Automatic 3D Registration of Trabecular Bone Images Using a Collection of Regional 2D Registrations

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Introduction Micro-MRI has shown potential as a modality for noninvasive assessment of trabecular bone (TB) architecture in response to drug intervention in patients with metabolic bone disorders [1]. Since the organization of the TB network is highly heterogeneous it is essential that in follow-up studies precisely the same volume is examined, which requires that the images be registered accurately in 3 dimensions. A complication is that the soft tissue adjacent to bone is not rigidly connected to the TB region of interest (ROI) (see **Fig. 1**). Thus, a successful technique must isolate and register only the ROI. Segmentation errors caused by aliasing or other artifacts can make it difficult to perform automatic registration based on the shape of the ROI and manual intervention may be required [2]. Instead, the proposed algorithm uses the local trabecular pattern near 100 randomly selected points in the ROI to register the 3D data sets. This is different from other 3D techniques which typically search the six directions of rigid body motion [3]. The algorithm assumes that the through-plane tilt is relatively small (20° or less).

Algorithm *Step 1*: The ROI is roughly determined in each of the two scans using an automatic segmentation algorithm [4]. This initial step is *not* required to be exact in order for registration to be successful.

Step 2: The slice shift between the two data sets is determined approximately (to within 5 slices out of 32 in either direction). This is done by roughly matching the ROIs (from Step 1) in each slice.

Step 3: A pixel p_0 is chosen toward the center of the ROI in the central slice of the baseline scan. The 40x40 square region, R_0, centered at p_0 is matched to a 2D patch of the same size in the follow-up scan by searching the nearest 11 slices, and stepping through XY rotation angles ranging from -30 to +30 degrees in increments of 3 degrees. The match is determined by maximizing the cross correlation between rotated versions of R_0 and 2D patches within the follow-up scan. The rotations of R_0 were implemented by applying a series of shear transformations [5]. The output of this step is a pixel q_0 in the second scan as well as a rotation angle $_0$. The accuracy of the match is tested by checking for consistency in neighboring pixels. Upon failure, Step 3 is repeated with a different central pixel.

Step 4: Ten pixels (p_1, …, p_{10}) are randomly selected within the ROI. The output of Step 3 defines a 2D transformation T_0 (a translation and a rotation) that serves as an approximation to the true 3D transformation. This 2D transformation is used to find pixels (q_1•, …, q_{10}•) in the follow-up scan which approximately correspond to the randomly chosen pixels in the baseline scan. More accurate matches (q_1, …, q_{10}) are then found using the search procedure from Step 3, except that only a small neighborhood of each q_j• needs to be searched, and only a few rotation angles near $_0$ need to be implemented. At this point, a more accurate 3D transformation T_1 can be obtained by minimizing the sum of the squared distances between the T_1p_j and the q_j.

Step 5: Same as Step 4, except one hundred random pixels (p_{11}, …, p_{110}) are selected, and the transformation T_1 from Step 4 is used to find rough matches (q_{11}•, …, q_{110}•). This time only a very small neighborhood of each q_j• needs to be searched. The final 3D transformation T is selected to minimize the sum of the squared distances as in Step 4.

Methods The wrists of nine subjects were scanned twice within an interval of 1-3 months as part of a clinical study. Images were acquired with a 3D FLASE pulse sequence [6] on a 1.5 T scanner (GE Signa™). The voxel size was 137x137x410 μm^3 for 32 slices in a scan time of 12.5 minutes. The axial 3D slab was prescribed using the distal cortical endplate of the radius as a landmark.

The automatic 3D registration algorithm described above was applied to each pair of scans. Each follow-up scan was evaluated on a dense grid (using *sinc* interpolation) and then resampled on the transformed grid to match the baseline scan. The baseline scan was visually compared with the resampled follow-up scan in order to assess the accuracy of the registration transformation.

