

COMBINING MATCHING ALGORITHMS FOR HUMAN IDENTIFICATION USING DENTAL X-RAY RADIOGRAPHS¹

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ABSTRACT

The goal of forensic dentistry is to identify individuals based on their dental characteristics. In this paper we present a system for identifying individuals from their dental X-ray records. Given a dental record, usually a postmortem (PM) radiograph, the system searches a database of ante mortem (AM) radiographs and retrieves the best matches from the database. The system automatically segments dental X-ray images into individual teeth and extracts representative feature vectors for each tooth, which are later used for retrieval. The system integrates one method for teeth segmentation, and two different methods for representing and matching teeth. The first matching method represents each tooth contour by signature vectors obtained at salient points on the contour of the tooth. The second method uses Hierarchical Chamfer distance for matching AM and PM teeth to reduce the search space and accordingly reduce the retrieval time. Given a query PM image, and according to a matching distance, AM radiographs that are most similar to the PM image, are found and presented to the user using the two matching methods. The experimental results show that the system is robust. We studied the performance of the different modules of the system as well as the results of fusing the matching techniques.

Index Terms—Forensic dentistry, biometrics, fusion.

1. INTRODUCTION

Forensic radiology is a branch of forensics that deals with identifying people using postmortem radiological images of different parts of the body including skeleton, skull, and teeth. The branch of forensic radiology that relies on dental radiographs is called forensic odontology [1]. The identification is carried out by comparing postmortem (PM) images with antemortem (AM) records of missing people to find best matches. Dental features are regarded as the best candidates for postmortem biometric identification. Not only they represent a unique repository of identifying features, but also they are the most surviving postmortem part of the victim's body [2,3]. Currently, the identification relies on comparing manually extracted features of a PM dental record with the features of AM records archived in a database. Developing automatic dental identification systems caught the attention of few research groups [4-9]. They focus on developing biometric systems based upon dental X-ray images. Essentially, an automatic dental biometric system will facilitate for forensic odontologists to search through a large database of AM records and only manually verify the few best matches.

In this paper, we present a system for human identification using dental x-ray images. The system integrates modules for dental image segmentation of bitewing images, and teeth matching. We present a technique for dental X-ray image segmentation as well as two techniques for teeth matching. The matching techniques address the issues of representing each individual tooth by a set of

features and calculating the similarity between the AM and the PM teeth based on these features. Then, finding the best matching teeth from the AM database, and accordingly finding the best matched individuals using majority voting. Also, the second matching technique addresses the issue of reducing the retrieval time. The experimental results of the different modules and the results of fusing the matching techniques are presented.

The rest of this paper is organized as follows: Section 2 presents the segmentation method. Section 3 presents the matching techniques. Section 4 fuses the matching methods at the matching and the decision levels. Section 5 presents the experimental results. The conclusions and the future works are discussed in Section 6.

2. RADIOGRAPH SEGMENTATION

The goal of radiograph segmentation is to localize the region of each tooth in an X-ray image. Dental radiographs may suffer from poor quality, low contrast and uneven exposure that complicate the task of segmentation. Dental x-ray images have three different regions: soft tissue regions and background with the lowest intensity values, bone regions with average intensity values, and teeth regions with the highest intensity values. In some cases the intensity of the bone areas is close to the intensity of the teeth, which makes it difficult to use a single threshold for segmenting the entire image. The method starts by applying iterative thresholding followed by adaptive thresholding to segment the teeth from both the background and the bone areas. After thresholding, horizontal integral projection followed by vertical integral projection are applied to separate each individual tooth [8]. The contour pixels for each tooth are then extracted and sampled to represent each tooth by equal number of contour pixels.

3. DENTAL X-RAY TEETH MATCHING

This section presents the dental radiograph matching techniques. Given a PM dental image, the matching techniques retrieve the best matches from an AM database. Each technique extracts a set of features from the previously segmented X-ray images. Section 3.1 presents the teeth matching using signature vectors. Section 3.2 presents teeth matching using hierarchal contour matching. For all the images in the database, the segmented teeth are automatically classified and numbered according to the universal teeth numbering system using the algorithm described in [7]. This eliminates the possibility of matching teeth that have different numbers.

