Segmented total disease volume and associated apparent diffusion coefficient on whole body diffusion-weighted MRI show good interobserver agreement

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Introduction: Studies conducted using the whole body DWI (WBDWI) technique have shown high sensitivity for detecting bone marrow and soft tissue diseases, and high diagnostic accuracy for disease staging. As the background signal is relatively suppressed compared with diseased tissue on WBDWI, it is possible to apply segmentation techniques to obtain DWI based volumes of disease throughout the body [1]. From this segmented disease volume, it is not difficult to derive the global mean or median apparent diffusion coefficient (ADC) in the diseased areas. Initial work has shown this to be feasible, which can be applied to evaluate treatment response. The ability to derive two quantitative imaging biomarkers: disease volume and ADC from a single radiological examination is highly attractive. This may prove to be of particular value for the evaluation of metastatic bone disease, for which current assessment using morphological imaging is unreliable. However, it is not yet clear how variable diffusion volume segmentation and global tumour ADC estimation is between observers. Knowledge of intra-observer variability is critical for the wider adoption of the technique for disease evaluation.

Purpose: The aim of this study is to determine the interobserver variability of diffusion volume and global ADC estimation of total disease burden in patients with metastatic bone disease.

Materials and Methods: \textit{Study population} 10 patients with metastatic bone and soft tissue disease from cancers of the prostate (n = 6), breast (n = 3) and ovary (n = 1) underwent WBDWI. MR Imaging Axial, fat-suppressed, free-breathing EPI DWI was performed on a 1.5T MR system (Siemens Avanto, Erlangen, Germany) from skull vertex to mid-thigh in each patient (TR = 14000ms, TE = 67ms, matrix size 128x104x150, 430 cm field of view, slice thickness 5mm, receiver bandwidth 1628 Hz/pixel, STIR fat suppression, 6 signal averages, b-values 50 and 800 s/mm\(^2\)). ADC maps for all stations were generated covering each voxel location using a monoexponential model for the two b-value data. Image analysis Images were reviewed by two independent radiologists with 7 and 3 years experience in body DWI respectively. Analysis was performed offline on a workstation using self-scripted software in IDL (Exelis inc.) in the presence of a clinical scientist. Image Segmentation Each reader applied the computed DWI [2, 3] technique to maximize lesion conspicuity and background signal suppression. Once a threshold is selected, a Markov random field (MRF) model is applied such that the MRF posterior is maximized using the iterated conditional modes algorithm [1]. The estimated total disease diffusion volume (DV), global mean ADC value (ADCmean) and global median ADC (ADCmedian) value were recorded in each patient for each observer. Statistical and data analysis The intraclass correlation coefficient (ICC) of DV, ADCmean and ADCmedian was determined for the readers and reported with the 95% confidence intervals. Selected frequency density functions of ADCmean and ADCmedian are presented.

Results: Diffusion Volume The natural logarithms of diffusion volume segmented by Readers 1 and 2 are presented in Figure 1e. The ICC was 0.93 (95% CI: 0.75 – 0.98), suggesting a good agreement between readers. ADCmean and ADCmedian The global ADCmean determined by Readers 1 and 2 are displayed in Figure 1d. The ICC was 0.77 (95% CI: 0.34 – 0.93). For the global ADCmedian the ICC was 0.89 (95% CI: 0.58 – 0.97). There was generally good agreement in the selected frequency density plots between the two readers (Figure 1a-b).

Discussion: In this study, we found excellent interobserver agreement (ICC 0.93) for diffusion volume segmentation based on our described methodology, suggesting that the technique could be adopted in future studies for estimating total body disease burden in patients with cancers. In addition, there was good interobserver agreement for the global ADCmean (ICC 0.77) and ADCmedian (ICC 0.89) from the segmented disease volume. The interobserver agreement was better for ADCmedian, suggesting that ADCmedian is likely to be more robust as a central tendency value across a large number of imaging voxels throughout the body. We are currently evaluating the intraobserver variability of the technique.

Conclusions: Whole body diffusion volumes and global ADCmedian values of disease have very good interobserver agreement. These metrics appear robust for wider application in clinical research.