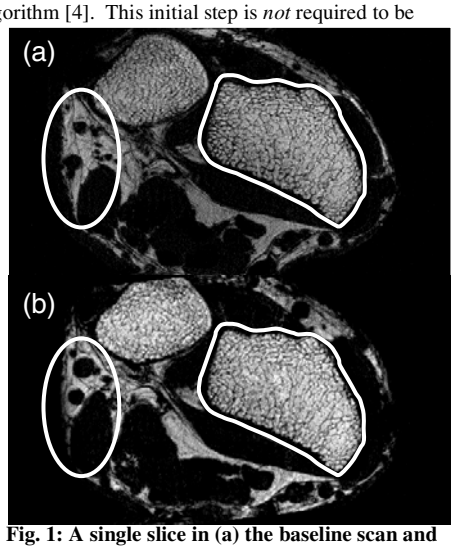

Fig. 1: A single slice in (a) the baseline scan and (b) the 3D resampled follow-up scan. The outlined TB regions have matching trabecular patterns suggesting that the 3D registration was successful. Outside of the TB region, the anatomy does not match (see the circled regions on the left), reflecting the fact that the wrist is not a rigid structure. Thus any rigid global registration technique would likely fail.

Results and Conclusions Each scan was registered successfully within 30 seconds on a Pentium IV, 3.06 GHz CPU. The through-plane tilt ranged between 1 and 10 degrees. The fit was accurate to within a pixel for most of the randomly chosen data points (see **Fig. 2**). **Fig. 1** shows the non-rigid structure of the surrounding anatomy, reflecting the importance of using a regional registration technique. **Fig. 3** illustrates the importance of correcting for through-plane tilt.

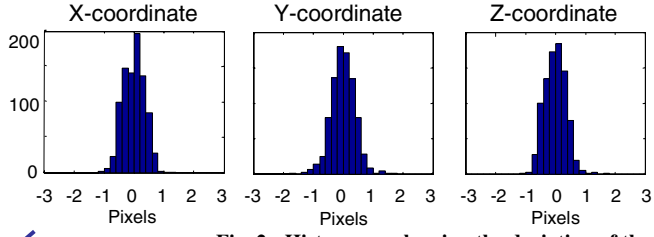

Fig. 2: Histograms showing the deviation of the 3D transformations in fitting the x-, y-, and z-coordinates of the 900 randomly chosen points (100 points for each of the 9 subjects). Most of the data lies within a half pixel, suggesting sub-pixel accuracy of the fit. An additional 29 points are not shown in the histograms because they are off by more than 3 pixels (these points were regarded as outliers, and were not used to determine the 3D transformations).

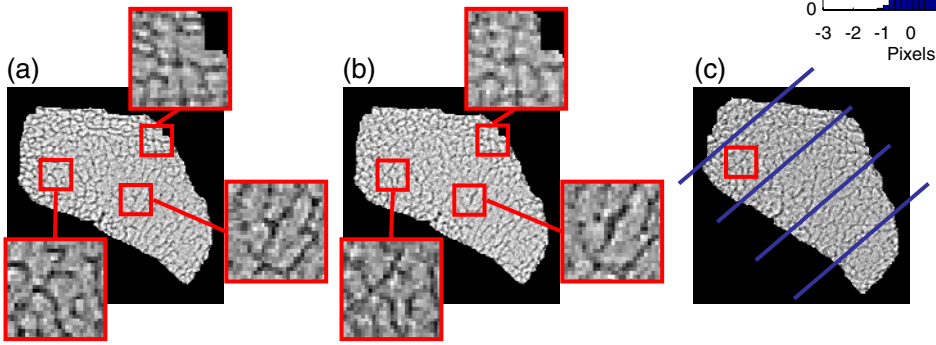

Fig. 3: Single masked slice in (a) the baseline scan, (b) the 3D resampled follow-up scan and (c) the follow-up scan before resampling. The magnified squares in (a) and (b) show the matching trabecular patterns throughout the bone. In the unregistered image (c), only a portion of the bone can be matched to the base scan. This is due to tilting in the slice direction (5 degrees in this case). The diagonal lines in (c) show where the corresponding slices in the base scan would begin and end. The spacing of these lines reflects the severity of the tilt deviation.

References:

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