Evaluation of Motion Corruption on Image Quality in Micro MRI of Trabecular Bone: Impact on Structural Parameters

Y. A. Bhagat[1], M. J. Wald[1], C. S. Rajapakse[1], H. Saligheh Rad[1], J. F. Magland[1], M. B. Leonard[2], and F. W. Wehrli[1]

[1]Laboratory for Structural NMR Imaging, Radiology, University of Pennsylvania, Philadelphia, PA, United States, [2]Nephrology, Children's Hospital of Philadelphia, Philadelphia, PA, United States

INTRODUCTION: Given the lengthy scan times (~10-17 minutes), motion corruption is a significant source of error in high resolution magnetic resonance imaging of trabecular bone (TB) [1], as it leads to blurring of the TB microstructure and results in a loss of sensitivity and reproducibility of the structural parameters [2]. Sub-millimeter in–plane translational motion can be effectively detected using navigator-projections and subsequently corrected in the high resolution images [3]. To address the level of motion corruption acceptable for *in vivo* scans and establish a standard of optimized image quality in our clinical studies, a comprehensive image rating scheme employing a group of 4 raters was developed to characterize the degree of motion corruption within a given scan complementing other image quality metrics like signal-to-noise ratio (SNR) and the level of artifacts. We aimed to evaluate the robustness of the image evaluation with respect to translational motion corruption by applying several translational motion trajectories to a relatively motion-free high quality TB image. The mean scores (from 4 raters) for the level of motion corruption were compared to an objective image sharpness criterion chosen as the normalized gradient squared (NGS), and quantitative parameters of the TB microstructure. We hypothesized that the motion scores for images degraded by variable extents of *in vivo* and simulated motion would correlate with the computed NGS values [4]. Furthermore, this would permit us to establish a relationship between the motion scores and TB structural parameters in a manner so as to designate a cutoff score for motion beyond which the reliability of the structural parameters comes into question.

METHODS: A high quality 3D fast large angle spin echo (FLASE) [5] image (SNR = 12.7, **Figure 1A**) obtained at 1.5T (Siemens Sonata, Erlangen, Germany) with a voxel size of 137 x 137 x 410 μm^3, serving as a reference. This image was subjected to 14 x- and y- translational motion trajectories: 9 simulated trajectories that model abrupt patient movements and 5 *in vivo* trajectories derived from retrospective analysis of patient scans. Each point within an input motion trajectory (460 total points for each y- phase encoding in the FLASE acquisition) represented the average shift for a given 2 second period during a scan. The x- and y- shifts were applied as phase factors to the k-space data of the "high quality" scan resulting in motion-corrupted images upon Fourier transformation. Each motion-corrupted image was then independently rated by four experienced raters on a scale of 1-4 for the level of motion corruption (1: optimal, 2: slight blurring, 3: significant blurring and 4: severe blurring). Additionally, the NGS was computed for each image followed by masking of the TB region and virtual bone biopsy processing [6] to quantify the effect of the motion on the topological parameters such as bone volume fraction (BVF, bone volume/total volume), surface-to-curve (S/C) ratio, a measure of the ratio of plates to rods in the analyzed volume. Fleiss' κ coefficient test [7] was used to measure the inter-rater agreement from the image evaluations. The κ coefficient is the ratio between the observed and expected frequencies and ranges from -1 (no agreement) to 1 (perfect agreement).

RESULTS AND CONCLUSIONS: A κ coefficient value of 0.31 was obtained from the evaluation of the level of motion corruption in the images, signifying fair agreement between the 4 raters [7]. **Figure 1** shows 3D FLASE distal tibia images from a 43-year-old normal female. The uncorrupted image was graded by a mean score of 1.0 for motion. The native translational x- (blue) and y- (blue) motion trajectories are displayed below the NGS value of the image. Increases in translational motion along x and y yielded consistently higher motion quality scores and lower NGS values that were associated with not only the degree of motion corruption applied to the image, but also the k-space interval during which the shifts were introduced (**Figure 1** B, C). **Figure 2** displays a plot of the mean motion scores versus the NGS values for all 15 cases evaluated in the study. Higher motion scores (poor) correlated negatively with the corresponding NGS values. Images corrupted using *in vivo* motion trajectories (yellow) demonstrated better motion scores and NGS values compared to images degraded with simulated motion trajectories. **Figure 3** displays a plot of the percentage changes in the TB structural parameters for two cases shown in Fig. 1 (images B and C). BVF was reduced by 8.5% and 13% for decreases in NGS of 1.1% and 3.5%, respectively relative to image A. The surface to curve (S/C) ratio demonstrated steeper declines of 21% and 39% for images B and C, respectively compared to A (**Fig. 1**), as evidenced by the increase in curve voxels and decrease in surface voxels. On average, based on the 14 cases where the level of translational motion corruption was varied, a mean motion score of 2.0 or higher yielded ~9% change in a topological parameter such as BVF.

