Computation of Structure Model Index in the Spatial Resolution Regime of *in vivo* Trabecular Bone MRI

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Background and Motivation: Trabecular bone (TB) can be regarded as a meshwork constituted by two classes of structural elements, modeled as plates and rods. The inter-linked configuration of these structural elements provides mechanical support to body at minimal weight. A common feature of osteoporotic bone loss is transformation of plates to rods [1]. One metric for quantifying TB morphology is the Structure Model Index (SMI) [2], which quantifies the relative plate- and rod-"likeness" of the TB network. The SMI has been used widely in high-resolution μCT images of specimens obtained at voxel sizes of 5-20 μm, which is far below trabecular thickness thus allowing accurate binarization of the image into bone and marrow phases by simple thresholding. In contrast, the voxel size of *in vivo* MR images is at best in the order of trabecular thickness (100-150 μm).

Here, we explore two up-sampling methods for *in vivo* MR images from which SMI can be computed. The first is sinc-interpolation, based on zero-filling k-space to decrease apparent voxel size. The second method is a method denoted "subvoxel processing", in which the image is up-sampled onto a finer grid and the signal intensities of up-sampled voxels are redistributed based on their local neighbors [3]. For both methods, SMI was calculated from the up-sampled images using various binarization thresholds. The objective of this study was to determine the relative agreement of SMI from up-sampled *in vivo* resolution MR images with the data from the gold-standard μCT images and investigate the sensitivity of the two up-sampling methods with respect to binarization thresholds.

Methods: Images from 18 trabecular bone specimens of the distal tibia obtained previously [4] by μCT and MR imaging at 1.5T at isotropic voxel sizes of 25μm^3 and 150μm^3, respectively, were processed. MR images were corrected for receive coil shading and inverted to generate bone volume fraction (BVF) maps [5] representing the fractional bone volume in each voxel. Pairs of μCT and MR BVF maps were registered to each other. Micro-CT BVF maps were binarized with a threshold value selected using Otsu's method [6] and treated as the ground-truth. Seventy-two (72) pairs of registered volumes (μCT: 216x216x216 voxels; MR: 36x36x36 voxels) were selected from these 18 specimens. MR BVF maps were up-sampled via subvoxel processing (sv-MR) and sinc-interpolation (sinc-MR) followed by binarization at threshold values ranging from 95% to 50% of BVF. Fig 1 shows the 3D renderings of the μCT, sv-MR and sinc-MR BVF map thresholded at 70% BVF of the registered subvolumes of one of the bone samples.

SMI was calculated as $6S'V/S^2$, where $S=S(r)$ is the surface area and V is the volume of TB. $S(r)$ was obtained by summing the areas of all patches with vertices generated with the marching cube algorithm [7]. $S'=(S(r+\Delta r)-S(r))/\Delta r$ and $S(r+\Delta r)$ was obtained from summing the areas of all patches with vertices moving outward along the normals from the current ones by Δr. V was obtained from the surface integral of the dot product between the area of each surface patch and its outward pointing normal using the divergence theorem of Gauss. SMI thus yields numbers ranging from 0 to 3 in which 0 and 3 correspond to ideally plate- and rod-type architectures, respectively.

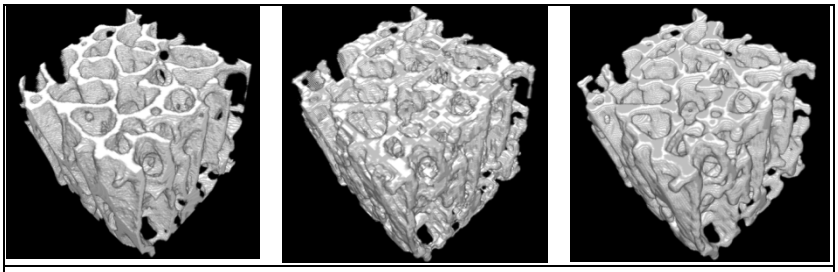

Fig 1. 3D renderings of HR-μCT (left), sv-MR thresholds at 70% BVF (middle) and sinc-MR thresholds at 70% BVF (right). The SMIs are 0.535, 0.504 and 0.662 respectively. SMI of 0 and 3 corresponds to completely plate- and rod-type structure respectively.

