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SEGMENTATION OF MAGNETIC RESONANCE MICROIMAGES OF TRABECULAR BONE: CLASSIFIERS AND MARKOV RANDOM FIELD MODEL

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Abstract: *Quantitative assessment of trabecular bone structure based on magnetic resonance microimages requires a segmentation step, which is difficult to perform because of low signal-to-noise ratio and spatial signal inhomogeneities in these images. In this paper, we present the design of voxel classifiers based on statistical mixture models and classifiers using the feed-forward artificial neural networks (ANN). In both cases a Markov random field (MRF) prior model is used to enhance the reliability of the segmentation process.*

Introduction

The most commonly used criterion for the fracture risk prediction has been based on bone mineral density (BMD) measurements. Several studies have shown, that this measure alone typically is the best predictor of trabecular bone strength, anyhow the density measurements explain just 30%-80% of the variation in Young's modulus [1, 2]. It has been suggested, that morphologic features of trabecular bone may help improve the assessment of the bone strength.

Magnetic resonance microscopy or μMRI is capable of providing ex-vivo 3D MR images of trabecular bone with resolutions below 50 μm, however, the low signal-to-noise ratio and the signal inhomogeneities make an accurate segmentation of these images a demanding task [3]. When in-vivo MR images are processed, the corresponding lower resolution and resulting partial volume effect makes this task even harder.

In this work, we describe the construction of two different voxel classifiers. The first one is based on a density function mixture model, whereas the other is using an artificial neural network to estimate the conditional probabilities of obtaining the input patterns if given voxel belongs to the bone or to the bone marrow. The Markov Random Field prior model is used to express the belief, that clusters of voxels belonging to the same class have a higher probability than configurations with many isolated voxels. This prior belief is incorporated into the segmentation method using the Bayes' rule.

MATERIALS AND METHODS

Sample

A trabecular bone sample of bovine origin was investigated by means of 3D X-ray computed micro-tomography. The voxel resolution of the images was 14x14x14 μm^3, each slice contained 2048x2048 pixels and the image consisted of 505 slices. The experiment was performed at the SYRMEP beamline of Elettra Synchrotron Light Source (Trieste).

The mixture model

The conditional model (likelihood function) is based on the probability of acquiring a brightness value *x*, when the voxel in the measured specimen actually belongs to the class *k* (in the case of trabecular bone image segmentation the voxel can be marked as bone or marrow voxel). In our model we assumed, that the probability distribution of brightness values $p_I(x)$ in an ideal "noise free" image is characterized as a mixture of three different probability distributions: i) the distribution of pure

bone voxels, modeled as a Dirac Delta function with zero brightness value, ii) the pure marrow voxels, following the Gaussian distribution with mean μ_{marrow} and a small variance σ^2_{marrow}, iii) the distribution of boundary voxels, derived from bone and marrow voxels density functions, assuming the uniform distribution of marrow volume fraction in boundary voxels. Since after some initial tests we found out that it is impossible to estimate all parameters controlling these distributions from a single measurement, we use a fixed mean value μ_{marrow} and variance σ^2_{marrow} for the distribution of marrow voxels. These values were estimated through the analysis of a typical trabecular bone MR microimage, which was filtered using a nonlinear diffusion filter. In this way we formed a model of brightness distribution in an image non corrupted by noise. The probability density function $p_N(x)$ of voxel brightness in the noisy image is derived as the integral $\int_0^1 p_{rice}(x \mid \alpha, \sigma) p_I(\alpha) d\alpha$, where $p_{rice}(x \mid \alpha, \sigma)$ is the Rice probability distribution and σ^2 is the noise variance estimated from image regions containing no signal. The model probability density function $p_N(x)$ was fitted to the histogram of the acquired image using the steepest gradient optimization procedure in order to estimate the unknown parameters (the weighting coefficients) (Fig. 1a). When all the parameter of the mixture model are known, it is possible to estimate the conditional probabilities of measuring the given brightness value of the classified voxel assuming the voxel belongs to a given class (Fig. 1b).

MRI intensity inhomogeneities are modeled with a spatially varying factor called the gain field. In order to estimate the gain in some voxel, the average brightness value in *k*-pure marrow voxels (which is not corrupted by the partial volume effect), which are spatially nearest to the evaluated voxel, is computed. The ratio between this value and the average brightness value of pure marrow voxels in the whole image gives the gain estimate. The constant *k* should be large enough to obtain the gain estimate with a low variance, but small enough to incorporate even the fastest spatial gain changes. The pure bone voxels are selected using an auxiliary segmentation procedure (simple thresholding after nonlinear diffusion filtration) as marrow voxels with all neighbors belonging to the marrow. The estimated gain is used to scale the probability density function $p_N(x)$ (it would be more correct to weight the value μ_{marrow} however this computation would be very demanding).

