-of-fit measure consisted of two parts that were combined to obtain an overall measure. One part was based on a chamfer distance measure, and the second part was based on a measure of the amount of overlap of the two filled contours.

The chamfer distance was calculated as given by Gavrila (14) and was used for the contour matching. For a given 2D alignment of the two contours, U and V, the average minimum distance between the two contours was identified; U and V represented discrete values along the contours. Given two point sets, $U = \{u_i\}, i = 1, \ldots, n$ and $V = \{v_j\}, j = 1, \ldots, m$, the chamfer distance function was the average of the distance between each point, $u_i \in U$ and its closest point on V:

$$d_{\text{chamfer}}(U, V) = \frac{1}{n} \sum_{u_i \in U} \left(\min_{v_j \in V} |u_i - v_j| \right) \qquad (1)$$

where |.| denotes the Euclidian distance, and n is the number of points in U. In the case of a perfect match, the two contours U and V would be perfectly aligned. In that case, all of the distances $\min_{v_j \in V} |u_i - v_j|$ along the contour U would be 0, thus giving a measure of similarity $d_{\text{chamfer}} = 0$. Finding the 2D translation that resulted in the ideal alignment of the two contours required a search of all 2D translations in the plane. Although we did not use it in this work, the computational burden of this search can be greatly reduced by using distance transforms (15).

Measure of Overlap—Another part of the goodness-of-fit measure was based on the amount of overlap between the two contours after they were aligned for the best match. This measurement was computed as the fraction of overlap between the filled bite mark contour and the filled dental model contour. The overlap measurement was computed as:

$$d_{\text{overlap}}(U_{\text{fill}}, V_{\text{fill}}) = \frac{|U_{\text{fill}} \cap V_{\text{fill}}|}{|U_{\text{fill}}|} \qquad (2)$$

where the notation $|S|$ denotes the cardinality of a set S and, in our case, represented the number of pixels in the appropriate set in the aforementioned formula. The computed overlap measure would have been 1 for a perfect alignment and approach 0 for a poor alignment.

Once the translation was found for the ideal alignment, the chamfer distance was computed and normalized. The $d_{chamfer}$ was $c.$ 3 for a typically good alignment but was <10 for a poor alignment. Thus, a normalized overall goodness measure based on $d_{chamfer}$ was $d_{chamfer}$ computed as

$$\text{goodness}_{\text{chamfer}} = \begin{cases} 1 - d_{\text{chamfer}}/10 & \text{if } d_{\text{chamfer}} < 10 \\ 0 & \text{if } d_{\text{chamfer}} > 10 \end{cases} \quad (3)$$

The overall goodness of fit was calculated as a linear combination of the two measures of goodness of fit:

$$\text{goodness of fit} = \alpha \times d_{\text{overlap}} + \beta \times \text{goodness}_{\text{chamfer}} \quad (4)$$

The values of α and β were determined empirically through experimentation. It was determined that finding the initial alignment maximizing the overlap amount was most successful ($\alpha = 1, \beta = 0$). Once the best alignment of the bite mark contour with the dental model contour was found, the result was refined and the overall goodness of fit was computed by including the $d_{chamfer}$ with $\alpha = 0.25$ and $\beta = 0.75$.

Obtaining 2D Contours from the 3D Dental Model

Once the digitized, 3D, dental models are created, the 2D contours that capture the tooth edges are computed. The process is as follows. The 3D model is imported into the volume editing software Rapidform (Rapidform 2006 with Object Linking and Embedding (OLE) automation; INUS Technology, Inc., Rapidform Global Headquarters, Seoul, Korea) and initially aligned using the Rapidform trackball transformation function. The model is oriented lengthwise along the y-axis with the teeth in the x–z plane approximately symmetric about the x-axis. Once the model is initially oriented by the user, the teeth contours are automatically captured using OLE automation with Rapidform as follows.

First, a bounding box is created around the model using the Rapidform function "GetMinMaxBox." The box is used as the search space for the teeth contour. A brute force search is conducted to find the ideal contour by intersecting the model with several planes at multiple orientations. The plane–model intersection was computed by using the Rapidform function, "GetCrossSectionOfShell" in the "MeshTools" toolbox.

The top plane of the bounding box is used as the initial plane, and the plane is decremented by 0.25 mm along the bounding box until 5 mm has been searched. Also, for each height, the plane is rotated by −2.5°, 0°, or 2.5°. At each plane location, the number of line segments of the intersection is counted, and the most complex contour (the contour with the most line segments) is considered the best contour as containing the most shape detail.