3.1 Teeth matching using signature vectors

This technique relies on selecting a set of salient points from the tooth's contour and generating a signature vector for each salient point [8]. The signature vectors capture the curvature information for each salient point. Each element in the vector is the distance between the salient point and a point on the contour. Salient points are the contour points of high curvature. The algorithm calculates the curvature for every contour point and then selects a set of N points with the highest curvature as the salient points. For each

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salient point, p , defined by its 2D coordinates, each other point p_i on the contour can be related to p by the distance

$$d_i = \|p - p_i\| \quad (1)$$

and the signature vector V_p of the point p is defined as

$$V_p = [\|p - p_i\|], i = 1 \dots M \quad (2)$$

where M is the number of points on the tooth contour.

During matching, the image of a PM tooth is aligned with that of a corresponding AM tooth [10] (they should have the same universal tooth number). The alignment step assumes that the image of the PM tooth is transformed with respect to the image of the AM tooth by a transformation T

$$T(Q) = A \times Q + \tau \quad (3)$$

where $Q = (x, y)^T$ represents a point in the query contour, $T(Q)$ is the result of applying the transformation on Q . A is a transformation matrix includes both rotation and scaling, and τ is a translation vector. A and τ can be represented as

$$A = \begin{pmatrix} \cos \theta & \sin \theta \\ -\sin \theta & \cos \theta \end{pmatrix} \times \begin{pmatrix} S_x & 0 \\ 0 & S_y \end{pmatrix}, \tau = \begin{pmatrix} \tau_x \\ \tau_y \end{pmatrix} \quad (4)$$

Where θ is the rotation angle, S_x and S_y are vertical and horizontal scale factors, and τ_x and τ_y are vertical and horizontal translations. The parameters (i.e., θ , S_x , S_y , τ_x , τ_y) are optimized to obtain minimum matching distance between the transformed contour of the query tooth and the contour of the AM database tooth.

Now, suppose we have a query tooth contour, q , and a database tooth contour, k , the signature vectors Q_i and K_i are defined as

$$Q_i = [\|qc_i - q_j\|], K_i = [\|kc_i - k_j\|], i = 1 \dots N, j = 1 \dots M \quad (5)$$

Where qc_i , kc_i are high curvature points, q_j , k_j are contour points, N is the number of high curvature points, and M is the number of the tooth contour points. The matching distance to be minimized for each pair of query contour, q , and database contour, k , is

$$D = \sqrt{\sum_{i=1}^N \frac{1}{k_i} \sum_{j=1}^M (Q_{i,j} - K_{i,j})^2} \quad (6)$$

Where $Q_{i,j}$ is element j in signature vector Q_i , $K_{i,j}$ is element j in signature vector K_i , and k_i is the mean value for the database's signature vector i . k_i is used to normalize the distance between each two corresponding signature vectors, i , for the distance D to be independent of the scale. The best matching AM tooth will correspond to the minimum D . In order to obtain the best matching image, majority voting is used so that the best matching AM image is with the maximum number of teeth ranked first. For a given PM image, we order the matched AM images according to the maximum number of teeth that ranked first, then to the maximum number of teeth that ranked second and so on. The best AM match is the first image in the list. If there is a tie, the one that has the minimum average matching distance for the whole AM image is chosen.

3.2 Hierarchical Dental X-ray Contour Matching

This technique is based upon the Hierarchical Chamfer Matching [9]. The idea of this technique is to perform matching at different resolution levels to reduce the retrieval time. Starting at the lower resolution level, the search space is large, i.e. contains all the images, while the matching between two teeth is fast. At each resolution level, the distance is calculated from the AM tooth distance map (DT) and a PM tooth's contour. As a result, the search space is decreased by eliminating images from the search

space as moving to higher resolution levels. This is one of the advantages of using the hierarchical matching technique.

