

COMBINED SEGMENTATION AND SEQUENTIAL REGISTRATION METHOD FOR ARTIFACT REMOVAL IN ADC MAPS IN LIVER

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Introduction: It is known that bulk motion artifacts adversely impact the reproducible measurement of ADCs in the liver¹. In this work, we present a combined registration and segmentation approach to align multiple b-value DWI sequences to compute artifact free ADC mapping with more repeatable measurements compared to using either no registration or simultaneous affine registration between all sequences.

Materials and Methods: 14 patients imaged between (September 2011 and September 2013) were analyzed retrospectively under an institutional review board approved retrospective waiver compliant with the Health Insurance Portability and Accountability Act. All patients were imaged using breath-hold fat suppressed DWI using 3.0T GE MR 750 scanners with the following b-values: 0, 50, 250, 300, and 500 s/mm². An experienced radiologist identified the tumors of interest on one of the DWI or related anatomical images.

Method: Our approach combines segmentation of structures of interest with a sequential registration using a three-step procedure. First, a user selects a reference image and places a set of strokes to identify structures of interest as shown in Fig.1 (a) from which an automatic segmentation of those structures is obtained using an interactive segmentation method². Second, the remaining b-value images are registered to the reference, and the corresponding structures are segmented in the aligned images. The individual images are registered using affine transform and Mattes mutual information metric. Third, the closest image to a given reference is determined using the modified Hausdroff distance between the contours of the segmented structures in the reference and those in the aligned images. The closest image is then designated as the new reference and the afore-mentioned procedure is repeated until all the b-valued images are aligned to the initial reference image. Our registration approach is not adversely impacted by large differences in the intensities between the diffusion images of different b values, removing the need for careful fine-tuning of the registration parameters. Second, the approach focuses the registration to structures of interest thereby, removing any artifacts around those structures.

Results and Discussions: We analyzed the efficacy of our approach on tumors selected from the 14 patients and compared the results to 1) no registration and 2) simultaneous registration of all sequences. Fig.1 shows some examples of artifact (dark boundaries on the edge of structures of interest) appearing in the ADC map with no registration Fig.1(b) which are reduced the most using our sequential registration approach Fig.1(d). We also analyzed the variability in the computation of mean ADC values inside the tumors by artificially introducing random motion between the different DWI images. Table 1 shows the mean ADC values computed from the volumetrically segmented tumors and the computed standard deviation over 5 different trials. Motion was randomly simulated in DWI images in four out of five trials. The first trial corresponded to the baseline images with associated intrinsic motion or distortion. As shown, our sequential registration approach shows the lowest standard deviations in the computed ADC 11 out of 14 patients.

Conclusions: Sequential registration guided by segmentation of structures of interest reduces artifacts and obtains repeatable ADC measurements.

References: 1. Mazaheri et.al Acad Radiol 2012; 19:1573-1580 2. Vezhnevets, Graphicon, 150–156, 2005

	No registration	Affine Registration	Sequential Registration
1	1.56(0.007)	1.55(0.01)	1.56(0.005)
2	1.20(0.17)	1.26(0.09)	1.29(0.08)
3	1.40(0.21)	1.35(0.22)	1.40(0.10)
4	1.40(0.06)	1.31(0.08)	1.35(0.03)
5	1.56(0.11)	1.70(0.05)	1.67(0.05)
6	2.12(0.47)	2.30(0.09)	2.35(0.09)
7	2.30(0.06)	2.37(0.05)	2.38(0.04)
8	0.85(0.11)	0.80(0.01)	0.81(0.01)
9	1.05(0.15)	1.09(0.11)	1.13(0.06)
10	1.12(0.10)	1.14(0.08)	1.09(0.06)
11	1.60(0.40)	1.39(0.17)	1.36(0.09)
12	1.81(0.13)	1.84(0.13)	1.86(0.10)
13	1.61(0.40)	1.39(0.17)	1.36(0.09)
14	1.80(0.13)	1.84(0.13)	1.86(0.11)

Table 1. Mean ADC values (standard deviation) computed inside tumor volumes over 5 different trials with introduced motion for 14 patients.

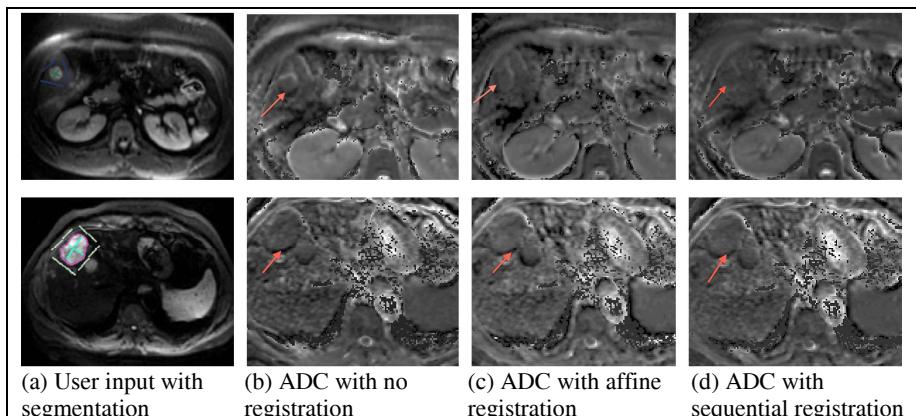


Fig.1 Comparison of the ADC computation using no registration, affine registration of all sequences, and sequential registration with segmentation for two different patients. Regions with artifacts are indicated with an arrow in (b) and the corresponding regions are highlighted in (c) and (d). As seen, the artifacts progressively disappear using simultaneous registration and more so with sequential registration.