# Translational Motion Self-Navigation in Center Out Radial Micro-MRI of Trabecular Bone 

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Introduction: While noninvasive assessment of trabecular bone (TB) architecture by MRI at selected anatomic locations has been shown to be feasible [1,2], full 3D isotropic scanning at a resolution sufficient to resolve individual trabeculae continues to be an unmet challenge. Recently, a hybrid radial variable echo time (HR-VTE) pulse sequence (shown in Figure 1) was proposed [3] as an alternative to the spin-echo based FLASE [4] pulse sequence for imaging TB. This new sequence has some important advantages when pursuing in-vivo 3D isotropic resolution. The sequence features a short echo time ( $<1 \mathrm{~ms}$ ), and therefore shares some of the advantages of spin-echo techniques, including having a high SNR efficiency and being less susceptible to off-resonance effects [5]. In addition, HR-VTE offers the following advantages over spin-echo protocols which may be particularly important when collecting isotropic data at field strengths above 1.5T: (a) lower power deposition (small flipangle excitation); (b) no stimulated echo artifacts caused by imperfect refocusing pulses (particularly important for high z-resolution imaging); (c) improved motion correction (via subaperture image registration); and (d) shorter TR enabling the acquisition of more slices within the same scan time.

With scan times on the order of 10-15 minutes and a voxel size of 100-300 microns, micro-MRI TB protocols are sensitive to even very slight (submillimeter) patient motion [6]. It is well known that, in a PR sequence, rigid in-plane translational motion can be corrected by aligning the center-of-mass of each 1D projection to the center of the field of view. However (as explained below) this technique is theoretically imperfect when only half of 1D k-space is acquired within each view, which is the case in HR-VTE. Here we propose an alternative to the center-of-mass correction technique that uses only two acquired data points per view (one on either side of the $\mathrm{k}=0$ sample) to perform the translational motion correction. The technique requires an interleaved view ordering (such as the golden angle step [7,8]). It is robust with respect to a number of experimental factors, including spatial phase modulation, chemical shift, and phase and amplitude fluctuations during the scan.
Theory: Difficulty with center-of-mass strategy for center out acquisition schemes: The center-of-mass technique involves computing the first moment of each 1D projection. Ideally, this measurement should depend sinusoidally on the view angle, with the fit reflecting the location of the 2D center of mass of the object relative to the center of the field of view. However, if only half of 1 D k -space is acquired in each view (the case in center out radial scanning), then it is impossible to accurately reconstruct 1D projections (except in the rare case where the reconstructed image has constant phase). Consequently, there will be a systematic deviation from a sine curve (see Figure 2), potentially leading to inaccurate motion detection.
Alternative technique: As an alternative to center-of-mass we propose computing the following quantity (with units of pixels): $f(\theta)=\frac{N}{2 \pi} \arg \left(\frac{k_{+1, \theta}}{k_{-1, \theta}}\right)$
Here $\mathrm{k}_{+1,0}$ and $\mathrm{k}_{-1,0}$ are the two complex k -space measurements immediately adjacent to the central ( $\mathrm{k}=0$ ) measurement at readout angle D , and N is the number of readout data points. This simple measurement is very robust since it is inherently unaffected by phase and amplitude fluctuations in signal during the scan.

Like the first moment measurement, this quantity is an approximately sinusoidal function of D (Figure 4a) (with an exact fit as the field of view becomes much larger than the object). Translational motion can be tracked using $f(\theta)$ exactly as in the center of mass method. In order to compensate for deviations from a sine curve, the data from the entire scan is fit to a smooth curve, and translational motion is measured as small deviations from the fitted curve.

It should be noted that other similar quantities could also be used in place of equation (1) to track the motion. This particular function was chosen because of its simplicity as well as its high signal-to-error ratio.
Methods and Results: The HR-VTE pulse sequence was used to acquire in-vivo images of the distal tibia at a resolution of $150 \times 150 \times 450 \mu \mathrm{~m}^{3}$ using a 2 -element custom receive coil on a 1.5 T Siemens Sonata scanner. Scan parameters were: $\mathrm{TE}<1 \mathrm{~ms}$, $\mathrm{TR}=25 \mathrm{~ms}, 32$ slices, 1500 views, scan time $=20$ minutes (scan time will be reduced for use in clinical protocols). For the anisotropic acquisition, image quality was comparable to spin-echo acquired images with similar scan parameters. The motion correction technique described above provided a significant improvement in image sharpness at both resolutions (see Figure 3). Figure $4 b$ shows the detected X and Y motion throughout the scan in each of the two receiver channels. The plot suggests that the correction was accurate to within a half of a pixel ( $75 \mu \mathrm{~m}$ ), the slight inconsistency between the two channels could be due to rotational motion.
Conclusion: An alternative to the center-of-mass technique has been proposed for detecting in-plane translational motion for center out radial pulse sequences. The technique was applied to high resolution imaging of trabecular bone using the HR-VTE pulse sequence. The advantages of the new technique include simplicity of computation as well as practical robustness with respect to various experimental factors.


Figure 1. Hybrid radial variable echo time (HRVTE) pulse sequence.




Figure 4.
(a) $f(\theta)$ measured throughout the in-vivo scan. The black lines represent the smooth fit to this data.
(b) Translational in-plane motion throughout the scan detected using the data from (a).
Figure 3. In-vivo microMRI scan of the distal tibia before and after translational motion correction. The image was acquired using the HRVTE pulse sequence with a resolution of $150 \times 150 \times 450$ $\mu \mathrm{m}^{3}$.

1500

Figure 2. One-dimensional center of mass computed as a function of view angle in an in-vivo HR-VTE scan of the distal tibia. The deviation from the sine curve is a consequence of acquiring only half of 1D k-space in each view. A golden angle increment was used to collect 1500 views.

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