The technique extracts the contour pixels and builds a DT image for all the AM teeth in the database. The DT [11] is computed by setting each contour point to zero and non-contour points to infinity, we only compute the DT for an area around the feature points, which tremendously reduces the amount of computations. Each pixel obtains a new value $v_{i,j}^k$ equal to

$$v_{i,j}^k = \min \begin{cases} v_{i,j}^{k-1} \\ v_{i,h}^{k-1} + 3 & h = j - 1, j + 1 \\ v_{m,j}^{k-1} + 3 & m = i - 1, i + 1 \\ v_{m,h}^{k-1} + 4 & m = i - 1, i + 1; h = j - 1, j + 1 \end{cases} \quad (7)$$

Where $v_{i,j}^k$ is the value of the pixel at position i,j at iteration k .

This iterative procedure will continue until there are no changes in the values. From our experimental results, 10 to 15 iterations were sufficient for convergence. The distance between AM and PM teeth is computed by summing the $v_{i,j}$ values which correspond to the contour points of the PM tooth. Figure 1 shows an example. The zero entries represent the pixels' positions of an AM tooth contour. The dark-edge entries represent the pixels' positions of a given PM tooth contour.

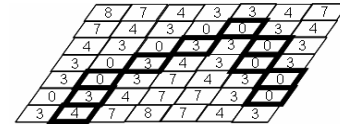


Fig 1: Example of the distance transformation image.

To allow for the multi resolution matching, the DT is calculated for the original contour image as well as a series of contour images, where each one is a representation of the original contour at a lower resolution. The image of the tooth contour at a given resolution is constructed from the contour image at the higher resolution by replacing each block of four pixels by a single pixel. This new pixel is the result of the "OR" of the four parent pixels. Due to the fact that there is no much details in lower resolutions and from our experimental results, it is sufficient to use around six levels.

Given a PM query image, the teeth are first segmented, and numbered. At any resolution level, the matching scores are generated based on the distance between the contours of the PM tooth and each AM tooth that have same tooth number. This is achieved by superimposing the contour pixels of the PM tooth on the DT of each AM tooth, and then, calculating the distance between the PM and the AM contours. The contour of the PM tooth at any resolution level is constructed from the contour at the higher resolution using the same idea of constructing the AM tooth contour images.

Before matching, the contour of each tooth in a PM image is aligned with the contour of a corresponding AM tooth using the same transformation in equations 3, and 4. The parameters are optimized to obtain the minimum matching distance between the AM and PM teeth, which is equal

$$D(q_j, k_j) = \sqrt{\frac{1}{m} \sum_{i=1}^m v_i^2} \quad (8)$$

where q_j is tooth j in the query image Q , k_j is tooth j in the AM image K , v_i is the value of the distance map at the position corresponding to contour point i of the PM tooth, and m is the number of contour points.

The matching procedure starts with the lowest resolution level and proceeds to the higher levels, where the results at the low level will guide the matching at the higher levels. This multi-resolution technique speeds up the computation. The matching starts from the coarse level in the hierarchy, where the computation is faster. The matching criterion defined at (8) was applied to search the best match for each PM tooth in the database with the same tooth number. The AM teeth are arranged in an ascending order according to the calculated distance. We reject 50% of the teeth with the largest distance. A limited number of AM teeth are marked as the possible candidates for further match. Then the matching process is moved to the upper resolution level with more points and less search space. This is one of the advantages of using the hierarchical algorithm, i.e., reducing the computational load significantly. In order to obtain the best matching image, majority voting is used as explained in the previous section.

4. FUSION OF THE MATCHING TECHNIQUES

In this section, the two matching techniques are fused together at the matching level as well as at the decision level to improve the overall performance of the system. Section 4.1 presents the fusion at the matching level and Section 4.2 presents the fusion at the decision level.

4.1. Fusion at the matching level

A typical scenario for fusing two or more matchers is often proprietary, where each matcher independently acquires inputs and makes an autonomous assessment of the match. The scores of an individual matcher are available for fusion while the features used by one matcher are not accessible to the other matcher. We present two methods for fusion the matchers.

1. Score Summation: The idea is to calculate the weighted average of the matching scores, produced by the different matchers. According to the weighted average scores, a decision of reject or accept will take place. First, the scores are normalized using the Min-Max method.