The method for capturing the teeth contour from the 3D dental model is summarized as follows:

- assuming the model is oriented lengthwise along the y-axis with the teeth in the x–z plane symmetric about the x-axis, create a bounding box about the model.
- the top plane of the bounding box is the initial position for the search plane with normal $\vec{\mathbf{n}}$ and point $P_0 = (p_x, p_{y0}, p_z)$.
- at each height, adjust the normal vector, $\vec{\mathbf{n}} = < \cos(\frac{\pi}{2} + \varphi)$, $\sin(\frac{\pi}{2} + \varphi), 0>$, for $\varphi = -2.5°, 0°, 2.5°$.
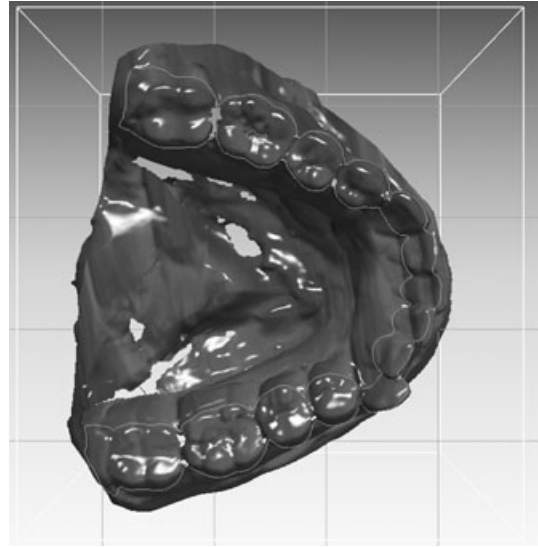

FIG. 5—*Digitized 3D dental model with intersecting plane and captured tooth contours shown as gray curves around the teeth.*

- for each plane orientation, compute the intersection between the plane and model and calculate the number of line segments of the contour.
- decrement P by 0.25 mm along y, so $P_i = (p_x, p_{y0} - i \times 0.25, p_z)$.
- repeat steps 3 through 5 for $i = 1$ to 20.

The desired contour is the plane–model intersection with the maximum number of line segments. An example contour obtained from a model is shown in Fig. 5.

Obtaining 2D Contours from the Bite Mark Images

The 2D contours from the bite marks were more difficult to extract because of the quality of the bite mark images. Two methods were explored to help the forensic analyst with this task. The first approach let a human expert interactively draw the teeth contours on the image. To capture the edge contours using this method, each bite mark image was opened in Adobe Photoshop. A transparent layer was then created over the original bite mark image, and the tooth edges were traced onto the transparent layer. The layer containing only the tooth edges (teeth contours) was saved as a separate binary image. In extracting the teeth contours, the correct placement of the edge seemed to be less important. The most important aspects of the contour retrieval were to capture the relative position of the teeth, the approximate shape and size of each tooth, and the orientation of each tooth. As expected, this was a time-consuming task, and even then, with some bite mark images, it was sometimes difficult to know where exactly the true bite mark contour was supposed to be.

The second approach we used automates this process to a degree. In this approach, the human expert indicated each of the teeth by clicking approximately in their centers. The contours then were identified by placing an oval-shaped, energy-minimizing snake on these points and deforming the snake curve according to the image data and an internal potential energy of the snake. The automated contour extraction methods we tried did not result in reliable detection and localization of bite mark image contours. Therefore, in the rest of this paper, we will focus on the results using the manual bite mark contour extraction method.

Method to Estimate Probability of Match

We will present a method to estimate the probability of a match between a dental model and a bite mark based on the goodness-of-fit measurement, i.e., the error distance, between the bite mark and dental model contours as described earlier. This method relies on an appropriate statistical model that links the error distance to the probability of a match based on the data we collected described elsewhere. Through model fitting, an estimation was made for the probability of a match for each pair of dental model and bite mark when given its error distance.

Statistical Model Used to Convert Error Distance to Probability

The population was considered to include all possible pairs of a dental model and a bite mark image. When one randomly chose a pair, there were only two possible outcomes: match or mismatch. We used Y to denote the binary match variable for a randomly chosen pair. If there was a match, then we let $Y = 1$, otherwise $Y = 0$. The problem of interest was to predict the probability of a match, $\pi = P(Y = 1)$, based on the goodness-of-fit measurement between the pair, denoted by X. In this work, the logistic regression model was used to study the relation between π and X. More specifically,

$$y \sim \text{Bernoulli}(\pi)$$

$$\text{logit}(\pi) = \beta_0 + \beta_1 X, \text{logit}(\pi) = ln\left(\frac{\pi}{1-\pi}\right)$$

