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Dental identification system based on unwrapped CT images

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Abstract—**Dental comparison of postmortem (PM) and antemortem (AM) radiographs provides one of the best avenues for the forensic identification of human remains. Nevertheless conventional dental comparison is labor-intensive, subjective, and has several inherent drawbacks. This paper presents a semi-automated image analysis system designed to assist the forensic dentist with the task of identifying human remains. This system overcomes the drawbacks of conventional dental comparison because it is based on the comparison of radiograph-like images reconstructed from PM computed tomography (CT) data with AM digitized conventional radiographs. The efficacy of the system is demonstrated using 4 dental CT data sets and 32 digitized bitewing radiographs obtained from routine clinical practice.**

I. INTRODUCTION

Forensic dentistry is a branch of forensics concerned with establishing the identity of a deceased individual from his/her post-mortem (PM) dentition using ante-mortem (AM) dental records. It is one of the best avenues for human identification because teeth are not only highly resistant to decomposition, but are also unique to an individual. Conventional dental comparison involves manually summarizing dental records and radiographs. A PM summary can then be compared to AM summaries to establish a shortlist of possible identities. Manual comparisons of the candidate AM radiographs with the PM radiographs are necessary to make a positive identification. In particular the forensic dentist commonly confirms the identity of the human remains based on tooth features such as tooth morphology.

Conventional dental comparison has several shortcomings [1]: it is very labor intensive, it is error prone because mistakes can be made collecting information and compiling summaries, it is subjective, and the shortlist of possible matches is based on summary information rather than features—e.g. tooth and root morphology—derived directly from the PM and AM radiographs. This has motivated research into, and development of, computer-assisted dental comparison methods/systems. They can be broadly classified into two groups: those that aim to improve the efficiency and accuracy of the conventional approach; and those that aim to extend the conventional approach. Software packages such as CAPMI [2], WinID [3], IDIS [4], and OdontoSearch [5] belong to the first group. These packages essentially permit the creation of AM/PM computer databases using standardized summary forms, and text-based searching of records. Candidate radiographs can then be visually compared, possibly using other software packages such as Adobe Photoshop® [6] and Digital Dental Radiographic Identification (DDRI) [7]. With regard to the second group, several approaches to content-based matching of digitized radiographs have been proposed: [8], [9], [10], [11], [12], [13], [14], and [15]. These approaches utilize image processing and statistical pattern recognition techniques to perform automated or semi-automated matching of digitized radiographs based on tooth shape.

The majority of existing computer-assisted dental comparison methods/systems use conventional x-ray radiographs—e.g. bitewing and periapical films—acquired PM for matching against AM conventional radiographs. The reason for this is that such radiographs are much more commonly acquired AM than panoramic radiographs or x-ray computed tomography (CT) images. However, the use of PM conventional radiographs is problematic for several reasons including: their inherently poor image quality, the difficulty matching the AM and PM viewing geometries, and the difficulty obtaining such radiographs when the state of the dental remains is poor. Recently we demonstrated that these problems can be overcome by acquiring PM CT data and using it to reconstruct 2D radiograph-like images for matching against AM radiographs [16]. This is the approach used in the dental identification system (DIS) presented in this paper. The system is able to reconstruct a 2D panoramic-like image from the PM CT data and to match this against a database of AM digitised radiographs. At the present time the system can perform matching against bitewing radiographs. Such radiographs contain up to ten teeth enabling the possibility of using both tooth morphology and the spatial inter-relationships between the teeth to establish identity.

This paper is organized as follows. Section II introduces the proposed DIS and describes the algorithms/methods therein for metal artifact reduction, unwrapping CT data, segmentation of the teeth, and image matching. Section III presents the results of an experimental evaluation of the system using CT data and bitewing images from routine clinical dental examinations. Finally Section IV critically examines the presented work and describes future research.

