Using Search Algorithms for Automating Alignment of Radiographs for Subtraction Radiography

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Subtractions of serial radiographic images of unchanged structures should in theory be uniformly grey. In practice, one observes in such subtractions varying sized and shaped aggregates of pixels which are lighter or darker than the remainder of the pixels in the subtraction image. Such aggregates are called structured noise and could be misinterpreted to represent anatomical change. The appearance of structured noise in a subtraction image may occur when there is lack of correspondence between the two images for a single or combination of reasons: non- uniformity in film processing producing differences in film contrast ; variation in film position and/or discrepancy in projection geometry of x-ray beam to anatomical structures of interest; misalignment of radiographic images wheng enerating the subtraction image; or different "best-appearing"alignments of images with discrepant geometry.

Even though the best presently available techniques for obtaining standardized radiographs for subtraction are utilized, there may still be pairs of radiographs with significant geometric discrepancy. This results in a problem more difficult to correct and/or manage. For such images there is no perfect alignment. Utilization of different reference areas for alignment, local or global could result in different alignments and consequent differences in the quality and/or quantity of structured noise. Even theuse of the same manual alignment procedure used repeatedly by the same aligner may produce different alignments on repeated attempts. An automated alignment procedure would enable one to achieve a reproducible alignment for pairs of radiographs with imperfect geometry.

Radiographs which served as the basis for digital subtraction images were taken at 32 alveolar crestal sites on 16 dried human skulls. The radio-graphs used represented an anterior and posterior mix of maxillary and mandibular crestal sites with 1/4 inch or 1 inch thickness of simulated soft tissue covering the range of cheek thickness anticipated in a group of adult subjects. A pair of x-rays was taken at each designated site. The angle difference between the pairs was experimentally controlled to be 2 degrees in the vertical direction. The x-rays were taken by placing a skull in a holding device, which is fixed to a sleeve in which the x-ray collimator fits. The 2 degree vertical angle discrepancy of the x-ray beam between two radiographs was obtained by moving the skull in the holding device relative to the fixed x-ray collimator in a vertical direction. The film was maintained at right-angles to the beam. This produces changes similar to those observed in clinical serial radiographs.

Subtraction images were obtained from 32 pairs of radiographs. Two sets of subtraction images were created. For one set, the pairs were manually aligned and for the other set, the pairs were automatically aligned utilizing the algorithm presented in this paper. Alignment was done using a locally defined procedure. A window was outlined with a cursor just apical to the crestal area of interest on the subtraction image. This window includes the subcrestal alveolar bone and the interface between the tooth root and the bone. For a given pair of radiographic images, the same window was used to achieve the desired alignment for manual and automatic alignment method. For the purpose of manual alignment, the aim was to minimize the range of gray levels in the window by subjective assessment.

The algorithm used in this study addressed the problem of fine alignment.The task of the automated alignment procedure was to shift (both vertically and horizontally) and rotate one of the images

so that the anatomical structures within the window of interest are aligned as well as possible with those of the other image. The amount of shift was limited to a translation of ± 20 pixels and a rotation of ± 5 degrees, made in 0.2 degree increments. The criterion for evaluating the quality of the match was the edges of difference (EOD), which is determined as the best method after evaluating several other methods. The position which produced the minimum edges of differences was considered the best alignment.

To evaluate the best alignment position we needed to search all the possible18,491 (41 vertical translations x 41 horizontal translations x 11 rotational translations) image positions which takes about 15 hrs. when we used a sun4/160 work station. Rather than exhaustively search all possible image positions, the algorithm proceeded in 2 stages. The coarse alignment was done on 1/4 scale images, searching ± 5 pixels and ± 5 degrees at 1 degree increments requiring 1331 (11x11x11) evaluations. Fine alignment was thencarried out in a search space of pm 5 pixels and ± 1 degree at 0.2 degree increments. This required another 1331 (11x11x11) evaluations, giving an effective rate of 2662 evaluations per image pair which consumes only 3 hrs.of calculation time.

In this case we have used the downhill simplex method. After giving three randomly selected shift positions, this method automatically converges the results to a minimum value point. In this particular situation we could not use the simplex method directly because of the possibility of converging to a local maxima instead of the true solution. Once a solution is achieved,another starting point was randomly selected (which is ± 1 pixel and ± 1 degree shifted from the solution) and the process is repeated until we achieve the same results three times in a row. This method gives the results in less than 45 minutes and has the same accuracy as the method 1.

For 24 observers the preference for automated alignment ranged from 19% to 91% of 32 observations. For the 32 subtraction pairs the preference for automated alignment ranged from 12% to 87% of 24 observations. The mean percentage of preference for the automatically aligned images for 24% observers was 49% with a standard error of 4%. Within 95% confidence limits it was calculated that the true mean must lie somewhere between 41% and 57%.

The results of this study indicate that automated alignment of pairs of radiographs produces subtractions which are indistinguishable in quality from subtractions aligned manually by an experienced aligner. In developing the algorithm for automated alignment, care was taken that the criteria used for establishing a window appropriate for testing the quality of alignment were the same for both alignment techniques. It should be noted that no claim is made that the algorithm corrects for the angle discrepancy between the pairs of images, but rather that it merely seeks to find the best possible alignment for a specific inter-proximal bone site.Furthermore, since at low resolution, the procedure is using the root edge as the primary feature, it did not miss the global minimum at high resolution with the given search space. Figure 3 shows the performance of the matching criteria for a typical radiograph.

This automated alignment procedure represents one step towards our present goal to completely automate this procedure. Two further steps must be automated: 1) placing completely unaligned images into approximatealignment 2) defining an alignment window for the procedure implemented in this study. This would permit identical alignment for any pair of images in different laboratories. Such uniformity of technique would allow for more effective comparison of results of digital subtractions performed in different laboratories.

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