Results: Correlation coefficients (R) of the SMI values derived from sv-MR relative to μCT were always greater than those between sinc-MR and μCT for all threshold levels (Fig 2). Fig 3 shows the plot of SMI values calculated from sv-MR thresholded at 75% BVF threshold versus μCT, revealing a good correlation between the two datasets. Furthermore, root mean square differences (RMSD) between the SMIs calculated from sv-MR and μCT were also always lower than those from sinc-MR and μCT (Fig 4). The data therefore suggest SMI derived from subvoxel processed image to be closer to the ground truth. Both R and RMDS values of sv-MR versus μCT were found to vary less compared to sinc-MR versus μCT (sv-MR vs μCT: R 0.73 - 0.80; RMSD 0.27 - 0.35. sinc-MR vs μCT: R 0.49 - 0.73; RMSD 0.42 - 1.08). These results suggest SMIs calculated from sv-MR to be less sensitive to binarization threshold choices.

Conclusions: Subvoxel processing of *in vivo* resolution trabecular bone images provides SMI values closer to the ground truth and are less sensitive to variations in threshold settings than SMI values obtained from sinc-interpolated images. The method should enable quantification of this important topological index from *in vivo* MR images in treatment studies.

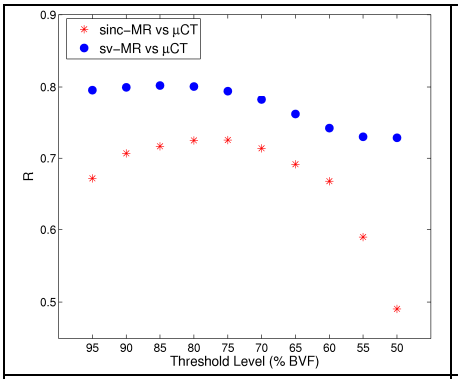

Fig 2. Correlation coefficient (R) of SMI values

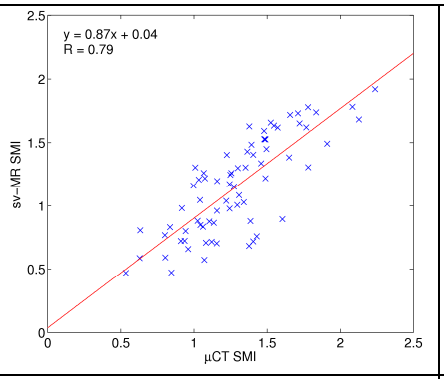

Fig 3. Correlation of SMI calculated from sv-MR at 75% BVF threshold versus μCT

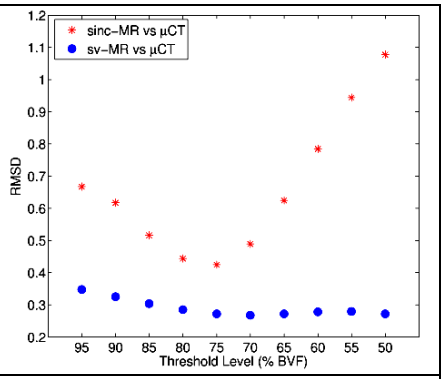

Fig 4. Root mean square difference (RMSD) of SMI values

References: [1] Hildebrand et al., JBMR 1999; [2] Hildebrand and Rüegsegger, CMBBE 1997; [3] Hwang and Wehrli, MRM 2002; [4] Rajapakse et al., J Orthop Res. 2009; [5] Vasilic and Wehrli, IEEE TMI 2005; [6] Otsu, IEEE Sys, Man, Cyber 1979; [7] Lorensen and Cline, SIGGRAPH 1987.

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