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II. METHODS

A. System components

The proposed dental identification system (DIS) has two modes of operation: archival and retrieval. In the archival mode, the system permits the user to enroll a new digitized AM radiograph into its database. The system automatically segments the individual teeth in the radiograph image and then provides the user with the opportunity to interactively make corrections before the image is committed to the database. In the retrieval mode, the system permits the user to upload a PM CT data set for which an identity is sought. It then automatically unwraps this data to create a 2D panoramic radiograph-like image, automatically segments the individual teeth, and provides the user with the opportunity to interactively make corrections before the database is queried for potential AM matches.

B. Metal artifact reduction

Using dental CT data for forensic identification is problematic because CT images can contain geometric and intensity artifacts—e.g. beam hardening, partial volume, patient motion—which seriously degrade the quality of the images [17]. Metal artifacts, originating from metal restorations, are the most significant of these. They present as pronounced dark and light streaks in the CT images reconstructed using the filtered back-projection method commonly used in commercial CT scanners. For this reason the DIS incorporates our own novel metal artifact reduction algorithm called metal artifact reduction by sequential substitution (MARSS). The algorithm is automatically applied to uploaded CT data before unwrapping, segmentation, and matching are performed.

The MARSS algorithm is a projection correction method; i.e. it attempts to correct those portions of the sinogram or projection data corrupted by the presence of the metal restorations. It is based on the idea that these portions can be substituted with the corresponding portions of the projection data from an unaffected or corrected adjacent slice. The rationale is that in reconstructed CT data there is spatial dependence or autocorrelation such that voxels in close proximity will have similar value. When the dental CT data are acquired so that the axial slices are parallel to the occlusal plane then metal artifacts will be predominantly intra-plane and not inter-plane. Therefore reconstructed axial slices containing the roots of the teeth will be free from metal artifacts. Thus, proceeding sequentially from the roots to the crown, when a slice with metal artifacts is encountered, its sinogram is corrected using data from the sinogram or corrected sinogram of the preceding slice.

MARSS processes each successive slice image in six steps. In the first step, the image is thresholded to obtain a binary mask (BM) containing as much of the metal restorations and streaks as possible. We have found that a suitable threshold value is one third of the maximum intensity value present in the CT data set. In the second step, the BM, the slice image, and the preceding slice image are forward projected to obtain the mask projection data (MPD), the target projection data (TPD), and the source projection data (SPD) respectively. The non-zero values in the MPD locate the areas of the TPD corrupted by the metal restorations. Hence in the third step, for every non-zero pixel in the MPD, the corresponding pixel in the TPD is substituted with its counterpart in the SPD. In the fourth step the corrected TPD is back projected. In the fifth step the metal restorations are superimposed. This is done by filtering the BM, using a morphological closing with a small disk structuring element, to retain only the metal restorations, and then replacing the corresponding pixels in the back projection in step four with their counterparts in the original slice image. Finally, in the sixth step the original slice is replaced with the corrected slice. This ensures that it can be used in the correction of the next slice image.

The efficacy of the MARSS algorithm is demonstrated in Figure 1.

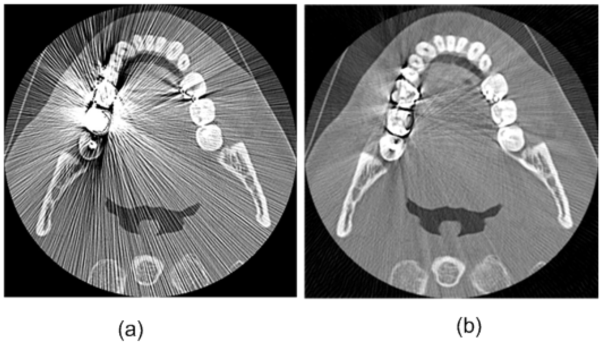


Figure 1: (a) Original axial slice image affected by metal artifacts. (b) Result after the application of the MARSS algorithm.