The above model indicated that

$$\pi = \frac{\exp(\beta_0 + \beta_1 X)}{1 + \exp(\beta_0 + \beta_1 X)}$$

The drawback of this model was that it did not account for variability among bite marks in terms of absolute distances. To reduce this variability, we standardized the error distance (goodness fit) for each bite mark by computing its Z-score as given below:

$$Z = \frac{X - \mu_X}{\sigma_X}$$

where μ_X and σ_X were the mean and standard deviation of X. This transformation of variables now allowed us to compare error distances across different models and bite marks. We then used the following model with the new variable, Z, for our statistical analysis:

$$Y \sim \text{Bernoulli}(\pi), \qquad \pi = \frac{\exp(\beta_0 + \beta_1 Z)}{1 + \exp(\beta_0 + \beta_1 Z)}$$

To predict π was then equivalent to estimating the unknown parameters β_0 and β_1 using the data we collected, performing a logistic regression analysis and estimating the maximum likelihood estimates (MLE) of these parameters using the goodness-of-fit measure computed between each candidate match of bite mark image and teeth model pair.

Experimental Results and Discussion

Our method of dental identification was tested on a set of 15 3D dental models with two or three bite mark images for each model for a total of 42 bite mark images. Therefore, there were a total of $15 \times 42 = 630$ possible 3D model and bite mark pairs. Figure 6 shows a typical alignment found using this method. The goodness-of-fit value in this case is 0.86 with model 6 matching bite mark

FIG. 6—*A correct match identified by the method using chamfer distance based on goodness-of-fit measure. Gray represents the bit mark contour, and black represents the contour from the 3D model. The goodness-of-fit measure for this match is 0.86.*
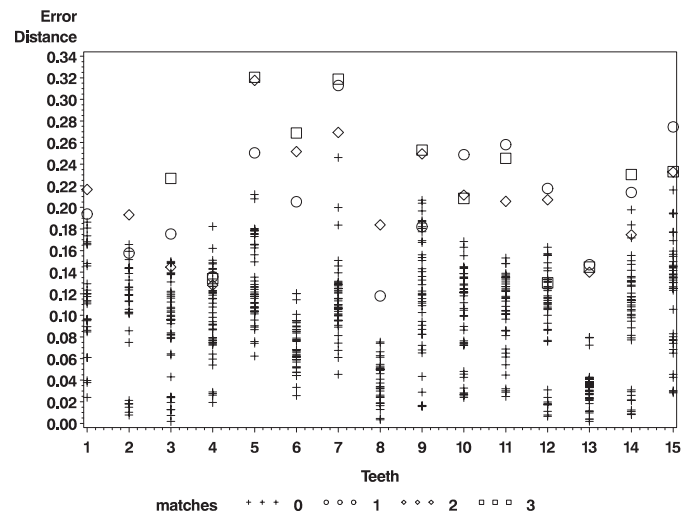

FIG. 7—*The goodness-of-fit measures calculated for each 3D teeth model and bite mark image pairing. The symbol plus "+" indicates mismatch, and the other three shape symbols—circle, diamond, and square—indicate the true match. The goodness-of-fit measure computed identifies most of the matches correctly as indicated by the three shapes being on top of each corresponding column in most cases.*

16. Using this goodness-of-fit data, we ran a set of automated matching tests that resulted in a goodness of fit for each such pairing. The details of this automated algorithm were reported (2). Figure 7 shows the resulting measures of goodness of fit for each such pair.

A more detailed discussion of these results is given elsewhere (2). In this paper, these results were used to estimate the probabilities of match from these error metrics for this given data set.

Model Fitting and Prediction of the Probability of Match

For the study reported here, we analyzed the data collected, which form 630 possible dental models to bite mark image pairings. Letting $Y_{i(j)k}$ be the binary match variable for the pair of ith repetition of bite mark image of the jth teeth and kth dental model

and letting $X_{i(j)k}$ be the goodness-of-fit measurement, or the error distance, between the given pair, the standardized error distance was then given by:

$$Z_{i(j)k} = \frac{X_{i(j)k} - \bar{X}_{i(j)}}{s(X_{i(j)k})}$$

where $\bar{X}_{i(j)}$ and $s(X_{i(j)k})$ were the mean and standard deviations as computed by:

$$\bar{X}_{i(j)} = \frac{1}{15}\sum_{k=1}^{15} X_{i(j)k}$$

$$s(X_{i(j)k}) = \left(\frac{1}{14}\sum_{k=1}^{15}(X_{i(j)k} - \bar{X}_{i(j)})^2\right)^{1/2}$$

[Correction added after online publication 30 Sept. 2010: Equation corrected.]

