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 25µm³ and 150µm³, 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 \(6S'V/S\), where \(S=\int(S(r+\Delta r)-S(\Delta r))/\Delta r\) and \(S'=\sum(areas\ of\ all\ patches\ with\ vertices\ moving\ outward\ along\ the\ normals\ from\ the\ current\ ones\ by\ \Delta r)\). \(V\) 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.

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 SMI values 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 RMSD 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.


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