C. Unwrapping the CT data

The algorithm used by the DIS to unwrap the MARSS-corrected CT data, to create a 2D panoramic radiograph-like image, is a modification of [16]. Specifically the algorithm was modified in two ways. Firstly, the manner in which a mask of the dental arch is specified has been changed. The user is now required to manually draw a rectangular mask enclosing the dental arch area (determined using a maximum intensity projection). The jaw mask is then determined automatically using a coarse threshold followed by an alternating sequential filter using disk-shaped structuring elements of increasing size (radius from 1 to 10 pixels). Secondly, the points along the medial axis are uniformly sampled to minimize the magnification artifacts.

An example of an unwrapped image created using this algorithm is shown in Figure 2.

Figure 2: Panoramic radiograph-like image obtained by unwrapping the CT data.

D. *Tooth segmentation*

The method implemented in the DIS for segmenting the individual teeth, in either a digitized bitewing radiograph or a radiograph-like image obtained by unwrapping the CT data, comprises four main steps: adaptive thresholding, tooth isolation, tooth contour extraction, and interactive correction.

In the first step, the original image is adaptively thresholded to separate the dental structures from the background.

In the second step, the horizontal/vertical projection method proposed by Chen and Jain [13] is applied to isolate each tooth in its own region-of-interest (ROI). The method involves summing pixel intensities along each row to produce a 1D projection on the vertical axis. The lowest regional minimum in the projection locates the line of separation between the upper and lower jaws. Similarly, the 1D projection vertically through the image reveals the location of the gaps between the neighboring teeth. In this way the image is partitioned into quadrilateral ROIs, each containing a tooth.

In the third step, the *active contours without edges* method of Chen and Vese [18] is applied to each ROI to obtain the contour of the tooth contained therein. The advantage of this method over classical active contour models is that the stopping term does not depend on the gradient image. It is therefore well-suited to segmenting objects with poorly defined edges. Each ROI is deemed to contain two regions: foreground (the tooth) and background. This model drives the evolution of the contour and is minimized when the contour divides the image in such a way that the difference between the mean intensity inside and outside the contour is maximized.

Finally, in the fourth step the individual tooth contours can be manually corrected. This is necessary because although the method of step 3 copes well with poor quality images, in some dental images parts of adjacent teeth may be erroneously included in the segmentation.

E. *Image matching*

The method implemented in the DIS for matching an AM bitewing radiograph (source image) in the database to the unwrapped CT image (target image) is based on contour matching rather than feature—e.g. crown height or the width of the tooth at the cemento-enamel junction—matching. The reason for this is that, in general, tooth contours can be reliably extracted in both image types.

A bitewing radiograph is typically used to investigate the posterior teeth for dental caries. Up to five teeth may be seen in both the upper and lower jaw: 3 molar teeth and 2 premolars. However the teeth at the left and right sides of the radiograph are usually only partially visible. For this reason the matching algorithm ignores the left and right (possibly partial) tooth contours leaving two or three complete tooth contours (assuming no teeth are missing) in both the upper and lower jaw. The algorithm seeks to match the upper jaw teeth and the lower jaw teeth separately. It attempts to match the source tooth contours to the target at two different tooth positions on the left and two different positions on the right (because the bitewing radiograph may have been acquired from either the left- or right-hand side). For example, if three complete lower jaw teeth can be seen in the source bitewing radiograph then there are four possible locations in the source image that they may match as shown in Figure 3.

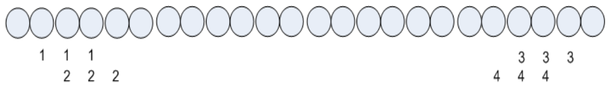


Figure 3: Four possible matching positions in the target image when the source bitewing image contains three complete teeth.

Contour alignment

For a candidate matching position, the source contours need to be aligned spatially with the target contours. To do this, a point-wise correspondence between the left-most complete tooth contour in the source and the complete tooth contour at the candidate position in the target is computed. More specifically, each point on the source contour is mapped to the nearest point (Euclidean distance) on the target contour. These point correspondences are then used to estimate the affine transformation needed to align the source to the target. The transformation is then applied to the group of source contours as a whole.

