AN AUTOMATED INTENSITY CORRECTION, REGISTRATION AND VOLUME STITCHING ALGORITHM FOR RECONSTRUCTION OF THE WHOLE SPINE FROM 7 TESLA MR DATA

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INTRODUCTION: Initial feasibility studies have shown the promise of 7T MRI for studying spine disorders. In particular, Vossen *et al.* [1] have developed a setup that enables imaging of the whole spine within clinically acceptable times. However, diagnosis based on such data is compromised by the presence of high intensity inhomogeneities and the need to analyze several separately acquired image stacks. In addition, the bed position in most 7T scanners does not have the standard clinical automatic displacement measurement, leading to positional uncertainties. In practice, both intensity inhomogeneity correction and volume stitching must be performed manually [1]. Here we present our novel algorithm for reconstructing a whole spine volume from a set of image stacks acquired on a 7T MR scanner. Our method consists of a number of consecutive image processing steps: 1) intensity inhomogeneity correction; 2) geometric transformation and cropping; 3) image registration; 4) volume stitching. To our knowledge, this work is the first to address the problem of reconstructing the whole spine volume from 7T MR data.

METHODS: In total 18 whole-spine data sets were acquired for this study on a commercial human whole-body 7T MR system (Philips Achieva, Philips Healthcare, Best, the Netherlands) according to the protocol described in [1].

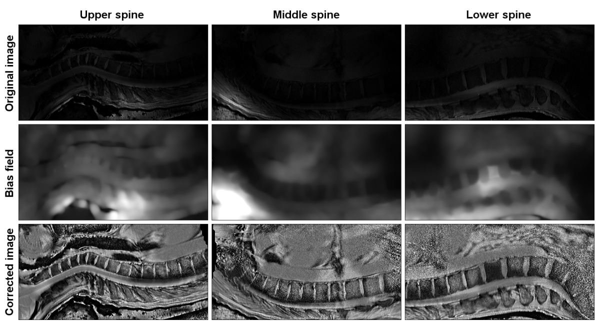

Fig. 1. Results of applying our intensity inhomogeneity correction algorithm. For one data set acquired in three stations (upper-, middle-, and lower-spine) the original image (top), the calculated bias field (middle), and the corresponding corrected image (bottom) are shown. One slice from the 3D image stack is shown in each case.

Intensity inhomogeneity correction is typically applied in order to remove both system-specific and patient-induced image artifacts. The main requirement for an efficient algorithm for bias correction in 7T whole-spine MR data is that it has to be capable of correcting rapidly varying intensity inhomogeneity while preserving fine details. In this work, we use the coherent local intensity clustering (CLIC) algorithm recently developed by Li *et al.* [2] for analyzing neuro MR image data. This method estimates the bias field by modeling the imaged object by a finite number of tissue classes, each of them ideally appearing having a fixed image intensity. Due to the intrinsic spatial smoothness of the bias fields estimated by such method, it is able to produce realistic results even for severe cases of intensity inhomogeneity. A sample result after applying the bias correction method, as illustrated in Figure 1, clearly shows that intensity distributions within each stack as well as between the different stacks become much more homogeneous.

Next, each image stack is transformed to patient coordinates to ensure that all the stacks have the same orientation. Since the displacement of each stack with respect to its predecessor is unknown, this coordinate transformation reduces to a three-dimensional rotation of each stack in accordance to the angulation information recorded by the scanner. Each stack is additionally cropped in order to remove the unsampled areas appearing either as a consequence of the applied coordinate transformation or due to the reconstruction filters.

The restoration of the correct position of each station with respect to its predecessor is equivalent to registering two image stacks to each other. For this type of data, the image gradient is the most complete and reliable source of information. The MR image has high contrast between different soft tissues, which, together with the presence of multiple well-defined interfaces in the whole-spine MR data (skin surface, boundaries of vertebrae and spinal cord, etc.), makes the gradient the primary information source for performing image registration. A gradient-correlation-based scheme was recently developed by Tzimiropoulos *et al*. [3] and shown to outperform traditional correlation methods on various 2D images. In this work, we extended their algorithm to 3D for detecting the most likely translation between any two image stacks, and developed a scheme for assigning a reliable quantitative measure to the estimated translation. Our method consists of two main steps: 1) finding the most probable translation between two arbitrary image stacks, and 2) recovering the correct sequence of the acquired sub-volumes (upper-, middle-, and lower spine).

Stitching the separate image stacks into a composite volume reduces in practice to finding the best way to combine each pair of overlapping images in order to obtain a seamless natural transition between the two. In this work, we used the multi-resolution approach of Burt and Adelson [4]. Initially, the bounding rectangle of the composite image is calculated based on the known sizes and displacements of each image stack. Next, the stacks are placed at their final locations. Finally, the average images within each of the overlap areas are calculated. Figure 2 shows the stacks placed at their correct location with the overlapping neighboring stacks and the final result for one of the data sets.

For validation of our registration method, we created a ground truth by manually segmenting the same structure (vertebra) in each pair of the co-registered images. For each pair of overlapping image stacks, we selected one vertebra that lies in the overlap area. Next, each selected vertebra was manually segmented in both overlapping images, resulting in 30 pairs of 3D image stacks containing binary masks of the outlined regions. Finally, the distance between the centers of the two segmented regions was calculated and used as a quantitative measure of the performance of our image registration algorithm.

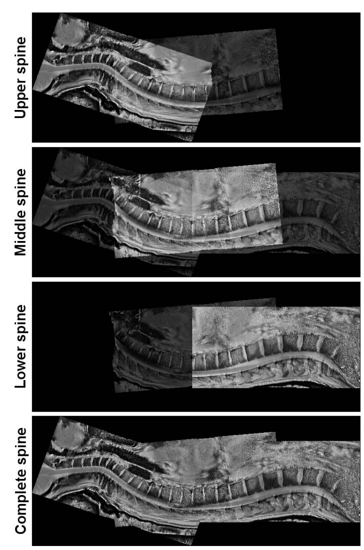

Fig. 2. Sample performance of our volume stitching algorithm. One slice from the correctly positioned upper-, middle-, and lower-spine parts and from the complete reconstructed volume is shown. Also the adjacent parts of the spine are shown (shaded areas).

RESULTS AND CONCLUSIONS: The results of the described validation analysis are summarized in Table 1 in both millimeters and number of pixels (obtained by dividing the corresponding measure in millimeters by the in-plane distance between two neighboring pixels). In all 30 cases our algorithm was able to produce high-quality registration of the two sub-volumes. The mean error value (distance between the two centers) is found to be 0.53 mm and the corresponding value in pixels is less than unity and equals 0.89, which confirms high accuracy of the restoration of the inter-scan bed translations. Thus, our method can fully substitute human interaction in performing recovery of the whole-spine 7T MRI volumes, which will result in better visual inspection of such data and facilitate its further analysis and diagnosis.

Table 1. Summary of the Results of the Registration Performance of our Algorithm.

Error	Mean	Std	Min	Max
Millimeters	0.53	0.31	0.04	1.42
Pixels	0.89	0.57	0.06	2.79

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REFERENCES: [1] Vossen et al. *J.Magn.Reson.,* 208:291-297 (2011); [2] Li et al, *IPMI 2009,* 5636:288-299; [3] Tzimiropoulos et al. *IEEE TPAMI,* 32:**1899**-1906 (2010); [4] Burt and Adelson. *ACM Trans.Graphics,* 2:217-236 (1983).