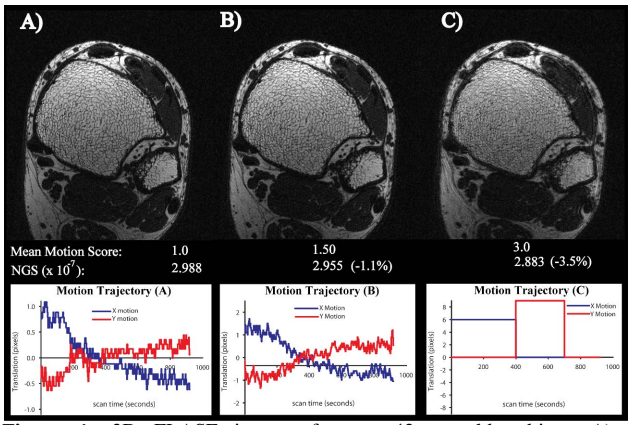

Figure 1: 3D FLASE images from a 43-year-old subject. A) Original uncorrupted image. B) The original image was subjected to an *in vivo* translational motion trajectory (1.5 to -1.25 pixels along x and -1.25 to 1.0 pixel along y shown below). This yielded a mean motion score of 1.5 with a reduction in NGS of 1.1% relative to the original image (A). C) A simulated abrupt motion trajectory of 6 pixels along x and 9 pixels along y was applied yielding a poorer motion score (3.0) and NGS value (3.5% decrease relative to A).

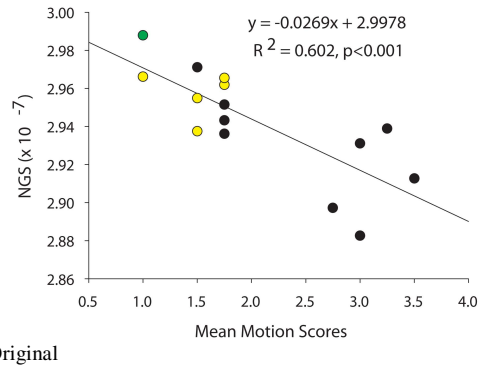

Figure 2: Mean motion scores (based on evaluations by 4 raters) versus NGS for the original image (green) and 14 images with varying levels of induced translational motion. Values from images corrupted using retrospective *in vivo* translational motion trajectories are shown in yellow.

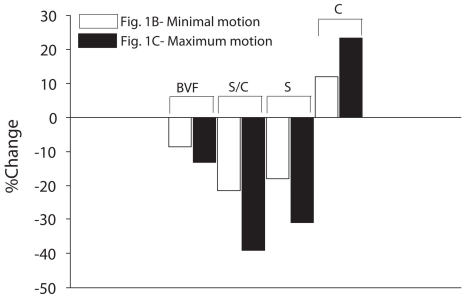

Figure 3: The percent changes in TB structural parameters for images B and C relative to A from **Fig. 1** are shown.

REFERENCES: [1] Majumdar. Top Magn Reson Imaging 13:323 (2002). [2] Gomberg *et al. Bone* 35:1 (2004), [3] Song & Wehrli. *MRM* 41:5 (1999). [4] Lin *et al. JMRI* 26:1 (2007). [5] Ma *et al. MRM* 35:903 (1996). [6] Magland and Wehrli. *Acad Radiol* (in press). [7] Landis & Koch. *Biometrics* 33:159 (1977).

ACKNOWLEDGEMENTS: NIH RO1 AR41443, RO1 AR53156, RO1 DK75648