2. Weight Adaptation: The idea is to use a set of training data and search for the weights such that the total error rate on the training set of the fused scores is minimized. The weights are multiples of 0.01 over the range [0, 1]. By adapting these initial weights we obtain a final weight for each matcher. First, the scores are normalized using the Tanh method. Applying all possible weight combinations, and choosing the set of weights that minimizes the total error. The total error is in the form of costs associated with two types of errors

$$E = C_{FA}F_{AR} + C_{FR}F_{RR} \quad (9)$$

where C_{FA} is the cost of accepting a false match, F_{AR} is the false acceptance rate, C_{FR} is the cost of falsely rejecting a true match, and F_{RR} is the false rejection rate. For simplicity, we assign equal costs ($C_{FA} = C_{FR} = 1$), the risk is equivalent to the total error. This scenario needs many iterations to choose the final weights.

4.2. Fusion at the decision level

Many different strategies are available to combine the distinct decisions into a final decision. These range from majority votes to sophisticated statistical methods. In practice, however, developers seem to prefer the easiest method: Boolean conjunctions. We implemented two Boolean scenarios for fusing our matchers at the decision level, given the decisions from the two matching techniques, DM_1 , DM_2 , the two matching techniques are fused together using the Boolean functions:

1- AND: (DM_1 .AND. DM_2): requires a positive decision from the two matchers, otherwise it fails to identify.

2- OR rule (DM_1 .OR. DM_2): this scenario requires positive decision from at least one matcher.

These scenarios are implemented and their performances are listed in the experimental results section.

5. EXPERIMENTAL RESULTS

Our database was provided by the FBI. The segmentation technique was applied to 187 bite-wing images. It always correctly segments the upper jaw from the lower jaw for all the images. The results are shown in Table 1. A few teeth segmentation/separation results are shown in Figure 2. The cases where teeth were not correctly separated are due to the poor quality of the images.

	Upper jaw	Lower jaw
# of teeth in 187 images	627	569
# of correctly separated teeth	519	456
% of correctly separated teeth	83%	80%

Table 1: The results of the segmentation technique.

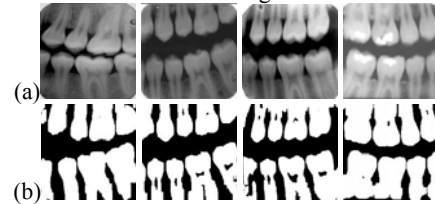


Fig 2: Teeth segmentation and separation results; (a) The original images (b) The segmented teeth.

We tested the matching techniques on a set of bitewing AM dental images. The AM database contains 162 AM images. The AM images are segmented, and numbered. During matching, Given a PM image, the teeth are also segmented and numbered. Then, the matching distance for the matching techniques are calculated between each PM tooth and each AM tooth in the database with the same number. The best matched AM tooth is the one with minimum matching distance. The matching techniques were evaluated using 50 PM query images, the correct matches were always retrieved for the 50 PM query images using the two matching techniques. Table 2 shows the results.

PM		Signature vectors		Hierarchical technique	
		Correct matches	%	Correct matches	%
# of teeth	217	172	79	182	83
# of images	50	40	80	42	84

Table 2: The results of the matching techniques.

The matching performance curves for both matching techniques are shown in Figures 3, and 4 respectively.

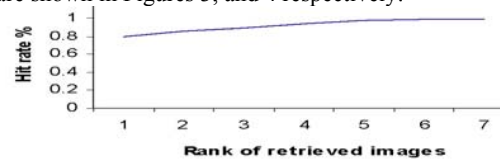


Fig 3: The performance curve of the signature vectors matching.

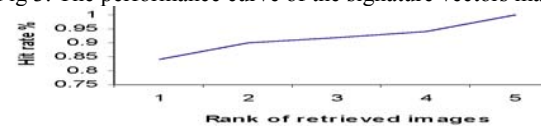


Fig 4: The performance curve of the hierarchical matching.

Studying the experimental results of the matching techniques, the hierarchical technique outperforms the signature vector technique. The advantage of the hierarchical technique is that the

matching is applied using multi-resolution algorithm. This speeds up the computations by reducing the search space. We also compared the retrieval time for both methods; the hierarchical method is 20% faster than the signature vector method, on average. We also applied the hierarchical matching technique to our test set, but only for the original images without applying the hierarchical technique. Comparing the retrieval time of both methods, the hierarchical method reduces the retrieval time by 23%, on average.