Contour matching/comparison

Progressing from left to right, the similarity between corresponding pairs of tooth contours is computed. More specifically, each point on the source tooth contour is mapped to the nearest point (Euclidean distance) on the target tooth contour. The average distance between the corresponding pairs of points then yields a measure of similarity between the contours. These similarity measures are tabulated in two rows of a $2n \times 10$ matrix where n is the number of AM images in the database. The first row holds measures for the first candidate matching positions on both the left and right (1 and 3 in Figure 3) for the upper jaw and the left and right for the lower jaw. The second row holds measures for the second candidate matching positions.

Image matching

For each column of the similarity matrix, the mean and standard deviation is computed, and each element that lies within a prescribed number of standard deviations of the mean is flagged. The number of flags per row is then computed. The row with the maximum flag count is considered to be the best match. If there are several candidate best rows, then the similarity values are summed for each and used to rank them in ascending order.

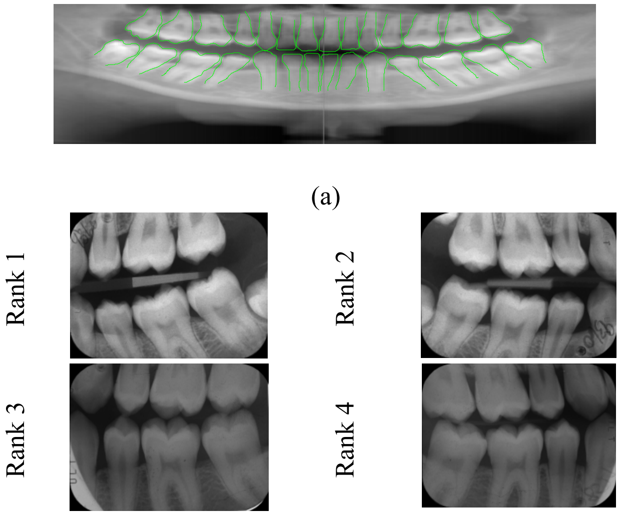
III. EXPERIMENT AND RESULTS

The DIS was evaluated using four dental CT data sets (from four different subjects) and 32 bitewing images (from 12 different subjects including the four from which the CT data was acquired). The data were obtained from routine clinical dental examinations performed by staff at Queensland Diagnostic Imaging (QDI). The study was approved by the Human Research Ethics Committee of the University of Queensland.

Each bitewing image was enrolled in the DIS. For each CT data set in turn, the DIS was queried to find the best match/matches (using a prescribed standard deviation of 2). The results are shown in Table 1. They show that for all four CT data sets at least one of the corresponding bitewing radiographs was correctly identified within the top 4 matches. In fact all of the bitewing images belonging to these CT data sets were correctly identified within the top ten ranked matches (not shown). Figure 4 shows the matching results for CT data set 1.

Table 1: Matching results.

CT data set	Corresponding bitewing radiographs	Matched bitewing radiographs	Highest rank
1	2	2	1
2	2	2	1
3	2	2	2
4	6	3	4



(a)

(b)

Figure 4: Top 4 matches for CT data set 1 (a) Unwrapped CT image, (b) Matching bitewing radiographs (rank 1 and 2 are the correct matches).

IV. DISCUSSION AND CONCLUSION

In this paper we presented a novel dental identification system based on matching unwrapped CT data (of unknown identity) to digitized bitewing images (of known identity). The system incorporates a new method for metal artifact reduction (MARSS) as well as purpose-designed algorithms for teeth segmentation and image matching. The matching methodology has been designed to permit the matching of AM and PM images in which one or more teeth may be missing. Our results, based on a limited data set of 4 clinical CT data sets and 32 bitewing radiographs) demonstrate the efficacy of the CT-based approach to computer-assisted dental matching. The identity of each of the CT data sets could be established on the basis of the top 4 matches. We are presently gathering more data, including 30 PM CT data sets and associated AM radiographs, to better evaluate the system and to incorporate matching based on periapical films.

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