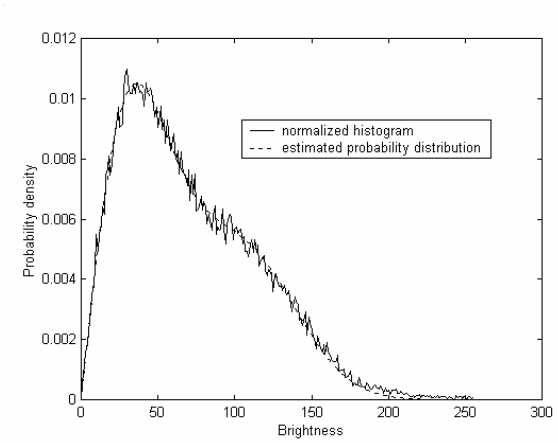

Fig. 1a. Normalized intensity histogram of the acquired image and the estimated probability distribution

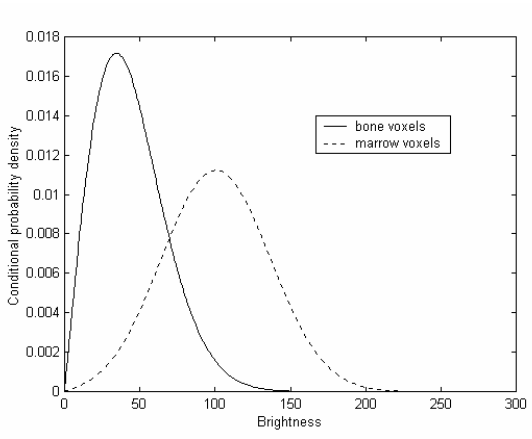

Fig. 1b. Conditional probabilities for voxels belonging to the bone or to the marrow classe

Artificial neural network

The feed-forward artificial neural network with a single hidden layer can be used as a classifier estimating the posterior probabilities of input patterns being of given class, assuming the noise present in target values of training data, the sum-of-squares error function and the one-of-k encoding of network outputs [4]. In our work we apply such a network with input given by brightness values of the classified voxel and voxels lying in defined neighborhood of the classified voxel (typically 6- or 26-neighborhood).

The training set is generated using the X-ray computed micro-tomography (μCT) trabecular bone images with a low noise level and high spatial resolution (14×14×14μm). Because of these properties the segmentation of μCT images is accurate. The segmented images are downsampled to the resolution level of microMRI images (from 42×42×42μm for modeling the in-vitro measurements to 126×126×126μm for in-vivo measurements). In this way also the partial volume effect is simulated. The input patterns are picked up from the downsampled image after adding the Rice noise and the target vectors are given by the brightness of the classified voxel without noise. The backpropagation learning algorithm is applied.

In this case the noise is present in input patters and not in the target values of training data. However, for the sake of simplicity, we still assume that the neural network estimates the posterior probabilities. The training set is generated using just the voxels lying in the boundary between the bone and marrow. Then the probabilities of a voxel being classified as bone or marrow (class probabilities) are equal, and the estimated posterior probability is equal to the conditional probability.

The resistance of the designed classifier to the spatial signal inhomogeneities is enhanced through varying the μ_{marrow} values in the training sample. In this way we would like to emphasize the edge information contained in the input pattern and suppress the importance of the brightness value of the classified voxel in the classification process.

The prior model

The Bayesian segmentation method incorporates a prior model, which should express the belief that clusters of voxels belonging to the same class have higher probability than configurations with a large number of isolated voxels. The probability of any configuration of the segmented image is given by the Gibbs distribution [5,6], which is a function of potential energies assigned to local voxel configurations (therefore this prior model is a MRF). We use the simple Ising model to define these energies [5].

The Gibbs distribution is controlled by a parameter τ, which measures the rigidity of the configuration. The higher τ, the steeper is this distribution, leading to a "smoother" segmentation of the image (Fig. 2). Estimation of this parameter is thus an important point in the design of the Bayesian segmentation algorithm.

The posterior probability of a segmented image configuration is proportional to the product of a given configuration's prior probability and likelihood value. A Monte Carlo method with a Metropolis stochastic sampler, which takes advantage from the Gibbs distribution properties, is used to find the configuration of the segmented image according to the Maximum Marginal Posterior (MMP) rule [5].

RESULTS AND DISCUSSION

The evaluation of the designed image segmentation algorithms is based on the comparison of trabecular bone morphologic parameters [2] estimated from the segmented and downsampled μCT images and from the corresponding MR phantoms processed by both designed methods. The synthetic images (phantoms) derived from μCT images present a realistic representation of trabecular bone structure and simulate the noise distribution and intensity inhomogeneities typical of the MR images.

Until now only a few samples were processed in this way, therefore no reliable quantitative comparison of both designed methods with more classical approaches (e.g. nonlinear diffusion filtration followed by a simple thresholding procedure) could be done. However some preliminary results have shown, that implemented algorithms can be useful in the trabecular bone structure analysis. In the future, we intend to estimate the robustness of designed methods to the various levels of noise and signal inhomogeneities in processed images, as well as try to investigate the influence of the MRI data acquisition process (resolution, number of averages, spin warp or backprojection image encoding etc.) on the morphologic parameters estimated from processed images.

Fig. 2a. A single slice of a MR phantom. Resolution 84×84μm.

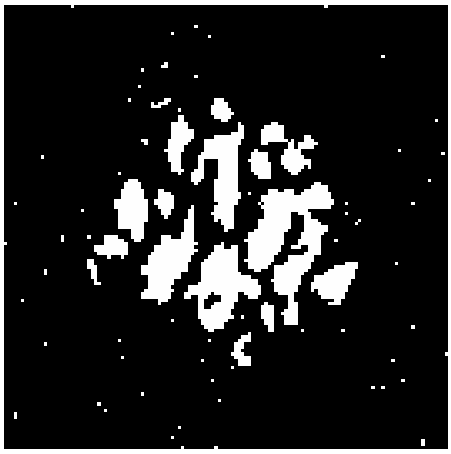

Fig. 2b. A single slice of the image after segmentation using the mixture model classifier (the same slice as in Fig. 2a).

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