Simulations of *in vivo* 3D Structural MRI of Trabecular Bone using High Resolution µCT

C. S. Rajapakse[1], J. Magland[1], X. H. Zhang[2], X. S. Liu[2], X. E. Guo[2], and F. W. Wehrli[1]

[1]Laboratory for Structural NMR Imaging, Department of Radiology, University of Pennsylvania School of Medicine, Philadelphia, Pennsylvania, United States,
[2]Department of Biomedical Engineering, Columbia University, New York, New York, United States

Introduction Osteoporotic bone fractures are primarily initiated in regions with large fractions of trabecular bone (TB) such as the vertebrae and ends of long bones. Currently, bone densitometry, which provide information on bone mineral density in these regions, are used to predict fracture risk. However, studies have shown that prediction of bone strength can be greatly improved by including the bone's structural and mechanical properties in the analysis [1]. Recent advances in *in vivo* µMRI have led to the "virtual bone biopsy" (VBB) as a means for noninvasive assessment of TB architecture [2]. Even though resolution and signal-to-noise ratio (SNR) of these techniques are clearly inferior to those of µCT, it provides valuable information about the TB architecture. The aim of this work was to address to what extent, with appropriate processing strategies, fundamental structural properties can be recovered at in vivo resolution. To answer this question thirteen TB samples were imaged using µCT, representing the gold standard. To simulate the *in vivo* µMRI resolution, these samples were downsampled in k-space. Subsequently, 3D reconstructions of the TB architecture were made for both sets of images for comparison. TB parameters such as bone volume fraction (BVF) and surface density were also compared.

Methods Thirteen TB samples (seven femur, three lumbar and three tibia) were cored using Core Drills 102057 (Starlite Industries, Inc.) with inner diameter 5.20mm and scanned with vivaCT 40 (Scanco Medical) µCT scanner at 21x21x22µm resolution using the protocol described in [3]. The images were binarized by setting a threshold at the midpoint of the two modes. The segmentation of a gray scale image generally results in creation of elements disconnected from the main structure. These unconnected parts were removed by a clustering algorithm. The resulting images were downsampled in k-space by a factor of 6x6x18. The downsampled image resolution was 126x126x396µm, which is of the order of resolution that can be obtained from *in vivo* VBB [2]**.** These simulated, partial volume blurred, MR images, were subvoxel processed by 2x2x4 to 63x63x99µm [4] which is a standard algorithm used in the VBB to enhance apparent resolution. Figure 1 illustrates the result of VBB processing, including skeletonization which converts the image to a map consisting of surfaces and curves [2].

Results and Conclusions Figure 2 shows 3D renditions of the skeletons derived from the original µCT scans and the "*in vivo* MR" images. It is visually apparent that the images reconstructed after downsampling and subvoxel processing compare favorably with those derived from the high-resolution µCT images. BVF and other structural parameters compared well as shown by the correlations of parameters extracted from pairs of low and high-resolution images (Figure 3). It was found that the gold-standard parameters were underestimated at *in vivo* resolution. Therefore, some kind of correction factor would be needed to get the correct value of these structural parameters from images at µMRI resolution. See Figure 3.