Figures 7 and 8 show the scatterplots of the error distance and standardized error distance against dental models. There were 15 dental models that made repeated bite marks, and the columns show the data for each. The error distance (standardized error distance for Fig. 8) between the pair comprised of each dental model and bite mark made by these teeth is plotted on the vertical axis. The shape symbols represent the distance for the correct match (i.e., that the dental model was made from these teeth). The different shapes—circle, diamond, and square—represent the three repetitions of bite marks made by these teeth, respectively. The symbol plus "+" represents the distance for the mismatch (dental model was from other teeth).

The sample $\{(Y_{i(j)k}, Z_{i(j)k}), i = 1, 2, 3; j, k = 1, \ldots, 15\}$ is then assumed to follow the logistic regression model:

$$Y_{i(j)k}|Z_{i(j)k} \sim \text{Bernoulli}(\pi(Z_{i(j)k})), \text{independently}$$

$$\pi(Z_{i(j)k}) = \frac{\exp(\beta_0 + \beta_1 Z_{i(j)k})}{1 + \exp(\beta_0 + \beta_1 Z_{i(j)k})}$$

To predict π is then equivalent to estimating the unknown parameters of the polynomial regression function in the model given above. PROC GENMOD of the statistical software SAS version 9.1 (SAS Instit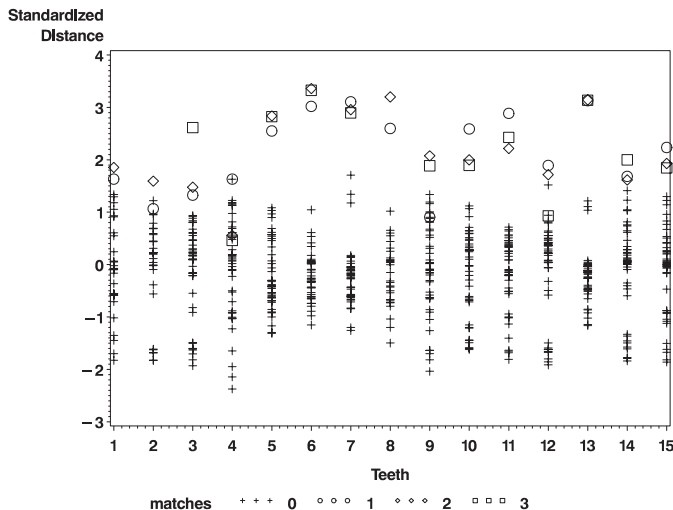ute Inc., Cary, NC) was used to obtain the MLE of the parameters β_0 and β_1 using the empirical data and the computed goodness-of-fit measures described above for the matches. The calculated MLE of the two parameters were

$$\hat{\beta}_0 = -7.6305, \quad \hat{\beta}_1 = 5.0589$$

Hence, the predicted probabilities are

$$\pi(Z_{i(j)k}) = \frac{\exp(-7.6305 + 5.0589 Z_{i(j)k})}{1 + \exp(-7.6305 + 5.0589 Z_{i(j)k})}$$

Figure 9 shows the plot of the predicted probability against the identity (one of 15) of the dental cast for our data. Again, the shape symbol represents a match, and the symbol plus "+" represents a mismatch. Of the 630 dental/bite mark pairs, there are 42 matches and 588 mismatches. Based on the classification cutoff point of 0.5, the model correctly predicted (35 + 585)/630 = 98.4% of the matches and mismatches. Specifically, the model correctly predicted 35 of the 42 matches and 585 of the 588 mismatches.

Now, we employ cross-validation procedure to validate our model. More specifically, we use jack-knife procedure, whereby single observations are withheld from the data set while fitting the model, and the observation then tested with the fitted model. This process continues until all observations have been tested. The cross-validation accuracy was estimated again as (35 + 585)/630 = 98.4%, the same as the above computed model accuracy. That both accuracies were high and similar suggests the model is fairly robust and is not overly influenced by characteristics of the model building data.