There are different reasons for the misclassified subjects. In some cases the tooth contour is not correctly extracted during the segmentation step because of the image poor quality. In other cases, because the X-ray image is a 2D projection of a 3D object, the 2D shapes of the contours were similar which leads to wrong matches. It is also important to note that if the PM images are captured long after the AM images were captured, the shapes of the teeth can change because of artificial prosthesis, teeth growth, and teeth extraction.

The matching techniques are fused using the scenarios introduced in Section 4. Figures 5, and 6 show the fusion of the two matchers at the matching level. Also, Figure 7 shows the fusion of the two matchers using the Boolean functions.

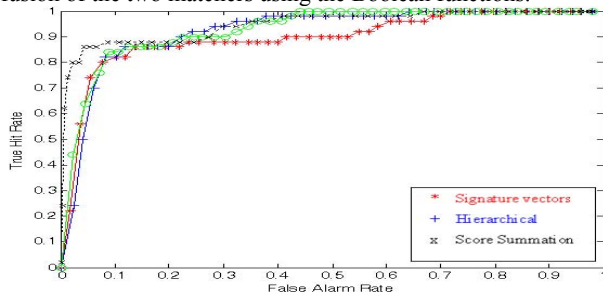


Figure 5: the ROC curve for the Score Summation method

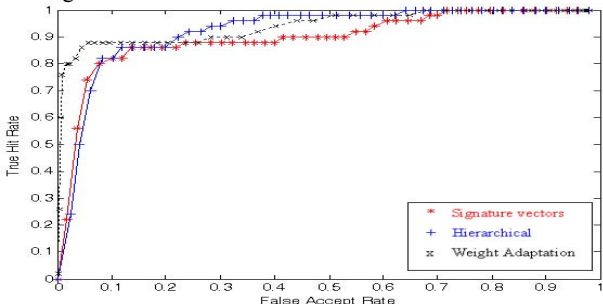


Figure 6: the ROC curve for the Weight Adaptation method

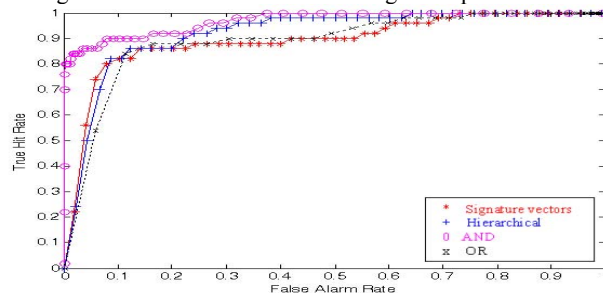


Figure 7: the ROC curve for AND, and OR functions.

From these two ROC curves, the fusion at the matching level improves the system performance and also the weight adaptation method outperforms the score summation method. Also, from the ROC curve, we can notice that, when we use the AND rule, the F_{RR} (false rejection rate) for the fused matchers is higher than it is for any individual matcher. Also we can notice that, when we use

the OR rule, the F_{AR} (false acceptance rate) for the fused matchers is higher than the F_{AR} for any individual matcher.

6. CONCLUSION

In this paper we presented a system for identifying individuals based on their dental X-ray records. The system archives the AM images into the database by segmenting the teeth, extracting their contours, numbering the teeth, and representing each tooth by a set of features. We presented a segmentation technique to segment the bite-wing dental images and two matching techniques. The first matching technique relies on selecting a set of salient feature points with high curvature from the contour of a tooth and generates a signature vector for each salient point. The second matching technique uses Hierarchical Chamfer distance transformation to reduce the search space is reduced significantly as well as the computational load. Given a PM image, the system segments the teeth, extracts their contours and represents each tooth a set of feature vectors. The matching modules search the database for the best matching candidates. Matching scores are calculated based on the distances between the feature vectors of AM and PM teeth. We have presented the experimental results for evaluating the performance of the different modules of the system. The two matching methods are fused at the matching level as well as the decision level to improve the overall performance of the system. The results show that the hierarchical technique outperforms the signature vectors technique. The system performance was tested on images of different qualities. In our future work we will develop algorithms for fast retrieval. We will also extend our system to handle panoramic and periapical radiographs.

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