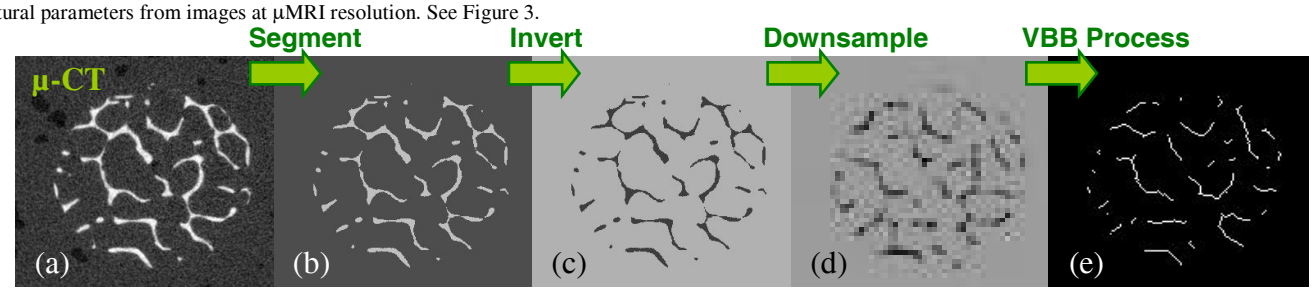

Figure 1: (a) Single slice of high-resolution (21x21x22 μm^3 voxel size) µCT image from a distal tibia specimen; (b) segmented; (c) intensity inverted to mimic MRI; (d) Fourier transform of low-pass filtered k-space data to *in vivo* resolution; (e) VBB processed skeleton map.

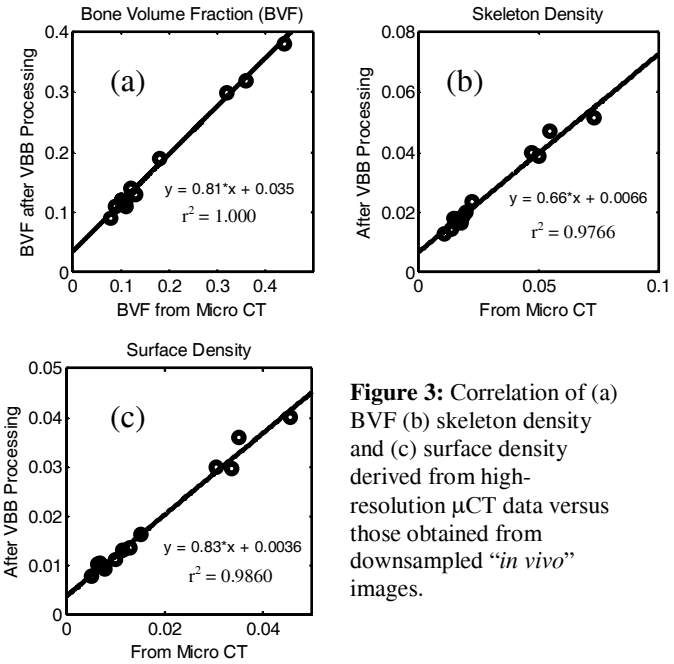

Figure 3: Correlation of (a) BVF (b) skeleton density and (c) surface density derived from high-resolution µCT data versus those obtained from downsampled "*in vivo*" images.

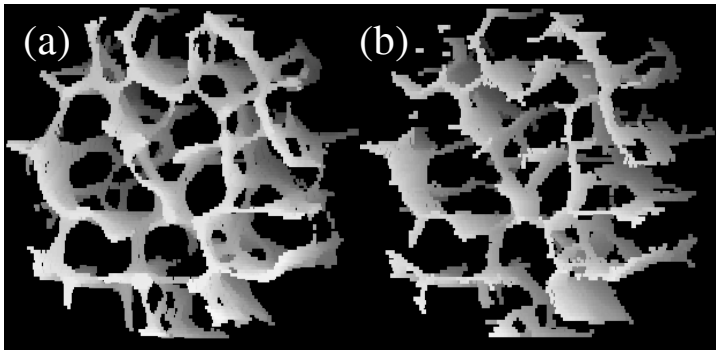

Figure 2: 3D view of TB architecture of small portion of tibia sample from (a) high-resolution µCT data and (b) after VBB processing of downsampled images.

References
[1] Müller, The Harvard Orthopedic J, 2002:2
[2] Wehrli et al., Proc IEEE, 2003:91
[3] Keaveny et al., J Biomech, 1994:27
[4] Hwang et al., Magn Reson Med, 2002:47
Aknowledgement: NIH R01 AR41443, R01 AR53156 and R01 AR49553