Next, using the probabilities predicted from our model, we computed the true-positive rate (sensitivity) and the false-positive rate (specificity) for a variety of probability thresholds. For example, if the probability threshold is 0.6, our model correctly predicted 35 of the 42 matches and 586 of the 588 mismatches. Then, the sensitivity of the model is 35/42 = 0.833, and the specificity is 1–586/588 = 0.003. Table 1 gives the sensitivity and specificity of our model for various probability thresholds ranging from 0.005 to 0.9. Based on Table 1, we further plot the receiver operating characteristic curve (or ROC curve) in Fig. 10 to evaluate the performance of our model. ROC curve is a plot of the true-positive rate against the false-positive rate for the different possible cutoff points of a diagnostic test. Accuracy of the test is measured by the area
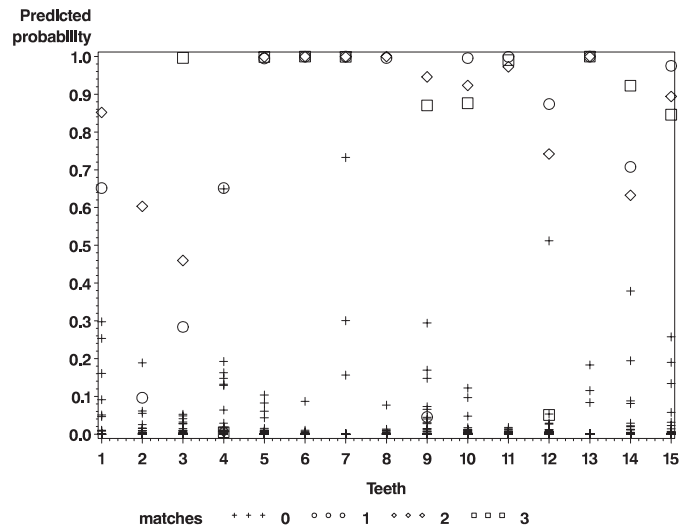

FIG. 8—*The standardized distance Z plotted for each pairing of 3D teeth model and bite mark image.*

FIG. 9—*The predicted probabilities of the bite mark to teeth model matches.*

TABLE 1—*The sensitivity and specificity of the model.*

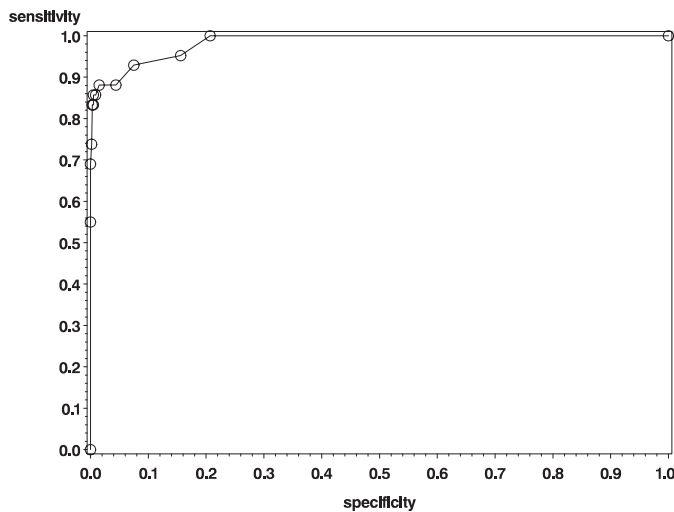| Probability Thresholds	Sensitivity	Specificity
0.005	1.000	0.21
0.01	0.952	0.156
0.05	0.929	0.075
0.1	0.881	0.044
0.2	0.881	0.015
0.3	0.857	0.009
0.4	0.857	0.005
0.5	0.833	0.005
0.6	0.833	0.003
0.7	0.738	0.002
0.8	0.690	0.000
0.9	0.548	0.000

FIG. 10—*The ROC curve of the model.*

under the ROC curve. An area of 1 represents a perfect test; an area of 0.5 represents a worthless test. A rough guide for classifying the accuracy of a diagnostic test is the traditional academic point system: 0.90–1 = excellent (A); 0.80–0.90 = good (B); 0.70–0.80 = fair (C); 0.60–0.70 = poor (D); and 0.50–0.60 = fail (F). The area under our ROC curve is much larger than 0.90. Hence, we claim the predicted probability calculated through the proposed logistic model did an excellent job in distinguishing the correct match and mismatch.

Conclusions

In this paper, we presented a computational framework for forensic identification based on bite marks and an empirical method for estimating the probability of match from a given population sample of teeth. The automated match results using the 3D teeth models and bite mark contours were also compared to the human odontologists' performance in Eq. 2. The analysis there indicated that the matches missed by our distance measure were also missed by the odontologists in certain instances, indicating that there was not sufficient distinctive information in the teeth to allow individualization of the bite marks. We conclude that the proposed method of automated computation of the match and the assignment of a probability value is a promising approach that yielded initial good results as discussed in the Results section. Furthermore, the same methodology can be adapted to other forensic identification applications.

Future improvements would include a more realistic set of bite marks to use in the logistic function estimation. This might also result in improved automated bite mark contour extractions and, therefore, better match results.

Conflict of interest: The authors have no relevant conflicts of interest to declare.

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