A Novel Method for Determining Bone Volume Fraction Using a Local Threshold Criterion

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Fig.1a) A single slice of the distal tibia $(137x137x410 \ \mu m^3 \text{ voxel size})$. b) Marrow volume fraction (MVF) image obtained with the proposed algorithm; c) threshold map; d) image thresholded using only the LoG zeros as a classification criterion, showing that it is noise dominated. Also shown are magnifications of the same region in b) and d).

INTRODUCTION There is considerable interest in the noninvasive measurement of trabecular bone architecture as a metric for assessing the mechanical competence of the bone. High-resolution MRI has proven its potential to provide images from which architectural measures can be derived [1,2]. Since the achievable resolution of these images is on the order of trabecular thickness, the intensity histogram is monomodal which complicates binarization of the images. Instead, bone volume fraction (BVF) maps have been generated in which the grayscale at each pixel location represents the fraction of the voxel occupied by bone [3]. The two major problems in determining BVF from micro-MRI images are (a) the distinction between bone and marrow to correctly estimate the volume of bone in the presence of noise; (b) dealing with intensity inhomogeneities (shading) due to the inhomogeneous reception field of the receive coil, which is exacerbated when surface coils are used. Here, we introduce a method that calculates a local threshold for the image intensity that is then used to classify pixels into bone or marrow.

THEORY AND METHOD

In short-TR spin-echo images trabecular bone appears dark while marrow gives a bright signal due to its concentration of mobile protons. The Laplacian of Gaussian (LoG) [4] is a second order differential operator whose zeros are related to the edges of the image to which it is applied. In the crudest approximation one would look for zeros of the LoG to determine the boundary between bone and marrow. However, this method is well known to be sensitive to noise and does not provide satisfactory results as illustrated by Fig. 1. We propose a way to find a local *intensity* threshold derived from statistics of the LoG in a neighborhood of a pixel, making this threshold less sensitive to noise and local changes in the image shading. Toward this goal we first calculate the two-dimensional (2D) LoG, L(i,j), of each slice:

L(i,j)=8*I(i,j)-I(i-1,j)-I(i+1,j)-I(i,j+1)-I(i,j+1)-I(i-1,j-1)-I(i+1,j+1)-I(i-1,j+1)-I(i+1,j-1),where indices *i* and *j* represent pixel in-slice position. We then find the conditional probability $p_{ij}(L/I)$ that a pixel of intensity *I*, in a disk of radius *r* centered at pixel (i,j), has a LoG value of *L*. The function $<L>_{ij}(I)$, that is the average of the LoG for a given pixel intensity *I* in the disk, is $<L>_{ij}(I) = \sum_{L} L p_{ij}(L/I)$. The functions $<L>_{ij}(I)$ relate the intensity of each pixel to its local probability that the pixel is in the bone or marrow region. We define the local threshold intensity, $I_{TH}(i,j)$, as the intensity for which $<L>_{ij}(I_{TH})=0$. For a pixel with intensity *I*, instead of checking its value of the LoG we check whether $<L>_{ij}(I) \leq 0$; if so, we classify that pixel as marrow and set its intensity to I_{MARROW} ; if not, we classify it as bone and set its intensity to $I(i,j)=I_{MARROW}(I(i,j)/I_T(i,j))$.

The marrow volume fraction (MVF) is obtained by averaging the new intensities over a volume of interest and dividing the average by I_{MARROW} , with the BVF then equal to 1-MVF.

RESULTS AND CONCLUSION

The new algorithm is implemented as follows. First the 2D LoG is calculated for each slice. Then, for each pixel (i,j) in a given slice a disc of 15-pixel radius is analyzed. The function $\langle L \rangle_{ij}(I)$ is calculated as $\langle L \rangle_{ij}(I) = (1/N_I) \sum_{I(k,l)=I} L(k,l)$ where N_I is the number of pixels, I(k,l), with intensity I within the disk centered at pixel (i,j). This function is then smoothed by averaging over a 12 point interval around each intensity value. The thresholds, $I_{TH}(i,j)$, are then determined as the values of I for which $\langle L \rangle_{ij}(I)$ changes sign. This criterion is used, since due to noise this discrete function almost never takes zero as a value. All pixels with intensities above the threshold value are set to 255 (8-bit precision). Pixel with intensities below the threshold value are not modified. If the thresholding produces isolated pixels of bone their intensity is set to 255 (marrow). Fig. 1a shows the original image and Fig 1b the thresholded result. The MVF was obtained as the average value of the thresholded image intensity in the trabecular bone region divided by 255.

The method's performance was evaluated by comparison with a previously established method based on histogram deconvolution [3] used to determine the BVF. Fourteen wrist and 34 tibia scans of perimenopausal women who are part of an ongoing longitudinal study, were analyzed with both methods. Fig. 2 shows a correlation of BVF values obtained with the two algorithms. The BVF values obtained with the new method are strongly correlated with the established histogram deconvolution algorithm (r^2 =0.73 for the tibia and r^2 =0.86 for the wrist). For the wrist scans a birdcage coil was used that has high B₁ field homogeneity in the region of interest. The tibia scans were obtained with a surface coil, placed anteriorly. The shading produced by the signal variation in the anterior-posterior direction is reflected in the local threshold as shown in Fig. 1c and the larger spread of BVF values BVF values that are on average 8% lower than the histogram deconvolution values. The local threshold algorithm is about 5 to 7 times faster than histogram deconvolution. Planned enhancements comprise the inclusion of means to eliminate isolated bone islands using connectivity arguments.

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Fig. 2 Distal tibia BVF calculated calculated using the proposed algorithm (LTH) plotted versus BVF calculated with the histogram deconvolution algorithm (HDC) described in [3]. The line is a linear fit to the data.