

Traditional Bone Structural Parameters on Different Resolutions in Magnetic Resonance Imaging

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Introduction

It is known that trabecular bone structure gives more information to the prediction of bone strength compared to bone mineral density (BMD). In order to assess the trabecular bone structure, it is necessary to obtain high resolution trabecular bone images. However, the resolution of the image for human is limited due to scan time. Thus, the evaluation of the trabecular bone structure has been performed the images with resolution less than trabecular bone thickness. In this study we have developed bone structural analysis program and investigated the effect of MR images with different resolutions for the calculation of trabecular bone parameters

Materials and Methods

MRI: Bone specimens were removed at distal femoral condyle during knee joint replacement procedure. They were cut by a saw (1x1x1 cm³) and then fixed in formalin for storage. In preparation for scanning, the bone specimens were defatted, degassed, and immersed in 0.5% volume-% gadopentetate doped water. Three dimensional trabecular bone images of the bone specimens were obtained on a 4.7T Bruker BioSpec MRI with 40cm bore size. A 2.5cm birdcage coil with quadrature detection was used. Bone marrow susceptibility difference causes blurring at the trabecular bone marrow interface and it is also necessary to reduce scanning time to obtain high resolution 3D trabecular images. Thus, a 3D fast large-angle spin-echo (FLASE) sequence with 140° pulse (TR = 100 ms and TE = 10ms) was used to overcome the above two problems. The resolutions of the three 3D images were 65, 130, 160, 196, 230 and 260 μm isocubically. **Bone structural analysis:** We applied cubic interpolation to make each dataset have finer resolution. And then we segmented bone structure by using Otsu thresholding. The morphological thinning based centerline extraction algorithm was applied on this segmented bone region. The voxels on the centerlines could be considered as structural elements for bone analysis. So, we calculated trabecular thickness (TB.Th), bone density (BV/TV), trabecular number (TB.N) and trabecular spacing (TB.S) based on centerline points. For calculating TB.Th, we used full-width half maximum(FWHM) from directional intensity profile. TB.S was computed as the average distance to another neighboring centerline voxels on four directions. As the resolutions became coarser, our bone segmentation tended to segment more bone regions. To correct this, the linear regression was incorporated in TB.Th and BV/TV calculation. The average slope of 8 human bone samples was used in the correction process.

Results

	130μm (%) (mean±std. [min:max])	160μm (%) (mean±std. [min:max])	196μm (%) (mean±std. [min:max])	230μm (%) (mean±std. [min:max])	260μm (%) (mean±std. [min:max])
TB.Th	<i><u>99.4±3.3 [93.0:102.9]</u></i>	<i><u>98.8±4.5 [91.6:104.4]</u></i>	<i><u>100.0±6.7 [92.2:111.8]</u></i>	<i><u>99.0±6.6 [91.8:109.9]</u></i>	100.4±7.7 [91.0:110.9]
BV/TV	<i><u>97.8±5.5 [90.2:104.8]</u></i>	96.2±7.3 [87.1:104.1]	96.7±11.4 [82.9:114.6]	94.5±12.2 [80.1:112.7]	102.8±19.4 [71.9:133.7]
TB.N	<i><u>98.4±2.7 [93.7:101.9]</u></i>	<i><u>97.3±3.3 [91.5:101.0]</u></i>	96.4±5.4 [86.8:102.5]	95.2±6.7 [85.5:105.9]	101.7±12.5 [78.6:120.5]
TB.S	<i><u>99.7±2.0 [96.9:102.7]</u></i>	<i><u>99.8±2.8 [95.6:104.8]</u></i>	<i><u>100.2±4.6 [94.3:108.1]</u></i>	<i><u>102.2±5.8 [92.2:109.8]</u></i>	105.3±10.2 [91.9:126.3]

Table 1. The distribution of traditional bone structural parameters in reference to those of 65μm image, the bold, italic and underline data represents less than 10% difference to 65μm image result.

Table 1 shows the mean, std., min and max values of traditional bone structural parameters. These values were normalized to the reference values from 65μm resolution images. In TB.Th, there were less than 10% in difference from the results in 130μm to 230μm images. In BV/TV, the only 130μm result showed less than 10% difference. In TB.N, 130μm and 160μm results did so. And in TB.S, except 260μm result, all other results were not more than 10% different from reference value. Fig 1~4 shows the bone structural parameters calculated from 8 human bone specimens in different resolutions.

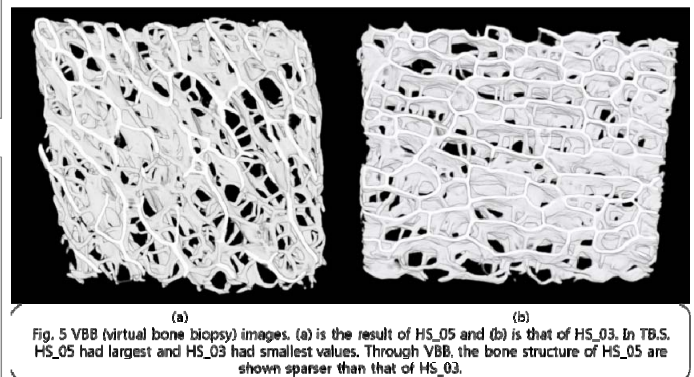
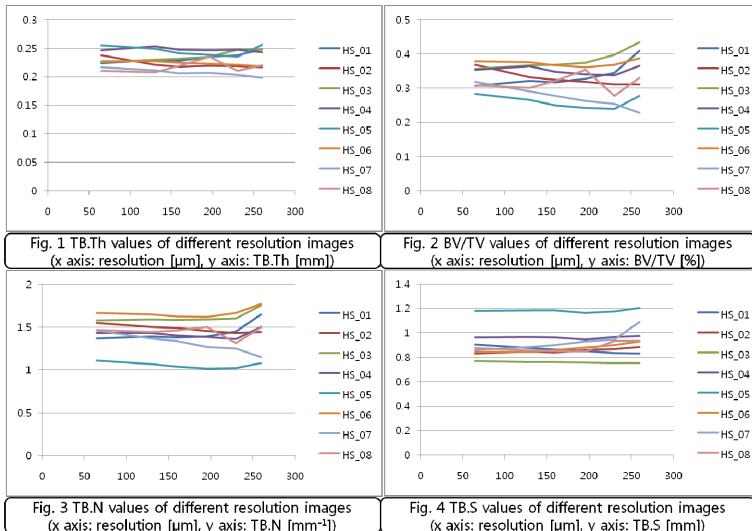


Fig. 5 VBB (virtual bone biopsy) images. (a) is the result of HS_05 and (b) is that of HS_03. In TB.S, HS_05 had largest and HS_03 had smallest values. Through VBB, the bone structure of HS_05 are shown sparser than that of HS_03.

Discussion

Through this study, we have developed automatic bone structural analysis software. By using this software, the traditional bone structural parameters like TB.Th, BV/TV, TB.N and TB.S could be calculated. The result shows that the calculation of TB.Th and TB.S was robust in relatively low resolutions. Our bone segmentation and structural analysis algorithms were robust in low resolution images.